Wheat Gene Catalogue – Introduction

This Catalogue is a WORD extension of the MACGENE (National Institute of Genetics Japan (*http://shigen.nig.ac.jp/wheat/komugi/genes/symbolClassList.jsp*) that was not continued after 2017. It is updated with all curated material up to 1 September 2024.

The Catalogue consists of the following sections:

- Introduction
- Trait list
- Section 1: Morphological and Physiological Traits – 107 pages
- Section 2: Proteins – 78 pages
- Section 3: Pathogenic Disease/Pest Reaction – 156 pages
- Section 4: References – 241 pages

The material in the Catalogue has been collated since 1968 and major contributions were made by numerous people including Mike Gale, Gary Hart, Katrien Devos, Olin Anderson, John Rogers, Jorge Dubcovsky, Xianchun Xia, Yukiko Yamazaki, and John Raupp and many others who have discussed individual trait material. This is gratefully acknowledged and appreciated.

The Catalogue is not free from errors in curation and the various cycles of editing over years – please advise problems or suggestions for updating.

The documents presented are working files – items highlighted are for checking or currently cannot be traced.

Some items listed as 'alleles' would currently fit the description 'haplotype' as defined in Boden et al. (2023) 'Updated guidelines for gene nomenclature in wheat'. Theoretical and Applied Genetics 136:72. *https://doi.org/10.1007/s00122-023-04253-w*.

References in the gene text can be traced by enclosing reference numbers below four digits in unique reference brackets, e.g. {1} to {999}; for reference numbers 1000 and above the number without brackets can be used, e.g. 1001 or 11700.

Until 2017 this Catalogue was prepared and maintained on behalf of the International Wheat Genetics Symposium.

R.A. McIntosh
1 September, 2024

Wheat Gene Catalogue – Trait Summary

1. Morphological and Physiological Traits

- **1.1 Gross Morphology: Spike characteristics**
  - **1.1.1. Squarehead/spelt**
  - **1.1.2. Club/Compact spike**
  - **1.1.3. Sphaerococcum**
- **1.2. Branched spike**
- **1.3. Elongated glume**
- **1.4. Ear length**
- **1.5. Multi-gynoecium; Multi-ovary**
- **1.6. Accumulation of abscisic acid**
- **1.7. Alkylresocinol content in grain**
- **1.8. Aluminium tolerance**
- **1.9. Anthocyanin pigmentation**
  - **1.9.1. Purple anthers**
  - **1.9.2. Purple/Red auricles. Purple leaf base/sheath**
  - **1.9.3. Red/purple coleoptiles**
  - **1.9.4. Purple/red culm/straw/stem**
  - **1.9.5. Purple grain/pericarp**
  - **1.9.6. Purple glume**
  - **1.9.7 Purple leaf blade**
- **1.10** Awnedness
  - **1.10.1. Dominant inhibitors of awns**
  - **1.10.2. Promotors of awns**
  - **1.10.3. Smooth awns**
- **1.11. Basal Sterility in speltoids**
- **1.12. Blue aleurone**
- **1.13. Brittle culm**
- **1.14 Brittle rachis**
- **1.15. Boron tolerance**
- **1.16. Cadmium uptake**
- **1.17. Chlorophyll abnormalities**
  - **1.17.1. Virescent**
  - **1.17.2. Chlorina**
  - **1.17.3. Striato-virescens**
  - **1.17.4. Yellow-green**
- **1.18. Cleistogamous flowering**
- **1.19. Copper efficiency**
- **1.20. Corroded**
- **1.21. Crossability with rye and *Hordeum* and *Aegilops*** spp
  - **1.21.1. Common wheat**
  - **1.21.2. Tetraploid wheat**
- **1.22. Dormancy (Seed)**
  - **1.22.1. Germination index**
  - **1.22.2. Vivipary**
  - **1.22.3. Pre-harvest sprouting**
- **1.23. Ear emergence**
- **1.24. Earliness *per se***
- **1.25. Embryo lethality**

- 2.2.14. Phosphodiesterase
- 2.2.15. Phosphogluconate dehydrogenase
- 23.2.16. Phosphoglucomutase
- 2.2.17. Shikimate dehydrogenase
- 3.2.18. Superoxide dismutase
- 2.2.19. Triosephosphate isomerase
- 3.2.20. Aromatic alcohol dehydrogenase
- 2.2.21. Aconitase
- 2.2.22. NADH dehydrogenase
- 2.2.23 Dipeptidase
- 2.2.24. Malic enzyme
- 2.2.25. Adenylate kinase
- 2.2.26. Glutamate-pyruvate transaminase
- 2.2.26. Glutamate-pyruvate transaminase
- 2.2.28. Beta-glucosidase
- 2.2.29. Starch branching enzyme I
- 2.2.30. Starch branching enzyme II
- 2.2.31. Benzoxinones
- 2.2.32. Acetohydroxyacid synthase (EC 4.1.3.18)
- 2.2.33. Phytoene synthase (EC 2.5.1.32)
- 2.2.34. Polyphenol oxidase
- 2.2.35. Protein disulfide isomerase (EC 5.3.4.1)
- 2.2.36. Isoamylase 1
- 2.2.37. Polygalacturonase-inhibiting proteins
- 2.2.38. Flavone 3-hydroxylase (EC 1.14.11.9)
- 2.2.39. Zeta-carotene desaturase
- 2.2.40. Carotenoid beta-hydroxylase (non-heme di-iron type)
- 2.2.41 Lycopene-zeta-cyclase
- 2.2.42 Dehydration-responsive element (DREB) proteins; Dehydration response factors (DRF)

2.3. Endosperm storage proteins

- 2.3.1. Glutenins
- 2.3.2. Gliadins
- 2.3.3. Other endosperm storage proteins
- 2.3.4. Enzyme Inhibitors
- 2.3.5. Grain softness protein
- 2.3.6. Histone H1 Proteins
- 2.3.7 Iodine binding factor
- 2.3.8 Lipopurothionins
- 2.3.9. Lectins
- 2.3.10. Puroindolines and grain softness protein
- 2.3.11. Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator alias Storage protein activator
- 2.3.12. Salt soluble globulins
- 2.3.13. Serine protease inhibitors *alias* serpins
- 2.3.14. Starch granule proteins
- 2.3.15. Starch synthase
- 2.3.16. Water soluble proteins
- 2.3.17. Waxy proteins

3. Pathogenic Disease/Pest Reaction

3.26. Reaction to *Sitodiplosis mosellana* (Gehin)
3.27. Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)
3.28. Reaction to soil-borne cereal mosaic virus
3.29. Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides* (Fron) Deighton)
3.30. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*
3.31 Reaction to *Tilletia indica* Mitra
3.32. Reaction to *Ustilago tritici* (Pers.) Rostrup
3.33. Reaction to wheat spindle streak mosaic bymovirus (WSSMV)
3.34. Reaction to wheat streak mosaic virus
3.35. Reaction to *Xanthomonas campestris* pv. *undulosa*
3.36. Resistance to colonization by *Eriophyes tulipae* (*Aceria tulipae*)
3.37. Reaction to wheat yellow mosaic virus

The Wheat Catalogue: 1. Morphological and Physiological Traits

Note: Levy and Feldman {797} studied the inheritance of more than 20 morphological and biochemical traits in crosses of four *T. dicoccoides* lines and T. durum. Similarly, Kuspira et al. {744} studied 12 qualitative characters in *T. monococcum*. The symbols applied to the characters examined in these studies are not being reserved and listed in the Catalogue. However, both studies should serve as base for future work.

1.1. Gross Morphology: Spike characteristics

Major hexaploid wheat types are categorized into groups with respect to three major gene pairs; viz. *Q, C* and *S1* {1038}.
1. Common wheat *Q c S1* **v:** vulgare group.
2. Club wheat *Q C S1* **v:** compactum group.
3. Shot wheat *Q c s1* **v:** sphaerococcum group.
4. Spelt wheat *q c S1 and q C S1* **v:** spelta group (including vavilovi).
The majority of hexaploid wheat stocks are already, or can be readily, classified into these groups. Diploid wheat is assumed to be *q*. Durum and carthlicum groups have the genotype *Q* {1049}.

1.1.1. Squarehead/spelt

Q

Q {881}. [*k* {1550}; *Ap2-5A*]. 5AL {1293}. **bin:** 5AL-17 {10541}. **v:** Common wheats. CS; Iranian spelts {140}. **tv:** *T. turgidum* ssp. *carthlicum, durum* and *polonicum* {10457}. **ma:** Complete linkage with cDNA clone PtAq22 {0127}. **c:** *Q* was cloned and shown to have similarity to *AtAP2* (APETALA 2), the *Q* allele was more abundantly transcribed than the *q* allele transcription factors {10457}. GenBank AY02956.1.

q {881}. [*K* {1550}]. **v:** Macha wheats; European spelt wheats {10457}; *vavilovi* wheats. **s:** CS*8/White Spring Spelt 5A {1048}. **tv:** *T. turgidum* ssp. *dicoccum, dicoccoides* {10457}. **ma:** Cent – *Xrsq805(Empb)-5A* – 4.6 cM – *Q* – 4.3 cM – *Xpsr370-5A* {419}; *Q* was physically mapped in 5AL, fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23 {446}; *Q* – 9.3 cM – *Xpsr370-5A* {9903}. The speltoid phenotype of at least some spelts may be caused by genes at other loci {0140}. Fine mapping of the 20 cM region possessing Q and delimited by deletions 5AL -7 and -23 is reported in {0324}.

A nucleotid change in the microRNA172 binding site of the Q locus played a critical role in wheat domestication and the origin of free-threshing modern wheats {11192}.

Pleiotropic features of the *Q* locus include effects on glume toughness, threshability, rachis fragility, spike length, flowering time, and plant height {11342}.
Final spike and reproductive morphology is affected by the *Q/q* sequence and its regulation by miR172 {11344} along with direct or indirect interaction with the homoeologues {11344}.

Homoeologues of *Q* were described in {11192}. Both have miRNA172 target sites close to the 3' ends of the coding region. These genes were referred to as *Ap2-5B*, a transcriptionally active pseudogene, and *Ap2-5D* that encodes a functional protein that contributes to suppression of the speltoid phenotype {11342}. Reduced height gene *Rht23*, a mutationally derived allele in NAUH164, was caused by a SNP (G3147A, Ala416Thr) within the miR172 target site in 5DL that permitted up-regulation of *Ap2-5D* due to down-regulation of miR172 in leaves, stems and spikes {11345}.

1.1.2. Club/Compact spike

C

C {1517}. [*Cd* {47}]. 2DL {1192, 1517}. probably 2DL {10578}. 2D {1192}. **bin:** C-2DS1 - C-2DL3, markers flanking *C* were located on either side of the centromere {10578}. **i:** S-615*11/Elgin {1500}. **s:** CS*6/Poso 2D {1304}; CS*5/Red Egyptian 2D {1304}. **v:** Club wheats; Coda {10578}; Corrigin {10578}. **ma:** Coda / Brundage: *Xwmc144-2D* – 1 cM – *C* – 8 cM – *Xwmc18-2D*; Corrigin / CS (*Ae. tauschii* 2D): *Xwmc245-2D* – 1 cM – *Xcfd16-2D/Xgwm358-2D/C/Xcfd116-2D* – 1 cM – *Xbarc145-2D* {10578}.

C$_g$ {11114}. 2BL {11114}. **bin:** 2BL-0.48-0.89, near breakpoint 0.69. **v:** Akage Gumbai {11114}; Akage Gumbai 22 {11114}; Gumbai 22 {11114}; Kinoshita Komugi {11114}; Nakote Gumbai {11114}. **ma:** *Xhbg410/Xhbg440-2B* – 18.1 cM – C$_g$ – 15.3 cM – *Xgwm47-2B* {11114}.

Although gene C may be present in some forms of group *macha* {1447} and *spelta* {0623}, it is not universally present. Tsunewaki {1500} found that compact spike in one form was controlled by polygenes.
C may be orthologous to gene *Sog* for soft glumes on chromosome 2A^m {10578} Tetraploid wheat: A compact spike gene *C*^{17648} in mutant line MA 17648 wad located in chromosome 5AL {10541}. *Xbarc319-5A* – 9.7 cM – *C*^{17648} – 24.8 cM – *Xgwm179-5A* {10541}. *C*^{17648} was distal to the *Q* locus {10541}.

QTL

Courtot/Chinese Spring: Six QTL for spike compactness were detected but only 4 on chromosome arms 1AL, 2BS, 2DS and 4AS were consistent for at least two years {0114}. Two additional QTLs for spike compactness were detected in Courtot/Chinese Spring {10080} on chromosome arms 5DL (*QCp.icf-5D*) and 6DL (*QCp.icf-6D*). Markers *Xcfd26-5D* and *Xcfd38-6D* explained 13.6% and 12.2% of the variance in spike compactness, respectively {10080}.

1.1.3. Sphaerococcum

The naturally-occurring sphaerococcum gene in chromosome 3D and various mutant alleles conferring a similar phenotype form a homoeologous series. The sphaerococcoid alleles are either recessive or incompletely dominant. All three mapped loci are closely linked to the respective centromeres {0030}. The "a" alleles are allocated to Chinese Spring or "normal" wheats.

S1

S-A1 {0029}. 3A {0056}. **v:** CS {0029}.

S-A1a {0029}. **v:** CS {0029}; common wheats {0029}.

S-A1b {0029}. [*S3* {0056}]. **v:** MS 1453 {0056}. **ma:** *Xgwm2-3A*(S) – 5.1 cM – *S-A1* – 6.6 cM – *Xgwm720-3A*(L) {0030}.

S-B1 {0029}. 3B {0030}. **v:** CS {0029}.

S-B1a {0029}. **v:** CS {0029}; common wheats {0029}.

S-B1b {0029}. [s^{16219} {10541}, *S2* {0030}]. **v:** MSK 2452 {0056}; MSK 2454{0056}. **tv:** MA 16219 {10541}. **ma:** *Xgwm685-3B*(S) – 4.2 cM – *S-B1* – 0.5 cM – *Xgwm566/Xgwm845/*cent {0030}.

S-D1 {0029}. *TraesCSD01G137200*. 3DL {692}. 3D {0030, 1292}. 3DS {1193, 1194, 11415}. **v:** CS {0029}.

S-D1a {0029}. **v:** CS {0029}; common wheats {0029}.

S-D1b {0029}. [*s1*, *sp1* {1286}, *Tasg-D1* {11415}]. **i:** S-615*11/*T. sphaerococcum* var. *rotundatum* {1500}. **s:** CS*7/*T. sphaerococcum rubiginosum* 3D {1304}. **v:** Nongda 4332 {11415}; Sphaerococcum wheats {0029}; *T. antiquorum* K056397 & K56398 {10234}. **ma:** Located between markers *Xgwm341-3DS* and *Xgdm72-3DS* {11415}. **c:** The sphaerococcum phenotype is caused by a gain of function mutation in serine/threonine kinase glycogen synthase kinase 3 (STKc_GSK3) that in rice affects the brassinosteroid signaling pathway and grain shape {11415}. There is a Lys286Glu substitution in the ninth exon of *TraesCSD01G137200* {11415}.

S-D1c {0029}. [*S1* {0056}]. **v:** MS 3287 {0056}. **ma:** *Xgdm72-3D*(S) – 8.0 cM – *S-D1* – 2.9 cM – *Xgwm456-3D/*cent {0030}.

S2

s2. Partially dominant {1286}. [*sp2* {1286}]. **v:** Sphaerococcoid wheats. "*Sphaerococcum simulator*" {1286}.
Sphaerococcum-like tetraploid wheats were reported {122}, {475}, {1282}, {1286}, but comparisons between them, or with *s2*, were not made. Whereas Schmidt & Johnson {1281} reported a single recessive controlling the sphaerococcum character in tetraploid wheat, Joppa {621} using the same stock found that two recessive genes were necessary to produce this phenotype.

1.2. Branched spike

Synonyms: branched spike, four-rowed spike, multi-rowed spike, supernumerary spikelet, tetrastichon spikelet.
Branched spike and multi-rowed spike are phenotypes involving the presence of supernumerary spikelets,

or the presence of additional spikelets at rachis nodes. A similar condition in rye is known as 'monstrosum ear' (reviewed in {10637}). Genetic studies of branched spike in tetraploid and hexaploid wheats indicate that the phenotype is recessive, involves one or more genes, and is strongly influenced by environmental effects. Comparative genetic studies suggest an orthologous gene series in homoeologous group 2 {10637}.

BH1

bh-A1 {10637}. [*bh* {665}]. 2AS {665}. **tv:** PI 349056 {665}.

bh-D1{10637}. [*mrs* {10637}]. 2DS {10637}. **bin:** 2DS5-0.47-1.0 {10637}. **v:** Ra1 {10637}; Ruc163167-1-02 = Ra1 / ZGK242-81 {10637}; Ruc163167-1-02 = Alana /3/ Ra1 / ZGK242-82 // Ra1 {10637}. **ma:** *Xwmc453-2D/bh-D1* – 7.8 cM – *Xgwm988-2D*{10637}; *Xwwm484-2D* – 3.3 cM – *Xwmc453-2D/bh-D1* – 3 cM – *Xwgm988-2D* {10637}.
Ra1 is a mutant stock maintained at the NI Vavilov Research Institute of Plant Industry, St Petersburg, Russia.
A chromosome 2B gene of minor effect was identified {9907}. In a monosomic analysis of the hexaploid line LYB with supernumerary spikelets, Peng et al. {9908} located recessive genes in chromosomes 2A and 4A that promote the development of supernumerary spikelets and a gene in chromosome 2D that prevents their expression.

bh-R1 {10637}. [*mo* {10637}]. 2R {10637}. **al:** *S. cereale* D40 {10637}. **ma:** *Xrms056-2R* – 15.7 cM – *bh-R1* – 10.7 cM – *Xcfe209-2R* {10637}.

1.3. Elongated glume

Elongated glume is the phenotype associated with the polonicum group of tetraploid wheats. Expression in hexaploid wheat is much reduced compared with tetraploids. Matsumura {911} reported linkage of gene *P* and a gene for red coleoptiles implicating chromosomes 7A or 7B. A different gene was subsequently located in chromosome 7B {9990}.

P1

P1. [*P-A*^{pol}*1* {0254}, *P* {911}, *Eg* {922}, *P-A*^{pet}*1* {0254}]. 7AL {922, 1547}. 7A or 7B (based on linkage of 0.2 with a gene for red coleoptile) {922}. 7AS {11606, 11587}. **i:** Saratovskaya29*8//Novsibirskaya 67*2/*T. polonicum* {922, 0066}. NILs developed in {11606, 11587}. Paragon derivative {11606}. **itv:** P-LD222 = LD222*11/*T. turgidum* var *polonicum* {1547, 1546}. **tv:** *T. polonicum* {0254}; *T. petropavlovskyi* {0254}. NILs developed in {11587}. *T. petropavlovskyi* {add: 11587}; Tall and dwarf (with *Rht22*) Polish wheat accessions from Xinjiang {11587}. **ma:** *Xgwm260* – 7A(S) – 2.3 cM – *P1* – 5.6 cM – *Xgwm1083-7A*(L) {0254}; *Xgwm890* -7A – 2.1 cM – *P1* {0254}; *Xgwm260-7AS* – 2.3 cM – *P1*^{pol} – 5.6 cM – *Xgwm1083-7AL* {0254}; *Xgwm890-7AS* – 2.1 cM – *P1*^{pet} {0254, 11587}. Located between SSR markers *XP25* (128.79 MB) and *XP87* (128.92) in CDSREFSeq_v1 {11587}. **c:** An insertion in intron 1 causes alternate splicing and >50fold up-regulation of the *P1* allele affecting kernel length, glume length, and flowering date through the brassinosteroid pathway {11587}. The *VRT-A2a*

allele {11606} is present in Chinese Spring and other non-long-glume tetraploid and hexaploid accessions; The *VRT-A2b* in long-glume accessions has a 160 bp sequence replacing a 563 bp sequence in intron 1 in all *T. polonicum*, *T. petrapavlovkyi* and hexaploid Arrancada landraces {11606}. Loss-of-function mutations in both *VRT2* homoeologs in tetraploid wheat delay heading time, reduce plant height, and increase number of spikelets per spike {11607}.
Note: The loci determining elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* are not homoeologous to the *P* loci in the centromeric region of the group 7 chromosomes {0254}. According to {11606} *T. petropavlovskyi* is hexaploid.

P2 {9990}. 7BL {9990}. **itv:** LD222*7/*T. ispahanicum* {9990}. **tv:** *T. ispahanicum* {9990}. According to {0254} the loci of *T. polonicum, T. petropavlovsky* and *T. isphanicum* are allelic ('homoeoallelic') whereas other workers had claimed genes in the first two forms were not allelic. Wang et al. {0254} however concluded that loci bearing alleles for elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* were not part of the above series.

1.4. Ear length

QEl.ocs-5A.1 {0068}. 5AL {0068}. **v:** CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population {9903}. **ma:** Associated with *Xbcd9*-5A {0068}.

1.5. Multi-gynoecium; Multi-ovary

Synonym: three pistils (TP).
This trait describes a dominant phenotype consisting of 3 kernels within each wheat floret; that is, the flower consists of 3 separate ovaries, 3 anthers and 2 lodicules.

PIS1

Pis1 {10636}. 2DL {10636}. **bin:** C-2DL3-0.49 {10636}. **i:** CM28TP {11228}. **v:** TP Mutant {10636}. **ma:** *Xgwm539-2D* – 17.6 cM – *Pis1* – 19.5 cM – *Xgwm349-2D* {10636}. *KM69_132294739* – 3.5 cM – *KM70_136805221* – 3.0 cM – *PIS1* – 1.1 cM – *KM71_140258883* {11228}.

A gene designated *Mov-1* (multi-ovary) mapped to bin 2DL-9 in a CIMMYT line is assumed to involve the same locus as *Pis1*. *Mov-1* was mapped to a 3.5 cM interval (589.3 – 590.4 Mb) {11636}.

1.6. Accumulation of abscisic acid

A QTL was mapped on 5AL between *Xpsr575-5A* {proximal} and *Xpsr426-5A* {distal} {1180}.

1.7. Alkylresocinol content in grain

AR

Ar1 {0281}. High alkylresocinol content is dominant {0281}. 5AL {0281}. **tv:** Langdon{0281}.

ar1 {0281}. **tv:** Ardente {0281}; this cultivar has a low content compared to all tested durum and common wheats {0281}.

1.8. Aluminium tolerance

ALT1

Alt1 {234}. **v:** ET3 = Carazinho/4*Egret {234}.

alt1 {234}. **v:** ES3 = Carazinho/4*Egret {234}.

ALT2

Alt2 {848}. [*Alt$_{BH}$* {1213}]. 4DL {848}. **su:** *T. turgidum* cv. Langdon 4D(4B) {848}. **v:** BH1146{0115, 1213}; IAC-24 {0115}; IAC-60 {0115}; 13 induced mutants of Anahuac {0115}. **ma:** *Alt2* was mapped to a 4 cM interval flanked by *Xpsr914-4D* and *Xpsr1051-4D* {848}; on a consensus 4B-4D map of *T. aestivum; ALT2* – 1.1 cM – *Xbcd1230-4D* {1213}; *Alt2* cosegregated with *Xbcd1230-4D* and fell within the interval *Xgdm125-4D* – 4.8 cM – *ALT2 – 1.1 cM – Xpsr914-4D* {248}.
Malate transporter *AlMT-D1* gene (GenBank AB081803) is completely linked to aluminium tolerance in chromosome arm 4DL between SSR markers *Xwmc48b* and *Xwmc331* in a similar region to *ALT2* {10285}. *Almt1* transgenic expression in barley conferred and Al-activated efflux of malate with properties similar to those of *Al*-tolerant wheat {10286}. Allelic variation at the promoter of *Almt-D1* was associated with differences in Al tolerance. Molecular and pedigree analysis suggest that Al resistance in modern wheat germplasm is derived from several independent sources {10532}.

Almt1. *TaALMT1* {11242}. 4DL {11242}. 4DL {11242}. **v:** CAR3911 {11242}. **ma:** *Xwmc457-4D* – 4.0 cM – *Almt1* – 2.0 cM – *Xwmc331-4D* {11242}.

QTL

Atlas 66 / Century: A QTL in the region *Xdgm125-4DL – Xwmc331-4DL* accounted for nearly 50% of the phenotypic variation in root growth rate in hydroponic solution {10265}. An Al-activated malate transporter (*LMT1*) was earlier mapped to the same location {10266}.
Atlas 66 (insensitive)/Chisholm (sensitive) RILs: One QTL, located in chromosome 4DL, corresponded to ALMT1 and accounted for 50% of the phenotypic variation {10483}. A second QTL was located on 3BL (R^2 = 0.11); nearest marker *Xbarc164-3B* {10483}. Both QTLs were verified in Atlas / Century {10483}.
FSW (A1 tolerant) / ND35 (A1 sensitive): 3 QTLs for tolerance, *Qalt.pser-4DL* co-segregating with *Xups4*, a marker for the promoter of the *ALMT1* gene, *Qalt.pser-3BL* (*Xbarc164-3B – Xbarc344-3B*) and *Qalt.pser-2A* (*Xgwm515-2A – Xgwm296-2A*) {10605}.
In D genome introgression lines of Chinese Spring a major QTL was located in the interval *Xgwm125-4D – Xgwm976-4D*, R^2=0.31 {10598}, probably coinciding with *Alt2*. A second QTL from CS, *Qalt*$_{cs}$ipk-3B, R^2=0.49, occurred in interval *Xgwm1029-3BL – Xgwm1005-3BL* in a CS / CS (Synthetic 3B) population {10598}.

1.9. Anthocyanin pigmentation

The genetic determinants of anthocyanin pigmentation of various tissues are largely located in homoeologous regions in group 7, viz. 7BS (*Rc-B1, Pc-B1, Plb-B1, Pls-B1*) and 7DS (*Rc-D1, Pc-d1, Plb-D1*), and appear to be linked clusters rather than multiple alleles on each chromosome {10700}. Their relationship with genes for purple auricle and purple pericarp are still not clear.

1.9.1. Purple anthers

A single, dominant factor was reported {1326}.

PAN

Pan1 {921}. 7DS {921}. **v:** Ilyitchevka {921}; Mironovskaya 808 {921}; Novosibirskaya 67 {921}; Pyrothrix 28 {921}; Saratovskaya 210 {921}; Strela {921}; Ukrainka {921}. **tv:** *T. polonicum* {921}.

Pan2. 7AS {9959}. **tv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}. **ma:** *PAN2* – 9.2 cM – *RC1* – 12.2 cM – *Xutv1267-7A* (proximal) {9959}.

1.9.2. Purple/Red auricles. Purple leaf base/sheath

For review see {1641}.
Melz and Thiele {983} described a "purple leaf base" phenotype where anthocyanin pigmentation extended to the leaf base as well as auricles. Purple leaf base was expressed only when pigmentation occurred in the coleoptiles.

An5 {983}. 5R {983}.

Pc/Pls/Plb {10692}. 7B {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}. **ma:** *Xgwm951-7B* – 6.7 cM – *Pc/Pls/Plb* – 8.2 cM – *Pp1* – 8.9 cM – *Xgwm753-7B*{10692}.

Ra1. [*Ra* {1645}]. 1D Gulyeeva {474, 983}. 2D {1645}. **v:** Kenya 58 {1645}.

Ra2 {983}. 4B {983}.

Ra3 {983}. 6B {983}.

1.9.3. Red/purple coleoptiles

There is an orthologous gene series on the short arms of homoeologous group 7. The 'a' alleles confer red coleoptiles. In chromosome substitution lines of wild emmer to common wheat both the 7AS and 7AL derivatives had red coleoptiles, placing *Rc-A1* in the centromeric region {10974}.

RC1

RC-A1 {10451}. [*Rc*]. 7AS^3 {10451}. **dv:** PAU14087 {10451}. **ma:** *Xcfa2174-7AS* – 11.1 cM – *RC-A1* – 4.3 cM – *Xgwm573-7A/Xwmc17-7AL* {10451}.

Rc-A1a {0250}. [*Rc1*, *R* {401}]. 7A {769, 1293}. 7AS {0250}. **s:** CS*6/Hope 7A {1293}. **v:** Hope *Rc-B1a* {1293}. **tv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}. **ma:** *PAN2* – 9.2 cM – *RC-A1* – 12.2 cM – *Xutv1267-7^a* (proximal) {9959}; *RC-A1*(distal) – 11.9 cM – *Xgwm913-7A* {0250}.

RC-B1

Rc-B1a. [*Rc2*, *R2* {401}]. 7BS {769, 401, 250}. 7B {742}. **s:** CS*6/Hope 7B {769}. **v:** Hope *Rc-A1*. **ma:** *Xgwm263-7B* – 26.1 cM – *RC-B1* – 11.0 cM – *Xgwm1184-7B* {0250}.

RC-D1

Rc-D1a {0250}. [Rc 3]. 7D {596}. 7DS {1444, 1241, 0250}. **v:** Gaoyuan 115 {11160}; Mironovskaya 808 {1444}; Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404 {1240}; Tetra Canthatch/*Ae. squarrosa* var. *meyeri* RL 5289, RL 5406 {1240}; Sears' *T. dicoccoides* /*Ae. squarrosa* = Sears' Synthetic {596}. **ma:** *RC-D1* (distal) – 3 cM – *Xpsr108-7D* {180}; *Xgwm44-7D* – 6.4 cM – *RC-D1* – 13.7 cM – *Xgwm111-7D* {0250}. **c:** *TaMYB-D1* isolated from Gaoyuan 115 was proposed as the candidate gene {11160}.

Tahir & Tsunewaki {1453} reported that *T. spelta var. duhamelianum* carries genes promoting pigmentation on chromosomes 7A and 7D and genes suppressing pigmentation on 2A, 2B, 2D, 3B and 6A. Sutka {1444} reported a fourth factor in chromosome 6B and suppressors in 2A, 2B, 2D, 4B and 6A. The *Rc* allele appears to encode a transcription activator of late biosynthesis genes involved in the light-regulation of anthocyanin systhesis (studies carried out on CS(Hope 7A) substitution line) {10317}.

1.9.4. Purple/red culm/straw/stem

Purple or red colour is dominant.

PC1

PC1 {743}. [*Pc* {743}]. 7BS {768}. 7B {743}. **s:** CS*6/Hope 7B {743, 768}. **itv:** LD222*11/CS (Hope 7B) {1546}. **ma:** *Pc* (proximal) – 5.7 cM – *Xpsr490(Ss1)-7B*.

PC2

Pc2 {921}. 7DS {921}. **v:** Ilyitchevka {921}; Mironovskaya 808 {921}; Novosibirskaya 67 {921}; Pyrothrix 28 {921}; Saratovskaya 210 {921}; Strela {921}; Ukrainka {921}.

Pc/Pls/Plb {10692}. 7B {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}. **ma:** *Xgwm951-7B* – 6.7 cM – *PC/PLS/PLB* – 8.2 cM – *PP1* – 8.9 cM – *Xgwm753-7B* {10692}.

1.9.5. Purple grain/pericarp

Genes for purple pericarp were transferred from tetraploid wheats to the hexaploid level {112}, {214}, {941}, {1138}. At the hexaploid level duplicate genes {112}, {941} and complementary genes {112}, {939}, {1138}, {438} were reported. At the tetraploid level, duplicate-gene {941} and single-gene {1327} inheritances were observed. Purple colour is dominant and may be affected by environment and genetic background. Complementary

genes were located in chromosomes 3A and 7B {1138}. Possible pleiotropic relationships of genes affecting pigmentation of various tissues have not been studied in detail. *Pc2* and *Rc-B1a* may be the same gene {769}. Also, complementary genes involved in determination of purple pericarp could be related to culm colour {112}. The location of the second complementary gene is confusing: the three group 7 homoeologues might be involved in different materials.
For review, see {1643}.
Complementary dominant genes. A purple line PC was obtained from a cross of non-purple Line 821 (a 7S(7B) substitution from *Ae. speltoides*) and Line 102/00, a chromosome 2A introgression from *T. timopheevii* {10946}. Purple grained accessions are unknown in both *Ae. speltoides* and *T. timopheevii*.

PP1

Pp1 {41}. 7BL {10392}. 6A {41}. **i:** Saratovskaya 29*8/Purple {Australia} *Pp2* {40}. **v:** Novosibirsk 67 (this cultivar has white pericarp) {10392}. **v2:** Purple K49426 *Pp3a*{10392}; Purple Feed *Pp3b* {10392}. **ma:** *Xgwm983-7B* – 15.2 cM – *PP1* – 11.3 cM – *Xgwm767-7B* {10392}.

PP2

Pp2 {41}. 7A {41}. **tv:** *T. durum* Desf. subsp. *abyssinicum* Vav {40}.
Piech and Evans {1138} located complementary genes on chromosomes 3A and 7B. *Pp2* was renamed *Pp3b*.

PP3

Pp3 {10392}. 2A, not 6A {10392, 0066}.

Pp3a {10392}. **v2:** Purple K49426 *Pp1* {10392}. **ma:** *Xgwm328-2AS* – 2.7 cM – *PP3a* – 3.2 cM – *Xgwm817-2AL* {10392}.

Pp3b {10392}. [*Pp2*]. **v2:** Purple Feed {10392}, {66}. **ma:** *Xgwm328-2AS* – 5.2 cM – *PP3b/Xgwm817/Xgwm912-2A* – 3.6 cM – *Xgwm445-2A* {10392}.

pp1pp3. **v:** Saratovskaya 29 (this cultivar has red pericarp) {10329}.

A set of Saratovskaya 29 NILs is described in {11136}.

A homoeologous sysyem was later proposed:

PP1

PP-A1. [*Pp-A1*] 7AS. **v:** Saratovskaya 29 (not purple) {11312}.

PP-B1. [*Pp-B1*] 7BS. Later renamed as *Pp3b*.

PP-D1. [*Pp-D1*]. *TaPpm1a* {11313}. 7DS {11312}.

Pp-D1a**.** **v** Heixiaomai 76 *Pp3* {11313}; Luozhen 1 *Pp3* {11313}; Nongda3753 *Pp3* {11667}. **c:** GenBank KM382421**,** a purple pericarp MYB 1, is strongly expressed in the pericarp {11313}. GenBank MG066451 {11313}.

PP2.

PP3 [*Pp3*]. *TaMyc1* {11312}, *TaPpb1a* {11313}. 2AS.

Pp3**.** **v:** Heixiaomai 76 *Pp-D1* {11313}; Luozhen 1 *Pp-D1* {11313}; Nongda3753 *Pp-D1a* {11667}. **c:** Encodes a protein with an anthocyanin bHLH regulatory factor {11313}. GenBank MG066455; has a 6x261 bp tandem repeat in the promoter {11313}. Specifically expressed in the seeds {11313}. The alternate allele has only a single 261 bp repeat {11313}.

Combinations of *Pp3* and one or other *Pp1* single purple allele gave light purple pericarp whereas combinations involving *Pp3* with multiple purple alleles gave a dark purple phenotype {11312}.

Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color {11285}. This may correspond to *TaPpm2* located on chromosome 4BL, one of three *Ppm* genes with no effect on purple pericarp {11313}.

1.9.6. Purple glume

PG

Pg {10692}. 2A {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}. **ma:** *Xgwm328-2A* – 19.2 cM – *PG* – 1.4 cM – *PP3* – 5.1 cM – *Xgwm817-2A* {10692}.

1.9.7. Purple leaf blade

PLB

Plb {10692}. 7B {10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben) {10692}. **ma:** *Xgwm951-7B* – 6.7 cM – *PC/PLS/PLB* – 8.2 cM – *PP1* – 8.9 cM – *Xgwm753-7B* {10692}.

Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color {11285}. This may correspond to *TaPPM2* located on chromosome 4BL, one of three *PPM* genes with no effect on purple pericarp {11313}.

1.10. Awnedness

In cereals such as barley and rice awns are conferred by dominant genes. No homologous genes have been reported in wheat.

hd b1 b2. Bearded or fully awned genotype

1.10.1. Dominant inhibitors of awns

Hooded

HD

Hd {1551}. 4AS {1195, 1293}. **i:** S-615*11/CS {1500}. **v:** Chinese Spring *B2* {1293}. **ma:** *Xcdo1387-4A* – 8.2 cM – *HD* – 7.2 cM – *Xpsr163-4A* {0047} was mapped as a QTL with a peak on *Xfba78-4A* {0309}.

hd. **s:** CS*6/Hope 4A; CS*5/Thatcher 4A; CS*6/Timstein 4A.

Tipped 1

B1
TraesCS5A02G542800 (*b1* allele), annotated as a C2H2 zinc finger gene with an EAR domain (11570, 11571, 11581, 11582, 11596). Located in the terminal region of chromosome 5A that originated from homoeologous group 4 {11571}. Expression of *TraesCS5A02G542800* was higher in awnless genotypes {11571, 11581, 11582}.

B1 {1551}. *ALI-1* {11581}. 5AL {0242, 1293}. **i:** S-615*11/Jones Fife {1500}. **v:** Timstein {741}; Redman {160}; WAWHT2046 {10040}. **tv:** LD222 {10541}. Glossy Huguenot {11570}. **ma:** *Xgwm410.2-5A* – 8.2 cM – *B1* – 12.2 cM – *YR34* {10040}; Terminally located {10189}; *Xgwm291-5A.3* – 5.3 cM – *B1*{10330}. **matv:** *Xgwm291-5A* – 8.0 cM – *B1* {10541}. **c:** Functionally confirmed by transforming awned Kennong 199 with a 2,017 bp fragment containing *TraesCS5A02G542800* and UTRs from YMZ {11581}.
B1 was mapped as a QTL with a peak on *Xwmc182-6B* {0309}. Associated with increased number of spikelets per spike and decreased kernel size in a survey of global bread wheat germplasm {11571}. Associated with lower grain length and 1000 grain weight {11581}.

B1a {42}. **s:** Saratovskaya 29*8/Festiguay 5A {42}.

B1b {42}. **s:** Saratovskaya 29*8/Aurora 5A {42}.

B1c {42}. **s:** Saratovskaya 29*8/Mironskaya 808 5A {42}.

b1. *ali-1* {11581}. **v2:** Chinese Spring *B2 Hd* {1293}.

In a common genetic background, carriers of *B1a* have the shortest tip-awned phenotype; carriers of *B1b* and *B1c* have awns 2 to 3 times longer depending on environment. In F_1 hybrids, differences between the substitution line combinations are significant. The postulation of *B1* in both CS and Courtot {0309} based on the phenotype of a CS deletion stock was not supported by genetic observation.

Tipped 2

B2

B2 {1551}. 6BL {1297, 1293}. **i:** S-615*11/CS {1500}. **v:** Chinese Spring *Hd* {1293}.

b2. **s:** CS*6/Hope 6B; CS*5/Thatcher 6B; CS*9/Timstein 6B.

A GWAS of 364 wheat accessions identified 26 loci associated with awn length {11581}.

Awnless

Genotypes *Hd B2* (e.g., Chinese Spring) and *B1 B2* (e.g., Federation) are awnless. Presumably *Hd B1* is awnless. Watkins & Ellerton {1551} noted the probability of a third allele "*b1a*" leading to a half-awned condition, and in discussion they considered the possibility of a similar third allele at the *B2* locus. In view of more recent cytogenetic analyses, it seems that the half-awned condition could result from epistatic interactions between the alleles *B1* and/or *B2* and various promotor genes.

Although hooded, half-awned, tip-awned and awnless variants occur among tetraploid wheats, these are relatively infrequent. It has not been established with certainty that the above inhibitors are involved.

The inhibitor alleles have a pleiotropic effect on glume-beak shape {1348}. Acuminate beak is associated with full beardedness and occurs only in *b1 b2* types. *B2* reduces beak length producing an acute beak shape. *B1* reduces beak length producing an obtuse beak shape. In this effect *B1* is epistatic to *B2*.

1.10.2. Promotors of awns

The effects of (recessive) awn-promoting genes were documented in a number of studies, mainly through monosomic and disomic F_1 comparisons, and in tetraploids, whereas Heyne & Livers {549} provided genetic evidence of their effects. A series of "a" genes was documented, but the evidence for the existence of at least some of these was not well supported. Hence symbols for this gene series are not recognized.

1.10.3. Smooth awns

Smooth-awned tetraploid wheats were reported {16}, {45}, {690}, {1259} and genetic analyses {16}, {45}, {690} suggested a single recessive factor, with modifiers in most instances, relative to rough awns. The phenotype has not been reported in hexaploid wheats. No gene symbol is applied.

1.11. Basal sterility in speltoids

The presence of gene *Q* ensures the fertility of the first and subsequent florets in wheat spikelets {378}. In speltoids lacking *Q*, fertility of the second and subsequent florets is ensured by the dominant allele *Bs* (designated *A* in {378}) located on chromosome 5D {377}. In the presence of *Bs* the fertility of the first floret is under polygenic control.

In *bs bs* speltoids floret development is under polygenic control, and stocks with varying levels of basal fertility were isolated.

All group *vulgare* genotypes so far studied carry *Bs*.

The following stocks were described {378}:

GenotypeApprox. sterile-base scoreGroup *vulgare*----*QQ Bs Bs*0.00Speltoids StFF*qq Bs Bs*0.00StF*qq Bs Bs*0.08St1A*qq Bs Bs*0.39St1*qq Bs Bs*0.96St2*qq bs bs*1.41

	Genotype		Approx. sterile-base score
Group *vulgare*	----	*QQ Bs Bs*	0.00
Speltoids	StFF	*qq Bs Bs*	0.00
	StF	*qq Bs Bs*	0.08
	St1A	*qq Bs Bs*	0.39
	St1	*qq Bs Bs*	0.96
	St2	*qq bs bs*	1.41

1.12. Blue Aleurone

The *Ba* allele in *T. monococcum* spp. *aegilopoides* acc. G3116 determines a half-blue seed phenotype and is different from the allele present in *Elytrigia pontica* that determines a solid blue phenotype {282}. They are treated as different genes.
For review see {1643}.

BA1

Ba1 {643}. Derived from *Elytrigia pontica* (2n=70). [*Ba* {643}]. 4B [4BS-4el$_2$] {594}. **tr:** UC66049B (currently UC66049, PI 633834) {643}.

BA2

Ba2. [*Ba* {10451}]. 4A^{m}L. **dv:** G3116 {282}; PAU5088 = G2610 = PI 42783le9 {10451}. **ma:** *BA2* cosegregated with *Xcdo1387-4A, Xmwg677-4A* and *Xbcd1092-4*^{a} {282}; *Xcfd71-4A* – 10.3 cM – *BA* – 16.5 cM – *Xcfa2173-4A*.

1.13. Brittle culm

Three independent mutants with brittle tissues were obtained as EMS-induced mutants in *T. monococcum* accessions PAU 14087 {11002}. The mutations likely affected cellulose synthesis and involved all tissues {11002}.

BRC1

brc1 {11002}. 6AS {11002}. **dv:** *T. monococcum* mutant *brc3* {11002}. **ma:** *Xbarc37-6A* – 1.9 cM – *BRC1* – 10.3 cM – *Xbarc113-6A* {11002}.

BRC2

brc2 {11002}. 3AL {11002}. **dv:** *T. monococcum* mutant *brc2* {11002}. **ma:** *Xcfa2170-3A* – 2.9 cM – *BRC2* – 0.8 cM – *Xcfd62-3A* {11002}.

BRC3

brc3 {11002}. 1AL {11002}. **dv:** *T. monococcum* mutant *brc1* {11002}. **ma:** *Xwmc470-1A* – 3.9 cM – *Brc3* – 2.1 cM – *Xgwm135-1A* {11002}.

A further recessive mutation in *T. monococcum* accession Pau 5088 was named *brc5* (11505). **ma:** *Xcfd38*-5AL – 2.6 cM – *BRC5* – 4.8 cM – *Xgwm126-5AL* {11505}.

1.14. Brittle rachis

Brittle rachis in *T. durum* was defined as a spike that disarticulated when the tip was bent by 45 degrees relative to the peduncle {10242}. In chromosome substitution lines of wild emmer to common wheat, the 3AS derivative was more brittle than the 3BS derivative {10974}.
Wedge (W) type disarticulation is associated with the *Br-1* gene set whereas barrel (B) type disarticulation is caused by a different gene and is limited to species with the D genome {11080}.

BR1

BR-A1

Br-A1 {10061}. [*Br2* {10061}, *Br-A2* {10280}]. 3A {0130}. 3AS {10061}. **sutv:** LDN(DIC 3A) {0130}. **itv:** ANW10A=LD222*7/LDN-DIC DS 3A {10242}. **ma:** *Xgwm2-3A* – 3 cM – *BR-A1* – 8 cM – *Xgwm666-3A.1/Xbarc356-3A/Xbarc19-3A/Xgwm674-3A/Xcfa2164-3A* {10280}.

BR-B1

Br-B1 {10061}. [*Br3* {0130}, *Br-A3* {10280}]. 3BS {10061}. 3B {0130}. **sutv:** LDN(DIC 3B) {0130}. **itv:** ANW10B=LD222*7/LDN-DIC DS 3B {10242}. **ma:** *Xbarc218-3B* – 22 cM – *BR-B1* – 2 cM – *Xwmc777-3B* {10280}. **tv:** Senatore Cappelli PI 342646 {10242}; Sammartinara {10242}; others {10242}.
The presence of *Br-B1* in some durums apparently does not lead to significant shattering under conditions of Mediterranean agriculture {10242}.

BR-D1

Br-D1 {10061}. [*Br1* {9970}, Br^{61} {10362}]. 3DS {9970}. **v:** KU510, KU511, KU515 {10061}; R-61 {10362}; *T. aestivum* var. *tibetanum* {9970}. **dv:** *Ae. tauschii* KU2126 {10227}. **ma:** In *Ae. tauschii:* Br^{t} – 7 cM – *Xgdm72-3D* {10227}.
Evidence for an orthologous series extending to many related species is discussed in {0130} and {10061}.

BR-S1

Br-S1 {11080}. 3SS {11080}. **v:** Iranian spelts {11080}. **tv2:** *Triticum timopheevii* {11080}. **dv:** *Aegilops tauschii* {11080}. **ma:** *Xpsr1196-3S* – 32.3 cM – *BR-S1* – 1.5 cM – *Xabg471-3D* {11080}.

Br-D2

Br-D2 {11080}. 3DL {11080}. **v:** Common wheat {11080}; European spelts {11080}. **dv:** AL8/78 (shattering) {11080}; TA1604 (non-shattering) {11080}. **ma:** *Xmwg2013-3D* – 1.5 cM – *BR-D2* – 2.9 cM – *Xpsr170-3D* {11080}.

BR4

Br4 {10082}. 2A {10082}. **tv:** *T. dicoccoides* {10082}. **ma:** 33 cM distal to *Xgwm294-2A* (LOD=6.3, R^2=14.4%) {10082}.

1.15. Boron tolerance

Genes controlling tolerance to high concentrations of soil boron act additively.

BO1

Bo1 {1113, 1111}. [*Bot-B5b* {11432}]. 7BL {10460}. 7B {177}. **v:** Carnamah {10460}; Frame {10460}; Krichauff {10460}; Yitpi {10460}; Additional genotypes {10833, 10834}. **v2:** Halberd *Bo2Bo3*. **tv:** Kalka {10834}; Linzhi {10834}; Niloticum {10834}; Additional genotypes {10834}. **ma:** *Bo1* co-segregated with several STS-PCR markers, including *Xaww11-7BL*, falling within a 1.8 cM interval {10460}; The AWW5L7 (*Xaww11*) PCR marker allele was a good predictor of boron tolerance {10460}; Co-dominant PCR marker AWW5L7 co-segregated with *Bo1* and was predictive of the response of 94 Australian wheat genotypes {10833}; *Xbarc32-7B* – 2.4 cM – *Xaww5L7* – 1.2 cM – *Xbarc182-7B/BO1* – 1.2 cM – *Xpsr680/Xmwg2062-7B* {10833}; *Xbarc32-7B* – 2.6 cM – *Xaww5L7/BO1* {10834}. **c:** Boron transporter-like gene {11432}. GenBank KF148625.
Bo1 functions as a boron transporter {11432}.

BO2

Bo2 {1113, 1111}. **v2:** (W1*MMC)/Warigal *Bo3*. Halberd *Bo1 Bo3*.

BO3

Bo3 {1113, 1111}. 4A {0012}. **v2:** Warigal *Bo2*. Halberd *Bo1 Bo2*.

BO4

Bo4 {11432}. [*BOT(TP4A-B5C)* {11432}]. 4AL {11431}. **v:** G61450 {11431}. **c:** *Bo4* is a dispersed duplication of *Bo1* {11432}.

A homoeologous nomenclature based on annotated boron transporters inferred from the IWGS CS sequence is provided in Extended Data Table 1 in {11432}.

Very sensitive genotype: Kenya Farmer *bo1 bo2 bo3*.

Boron efficiency: In contrast to tolerance, boron efficiency was studied in {10135}. Monogenic segregation occured in Bonza (B inefficient)/SW41 (moderately B inefficient) and SW41/Fang60 (B efficient). Two genes, designated *Bod1* and *Bod2*, segregated in Bonza/Fang60.

QTL

Cranbrook (moderately tolerant) / Halberd (tolerant): DH population; QTLs for tolerance were identified on chromosomes 7B and 7D {10832}.

For a review of boron tolerance in wheat, see {10835}.

1.16. Cadmium Uptake

Low uptake is dominant.

Low cadmium uptake

CDU1

Cdu1 {963}. [*Cdu* {1128}]. Corrected to 5BL {10894}. 5BL {10104}. **itv:** Kyle*2/Biodur {10104}. **tv:** Biodur {1128}; Brigade {11044}; CDC Desire {11044}; CDC Verona {11044}; CDC Vivid {11044}; Enterprise {11044}; Eurostar {11044}; Fanfarran {10894}; Hercules {1128}; Napoleon {11044}; Nile {1128}; Transend {11044}; Strongfield {11044}. **bin:** 5BL9-0.76-0.79. **ma:** *CDU1* – 4.6 cM – *OPC-20* {1128}; *CDU1* – 21.2 cM – *UBC-180* {1128}; *Xfcp2-5B* – 12 cM – *CDU1* – 3 cM – *ScOPC20*{10894}; *ScOPC20/Xrz575-5B/XBG608197* – 0.5 cM – *Cdu1/XbF293297/XBF474090/Os03g53590(Xusw15-5B)* – 0.2 cM – *XBF474164*{10895}; *CDU1* is close to *VRN-B1*{10895}.

cdu1 {963}. [cdu 1 {1128}]. **itv:** Kofa {10104}. **tv:** Kyle {1128}; DT369 {10894}.

1.17. Chlorophyll abnormalities

1.17.1. Virescent

V1

V1. 3BS {1423}. 3B {122}, {1294}, {1311}. **v:** CS.

v1a. [*v* {1294}]. **i:** S-615*11/Neatby's Virescent {1500}. **s:** CS*9/Neatby's Virescent {1304}. **v:** Neatby's Virescent {1055}.

v1b. **i:** CS*/Hermsen's Virescent *v2b* {1304}. **v:** Hermsen's Virescent *v2b* {1311}.

V2

V2. 3A {1545, 1311}. **v:** CS.

v2a. **v:** Viridis 508 {1545}.

v2b. Expressed only when combined with *v2b*. **i:** CS*/Hermsen's Virescent *v1a* {1304}. **v:** Hermsen's Virescent *v1a* {1311}.
v1b and *v2b* are expressed only when both are present. Corresponding normal alleles are designated *V1* {3B} and *V2* {3A} following Sears' {1295} demonstration of their effects on the expression of *v1a*.

1.17.2. Chlorina

CN1

CN-A1. 7AL {1304, 1131, 1311}. 7° {1132}. **v:** CS.

cn-A1a. [*cn1a*]. **i:** ANK-32 {10820}; Chlorina-1 {1311}.

cn-A1b. [*cn1b*]. **i:** Cornell Wheat Selection 507aB-2B-21/6*CS {1133}.

cn-A1c. [*cn2*]. **i:** Chlorina-448 (CS background) {1545}.

cn-A1d {665}. **tv:** *CDd6* {665, 666}. **itv:** ANW5A-7A {10820}. **ma:** Hexaploid wheat: *Xhbg234-7A* – 8.0 cM – *CN-A1* – 4.3 cM – *Xgwm282/Xgwm332-7A* {10820}; Tetraploid wheat: *Xbarc192-7A* – 19.5 cM – *CN-A1* – 11.4 cM – *Xgwm63-7A* {10820}; Diploid wheat: *Xgwm748-7A* – 29.2 cM – *CN-A1* – 33.3 cM – *Xhbg412-7A* {10820}.

CN-B1. 7BL {1131}. **v:** Chinese Spring {1131}.

cn-B1a {665}. **tv:** *CDd1* {665, 666}; **v:** CBC-CDd1 {665}.

cn-B1b {665}. **tv:** CDd2 {665, 666}.

CN-D1. [*Cn3*]. 7D {1545}. 7DL {1131}. **v:** Chinese Spring {1131}.

cn-D1a. [*cn-D1, cn3*]. **i:** Chlorina-214 {1545}. **v:** CD3 {1583}.

Two mutants in diploid wheat are reported in {10820}.

13.17.3. Striato-virescens

A mutant of this type was described {376} but has been lost.

1.17.4. Yellow-green

YG

yg [{11238}]. Incompletely dominant. *y1718* {11238}. 2BS {11238}. **v:** Xinong 1718 mutant {11238}. **ma:** *Be498358* – 4.0 cM – *yg* – 1.7 cM – *Xwmc25-2B* {11238}.
The homozygous *ygyg* genotype is extremely yellow, stunted and sterile and the mutant is easily maintained as a heterozygote {11238}.

1.18. Cleistogamous flowering

Cleisogamy in barley is controlled by the *Chy1* allele that encodes an AP2 protein. The *Cly* and *cly1* alleles differ by a single nucleotide within the miR172 binding site. Three wheat homologues of *Cly1, viz, TaAP-2A, TaAp-2B* and *TaAp-2D* were located in the terminal bins of chromosomes 2AL, 2BL and 2DL, respectively in Chinese Spring and Shinchunaga {11013}. Cleistogamous flowering in durums Cleistogamy, a rare flowering habit in durum wheats, is controlled by a single recessive gene relative to chasmogamy {191}.

CL

Cleistogamous genotypes ***clcl***. **tv:** HI8332 {191}; WH880 {191}.
Chasmogamous genotypes ***ClCl***. **tv:** IWP5308 {191}; PWB34 {191}; WH872 {191}.

1.19. Copper efficiency

Copper efficiency is a genetic attribute that enhances plant growth in copper deficient soil.

CE

Ce {1276}. 4BL = T4BL.5RL {1276}. **v:** Cornell Selection 82a1-2-4-7 {462}; Backcross derivatives of Cornell Selection to Oxley, Timgalen, Warigal {464}; Hairy necked Viking {1276}.
5BS = T5BS.5RL. **ad:** CS+5R {463}. **su:** CS 5R {5D} {463}. **v:** Sears' stock HN-2 {464}; Backcross derivatives to Warigal and Timgalen {464}.

1.20. Corroded

CO1

co1. [*co* {1297}]. *wsl* {11535}. 6BS {1293}. **v:** }; Guomai Mutant {11535}; Sears' corroded mutant {1293, 1297, 11535{. **ma:** *Xgwm508-6B* – 5.1 cM – *Xgwm519-6B* – 8.2 cM – *CO1* {11535}; *Xgwm508-2* – 8.7 cM – *CO1* – *Xgpw7651-6B* {11534}.

CO2

co2. 6D {1570}. **v:** Kurrachee {1570}; Shannong 33 Mutant I30 {11534}. **ma:** *Xcfd190-6D – CO2 –* 9.1 cM – *6DS-5* {11534}.
A gene(s) in chromosome 6A acted as an inhibitor of corroded {1039, 1570}.

Corroded mutants are very frequent in EMS-treated populations {939}.

1.21. Crossability with Rye and *Hordeum* and *Aegilops* Spp.

1.21.1. Common wheat

High crossability of some wheats, particularly those of Chinese origin, viz. Chinese 446 {790}, Chinese Spring {1216}, and TH 3929 {939}, with cereal rye, weed rye (*S. segetale* L.) {1646}, and other species, e.g., *Aegilops squarrosa* {691}, *Hordeum bulbosum* {1387, 1397, 1469} and *H. vulgare* {349, 693], is determined by additive recessive genes. The *kr* genes influence crossability with *H. vulgare*. Allele *Kr1* is more potent in suppressing crossability than *Kr2*, which is stronger in effect than *Kr3* {1387}. According to Zheng et al. {1649}, the effect of *Kr4* falls between *Kr1* and *Kr2*.

KR1

Kr1. 5B {1216}. 5BL {762}. **ma:** Mapped to a 2.0 cM region flanked by *Xw5145-5B* and *CA1500122/Xw9340-5B* {10922}.
A second gene in 5BL distal to the *Ph1* locus and flanked by *Oshypl* and *Os09g36440*, but including *Xgwm371-5B*, affected the temperature sensitivity of seed-set in *Kr1* genotypes in wide crosses {10922}.

KR2

kr2. 5A {1216}. 5AL {1387}.

kr1 kr2. **v:** Chinese 446 {790}; Chinese Spring {1025, 1216, 762}; Martonvarsari $9^{*}4$/CS {1016}.

KR3 {11769}. 5DL {11769}. Published paper not available.

kr3. A very weak effect.

KR4

kr4. 1A {1649}.

KR5

Kr5 [{11387}]. *skr* {0134, 11352}. 5BS {11352, 11764}. ma: Linked marker *Cfb306-5B* {11764}.

kr5 **su:** Courtot (Fukuhokomugi 5B) {11352}. **v:** Balthazar-crossable {11352}; Deucendeu {11352}; MP98 {11764}; Ornicar-crossable {11352}.

Balthazar-crossable and Ornicar-crossable probably also carry *kr1* {11352}.

Kr1 kr2. **s:** CS*6/Hope 5B {1216, 762}. **v:** Blausamtiger Kolben {790}.

kr1 Kr2. **s:** CS*6/Hope 5A {1216}.

Kr1 Kr2. **v:** Marquis {790}; Peragis {790}.

kr1 kr2 kr3 kr4. **v:** J-11 {1649}.

Kr1 Kr2/Kr1 kr2. (heterogeneous). **v:** Martonvarsari 9 {1016}.
Using the Chinese Spring/Cheyenne chromosome substitution series, Sasaki & Wada {1265} found significant differences in crossability for chromosome 5B, 7D, 1D and 4B. Differences between rye lines were also reported {1265, 1458}. Allelic variation in the potency of the dominant suppressor genes was reported {1385, 343}. Evidence for allelic variation in dominant supressors is reported in {1386}. Lists of wheat/rye crossabilities:{1383, 1642, 850, 858}.

QTL

65% of the variability in a Courtot/CS population was associated with *Xfba-367-5A* (5AS), *Xwg583-5B* (5BL) and *Xtam51-7A* {0134}. Only the second QTL appeared to coincide with known locations of *Kr* genes. The former was *skr*.

1.21.2. Tetraploid wheat

The Chinese tetraploid, Ailanmai, possesses recessive crossability genes on chromosomes 1A, 6A and 7A with the 6A gene being the least effective {0017}.

1.22. Dormancy (Seed)

Seed dormancy in wheat has several components, including factors associated with vivipary and red grain colour. Dormancy is an important component of resistance/tolerance to pre-harvest sprouting (PHS). For a review of genes involved in preharvest sprouting see {11569}.

1.22.1. Germination index

TaSDR-1

Isolated using the seed dormancy related gene *OsSdr4*.

TaSDR-A1. [*TaSdr-A1* {11199}]. 2A {11199}. **ma:** *Xgwm95-2A* – 1.4 cM – *TaSDR-A1* – 1.5 cM – *Xgwm372-2A* {11199}.

TaSdr-A1a {11119}. **c:** GenBank KF021988 {11119}.

This allele is associated with lower germination index

TaSdr-A1b {11119}. **c:** GenBank KF021989 {11119}.

This allele is associated with higher germination index

TaSDR-B1. [*TaSdr-B1* {11119}]. 2B{11119}.

TaSdr-B1a {11119}. **v:** Yangxiaomai {11119}. **c:** GenBank KF021990 {11119}.
This allele is associated with lower germination index.

TaSdr-B1b {11119}. **v:** Zhongyou 9507 {11119}. **c:** GenBank KF021991 {11119}.
This allele was associated with higher germination index.

1.22.2. Vivipary

Orthologues of maize viviparous 1 (*Vp-1*) are located in chromosomes 3AL, 3BL and 3DL {9961} approximately 30 cM distal to the *R* loci. Variability at one or more of these loci may be related to germination index and hence to PHS {10468}.
Alleles at *VP-A1* were recognized using STS marker A17-19 {10919}.
Three sequence variants at *VP-B1* identified in {10468} were used to develop STS marker *Vp1B3* whose amplified products showed a significant, but not complete, association with germination index used as one measure of PHS.
Alleles of *VP-B1* were recognised using STS marker *Vp1B3* {10615, 10621}.

VP-1

VP-A1 {10919}. 3AL {10919}.

Vp-A1a {10919}. **v:** Nongda 311 {10919}. **c:** 599 bp {10919}.
Higher germination index.

Vp-A1b {10919}. **v:** Wanxianbaimaizi {10919}; Yannong 15 {10919}. **c:** 596 bp {10919}.
Lower germination index.

Vp-A1c {10919}. **v:** Jing 411 {10919}. **c:** 593 bp {10919}.
Higher germination index.

Vp-A1d {10919}. **v:** Xiaoyan 6 {10919}. **c:** 590 bp {10919}.
Lower germination index.

Vp-A1e {10919}. **v:** Zhengzhou 6 {10919}; Bainong 64 {10919}. **c:** 581 bp {10919}.
Higher germination index.

Vp-A1f {10919}. **v:** Yumai 34 {10919}. **c:** 545 bp {10919}.
Higher germination index.

Vp-A1g {11047}. [*Vp-1Ab* {11047}]. **v:** Kalyansona {11047}; Sonalika {11047}; Yaqui 50 {11047}; Yecora Rojo 76 {11047}. **c:** GenBank GU385899 {11047}.

Vp-A1h {11047}. [*Vp-1Ad* {11047}]. **v:** Attila {11047}; Glenlea {11047}; Tanori F71 {11047}. **c:** GenBank GU385901 {11047}.

Vp-A1i {11047}. [*Vp-1Af* {11047}]. **v:** Debeira {11047}; Kancahn {11047}; Rayon F89 {11047}. **c:** GenBank GU385903 {11047}.

VP-B1. 3B {11047}.

Vp-B1a {10615}. **v:** Charger {10616}; Zhongyou 9507 {10615}; 271 accessions {10616}. **c:** GenBank AJ400713 {10615}.

Vp-B1b {10615}. **v:** Altria {10616}; Recital {10616}; Yongchuanbaimai {10615}; 2 accessions {10616}. **c:** 193 bp insertion in third intron relative to *Vp-A1a*.

Vp-B1c {10615}. **v:** Scipion {10616}; Xinong 979 {10615}; 101 others {10616}. **c:** 83 bp deletion relative to *Vp-B1a*.

Vp-B1d {10616}. **c:** 25 bp deletion relative to *Vp-A1a*.

Vp-B1e {10998, 10621}. [*Vp-1Be* {10998}]. **v:** Fulingkemai {10999}; Hongheshangtou {10621}; Hongmangchum {10998}; Wangshuibai {10999}. **c:** 83 bp deletion, 4 bp insertion and 2 SNPs relative to *Vp-B1a* {10621}.

Vp-B1f {10998}. [*Vp-1Bf* {10998}]. **v:** Wanxanbaimaizi {10998}.

Vp-B1g {11047}. [*Vp-1Bg* {11047}]. **v:** HD2939 {11047}; Pavon 76 {11047}; Sonora 64 {11047}. **c:** GenBank GU385904 {11047}.

Vp-B1 allelic identifications for Chinese landraces, historical and current wheat cultivars are listed in {10621}.

VP-D1 {10919}. 3DL {10919}. **c:** AJ400714 {10919}.

Vp-D1a {10919}. 3DL {10919}. **v:** 81 Chinese wheat cultivars {10919}. **c:** 5 pairs of primers{10919}. There was a suggestion of a relationship between alleles and PHS response {10615}.

1.22.3. Pre-harvest sprouting

PHS1 **c** Encodes a mitogen-activated protein kinase kinase (*TaMKK3-A)* {11737} and orthologue of *SD2* (*Qsd2-AK*) in barley {11737}.
Phs1 {10500}. Semi-dominant {9960}. [*Phs* {9960}; *Phs1-4AL*; *Phs-A1* {11546}; *TaMKK-A* {11546}. 4AL {9960}. **i:** Haruyokoi*6/Leader {10500}; Haruyokoi*6/Os21-5 {10500}. **v:** Chinese Spring {11737}; Leader {10500}; Os21-5 {10500}; Soleil {9960}. **ma:** Associated with *Xpsr1327-4A* {10346}; *Xhbe03-4AL* – 0.5 cM – *Phs1* – 2.1 cM – *Xbarc170-4AL* {10500}.

phs1. **v:** Haruyokoi {10500}.

TaOsd1 {11738}. CRISPR-Cas 9 knockout of *TaQsd1* homoeologues in chromosomes 5A, 5B and 5D led to a 3-4-fold increase in dormancy in Fielder wheat {11738}. *Qsd1* encoding an alanine amino transferase controls dormancy in barley.

Genotypes with and without favourable haplotypes are discussed in {11546}.
According to {11547} red grain colour increases the time to dormancy release and has a cumulative effect when combined with other dormancy genes not associated with grain colour.
For a review of Preharvest Sprouting see {11595}.

QTL

Several QTL for falling number and alpha-amylase activity, two indicators for pre-harvest sprouting resistance, were identified in {0169}. The most significant were associated with *Xglk699-2A* and *Xsfr4(NBS)-2A*, *Xglk80-3A* and *Xpsr1054-3A*, *Xpsr1194-5A* and *Xpsr918-5A*, *Xpsr644-5A* and *Xpsr945-5A*, *Xpsr8(Cxp3)-6A* and *Xpsr563-6A*, and *Xpsr350-7B* and *Xbzh232(Tha)-7B* {0169}.

AC Domain / Haruyutaka: one major QTL in chromosome 4AL and two lesser possibly homomeologous QTLs for dormancy in 4BL and 4DL {0226}.

AC Domain (red seeded, PHS resistant) / RL4137 (white seeded, PHS moderately resistant): most measures of PHS occurred as clusters at the *R* loci. However, *QSi.crc-5D* for sprouting index, R^2=0.44, was independent of seed colour {10626}.

Annong 0711 (res) / Henong 825 (sus): RIL population. Differences in germination index were attributed to a 33 bp insertion in the promoter (possibly the AP2 binding site) of *TaMFT-3A* in Annong 0711 relative to Henong 825. *TaMFt-3A* encodes a phosphatidyl ethanolamine-binding protein {11410}.

Argent (non-dormant, white seeded) / W98616 (dormant, white seeded): 90 DH lines: Strong QTLs on chromosomes 1A, 3A, 4A and 7A and weaker QTLs on 2B, 5B, and 6B, all from W98616 {10740}.

CN10955 (PHS resistant white seeded) / Annuello (PHS susceptible, white seeded): F8 RIL population: *QPhs.dpivic-4A.2* in the *Xgwm637-4AS* – *Xgwm937/Xgwm894-4AL* region and *QPhs.dpivic-4A.1* in the *Xwmc48-4AS* – *Xgwm397-4AS* region {10599}.

SPR8198 (red seeded, PHS tolerant) / HD2329 (white seeded, PHS susceptible): Tolerance to preharvest sprouting (PHS) was associated with *Xwmc104-6B* and *Xmst101-7D* {0032}. In a further study 7 QTL were located on chromosomes 2AL, 2DL, 3AL and 3BL, the most important, on 2AL and 3AL {10670}.

SPR 8198 (dormant) / HD2329: *QPhs.occsu-3A* was located in the *Xgwm155-3A – Xwmc153-3A* region with $R^2 = 75\%$ across 6 environments {10261}.

Renan / Recital: QTL for preharverst sprouting were identified on chromosomes 3A (associated with *Xfbb293-3A* at P = 0.01), 3B (associated with *Xgwm403-3B* and *Xbcd131-3B* at P = 0.001), 3D (associated with *Xgwm3-3D* at P = 0.001) and 5A (associated with *Xbcd1871-5A* at P = 0.001) in the population {0347}. The resistant alleles on the group 3 chromosomes and on 5A were contributed by Renan and Recital, respectively. All QTL for preharvest sprouting co-located with QTL for grain colour {0347}.

RL4452 (red seeded, low PHS tolerance) / AC Domain (red seeded, high PHS tolerance): DH lines: Genes associated with falling number, germination index and sprouting index contributing to PHS were locatged on chromosomes 3A, 4A (locus-2) and 4B in AC Domain and 3D, 4A (locus-1) and 7D in RL4452 {10671}.

Rio Blanco (white seeded, PHS resistant) / NW97S186 (white seeded, PHS susceptible): RIL population: *QPhs.pseru-3AS*, R^2=0.41, *Xgwm369-3A – Xbarc12-3A*, and one minor QTL {10634}. This major QTL was confirmed in a Blanco / NW98S079 RIL population, R^2 up to 0.58 {10634}. *Qphs.pseru-3A* (*TaMFT*-3A) was fine mapped to a 1.4 cM region flanked by two AFLP markers and was tightly linked to *Xbarc57-3A* and seven other AFLP markers {10893}.

Sun325B (dormant white seeded) / QT7475 (semi-dormant white seeded): both parents with the chromosome 4A QTL: DH population: A QTL was located in the *Xgwm77-3B – Xwmc527-3B* interval ($R^2 = 0.19$) in the approximate region of the *R-B1* locus {10669}.

Totoumai (res) / Siyong (sus): RIL population: A QTL on chromosome 4AL was delimited to a 2.9 cM interval flanked by GBS109947 and GBS212432; nine and two SNP were associated with minor QTL on chromosomes 5A and 5B {11408}, respectively.

Zenkoujikomugi / CS: *Qphs.ocs-3A.1* on chromosome 3AS was associated with *Xbcd1380-3A* and *Xfbb370-3A* accounting for 38% of the phenotypic variation {10195}. *QPhs.ocs.3A-1* was localized to a 4.6 cM interval flanked by *Xbarc310-3A* and *Xbcd907-3A* {10245}. A weaker QTL, *Qphs.ocs-3A.2* in 3AL, was not associated with *TaVp1* {10195}, the wheat orthologue of the maize transcription factor Viviparous-1.

Zenkoujikomugi/Spica: White seeded wheats with the dormancy-related QTL, *QPhs-3AS* from Zenkoujikomugi were more resistant to PHS than counterparts with the contrasting allele from Spica {10377}. White seeded wheats with contrasting alleles of *QPhs-4AL* were not different {10377}.

Qphs.ocs-4A.1, may be the same as a QTL in AC Domain/Haruyutaka due to tight linkage with *Xcdo785-4A* {10245}.
QPhs.ocs.4B.1, a CS allele contributing to dormancy, was located in the region of *Xgwm495-4B* {10245}.

QPhs.sicau-3B.1, distally located on chromosome 3B in ***T. spelta*** **CSSR6 (res) / Lang (sus)**; nearest marker *wPt-6157*; transferred to durum cv. Bellaroi using SCAR markers {11246}.

QTL analyses in several crosses {10275} indicated a common region in chromosome 4A associated with dormancy, dormant genotypes included AUS1408, SW95-50213 and Halberd. The location was consistent with Japanese and U.K. work even though different flanking markers were involved.

Association mapping of 198 winter wheat genotypes detected 8 QTLs on 7 chromosomes, viz. 1BS, 2BS, 2BL, 2DL, 4AL, 6DL, 7BS and 7DS {10959}.

A GWAS identified 12 QTL for PBS resistance among which those on chromosomes 3AS and 4AL were most commonly detected {11409}.

Diploid wheat QTL

T. monococcum **KT3-5 (non-dormant) /** ***T. boeoticum*** **KT1-1 (dormant)**: RIL population: QTL on chromosome 5A^{m}L, *Xcdo1236c-5A – Xabc302-5A*), R^2 = 0.2-0.27. Weaker QTLs were found on 3A^{m} (*TmAB18 – Xwmc102-3A* and *Xrz444-3A – TmABF*) and 4A^{m} (*Xrz261-4A – Xrz141-4A*) {0892}. The 3A^{m} QTL co-located with *TmABF* and *TmAB18* {10417}, derived from orthologous ABA signaling genes in *Arabidopsis*. The 5A QTL may be orthologous to the barley dormancy gene *SD1* {10417}.
For a review of Preharvest sprouting see {11595}.

1.23. Ear emergence

QEet.ocs-4A.1 {0047}. 4AL {0047}. **v:** CS/CS(Kanto107 4A) mapping population. **ma:** Associated with *Wx-B1*{0047}.

QEet.ocs-5A.1 {0068}. 5AL {0068}. **v:** CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population {9903}. **ma:** Associated with *Xcdo584-5A* and morphological locus *Q* {0068}.

QEet.ocs-5A.2 {0026}. 5AL {0026}. **ma:** *Xcdo 412-5A – Xbcd9-5A* region {0026}.

QEet.inra-2B {10069}. 2B. **ma:** 2B linked to *Xgwm148* (LOD=5.7, R^2 = 11.9%.

QEet.inra-2D {10069}. 2D. **ma:** 2D linked to *XksuE3* (LOD=2.7, R^2 = 6.5%).

QEet.inra-7D {10069}. 7D. **ma:** 7D linked to *Pch1* (LOD=3.9, R^2 = 7.3%).

QEet.ipk-2D {255}. *QEet.ipk-2D* coincides with a QTL for flowering time, *QFlt.ipk-2D*. Both QTLs may correspond to *Ppd-D1* {0255}. 2DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Lateness was contributed by W-7984{0255}. **ma:** Associated with *Xfba400-2D* and *Xcdo1379-2D* {0255}.

QEet.ipk-5D {0255}. *QEet.ipk-5D* coincides with a QTL for flowering time, *QFlt.ipk-5D*. Both QTLs probably correspond to *Vrn-D1* {0255}. 5DL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}; Lateness was contributed by W-7984 {0255}. **ma:** Associated with *Xbcd450-5D* {0255}.

1.24. Earliness per se

Genes for earliness *per se* {0023} affect aspects of developmental rate that are independent of responses to vernalization and photoperiod.

EPS-A1

Eps-A1a {0024}. 3AL {0024}. 3A {0023}. **v:** Chinese Spring {0024}.

Eps-A1b {0024}. **v:** Timstein {0024}.

Eps-1A$^{\mathrm{m}}$ {0364}. [*Eps-A*^{m}1]. 1AL {0364}. **dv:** *T. monococcum* DV92 allele for late flowering, G3116 early flowering {0364}. **ma:** 0.8 cM distal to *Xwg241-1A* {0364}; within a 0.9 cM region within the *VAtpC – Smp* region{10246}; The circadian clock gene *Elf3* was identified as a candidate gene for *Eps-A*$^{\mathrm{m}}$1{11120}.

EPS-B1

Eps-5BL.1 {10075}. 5BL {10075}. **ma:** QTL mapped on chromosome 5BL, linked to *Xwmc73-5B* (this QTL explained 8% of the variance in flowering time, P <0.03 {10075}.

Eps-5BL.2 {10075}. 5BL {10075}. **ma:** QTL mapped on chromosome 5BL, linked to *Xgwm499-5B* (this QTL explained 6% of the variance in flowering time) {10075}.

EPS-D1

Eps-D1 {11193}. 1DL {11193}. **v:** Earliness allele: Cadenza and Spark {11193}; Lateness allele: Avalon and Rialto {11193}. **ma:** The earliness allele was associated with a subtelomeric deletion containing three candidate genes one of which was *TaELF-D1* {11193}.
A QTL for heading date co-segregated with *TaELF3-1DL* in a RIL population derived from **Gaocheng 8901 / Zhoumai 16** {11194}; a deletion of the *Eps-1D* region was associated with earlier flowering.

epsCnn {0025}. **v:** Cheyenne{0025}.

Eps Wi {0025}. 3A {0025}. **su: Cheyenne*****7 / Wichita 3A** {0025}. **ma:** Linked to QTLs for plant height, kernel number per spike, and 1,000-kernel weight in RSLs derived from CNN/CNN(WI3A) {0025}.

<u>QTL</u>

CS / *T. spelta* var. *duhamelianum* KT19-1: RIL population: Two QTL for narrow-sense earliness were detected on chromosome 2B in a {10057}. These QTLs were associated with markers *Xpsr135-2B* and *Xabc451-2B* {10057}. For both QTLs, earliness was conferred by the CS allele.

Courtot / CS: {0132}.

Cutler / AC Barrie: Three QTLs were mapped on chromosomes 1B (*QEps.dms-1B.1* and *QEps.dms-1B.2*) and 5B *QEps.dms5B*) {11039}.

Grandin / BR34: *QEet.fcu.5AL* identified in *Xfcp359-5A* – *Xfcp231-5A* interval ($R^2 = 0.38$), at or near the *Q* locus in {10256}. Grandin was the earlier parent.

1.25. Embryo lethality

The Chinese Spring (Imperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, R7) produced hybrid seeds with different proportions of differentiated embryos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74-100% differentiated embryos {10748}. A cross of R2 with the CS nulli-tetrasomics gave differentiated embryos only with N6AT6B and N6AT6D, indicating the presence of a complementary factor *Eml-A1* on chromosome 6A {10748}.

1.26. Flag leaf width

Two NILs in backgrounds of Mianyang 99-323 and PH691 possessing *Fhb5* in a *Xbarc303-5A* – *Xbarc100-5A* interval from Wangshuibai spanning the centromere had a narrow leaf phenotype. *QFlw.nau-5A*, re-designated as *TaFLW1*, was mapped to a 0.2 cM region, *Xwmc492-5A* – *Xwmc752-5A*: bin 5AL12-0.37-0.57, and was separated from *Fhb5*: bin 5AS3-C-0.75 {10934}.

1.27. Flowering time

The isolation of wheat genes orthologous to the Arabidopsis *Co* and rice *Hd1* genes was reported in {10054}. The genomic clones TaHd1-1, TaHd1-2 and TaHd1-3 originated from the long arms of chromosomes 6A, 6B and 6D, respectively. The orthology of the *TadHd1* genes with *Co/Hd1* was demonstrated by complementation of a rice line deficient in *Hd1* function with the TaHd1-1 genomic clone. The wheat *TaHd1* and rice *Hd1* genes were located in non-syntenic locations {10054}. To date, no variation for flowering time has been identified on wheat group 6 chromosomes.

QTL

QFlt.ipk-3A {0255}. 3AL {0255}. **v:** Opata/W-7984 (ITMI): RI mapping population{0255}; Lateness was contributed by W-7984 {0255}. **ma:** Associated with *Xbcd451-3A* {255}.

QFt.cri-3B.1 {10567}. Nearest marker *Xbarc164-3B*; identified in croses of substitution lines of Ceska Presivka and Zlatka or Sandra {10567}.

Arina (149 days) / Forno (150 days): winter wheat cross: Six QTL were detected over six environments. The 3 most important, all from Arina, were in chromosomes 6DL (R^2=16%), 3DL (R^2=14%) and 7BL (R^2=13%); 3 others in 2AL, 5BL and 6DL were from Forno {10172}.

CI 13227 / Suwon 92: RIL population: Heading date: AFLP marker – 2.6 cM – *QHd.pser-2DS* – 121.1 cM – *Xgwm261-2D* {10269}. This QTL could be *Ppd-D1* {10269}.

Ernie (early) / MO94-317 (late): winter wheat cross: days to anthesis (dta): *Qdta.umc-2D*, linked to *Xbarc95-2D*, R^2 = 0.74 {10456}.

Karl 92*2 / TA 4152-4: F_2:F_4 population: Two QTLs, *QHd.ksu-2D*, associated with *Xgwm261-2D* (R^2=0.17), and *QHd.ksu-3D*, associated with *Xgwm161-2D* 9 (R^2) {10273}.

Nanda 2419 / Wangshuibai: spring wheat cross: 7 QTL for flowering time identified with earlier alleles for five coming from Nanda 2419: *QFlt.nau-1B* (closest marker *Xbarc80-1B*, R^2=11 %), *QFlt.nau-1D* (*Xbarc62-1D, Xgwm232-1D*, R^2=6.13 %), *QFlt.nau-2B* (*Xwmc35-2B*, R^2=10 %), *XFlt.nau-2D* (*Xwmc601-2D*, R^2=10 %), *XFlt.nau-4A.1* (*Xcfd2-4A, Xmag1353-4A*, R^2=10 %), *XFlt.nau-4A.2* (*Xmag3386-4A, Xwmc161-4A*, R^2=18-19 %), *XFlt.nau7B (Xmag2110-7B, Xmag1231-7B, Xgwm537-7B, Xwmc218-7B*, R^2=18 %) {10566}.

1.28. Flour colour

Schomburgk/Yarralinka: RIL population: Regions in 3A and 7A accounted for 13% and 60% of the genetic variation, respectively, and *Xbcd828-3A*, *Xcdo347-7A* and *Xwg232-7A.1* were significantly associated with flour colour {9936}. The association was highly significant in all three replicates only for the 7A QTL. Symbols were not assigned to the flour colour loci. See also 29.2. Flour, semolina and pasta colour. Lutein is one of the carotenoids contributing to flour colour. Esterification of lutein contributes to its stability during storage. A locus controlling esterification was located in chromosome 7D.

Lutein esterification

LUTE

Lute {11189}. High lutein ester. 7DS {11189}. **bin:** 7DS4-0.61-1.00. **v:** Indis {11189}; Sunco*2/Indus Der. DM5685*B12 {11189}; Most bread wheat accessions. **ma:** *Xwmc438-7D* – 15.1 cM – *LUTE/XwPt-116/XwPt-3727* – 17.7 cM – *Xbarc154-7* {11189}.
Sunco is low lutein but high ester, whereas Haruhikari is low lutein and zero ester.

lute. Low lutein ester. **v:** Haruhikari {11189}.

Lutein esters were not detected in durum {11189}.

1.29. Free-threshing habit

QFt.mgb-5A {0046}. 5AL {0046}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population {0046}. **ma:** Associated with *XksuG44-5A* {0046}.

QFt.mgb-6A {0046}. 6A {0046}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population {0046}. **ma:** Associated with *Xpsr312-6A* {0046}.

1.30. Frost resistance

FR-1

Fr1 {1446}. 5AL {1446}. **v:** Hobbit{1446}. **ma:** Mapped to the mid-region of 5AL, 2.1 cM distal from *Xcdo504-5A* and *Xwg644-5A* and proximal to *Xpsr426-5A* {419}; Mapped 2 cM proximal to *Xwg644-5A* and *VRN-A1* {0291}; and flanked by deletion points 0.67 and 0.68 {0292}.

Fr2 {0291}. 5DL {0291}. **s:** CS*7/Cheyenne 5D {0291}. **ma:** *FR2* mapped 10 cM proximal to *VRN-D1*{0291}.

Studies using induced and natural mutants of *VRN-1* suggested that differences in frost tolerance previously attributed to *FR1* were pleiotropic effects of *VRN-1* {10708}.

FR-2

Fr-A2 {10079}. **dv:** *Triticum monococcum*. Frost tolerant parent G3116, frost susceptible parent DV92. **ma:** The QTL mapped on chromosome 5AL had a LOD score of 9 and explained 49% of the variation in frost tolerance. Closest markers: *Xbcd508-5A* and *Xucw90(Cbf3)-5A.* These markers are 30 cM proximal to *Xwg644-5A*, which is closely linked to frost tolerance locus *FR-1*. Eleven different *Cbf* transcription factors were identified at the *Fr-A2* locus {10302}; QTLs for frost tolerance in the *FR-A2* region were also identified in wheat chromosome 5B (*FR-B2* {10079}) and in barley chromosome 5H (*FR-H2* {10083}.

Fr-B2. [*Fr-B1* {10075}]. **ma:** QTL mapped on chromosome 5BL, linked to *Xgwm639-5B* (this QTL explained 12-31% of the variance in frost tolerance) {10075}. *Xgwm639-5B* mapped close to *Xmwg914-5B*, and to *Xbcd508-5B*, a marker located at the peak of the *Fr-A2* QTL {10075}. This data suggests that this locus is more likely orthologous to *FR-2* than to *FR-1*.

QWin.ipk-6A. 6AS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Winter hardiness was contributed by W-7984 {0255}. **ma:** Associated with *Xfba85-6A* and *Xpsr10(Gli-2)-6A* {0255}.

Responses to cold exposure and their genetics are reviewed in {0020, 0274}.

QTL

Norstar (tolerant) / Winter Manitou (non-tolerant): DH population: Norstar possessed major and minor QTL for tolerance on chromosomes 5A and 1D. The 5A QTL was 46 cM proximal to the *VRN-A1* locus (R^2=0.4); its peak co-incided with *Xwmc206-5A* and *Xcfd2-5A*, and expression of C-Repeat Binding Factor genes with strong homology to *Cfb14* and *Cfb15* located at the *FR-2* locus in *T. monococcum* {10414}.

1.31. Gametocidal genes and segregation distortion

1.31.1. Gametocidal activity

GC1-B1

Gc1-B1a {1485}. [*Gc1a* {1490}, *Gc1* {1487}]. 2B {1490}. **i:** CS*8/*Aegilops speltoides* subsp. *aucheri* {1487}.

Gc1-B1b {1485}. [*Gc1b* {1490}]. 2B {1490}. **i:** **C**S*8/*Ae. speltoides* subsp. *ligustica* {1490}.

GC1-C1

Gc1-C1 {0188}. 2CL {0189}. **ad:** CS/2C {0189}. **su:** CS2C(2A), CS2C(2B), CS2C(2D) {0189}.

GC1-S^l

Gc1-Sl1 {1485}. [*Gc-S^{l}3* {1485}]. *2S^l* {334}. **ad:** CS/*Ae. sharonensis* {334}.

GC2-S^{l}1

Gc2-S^{l}1a {1485}. [*Gc-S^{l}1* {1485}]. 4S^1 {866}. **ad:** CS/*Ae. longissima* {866}.

Gc2-S^{l}1b {1485}. [*Gc-S^{l}2* {1485}]. 4S^1 {1013}. **ad:** S/*Ae. sharonensis* {1013}. **ma:** An EMS-induced *Gc-2* mutant was mapped to a wheat-*Aegilops sharonensis* T4B-4S^{sh}#1 translocation chromosome {10068}.

GC-C1

Gc3-C1 {1485}. [*Gc-C* {1485}]. 3C {333}. **ad:** CS/*Ae. triuncialis* {338}.

Gc1-B1a, Gc1-B1b and *Gc1-S*^{1}, classified in the same functional group, are hypostatic to the genes *Gc2-S*^{1}*1a* and *Gc2-S*^{1}*1b*. *Gc3-C1* does not interact with the *Gc* genes in the other two groups.
In addition to these genes, chromosomes carrying gametocidal genes occur in *Ae. caudata* {337}, *Ae. cylindrica* {336} and other strains of *Ae. longissima* and *Ae. sharonensis* {335},{1484}.
Gametocidal genes in chromosomes in the same homoeologous group have the same gametocidal action {0190}. In monosomic additions of chromosomes with gametocidal effects, chromosome deletions and translocations are produced in gametes not having the gametocidal genes. This feature has been exploited to isolate genetic stocks suitable for physical mapping of wheat {0191} chromosomes, and of rye {0192} and barley {0193, 0194, 0195} chromosomes in a wheat background.

Genes with gametocidal activity (*Sd1* {1647} and *Sd2* {1161}) in wheat are present in homoeologous group 7 chromosomes of *Thinopyrum elongatum* {653, 1647}. A segment earlier believed to be derived from *Thin. distichum* {889, 892} is probably the same as that from *Thin. elongatum* {1162}.
In the presence of both *Sd1* and *Sd2, Lr19* is transmitted preferentially in heterozygotes, the degree of distortion being determined by genetic background. In heterozygotes with the same background, and in the presence of only *Sd2, Lr19* shows strong self-elimination. Based on these results, it seems likely that the Sears' translocation 7D-7Ag#7 does not carry *Sd1* {939}.
See also Pollen Killer.

1.31.2. Suppression of gametocidal genes

IGC1

Igc1 {1489}. Causes suppression of the 3C chromosome gametocidal gene of *Ae. triuncialis*. This alien gametocidal factor also promotes chromosome breakage {1486}. 3B {1488}. **v:** Norin 26 {1483, 1488}; Nineteen wheats listed in {1483, 1488}.

igc1. **v:** Chinese Spring{1483,1488}; Forty wheats are listed in {1483,1488}.

1.31.3 Segregation distortion

SD1

Sd1 {1647}. 7D {1647}. **v2:** Agatha *Sd2* {1647, 1161}. **ma:** Proximal to *Lr19* and distal to *Xpsr165-7D* {10255}.

SD2

Sd2 {1161}. 7BL {1163}. **v:** 88M22-149 {1163, 1161}.
Zhang et al. {10255} question the existence of this gene and alternatively suggested a duplication or deletion event influencing the transmission.

See also Pollen Killer

1.32. Gibberellic acid response (insensitivity)

GAI1

Gai1. [*GAI1* {1246}, {565}]. 4BS {980}. 4B {406}. **i:** See {408}. **v:** Norin 10 Der. {407, 565}. **ma:** *Xpsr622-4B* (distal) – 1.9 cM – *GAI1* – 8.3 cM – *Xbcd110-4B* (proximal) {9959}. **tv:** Messapia {9959}.

GAI2

Gai2. [*GAI2* {1246}, {565}]. 4D {411}. 4DS {980}. **i:** See {408}. **v:** Maris Hobbit {411}; Norin 10 Der. {565}; List in {407}.

GAI3

Gai3. [*GAI3* {1246}, {565}]. 4B {413}. 4BS {980}. **i:** See {408}. **v:** Minister Dwarf {413}; Selection D6899 {359}; Tom Thumb {405}; Tom Thumb Der. {565}, {567}.
In wheats with *Gai3*, the aleurone layer failed to respond to applied GA {405}

Two studies involving crosses between Tom Thumb derivatives and tall parents suggested that gibberellic acid insensitivity and reduced height were controlled by one gene, i.e., *Gai3* {359}, {413}. In a third study involving a Tom Thumb derivative, recombinants were isolated, indicating separate but linked genes, i.e., *Gai3* and *Rht-B1c* {565}, {567}. Further evidence was obtained for linkage between genes for gibberellic acid insensitivity and Norin 10 genes for reduced height in hexaploid {568} and durum {720} wheats. Hu & Konzak {567} reported 27% recombination between *Gai1* and *Rht-B1b* and 10% recombination between *Gai2* and *Rht-D1b* in hexaploid wheats involving Norin 10 and Suwon 92 derivatives. In durum derived from crosses involving Norin 10, 15% recombination was obtained between one of the genes for reduced height and gibberellic acid insensitivity {1246, 1247}. Gale & Law {403} considered *Gai1* and *Rht-B1b, Gai2* and *Rht-D1b, Gai3/* and *Rht-B1c* to be pleiotropic genes.

1.33. Glaucousness (Waxiness/Glossiness)

The *W* loci are complexes of closely linked genes involved in beta-diketone synthesis.

Glaucousness refers to the whitish, wax-like deposits that occur on the stem and leaf-sheath surfaces of many graminaceous species. The expression of glaucousness depends on the arrangement of wax deposits rather than the amount of wax {603}. Non-glaucous variants also occur and genetic studies indicate that non-glaucousness can be either recessive or dominant. Recessive forms of non-glaucousness are apparently mutants of the genes that produce the wax-like deposits. Dominant non-glaucous phenotypes (as assessed visually) appear to be due to mutations that affect the molecular structure, and reflectance, of the wax-like substances {10001}. The genes involved in wax production and the "inhibitors" are duplicated in chromosomes 2B and 2D. There appear to be independant genes for wax production and "inhibitors" {912}, {1493}, {10001}. In earlier issues of the gene catalogue the two kinds of genes were treated as multiple alleles {1432}. All forms of wild and cultivated einkorn are non-glaucous {10001}. Orthologous loci occur in barley chromosome 2HS (*gs1, gs6, gs8*) {467}, rye chromosome 7RL (*wa1*) {725} and maize (*gl2*) {211}. A gene for spike glaucousness, *Ws*, was mapped distally on chromosome 1BS in the cross *T. durum* cv. Langdon / *T. dicoccoides* acc. Hermon H52 {0171}.

1.33.1. Genes for glaucousness

W1. 2BS {1493}, {267}. **bin:** 2BS-0.84-1.00. **ma:** *Xgwm210-2B* – 0.77 cM – *XWGGC3197* – 0.81 cM – *W1* – 0.12 cM – *XWGGC2484* – 0.32 cM – *Xbarc35-2B* {11247}.

W1. **i:** Chinese Spring mono-2D/S615//10*wS615 {10001}. **v:** Bethlehem {11458}; Chinese Spring {1493}; P86 {11247}. **itv:** LD222*11/*T. turgidum* var. *pyramidale* recognitum {1546}. **v2:** S615 *W2* {10001}. **tv:** Kofa+Lr19 {11458}; AUS2499 {11458}. **c:** *W1* is a highly duplicated, variable gene cluster containing type III polyploid synthase, hydrolase and cytochrome P450 genes and is homologous to the *Cer-cqu* cluster in barley {11458}.

w1. Recessive allele for reduced glaucousness. 2BS {1432}. **su:** Bethlehem CASL*/*T. dicoccoides* TTD140 2BS(2B) {11458}. **v:** CS mono-4B mutant {1064}; J87 {11247}; Mentana {1432}; Salmon {1493}. **tv:** AUS2499 {11458}.

W2

W2. **i:** Chinese Spring mono-2B/S615//11*w-S615 {10001}. **v:** *T. compactum* cv. No 44 {10001}. **v2:** S615 *W1* {10001}.

W2a. **dv:** Glaucous forms of *Ae. tauschii*.

W2b. **v:** Chinese Spring - weak hypomorph recognized at increased dosage {1432}.
A non-glaucous spike phenotype in line L-592, a 7S(7A) substitution line, is described in {0113}.

w1w2 {10001}. **i:** w-S615 = S615*11/Salmon {10001}. **v:** Salmon {10001}; Mentana {1432}; CS mono-4B mutant {1064}.

W3

W3 {11456}. 3DL { 11457}. **dv:** *Aegilops tauschii* KU-2126 {11457}. **ma:** *Xgwm645-3DL* – 8.0 cM – *W3* – 8.9 cM – *Xbarc42-3DL* {11457}.

w4. **dv:** *Aegilops tauschii* KU-2104 {11457}; KU-2105 {11457}.

Glaucous synthetics LDN/KU-2104 and LDN/KU-2105 are presumed to have genotype *W1W1W4W4*.

1.33.2. Epistatic inhibitors of glaucousness

Each inhibitor inhibits all genes for glaucousness.

IW

IW1. 2BS {10001}. **bin:** 2BS3-0.84-1.00.

Iw1 {10001}. [*W1*^{1} {1493}, *I1-W* {1493}]. **i:** S615/Cornell 5075//10*S615 {10001}. **v:** WE74 {11094}; Shamrock {11090}. **tvsu**: LDN$_{\text{DIC521-2B}}$ {11245}. **tv** *T. dicoccoides* PI 481521 {11245}. **ma:** *JIC007* – 1.47 cM – *IW1* – 0.18 cM – *JIC010/JIC011* {11090}; Co-segregation with BF474014, CJ876545 and CD927782 and flanked by BE498358 and CA499581 within a 0.96 cM interval {11094}. **c:** *Iw1* encodes a long non-coding RNA (LncRNA) that putatively arose from an inverted repeat of a carboxylesterase gene (80% homology) in the *W1* cluster that consists of WI-COE (non-annotated carboxylesterase), WI-PKS (*Traes_2BS_9E10D26DB*, polykedide synthase) and WI-CYP (*Traes_2BS_163390FC4,* cytochrome P450-type hydroxylase) {11459}. GenBank C-DNA sequence, KX823910. The IR region has >94% identity to an IR region in *Ae. tauschii* chromosome 2 that also produces MiRNA and a marker-based location similar to that of *Iw2* {11459}. *Xgwm614-2B – IW1/Xbarc35-2B/CD893659/CD927782/BQ788707/CD938589 – Be498111* {11245}.

IW2

Iw2 {10001}. [*Iw3672* {10510}, *I2-W* {1493}, *IwT* {11207}]. 2DS {10001}. **bin:** 2DS5-0.47-1.00 {10578}; 2DS5-0.84-1.00. **i:** S615/Golden Ball Synthetic//10*S615 {10001}. **v:** Golden Ball Synthetic {10001}; Synthetic hexaploid line 3672 {10510}; TA4152-60 {11094}; Vernal Synthetic {10001}. **tv:** *T. dicoccoides* PI 481521 {11245}. **dv:** Non-glaucous forms of *Ae. tauschii* {1493}. **ma:** In *Ae. tauschii: IW2* – 30.1 cM – *Xgdm35-2DS* {10227}; *Xbarc124-2D* – 0.9 cM – *IW2* – 1.4 cM – *Xwe6(AL731727)* {10510}; *Xcfd56-2D* – 6 cM – *IW2* – 10 cM – *Xcfd51-2D* {10578}; Co-segregation with BF474014 and CJ876545 and flanked by CJ886319 and CJ519831 within a 4.4 cM interval {11094}. *Xgwm614-2B – IW1/Xbarc35-2B/CD893659/CD927782/BQ788707/CD938589 – Be498111* {11245}.

IW3

Iw3 {277}. [*IW3* {277}, I3-W {277}]. 1BS {277}. **sutv:** Langdon*/*T. dicoccoides* 1B {11455}. **tv:** *T. turgidum* var. *dicoccoides* {277}. **ma:** *XWL1967/Xfcp168-1B* – 0.15 cM – *XWL3096* – 0.015 cM – *IW3* – 0.12 cM – *Xpsp3000-1B* {11455}.

A non-glaucous spike phenotype in line L-592. A 7S(7A) substitution line, is described in {0113}. A dominant gene (*Vir*) for non-glaucousness was located in chromosome 2BL of cv. Shamrock, a derivative of *T. dicoccoides* {10543}. This gene mapped 2 cM distal to *Xgwm614-2B* {10543} whereas the *W1/Iw1* locus was placed distal to *Xgwm614-2B* in {10189}. Lines with *Vir* had delayed senescence ('staygreen') and an average yield advantage over their glaucous sibs {10543}. Although maps constructed from three tetraploid crosses suggested that *w1*, *W1* and *Iw1*$^{\mathrm{DIC}}$ = *Vir* remain unresolved {10815}.

1.33.3. Leaf glaucousness

<u>QTL</u>

RAC875 (non-glaucous leaf) / Kukri (glaucous leaf): *QW.aww-3A*, nearest marker *Xwmc264-3A*, accounted for 36-40% of the phenotypic variation; other QTL were located on chromosomes 1D, 2B (2 QTL), 4D, 5B and 2D {11131} = {11460}.

GWAS of flag leaf glaucousness in a large panel of genotypes identified major QTL on chromosome 2B (*W1/IW1*) and 3A {11482}.

1.33.4. Spike glaucousness

Spike glaucousness is recessive {10666}.

WS

Ws {10666}. 1AS {10666}. **bin:** 1AS1-0.47-1.00 {10666}. **v:** Svenno {10666}. **ma:** *BJ23702a* – 3.5 cM – *Tc95235* – 4.8 cM – *Bla* {10666}.

ws {10666}. **v:** Ciccio {10666}.

1.34. Glume colour and awn colour

1.34.1. Red (brown/bronze/black) glumes

The majority of studies report a single dominant gene for red glume colour. A few papers report two factors {1009, 1477, 1520}. Red glume colour in Swedish land cultivars is apparently associated with hairy glumes {1277} suggesting, because *Hg* is located in chromosome 1A, that a red glume factor different from *Rg1* is involved in the Swedish stocks. Nothing was known of the possible association of such a gene with *Bg*, another glume colour gene on chromosome 1A. See {1640} for review. A chromosome 1A gene, *Rg3*, was eventually identified by linkage with *Gli-A1* {1405} and shown to cosegregate with *Hg* {624}.

RG-A1

RG-A1 {10378}. [*Rg3* {923}, {924}, {562}]. 1AS {923}, {9906}, {924}, {562}.

Rg-A1a {10378}. **v:** TRI 542 {10378}; White glumed genotypes. **dv:** DV92 {282}; G2528 {10378}.

Rg-A1b {10378}. [*Rg3*]. **i:** Saratovskaya 29*3//F2 CS mono 1/Strela {924}. **v:** CS/Strela Seln {9906}; Iskra {9906}; L'goskaya-47 {1405}; Zhnitsa {9906, 10378}. **v2:** Milturum 553 *Rg-B1b* {9906}; Milturum 321 *Rg-B1b* {9906}; Strela *Rg-B1b* {9906}, {924}; Sobko & Sozinov {1405, 1406}; reported a further group of 30 international wheats which, by inference from their *Gli-A1* alleles, probably carry *Rg-A1b*. **ma:** A linkage order of *Rg-A1b* – *Hg* – cent – *Glu-A1* {1405}; *Xgwm1223-1A* / *Rg-A1* / *Hg* – 2.2 cM – *Xgwm136-1A* – 4.2 cM – *Xgwm33-1A* {10635}.

Rg-A1c {10378}. [*Bg* {1304, 282}, *Bg(a)*]. 1A {1304}, {282}. **i:** ANK-22A {10378}; S29BgHg {10378}. **s:** CS*7/Indian 1A {1304}. **v:** TRI 14341 {10638}. **v2:** Sears Synthetic *Rg-D1c* {10638}. **dv:** G1777 {282}; G3116 {282}. **ma:** *Rg-A1c(Bg)* and *Nor9* co-segregated in *T. monococcum*; *Xutv1391-1A* (distal) – 3 cM – *Rg-A1c(Bg)* – 1.6 cM – *Hg* – 2.4 cM – *Gli-A1* (proximal); *Xgwm1223-A1* – 0 & 0.6 cM – *Rg-A1c* – 4.7 & 4.6 cM – *Xgwm0136-1A* {10378}; Five of 6 wheats with *Rg-A1c* possessed a 264 bp allele at *Xgwm0136-1A* {10378}; *Rg-A1c* – 0.7 cM – *Xgwm1223-1A* {10638}.

Rg-A1d [*Bg(b)*]. **dv:** G3116 {282}.
At the diploid level *Rg-A1c (Bga)* and *Rg-A1d (Bgb)* were determinant and caused a solid black glume and a black line at the margins of the glume, respectively {282}.
A single factor for black glumes was reported in diploid, tetraploid and hexaploid wheats {1347}. Linkage with *Hg* was demonstrated at all levels of ploidy, indicating a common gene on chromosome 1A; *Bg* is epistatic to *Rg.**1***

RG-B1 {10378}. [*Rg1*, *Rg*]. 1B {1517}.1BS {369}. *TraesCS1B02G005200.*

Rg-B1a {10378}. **v:** TRI 542 {10378}; White glumed genotypes, including Chinese Spring. **dv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}.

Rg-B1b {10378}. [*Rg1*]. **s:** CS*5/Red Egyptian 1B {1304}. **v:** Diamant I {9906}; Federation 41 {1517}; Golubka {10635}; Highbury {1121}; Jagger {11538}; Norin 60 {11538}; Red Egyptian {1304}; Red glume spelts {11538}; *T. petrapavlovsky* {9906}. **v2:** Milturum 321 *Rg-A1b* {9906}; Milturum 553 *Rg-A1b* {9906}; Strela *Rg-A1b* {9906}. **tv:** Messapia {9959}; Ward {792}. **ma** *Xutv1518-1B* (distal) – 7.7 cM – *RG-B1* – 0.8 cM – *Gli-B1* (proximal) {9959}; *Xgwm1078-1B* – 1.5 cM – *RG-B1* – 3.1 cM – *Xgwm0550-B1* {10378}; *Xutv1518-1B* – (distal) – 7.7 cM – *RG-B1* – 0.8 cM – *GLI-B1* (proximal); *Xgwm1078-1B* – 4.6 cM – *RG-B1* – 2.0 cM – *MW1B002(Gli-B1)* – 4.1 cM – *Xgwm550-1B* {10635}. **c:** Encodes an R2R3-MYB transcription factor {11538}. *TraesJAG1B01G000800* and *TraesNOR1B01G001100* in red glume Jagger and Norin 40, respectively, carried the same *Rg-B1b_h1* sequence; haplotype comparisons revealed that a specific group of MYB alleles was conserved in red glume genotypes {11538}.

RG-D1 {10378}. [*Rg2*]. 1DS. 1DL {769}, {1241}.

Rg-D1a {10378}. **v:** Novosibirskaya 67 {10378}; L301 {10378}; White glumed genotypes.

Rg-D1b {10378}. Derived from *Ae. tauschii* [*Rg2*]. **i:** Saratovskaya 29*5//*T. timopheevii* ssp. *timoppheevii/T. tauschii* {9906}. **v:** ITMI Synthetic W7984 {10635}; Synthetic Hexaploid-11 {10218}; (*Triticum turgidum* ssp. *dicoccoides/Ae. tauschii*) {769}; (*Tetra Canthatch/Ae. tauschii* var. *strangulata* RL 5271); RL5404 {1240}; (*Tetra Canthatch/Ae. tauschii* var. *meyeri* RL5289); RL5406 {648, 1240}. **v2:** Sears Synthetic *Rg-A1c* {10638}. **dv:** *Aegilops squarrosa* accessions.

Rg-D1c {10378}. Brown or smokey-grey phenotype {729}. [*Brg* {729}]. **i:** ANK-23 = Novosibirskaya 67*10/K-28535 {729}. **v:** Golubka {10378}; K-28535 {729}; K-40579 {729}; *T. aestivum* botanical varieties cinereum, columbina and albiglaucum {10378}. **ma:** *Xgwm1223-1D* – 1.5 cM – *RG-D1* – 13.1 cM – *Xbarc152-1D* {10378}; *Xbarc149-1D* – 6.3 cM – *RG-D1* – 26.5 cM – *Xbarc152-1D* {10378}.

QTL

Opata / W-7984 (ITMI) mapping population: *QRg.ipk-1D* was mapped in the {0255}; Linkage with *GLI-D1* implied *RG-D1* (*Rg2*). This QTL coincided with a QTL for awn colour, *QRaw.ipk-1D* {0255}. **ma:** *Xpsp2000-1D* – 9.3 cM – *RG-D1* – 21.2 cM – *Xgwm106-1D* {10128}; *Xgwm1223-1D* – 6.6 cM – *RG-D1* / *Xksud14-1D* – 13.9 cM – *Xgwm33-D1*{10635}; *RG-A1* – 3.9 cM – *Xgwm1223-1D* {10638}.

1.34.2. Pseudo-black chaff

This is a blackening condition transferred from Yaroslav emmer to Hope wheat by McFadden at the same time as stem-rust resistance was transferred. The association of this condition with mature-plant stem-rust reaction (*Sr2*) has been noted in a number of papers. According to {742}, the condition is recessive. Pan {1102} considered linkage with stem-rust reaction could be broken, but this seems unlikely.

PBC

Pbc. 3B {742} 3BS. **s:** CS*6/Hope 3B {742}; CS*6/Ciano 5B {939}.

1.34.3. Black-striped glumes

This phenotype was reported in group *dicoccon*. **v:** E4225 {1417}.

1.34.4. Inhibitor of glume pigment

An inhibitor of glume pigment was reported on chromosome 3A {106}.

1.34.5. Chocolate chaff

CC

Cc {719}. 7B {719}. 7BS {665}. **tv:** Langdon mutant {719}; PI 349056 {665}. **dv:** CBC-CDd1 {665}.
The chocolate chaff phenotype was suppressed by a gene(s) in chromosome 7D {719}.

1.34.6. Awn colour

The literature on awn colour is not clear. In general, awn colour is associated with glume colour {045}. Occasionally, however, awn colour and glume colour may be different. According to Panin & Netsvetaev {1103}, black awns were determined by three complementary genes designated *BLA1, BLA2, BLA3. BLA1* was located in chromosome 1A and linked with *Gld 1A* (= *GLI-A1*) and *Hg*.

BLA1

Bla1 {10666}. 1AS {10666}. **bin:** 1AS1-0-0.47 {10666}. **v:** Svenno {10666}. **ma:** *TC95235* – 4.8 cM – *BLA1* {10666}.

QTL

QRaw.ipk-1A {0255}. 1AS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}; Awn colour was contributed by W-7984 {0255}. **ma:** Associated with *Gli-A1* {0255}.

QRaw.ipk-1D {0255}. 1DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}; Awn colour was contributed by W-7984 {0255}. **ma:** Associated with *GLI-D1* {0255}.

1.35. Grain Hardness/Endosperm Texture

Grain hardness or endosperm texture significantly influences flour milling, flour properties and end-use. The difference in particle size index between a hard wheat (Falcon) and a soft wheat (Heron) was reported by Symes {1452} to be due to a single major gene. Symes {1452} also found evidence for "different major genes or alleles" which explained differences amongst the hard wheats Falcon, Gabo and Spica. Using Cheyenne (CNN) substitution lines in CS and a Brabender laboratory mill, Mattern et al. {915} showed that the hard wheat milling and flour properties of Cheyenne were associated with 5D. Using Hope 5D substitution line in CS [CS(Hope 5D)] crossed to CS, and CS(Hope 5D) crossed to CS ditelosomic 5DL, Law et al. {777} showed that grain hardness was controlled by alleles at a single locus on 5DS. The dominant allele, *Ha*, controlling softness was present in Chinese Spring and the allele for hardness, *ha*, was present in the others. A similar study using CS (CNN5D)/CS recombinant inbred lines was reported by Morris et al. {03106}.
A pleiotropic result of hardness is the decreased level of a 15 kD starch granule protein, friabilin, on the surface of water-isolated starch {470}. In endosperm, soft and hard wheats have similar amounts of friabilin, consequently the distinction between the two textural types depends upon the manner in which the friabilin co-purifies with starch. Friabilin is also referred to by the name 'Grain Softness Protein' (GSP) {0384}, and was later shown to be comprised primarily of puroindoline a and puroindoline b {0295}. Grain hardness of reciprocal soft x hard F_1 kernels was well correlated with friabilin occurrence on starch in triploid endosperm {0381}. See IV, Proteins: 5.8 Puroindoline. GSP-1 genes, which are closely related to puroindolines, are also listed in the Protein section.

HA

Ha {777}. Soft phenotype. 5DS {777}. **i:** Falcon/7*Heron, Heron/7*Falcon{3109}; Paha*2//Early Blackhull/5*Paha {203}, {298}; Early Blackhull Derivative/5*Nugaines {203}, {298}. **v:** Chinese Spring {3106}, {777}; Cappelle Desprez {470}; Heron {470, 1452}; Paha, Nugaines{203}, {298}; NY6432-18 {241}.

ha {777}. Hard phenotype **i:** Falcon/7*Heron, Heron/7*Falcon {3109}; Paha*2//Early Blackhull/5*Paha {203}, {298}; Early Blackhull Derivative/5*Nugaines {203}, {298}. **s:** CS*6/Cheyenne 5D {915}; CS*6/Hope 5D {777}; Capelle Desprez*7/Besostaya 5D {470}. **v:** Falcon {470, 1452}; Holdfast {470}; Early Blackhull, Early Blackhull Derivative {203, 298}; Cheyenne {3106}; Clark's Cream {241}. **ma:** *Ha* was closely linked to *Xmta9(Pui1)-5D* {1414}.

Single factor effects on hardness were found for chromosomes 2A, 2D, 5B and 6D, and interactive effects were found for chromosomes 5A, 6D and 7A {1414}.
The addition of King II rye chromosome 5R converted Holdfast wheat from hard to soft {470}. A 14.5 kD rye analogue was also isolated from 6x triticales which have soft texture {470}. All ryes have soft texture.
Two genes for grain hardness were reported in {55}.
Hard and soft NILs are listed in {0298}.

QTL

Courtot / CS: DH population: a major locus in chromosome 5DS coincided with *Ha*; minor QTLs mapped in chromosomes 1A (associated with *Xfba92-1A*) and 6D (associated with *Xgwm55-6D*) {0141}.

Forno / Oberkulmer: Ten QTLs for kernel hardness (54% of the variation) were mapped in spelt {0280}.

Karl*2 / TA 4152-4: *QHa.ksu-3B*, associated with *Xksum9-3B* (R^2=0.09, and *QHa.ksu-5D (Ha)*, associated with *Xcfd-5D* (R^2=0.3), were identified {10273}.

Neixiang 188 (hard) / Yanshan 1 (medium hard): RIL population: *QGh.caas-1B.1* with hardness allele from Yanshan 1, $R^2 = 0.28$, *Xwms153-1BL – Xbarc81-1BL* {10640}.

Opata 85 / W-7984 Synthetic (ITMI population): RIL population: Two QTLs were detected {10051}. The QTL on the short arm of chromosome 5D was associated with *Xmta10-5D*, and increased hardness was contributed by Opata {10051}. The locus located proximally on the long arm of 5D was associated with *Xbcd450-5D* and increased hardness was contributed by the Synthetic allele {10051}.

Using proteomic analysis of 2D-protein gels applied to 101 lines of the population, and after a preliminary study of a sub-group of these lines {10086}, 446 amphiphilic protein spots were resolved, 170 specific to either of the two parents and 276 common to both {10087}. An important category of these proteins comprised the puroindolines. Seventy-two loci encoding amphiphilic proteins were conclusively assigned to 15 chromosomes. At least one Protein Quantity Locus (PQL) was associated with each of 96 spots among the 170 spots segregating; these PQL were distributed throughout the genome. The majority of the amphiphilic proteins were shown to be associated with plant membranes and/or play a role in plant defence against external invasions. Not only the puroindolines were associated with kernel hardness - a number of other amphiphilic proteins were also found to influence this trait.

1.36. Grain quality parameters

1.36.1. Sedimentation value

Qsev.mgb-6A {9920}. 6AL {9920}. **tv:** Nessapia/*T. dicoccoides* MG4343 mapping population {9920}.
ma: Associated with *Xrsq805-6A* {9920}.

Qsev.mgb-7A {9920}. 7BS {9920}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population {9920}. **ma:** Associated with *Xpsr103-7A* {9920}.

Cheyenne (high quality) / CS (low quality): RIL population: QTL were associated with *Glu-1* on chromosome arms 1AL and 1DL and *Gli-1/Glu-3* on 1BS {0251}. Cultivar Cheyenne contributed the higher SDS sedimentation values {0251}. The QTL on 1AL coincided with a QTL for bread loaf volume {0251}. The QTL on 1DL and 1BS coincided with QTL for bread mixing time {0251}.

1.36.2. Flour, semolina and pasta colour

QTL

Huapei 3 /Yumai 57: DH lines: 18 additive QTLs and 24 pairs of epistatic QTLs affected flour colour parameters; *qa-1B*, closely linked with *Xbarc372-1B* was associated with variation of a*, $R^2 = 0.256$ {10625}. A further study confirmed major QTL on chromosome 1RS (R^2=0.319) and 7A ($R^2 = 0.339$), minor QTL occurred on 1A and 4A {10716}.

Omrabi 5 / *T. dicoccoides* 600545: A major QTL was detected in the distal region of chromosome 7BL. The QTL explained 53% of the variation and was completely linked to microsatellite marker *Xgwm344-7B*. Omrabi 5 contributed the allele for high yellow pigment level. Two additional small QTLs were detected on 7AL {0365}.

PH82-2 (low) / Neixiang (high): RIL population: Analysis of yellow flour pigment revealed major QTL on chromosomes 7A co-segregating with marker *YP7A* (R^2 = 0.2-0.28) (see Phytoene synthase 1), and 1B (R^2 = 0.31-0.54) probably contributed by 1RS {10501}.

Schomburgk / Yarralinka: A QTL was detected on chromosome 7A {9936}. Cultivar Schomburgk contributed the yellow colour allele {9936}. Markers *Xcdo347-7A* and *Xwg232-7A* accounted for 60% of the genetic variation {9936}. A Sequence Tagged Site PCR marker wasdeveloped {0180}.

W9262-260D3 (low yellow colour) / Kofa (high colour): Four QTLs identified on chromosomes 2A (*Xgwm425-2A*), 4B (*Xgwm495-4B*), 6B (*Xgwm193-6B*) and *Psy-B1* (chromosome 7BL) {10230}. See also Enzymes Phytoene synthase.

Other references to flour colour are given under Flour Colour, *Lr19*, and *Sr25*.

Three QTL for peroxidase activity in the grain identified in a **Doumai (high POD activity) / Shi 4185 (low POD activity)** cross were named as *QPod.caas-3AL QPod.caas-4BS* and *QPod.caas-5AS* {11233}. Allelic variation was found at the *QPod.caas-3AL* locus {11233}.

TaPOD-1A

TaPod-A1a {11233}. 3AL {11233}. **v:** Doumai {11233}.

TaPod-A1b {11233}. **v:** Shi 4185 {11233}.

There was no apparent relationship to the *Per-* series identified by isozyme analyses and listed in the Protein section.

1.36.3. Amylose content

Amylose content has a significant effect on industrial quality; for example, reduced amylose wheats perform better in some types of noodles. The waxy protein genes have an important influence, but other genes are also involved.

QAmc.ocs-4A.1 {0047}. 4AS {0047}. **v:** CS/CS(Kanto107 4A) mapping population {0047}. **ma:** Associated with *Xbcd1738-4A* and *Xcdo1387-4A* {0047}.

1.36.4. Milling yield

QTL

NY6432-18 / Clark's Cream: RIL population: A QTL associated with *Pinb* on chromosome arm 5DS was detected {0241}. Cultivar Clarks Cream contributed the higher flour yield allele {0241}. This QTL coincided with QTL for hardness, hydration traits (dough water absorption, damaged starch and alkaline water retention capacity (AWRC) and baked product traits (cookie diameter and cookie top grain) {0241}.

Schomburgk / Yarralinka: A QTL was detected on chromosome 3A {0181}. Cultivar Schomburgk contributed an allele for the higher milling yield {0181}. RFLP markers *Xbcd115-3A* and *Xpsr754-3A* at LOD>3 were associated with this QTL {0181}.

1.36.5. Alveograph dough strength W

QTL

Courtot / Chinese Spring: QTLs for W were detected on chromosome arms 5DS (associated with *Xmta10-5D*), 1AS (associated with *Xfba92-1A*), and 3B (associated with *XksuE3-3B*) in cross {0141}. The first two QTLs coincided with those for hardness.

Forno / Oberkulmer spelt: Ten QTL for W (39% of the variation), nine QTL for P (48% of the variation) and seven QTL for P:L (38% of the variation) were mapped {0280}.

1.36.6. Mixograph peak time

QTL

NY6432-18 / Clark's Cream: RIL population: A QTL associated with *Glu-Dy1* on chromosome arm 1DL was detected {0241}. Clark's Cream contributed the higher mixograph peak time allele {0241}. This QTL coincided with a QTL for bread mixing time {0241}.

1.36.7. Starch characteristics

The Isoamylase-1 gene from *Ae. tauschii* (*Iso-1*) complemented the deficient rice sugary-1 mutant line {10295}.

QTL

Cranbrook (*Wx-B1a*) / Halberd (null *Wx-B1b*): QTLs for starch viscosity and swelling were associated with the *WX-B1* locus. An additional QTL for starch viscosity was found on 7BL between markers *Xgwm344-7B* and *Xwg420-7B* in the first parent. This QTL disappeared when amylase activity was inhibited indicating that it was determined by the late maturing a-amylase activity contributed by Cranbrook. A QTL for starch viscosity was associated with the *WX-A1* locus in the cross CD87 / Katepwa {0362}.

1.36.8. Loaf volume

LVL

Lvl1 {10312}. [*Lvl 1* {10312}]. 3A {10312}. **s:** Cappelle Desprez*7/Bezostaya 1 3A {10312}. **ma:** *Xgwm720-3A – Lvl1* appeared to be located in the *Xgwm2-3A – Xgwm720-3A* region {10312}.

QTL

Renan / Recital: RIL population: Loaf volume score was consistent across three environments and revealed major QTL on chromosomes 3A (flanking markers *Xfbb250-3A, Xgwm666-3A,* positive effect from Renan) and 7A (flanking markers *Xcfa2049-7A, Xbcd1930-7A,* positive effect from Recital) {10536}.

Thirty QTLs were located on 12 chromosomes, each of which explained between 5.85 and 44.69% of the phenotypic variation; the QTLs of largest effect were located on chromosomes 6B and 6D {10659}.

1.36.9. Dough rheological properties

QTL

Cranbrook / Halberd: DH population: environmental factors were a major determinant of dough extensibility whereas additive effects of alleles at the high and low molecular weight glutenin loci determined dough strength {10247}.

1.36.10. Grain fructan content

Fructans are non-digestible carbohydrates considered to have health benefits to consumers.

QTL

Berkut (high fructan concentration) / Krickauff (low fructan concentration): QTL detected on chromosomes 2B, 3B, 5A, 6D, and 7A of which *QGfc.aww-6D.2* ($R^2 = 0.17$, nearest marker, *Xbarc54-6D*) and *QGfc.aww-7A.1* ($R^2 = 0.27$, *Xgwm681-7A*) had the largest effects {10631}.

1.36.11. Water absorption

QTL

Neixiang 188/Yanshan 1: RIL population: *XAbs.caas-5D.1* with positive effects from Yanshan 1, $R^2 = 0.3$, *Xcfd18-5DS - Xcfd189-5DS* {10640}

1.36.12. Chinese dry noodle quality

QTL

Chuan 35050 / Shannong 483: RIL population: 3 QTL for noodle palate, elasticity and smoothness were clustered near *Glu-D1* with beneficial effects associated with subunits 5+10 coming from Chuan 35050. A very significant taste QTL, *QStas.sdau-4A.1* and positive QTLs for stickiness and total score also on chromosome 4A came from Shannong 483 {10647}

QTL Quality

AC Karma / 87E03-S2B1: DH population: 26 QTL were detected in 7 chromosomes in a large study of 11 seed quality traits {10434}; 6 were clustered in the *Glu-D1* region and 5 were clustered in the *Rht-D1* region.

Neixing 188 / Yanshan 1: RIL population: 75 QTLs for 5 quality-related traits are reported in {10640}.

Opata 85 / W-7984 Synthetic (ITMI population): RIL population: QTL analyses was undertaken of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility and mixograph properties) in the ITMI population grown in Mexico, France and USA (California) {10436}.

1.36.13. Grain Traits based on homolgyREQUIRES REVISION

Variation in grain traits based on genetic homology with other species.

TaBAS1

Tabas1-B1 {11198}. 2BL {11198}. **ma:** *Xbarc167-2B* – 10.38 cM – *Tabas1* – 5.23 cM – *Xcfa2278-2B* {11198}. **c:** BAS1 is a type of 2-Cys peroxiredoxin in a large peroxidase family.

Tabas1-B1a {11198}. **v:** Jing 411{11198}.
Associated with higher TGW.

Tabas1-B1b {11198}. **v:** Hongmanchun 21{11198}.
Associated with lower TGW

TaGASR

TaGASR7-A1 {11115}. Snakin/GASA gene family. 7AL {11115}. **ma:** *Xwmc301-7A* – 17.9 cM – *TaGASR7* – 10.6 cM – *Xwmc9-7A*{11115}. **c:** GenBank KJ000052 {11115}.
Hap1c in Lumai 14 and Xiaoyan 81 conferred higher grain length and grain weight than *Hap1g* in Hanxuan 10 and Xinmai 10 {11115}.

TaGS1

TaGS-D1 {11116}. 7DS {11116}. **ma:** *TaGs-D1* – 8.0 cM – *Xbarc184* {11116}.

TaGs-D1a {11116}. **v:** Doumai {11116}; Jingdong 8 {11116}. **c:** KF687956 {11116}.
Associated with higher TGW and grain length {11116}.

TaGs-D1b {11116}. **v:** Shi4185 {11116}; Yumai 21 {11116}. **c:** KF687957 {11116}.
Associated with lower TGW and grain length {11116}.

TaGW

TaGW-A2 {11121, 11122}. 6A {11121}. Orthologous to the rice RING-type E3 ubiquitin ligase *OsGW2* that functions as a negative regulator of grain weight. **ma:** *TaGW2* was mapped on the Spark x Rialto DH population to chromosome 6A and linked to markers *BS000072146, BS000105973* and *CA643341* at 46.8 cM {11121}. **c:** GenBank KP749901.1 {11122}.
A loss-of-function mutation in *TaGW2-A2* was associated with a 6.6 % increase in grain weight in tetraploid and hexaploid wheat {11122}.

TaSAP1

TaSAP1-A1 {11117}. Stress association protein gene family. 7A {11117}. **ma:** *Xwmc530-7A* – 2.1 cM – *TaSAP1-A1* – 13.9 cM – *Xbarc174-7A* {11117}. **c:** GenBank KC193579 {11117}.
Variation at this locus was associated with 1,000-grain weight, number of grains per spike, spike length, penuncle length and total number of spikelets per spike, but different haplotypes had different effects various traints {11117}.

TaTGW-7A

TaTGW-7Aa {11197}. **v:** Jing 411 {11197}.
Associated with higher TGW.

TaTGW-7Ab {11197}. **v:** Hongmanchun 21 {11197}.
Associated with lower grain weight.

TaTGW-A1

TaTGW-A1a {11196}. **v:** Doumai {11196}; Zhou 8425B {11196}.
Associated with higher TKW.

TaTGW-A1b {11196}. **v:** Chinese Spring {11196}.
Associated with lower TKW.

TaTGW6

TaTGW6-A1{11196}. 3AL {11196}. **ma:** *Gene-3665_61* – 2 cM – *TaTGW-A1* – 18 cM – *BobWhite_c47304_56* {11196}. **c:** TGW6 in rice encodes an indole-3-acetic acid-glucose hydrolase {11196}.

TaTGW6-B1 {11196}. 3BL {11196}. **c:** TGW6 in rice encodes an indole-3-acetic acid-glucose hydrolase {11196}.

TaTGW6-D1 {11196}. 3DL {11196}. **c:** TGW6 in rice encodes an indole-3-acetic acid-glucose hydrolase {11196}.

1.37. Grain weight

QTL

Renan / Recital: *QGw1.inra-2B*{10071}, favourable allele from Renan {10071}. (R^2 = 10.7-19.7%) {10071}. **ma:** *Xgwm374-2B – Xgwm388-2B*{10071}; *QGw1.inra-5B* {10071}**,** Ranan/Recital, favourable allele from Recital {10071}. (R^2 = 4.9-10.4%) {10071}. **ma:** *Xgwm639-5B – Xgwm604-5B* {10071}; *QGw1.inra-7A* {10071}, favourable allele from Recital {10071}. (R^2=5.2-10.3%) {10071}. **ma:** *Xcfa2049-7A – Xbcd1930-7A* {10071}.

RS111 / CS: RIL population: Variation at locus *QGw1.ccsu-1A* associated with *Xwmc333-1A*, accounted for 15% of the variation {0165}.

Rye Selection 111 (high GW) / CS (low GW) RIL: two definitive QTLs *QGw.ccsu-2B.1* and *QGw.ccsu-7A.1* and one tentative QTL, *QGw.ccsu-1A.1*, were detected by CIM analysis {10363}. The chromosome 7A QTL co-located with a QTL for early heading {10363}.

1.38. Grass-clump dwarfness/Grass dwarfness

Complementary dominant genes. Genotypes producing dwarfness: *D1-D2-D3-, D1-D2D2, D1-D4-D3-, D1-D2-D4* and *D1-D4D4*.

D1

D1 {534}. [*G* {972}]. 2D {939}, {534}, {1595}. 2DS {942}. **s:** CS*7/Kenya Farmer 2D {1000}; CS*6/Timstein 2D {534}. **v:** Big Club {534}; Burt {1000}; Federation {942}; Mus {534}; Ramona 50 {358}; Selection 1403 {1000}. **v2:** Hermsen's pure-breeding dwarf *D2* {1000}; Falcon *D3* {1172}; Gabo *D3* {944}; Timstein *D3* {534}; Metzger's pure-breeding dwarf *D2 D3* {1000}.

D2

D2 {534}. [*B 1* {972}]. 2BL {944}. 2B {574}, {536}. **s:** CS*7/Cheyenne 2B {1000}; CS*4/Red Egyptian 2B {1000}. **v:** Bezostaya 1 {1595}; Crete-367 {1029}; Desprez 80 {1595}; Florence {1000}; Kenya W744 {944}; Loro {1172}; Mara {1595}; Marquis {1000}; Poros {1595}; Redman {574, 534, 1001}; Riebesel {534}; Tobari 66 {358}. **v2:** Hermsen's pure-breeding dwarf *D1* {1000, 534}; Amby *D3* {358}; Cedar *D3* {1000}; Mendel *D3* {534}; Plantahof *D3* {534}; Spica *D3* {944}; Cappelle-Desprez *D4* {1595}; Brevor *D4* {1000}; Cheyenne *D4* {1000}; Metzger's pure-breeding dwarf *D1D3* {1000}.

D3

D3 {534}. [*A* {972}]. 4AL {939}. 4A {534}, {1595}. **s:** CS*6/Timstein 4A {1000}, {534}; CS*7/Kenya Farmer 4A{1000}, {534}. **v2:** Amby *D1* {358}; Falcon *D1* {1172}; Gabo *D1* {944}; Kenya Farmer *D1* {1000}; Timstein *D1* {534}; Metzger's pure-breeding dwarf *D1 D2* {1000}.

D4

D4 {1000}. 2D {1000, 1595}. 2DL {1598}. **s:** CS*7/Cheyenne 2D {1000}. **v2:** Cappelle-Desprez *D2* {1595}; Cheyenne *D2* {1000}; Brevor *D2* {1000}.

d1d2d3d4. **v:** Chinese Spring {1000, 534}.

Genotype lists in can be found in {358}, {534}, {972}. The effects of multiple allelism at *D2*, and possibly at *D1*, and modifying genes were demonstrated {1595}.

Knott {683} described a lethal dwarf condition controlled by a dominant gene closely linked with *Sr30* (chromosome 5D) in Webster and a complementary recessive gene in LMPG.

Phenotypes resembling grass clump dwarfs in hybrids carrying a 2BL.2RS translocation were reported in {916}. The complementary gene{s} in wheat was not *D1, D2 or D3*. The effect was suppressed at high temperature.

1.39. Growth rate and early vigour

QTL

Identified in *Ae. tauschii*: chromosomes 1D, 4D, and 7D carried QTLs for relative growth rate, biomass allocation, specific leaf area, leaf area ratio, and unit leaf rate. Chromosome 2D had QTLs for rate and duration of leaf elongation, cell production rate, and cell length. Chromosome 5D harbored QTLs for total leaf mass and area, number, and growth rate of leaves and tillers {10293}.

1.40. Hairiness/Pubescence traits

1.40.1. Pubescent auricles

PA

Pa {42}, {886}. 4BS{42, 886}. **s:** Saratovskaya 29*9/Yanetzkis Probat 4B {886}; Saratovskaya 29*5/Shabati Sonora 4B {886}; Saratovskaya 29*4/Siete Cerros 4B {886}. **v:** Diamant 1 {886}; Magali {886}; Pirotrix 28 {886}; Shabati Sonora {886}; Siete Cerros {886}; Ulyanovka 9 {886}.

pa. **v:** Gabo {886}; Saratovskaya 29 {886}. This phenotype was expressed in Diamant ditelo 4BL{886}.

1.40.2. Hairy glumes

HG1

Hg1 [{Hg {1494}]. *Hg* {1494}. 1A {1293}. 1AS {947}. **i:** S-615*11/Jones Fife {1500}. **s:** CS*7/Indian 1A {1293}. **v:** A well-known, widespread and easily identified dominant marker - only a few examples will be listed. Indian {1293}; Jones Fife {1494}; Prelude {1494}. **itv:** LD222*11/*T. turgidum* var. *durum melanops* {1546}. **tv:** Golden Ball {1342, 1494}. **dv:** *T. monococcum* lines {1494}. **ma:** *Xutv1391-1A* (distal) – 3 cM – *Bg* – 1.6 cM – *Hg* – 2.4 cM – *Gli-A1* (proximal) {9959}; Tel.........*Hg/BG605525* – 3.8 cM – *Xpsp2999(Glu3)-1A* {10193}. Mapped to region 1.337 – 2.162 Mb (CS Ref Seq v1) {11617}.

A 1A gene controlling hairy glumes was mapped in a cross between durum cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}.

hg1 {1405}. **v:** Ulyanovka {1405}; Pionerskaya {1405, 715}.

Evidence for multiple alleles in *T. monococcum* is given in {744}.
The likelihood of three alleles, *hg* (hairless), *Hg1* (weakly hairy) and *Hg* (very hairy), with *hg1* being recessive to *Hg* and causing a short (weak) hairy phenotype, was mentioned in {1405}.

HG2

Hg2 {11508}. 2BS {11508}. **v:** CIGM86.944 [syn. Croc_1 / *Ae. tauschii* 518] {11508}. **tv:** Croc_1 {11508}. **ma:** *XicsH020* – 1.18 cM – *HG2* – 0.84 cM – *XicsHS358,* corresponding to physical interval 740.0-741.1 Mb in cv. Svevo {11508}.

1.40.3. Hairy leaf

HL1

Hl1 {316}. Weakly hairy. [*Hl* {884}]. 4BL {760}. 4B {884}. **v:** Artemovka {925}; Caesium 111 {925}; Lutescens 53/12 {925}; Lutescens 62 {925}; Milturum 321 {884}; Poltavka {925}; Pyrothrix 28 {925}; Saratov 321 {884}; Saratovskaya 29 {760}, {884}; Sarrubra {925}. **ma:** *Xgwm375-4B* – 12.1 cM – *Hl1* – 2.1 cM {10516}.

HL2

Hl2 {316}. 7BS {316}. **v:** Hong-mang-mai {316}.
The hairy leaf gene (Hl^{Aesp}) in *Ae. speltoides* introgression line $102/00^{\mathrm{I}}$ was allelic with *Hl2* {10516}.

hl1 hl2. **v:** Chinese Spring {884}.
Kuspira *et al*. {744} provided evidence for at least three alleles at an *Hl* locus in *T. monococcum*.

A QTL analysis of the ITMI population identified loci determining hairiness of leaf margins and auricles in regions of chromosomes 4B and 4D orthologous to *Hl1* {10516}. Trichome number on leaf margins in *Ae. tauschii* was mapped to a 530 kb region in chromosome arm 4DL {11612}.

1.40.4. Hairy leaf sheath

HS

Hs {795}. [*Hls* {761}]. **v:** Certain hexaploid derivatives of G25 produced in Israel {939}. **tv:** *T. dicoccoides* G25 {761}.

hs. **v:** Most hexaploid wheats {939}. **tv:** *T. dicoccoides* G7 {761}.

Levy & Feldman {795} concluded that complementary genes determined hairy leaf sheath in *T. dicoccoides*.

1.40.5. Hairy neck/Pubescent peduncle

HP

Hp {275}. Derived from *Secale cereale*
4BL {T4B.5R} {274}, {275}. **i:** S-615[*]11/CS Derivative {1500}.
5BS {T5B-5R} {1298}. **v:** HN-2 (CS type) {1298}.
6D {T6D-5R} {1298} **v:** HN-1 (CS type) {1298}.
4BL {T4B.5R}. {274}, {275}. **v:** CS Derivative {1304}.

1.40.6. Hairy node/Pubescent node

Inheritance of hairy (glabrous) node versus non-hairy node was attributed to a single, dominant gene difference {396}, {837}, {910}, {914} and the *Hn/hn* locus was be linked with *B1* (awn inhibitor). Observations on 5A trisomics and telosomics of Chinese Spring confirmed this location. Love & Craig

{837} studied a cross involving Velvet Node CI 5877 and Gaines & Carstens {396} studied an offtype single plant designated Velvet Node Wash. No. 1981.

HN

Hn. 5AL. **v:** Aurore {722}; Fylgia {722}; Extra-Kolben II {722}; Marquis {910}; Tammi {765}; *T. vulgare erythrospermum* {910}. **tv:** *T. polonicum vestitum* {910}.

hn. **v:** Garnet {722}; Kimno {722}; Pika {722}; Timantii {722}.

Multiple alleles were reported in *T. monococcum* {744}.

1.41. Heat tolerance

QTL

Ventnor (tolerant) // Karl 92 (non-tolerant): QTLs contributing to grain-filling duration (GFD) under high temperatures were associated with *Xgwm11-1BS* (11% of variability) and *Xgwm293-5AS* (23% of variability) in {0327}.

1.42. Reduced height

1.42.1 Reduced height: GA insensitive

RHT1* [*Rht-1 {371}, {0019}].
The *Rht-1* homoeoloci are orthologous with the *D8* locus in maize and the *GAI* locus in Arabidopsis. They encode proteins resembling nuclear transcription factors and are involved in sensing gibberellin levels {0019}. Those proteins are DELLA proteins that repress plant growth, but repression is relieved by GA-induced DELLA repression. Common wheat and durum NIL pairs are listed in {02102}.

RHT-A1

Rht-A1a {0019}. 4A {10923}. 4AL {11017}. **v:** Chinese Spring {0019}. **ma:** *Xwmc48-4AS* – 2 cM – *Xgwm610-4A* – 1 cM – *Rht-A1* – 2 cM – *Xgpw4545-4AL* {11017}. **c:** GenBank KC767924. All common wheats are assumed to be monomorphic. A functional *Rht-A1a* allele is expressed at a similar level to its orthologues {10923}.
Haplotypes named as *Rht-A1b* to *Rht-A1g* are described in {11620}.

RHT-B1

Rht-B1a {116}. **v:** Tall wheats{116}; e.g. Chinese Spring{0019}. **c:** GenBank KC767925.

Rht-B1b {116}. Partially recessive {024}, recessive {357}, semi-dominant {408}. [*Rht1*{15}, *Sd1* {15}]. 4B {109, 406, 1040}. 4BS {89, 116}. **i:** See {414}, {2102}, {408}. **v:** Frontier {1597}; Guardian {1597}; Selection 14-53/Burt, 5 {15}; Siete Cerros {407}; Wren {1174}; WW15 {407}. **v2:** Norin 10-Brevor, 14 *Rht-D1b* {15}; Oleson *Rht-D1b* {357}; Selection D6301 *Rht-D1b* {357}; Shortim *Rht-D1b* {243}; See{1062}, {407}, {1386}, {415}. **tv:** Cocorit 71 {109}, {416}; Creso {109}, {451},

{416}; Malavika {1442}; Mida {450}; Sansone {109}; Valgerado {109}, {416}; Valnova {450}; Valselva {450}. **ma,tv:** *Gai1/Rht-B1b* – 1.8 cM – *Xpsr622-4B* {110}; Co-located with *Xbarc10-4B* {10189}.
The development of allele-specific primers for *Rht-B1b* was reported in {0378}.

An EcoTILLING study of >1,500 Chinese wheat accessions identified 7 sequence variations in *RHT-A1*, 8 new variants in *RHT-B1* and 4 new variants in *RHT-D1* {11697}.

QTL: QTL for reduced plant height, peduncle length and coleoptile length contributed by Cranbrook were associated with *XcsMe1-4B* (up to 49% of variability for plant height and peduncle length and 27-45% of variability for coleoptile length) in the cross **Cranbrook (semidwarf) / Halberd (tall)**. The dwarfing effect underlying the QTL was caused by the *Rht-B1b* allele {0379}.

Rht-B1c {116}. Semi-dominant {1040}. [*Sd3* {565}, *Rht3* {565}]. **i:** Tom Thumb/7* Kharkov//Lancer {1040}; See {408}. **v:** Minister Dwarf {404}; Selection D6899 (Tom Thumb-Sonora 64/Tacuari) {357}; Tom Thumb {405}; Tom Pouce Blanc {1634}, {407}; Tom Pouce Barba Rouge{1634}, {407}; Topo; Tordo. **ma:** *Xmwg634-4B* (distal) – 30.6 cM – *Rht-B1c* – 11.9 cM – *Xpsr144-4B* (proximal) {117}; Allele-specific markers were designed from the gene sequence {10923}. **c:** The *Rht-B1c* transcript carries a 90 bp in-frame insertion within the region encoding the conserved N-terminal DELLA domain plus two SNPs upstream of the insertion. A much larger insertion occurs in the gDNA {10923}.

Rht-B1d {116}. Semi-dominant {1599}, {116}. [*Rht1S* {1599}]. **v:** Saitama 27 {1599}; Occurs frequently in Italian and Yugoslavian wheats {1599}; Argelato, Centauro, Chiarano, Etruria, Farnesse, Gallo, Gemini, Lario, Pandas, Produttore, Orlandi, Orso, Salvia, Sprint, Strampelli. **c:** Has the same point mutations as in *Rht-B1b* - there is likely to be another mutation outside the coding region {10923}. *Rht-B1c* carries a 2,026 bp insertion of a *terminal repeat transposons in miniature* (TRIM) insertion at position 147 bp relative to *Rht-B1a*; this leads to an additional 30 amino acids in the DELLA domain affecting affinity between GID1 and Della {11390}. Genbank JN857970 (gDNA), JN859791 (cDNA) {11390}.

Rht-B1e {116}. [*Rht11* {718}, *Rht1*(*B-dw*) {1600}, *RhtKrasnodari1* {452}]. **v:** Karlik 1 PI 504549 {10924}; Krasnodari 1 (a spontaneous GA-insensitive offtype of Bezostaya 1) {1600}; Polukarlikovaya 49 and 11 derivatives {10924}. **ma:** A PCR marker distinguishes this allele from *Rht-B1a* and *Rht-B1b*{10923}. **c:** A stop codon occurs three codons upstream of the *Rht-B1b* mutation {10923}.

Rht-B1f {116}. Semi-dominant {116}. [*RhtT. Aethiopicum* {116}]. **tv:** *T. aethiopicum* accessions W6824D {116}; W6807C {116}.

Rht-B1g {0019}. **v:** Highbury mutants M3 103-3 and M3 103-9 {0019}.

Allele *Rht-B1g* is a fast neutron-induced mutation of *Rht-B1b* and produces a tall gibberellin responsive phenotype {0019}.

Haplotypes named *Rht-B1h* to *Rht-B1o* are described in {11620}.

Rht-B1p {11621}. *Rht17*. **v:** Chris Mutant CI 17241 {1129}. **c:** Contains a C-to-T substitution at position 178 leading to a stop codon {11621}. GenBank KT013263.

Rht-B1^{IC2196} {10144}. **tv:** *T. turgidum* var. *polonicum* IC12195 {10144}.

RHT-D1

Rht-D1 {116}. 4DS {1266} {980}, {116}. 4D {583}, {1544}, {411}. **bin:** 0.82-1.00 {11017}.

Rht-D1a {116}. **v:** Tall wheats {116}; e.g. Chinese Spring. **c:** KC767927.

Rht-D1b {116}. Partially recessive {024}, recessive {357}, semi-dominant {408}. [*Sd2*{15}, *Rht2*{15}]. 4D {411}. 4DS {980}. **i:** Common wheat and durum NIL pairs are listed in {2102}. See {414}, {2102}, {408}. **v:** Biscay {10574}; Combe {567}; Era {407}; Gaines Sib 2 {15}; Jaral {407}; Kite {1174}; Maris Hobbit {411}; Pirat {10574}; Pitic 62 {567}; Rubens {10574}; Songlen {243}. **v2:** Oleson *Rht-B1b* {357}; Norin 10-Brevor, 14 *Rht-B1b* {15}; Selection D6301 *Rht-B1b* {357}; List in {1386}. **ma:** *Xpsr1871(Pki)-4D* – 4 cM – *Rht-D1* – 6 cM – *Xubc821(PhyA)-4D* {410}; *Rht-D1* – 2.8 cM – *Xglk578-4D* {9966}; *Xpsr1871* – 1 cM – *Rht-D1b* – 4 cM – *Xpsr821*(PhyA) {0019}. The development of allele-specific primers for *Rht-D1b* was reported in {378}.

Rht-D1c {116}. Dominant {114}. [*Rht10* {1266}]. **v:** Ai-bian {1266, 1544}. **ma:** *Xpsr921-4D* (4DS) – 0.8 cM – *Rht-D1c* - 28 cM – *Xgwm165-4D* (4DL) {117}.

Rht-D1d {116}. Semi-dominant {116}. [*RhtAi-bian 1a* {115}]. **v:** Ai-bian 1a (spontaneous mutant of Ai-bian 1) {115}.

Haplotypes named as *Rht-D1e* to *Rht-D1h* are described in {11620}.

Line XN004, earlier considered to have *Rht21* {0230}, was shown to carry an allele at the *Rht-D1* locus {0231}.

Various common wheat and durum N1Ls differing at the *RHT-B1* and *RHT-D1* loci are listed in {02102}. Genotype lists in {402}, {1382}, {1612}, {1613}.
Rht-D1b, Rht-D1c and *Rht-D1d* are identical across the coding region, but *Rht-D1c* has a fourfold increase in copy number relative to *Rht-D1b*; *Rht-D1d* has a reduced copy number relative to *Rht-D1c* {10923, 11016}.

1.42.2. Reduced height : GA-sensitive

Borner *et al*. {116} found no evidence of orthologous GA-sensitive genes in rye, but reviewed evidence for orthologous GA-insensitive genes. The close linkage of *Rht8* and *Xgwm261-2D* permitted the use of the microsatellite as a marker for the detection of allelic variants at the *Rht8* locus {9962}.

RHT4

Rht4 {568}. Recessive. 2BL {10249}. **v:** Burt *ert* 937, CI 15076 {717, 566}. **ma:** Associated with *Xwmc317-2B* {10249}.

RHT5 *Traes3B02G025600* (predicted).

Rht5 {717}. 3BS {10249}. **v:** Marfed *ert* 1, M1, CI 13988 {1593}, {717}, {718}. **ma:** Approximately 10 cM from *Xbarc102-3B* {10249}. Located to an ~1 Mb interval flanked by *Kasp25* and *Kasp23* in the 0-30 Mb region {11625}. The predicted gene in Marfed M has a 30 bp deletion in the first intron {11625}.

RHT6

Rht6 {718}. Recessive. **v:** Brevor {569}; Burt {718}, {569}. **v2:** Norin 10-Brevor, 14 *Rht-B1b Rht-D1b* {569}.

RHT7

Rht7 {1602}. 2A {1602}. **v:** Bersee Mutant A {1602}; Bersee Mutant C {1602}.

RHT8. *TraesCS6A02G221900*; *TraesCSU03G0022100* (CS RefSeq v2.

Rht8. 2D {1601}, {1598}, {772}. 2DS. **s:** Cappelle-Desprez*/Mara 2D {1601}. **v:** Chuan Mai 18 {10249}; Novasadska Rana 1 {1604}; Sava {414, 1601}; Yumai 8679 {11624}. **v2:** Akakomugi *Rht9* {1191}; Mara *Rht9* {1191}. **ma:** *Xgwm484-2D* (proximal) – 19.9 cM – *Rht8* – 0.6 cM – *Xgwm261-2D* (distal) {727}; Close linkage with *Xgwm261-2D* {10249}; A survey of Chinese cultivars showed 13 alleles of *Xgwm261-2D* {10284}. **c:** *RHT8* contains two ORF with near-identical sequences. Encodes an unknown 808 aa protein containing a zinc finger BED-type motif and predicted Ribonuclease H-like domain {11624, 11642}. CRISPR-Cas9 editing of the *RNHL-A1* (*Traes2A02G059900*) and *RNHL-B1* (*Traes2B02G073600*) homoeologues caused reduced height {11624}.

rht8. *RNHL-D1* {11624}.

Close linkage of *Rht8* and *Xgwm261-2D* permitted the use of the microsatellite as a marker for the detection of putative allelic variants at the *Rht8* locus {9962}. Allele sizes for *Xgwm261* in U.S. eastern and central wheat cultivars are given in {10868}. A series of 'alleles' was based on variation in the closely linked marker *Xgwm261-2D*

Rht8a. Associated with a 165-bp fragment of WMS 261 {9962}. **v:** Autonomia {9962}; Bobwhite {9962}; Brevor {9962}; Chaimite {9962}; Ciano 67 {9962}; Chris {9962}; Dugoklasa {9964}; Federation {9962}; Frontana {9962}; Glennson 81 {9962}; Hope {0243}; Jupateco 73 {9962}; Kenya {9962}; Klein 32 {9962}; Lerma Rojo {9962}; Lusitano {9962}; Maringa {9962}; Marquis {0243};

Mentana {9962}; Michigan Amber {0243}; Nainari 60 {9962}; Newthatch {9962}; Opata 85 {9962}; Othello {9962}; Penjamo 62 {9962}; Quaderna {9962}; Rex {9962}; Riete {9962}; Saitama 27 {9962}; Spica {9962}; Veery S {9962}; Victo {9962}.

Rht8b. Associated with a 174-bp fragment of WMS 261 {9962}. **s:** Cappelle Desprez*/Mara 2D {1601}. **v:** Arthur {0243}; Balkan {9962}; Bunyip {9962}; Cappelle-Desprez {9962}; Carstens {0243}; Diakovchanka {0243}; Eureka {9962}; Festival {9962}; Fronteira {9962}; Fultz {9962}; Gabo {9962}; Heine VII {9962}; Inallettabile 95 {9962}; Jena {9962}; Klein Rendidor {9962}; Leonardo {9962}; Lutescens 17 {9962}; Mironovskaya 808 {9962}; Norin 10 {9962}; Norin 10/Brevor 14 {9962}; Oasis {243}; Odom {0243}; Podunavka {9962}; Purdue Abe {0243}; Record {9962}; Red Coat {9962}; Salzmunder Bartweizen 14/44 {0243}; Soissons {9962}; Talent {9962}; Tevere {9962}; Timstein {9962}; Tp114/65 {0243}; Wilhelmina {9962}; Wiskonsin 245 C/11226 {0243}.

Rht8c. Associated with a 192 bp fragment of WMS 261 {9962}. **v:** Akakomugi {1191}; Alfa {9962}; Aquila {9962}; Ardito {9962}; Argelato {9962}; Avrora {9962}; Banija {9964}; Baranjka {9964}; Beauchamps {9962}; Bezostaya {9962}; Biserka {9962}; Campodoro {9962}; Centauro {9962}; Chikushi-Komugi (Norin 121) {9962}; Chuanmai 18 {10512}; Damiano {9962}; Djerdanka {9964}; Dneprovskaya {9962}; Duga {9964}; Etoile-de-Choisy {9962}; Etruria {9962}; Fakuho-Komugi (Norin 124) {9962}; Farnese {9962}; Favorite {9962}; Fedorovka {0243}; Fiorello {9962}; Fortunato {9962}; Funo {9962}; Gala {9962}; Haya Komugi {9962}; Impeto {9962}; Irnerio {9962}; Jarka {9964}; Jugoslavia {9962}; Kavkas {9962}; Kalyan {0243}; Khar'kovskaya 50 {0243}; Khar'kovskaya 93 {0243}; Khersonskaya 86 {0243}; Kolubara {9964}; Kosava {9964}; Libellula {9962}; Lonja {9964}; Lovrin 32 {9962}; Macvanka-2 {9964}; Mara {9962, 119}; Marzotto {9962}; Mv 03-89 {0243}; Mv 06-88 {0243}; Mv 17 {0243}; Neretva {9962}; Nizija {9962}; Novasadska Rana 1 {1604}; N.S. Rana 1 {9962}; N.S. Rana 2 {9962}; N.S. 649 {9962}; N.S. 3014 {9962}; Obrii {243}; Odesskaya 51 {0243}; Odesskaya 117 {0243}; Odesskaya 132 {0243}; Odesskaya Krasnokolosaya {0243}; Odesskaya Polukarlikovaya{0243}; Orlandi{9962}; Osjecanka {9964}; OSK 5 5/15 {9964}; OSK 4 57/8 {9964}; OSK 3 68/2; Partizanka {9962}; Partizanka Niska {9962}; Poljarka {9964}; Posavka 1 {9964}; Posavka 2 {9962}; Pomoravka {9962}; Produttore {9962}; Radusa {9962}; Roazon {0243}; Salto {9962}; Sanja {9962}; San Pastore {9962}; Sava {414, 1601, 9962}; Siete Cerros {9962}; Sinvalocho {9962}; Simvol Odesskii {0243}; Sivka {0243}; Strumok {0243}; Skopjanka {9962}; Skorospelka 3B {9962}; Slavonija {9964}; Somorka{9964}; Sremica {9964}; Superzlatna {9962}; Svezda {9962}; Tira {0243}; Tisa {9964}; Transilvania {9962}; Ukrainka Odesskaya {0243}; Una {9962}; Villa Glori {9962}; Vympel {0243}; Yubileinaya 75 {0243}; Zagrebcanka {9964}; Zelengora {9964}; ZG 6103/84 {9964}; ZG 7865/83 {9964}; Zitarka {9964}; Zitnica {9962}; Zlatna Dolina {9964}; Zlatoklasa {9964}; Zolotava {0243}.

Although CS carries a 192 bp fragment, sequencing showed it was a different allele than other genotypes with *Rht8c* {02103}.

Although the 'diagnostic' association of *Rht8c* and *Xgwm261*$_{192}$ applied in many Strampelli derivatives and European wheats, there was no association between reduced height and this allele in Norin 10 and its derivatives {10512}. The pedigrees of a number of Chinese wheats postulated to have *Rht8c* on the basis of the marker traced to Italian sources {10515}.

Rht8d. Associated with a 201-bp fragment of WMS261 {9962}. **v:** Pliska {9962}; Courtot {9962}.

Rht8e. Associated with a 210-bp fragment of WMS261 {9962}. **v:** Chino {9962}; Klein Esterello {9962}; Klein 157 {9962}.

Rht8f. Associated with a 215-bp fragment of WMS261 {9962}. **v:** Klein 49 {9962}.

Rht8g. Associated with a 196-bp fragment of WMS261 [{0243}]. **v:** Mirleben {0243}

Rht8h. Associated with a 206-bp fragment of WMS261 [{0243}]. **v:** Weihenstephan M1 {0243}.

Genotypes of Indian semi-dwarf wheats based on the Ellis et al. {0378} markers are listed in {10404} and those for U.S. eastern and central and winter wheat cultivars are listed in {10868}.

RHT9

Rht9. 5AL {10249}. 7BS {1601}, {772}. **v:** Acciao {718}; Forlani {718}; Mercia 12 {10249}. **s:** Cappelle-Desprez*/Mara 5BS-7BS {1601}. **v2:** Akakomugi *Rht8* {1601}; Mara *Rht8* {1601}. **ma:** Close linkage with *Xwmc410-4A* {10249}.

RHT10. See *Rht-D1c*.

RHT11

Rht11 {718}. See *Rht-B1e*. **v:** Karlik 1 {718}.

RHT12. *TraesCS5A02G543100*

Rht12 {718}. Dominant. 5A {1606, 1445}. **bin:** 5AL-23, based on co-segregation with *B1*{1606}. **i:** N98-2105, Yangmai 5*5 / Karcagi 522M7K {11428}. **v:** Karcagi 522M7K {721}; Mercia, Vigour 18 and Halberd derivatives {11622}. **ma:** *Rht12* is located distally on 5AL cosegregating with *B1* and closely linked to *b-Amy-A1* {1606}; *Xgwm291-5A* – 5.4 cM – *Rht12* {726}. The *Rht12* phenotype was due to deletion of a 10.73 Mb terminal deletion of chromosome 5AL {11428). Reduced plant height might be due to activation of *TaGA2ox-A14* {11428}. **c:** Encodes a GA2oxA13 enzyme {11622} (previously predicted as GA2oxA14 {11428}. *Rht12* delayed ear emergence by 6 days {1606}.

RHT13

Rht13a. **v:** Magnif 41 PI 34466. **c:** Encodes a nucleotide-binding site leucine repeat (NBS-LRR) protein {11626}. Greatest sequence similarity to contig TGAC_Cadenza_U_ctg7180000823280 {11626.

Rht13b {M23019}. *Rht13* {718}. 7BS{10249}. **v:** Magnif 41M1 CI 17689 {718}. **ma:** Associated with *Xwms577*(*gwm577*)*-7B* {10249}. **c:** A serine-240-phenylalanine mutation caused autoactivation leading to transcriptional upregulation of pathogenesis-related genes including class III peroxidases associated with cell wall modelling {11626}. The same sequence was identified in TILLING line Cadenza0453 {11626}.

RHT14

Rht14 {718}. Allelic with *XRht16, Rht18* and *Rht24* {10767, 10818}. 6AS {10767}. **v:** Cp B 132 {123} = Castelporziano PI 347331{718}. **ma:** *Rht14* – 11.7 cM – *Xbarc3-6A* {10767}. Mapped to genomic region 383-422 Mb flanked by *GA20xA9* and *Xwmc753-6A* {11372}. *GA2oxA9* expression was higher in Castelporziano than in its tall parent Capelli – see *Rht18* {11301}. **c:** See *RHT24*.

RHT15

Rht15 {718}. **tv:** Durox {718}.

RHT16

Rht16 {718}. Allelic with *Rht14* and *Rht18* {10767, 10818}. 6AS {10767}. **v:** Edmore M1 {718}. **ma:** *Rht16* – 28.0 cM – *Xbarc3-6A* {10767}.

RHT17

Rht17 {718}. *Rht-B1p* {M23014}. **v:** Chris Mutant CI 17241 {1129}.

RHT18

Rht18 {718}. Allelic with *Rht14*, *Rht16* and *Rht24* { 10767, 10818}. 6AS {10767}. **tv:** Icaro{718}. **ma:** *Rht18* – 25.1 cM – *Xbarc3-6A* {10767}. Hexaploid derivatives in the backgrounds of Fengchan 3, Jinmai 47 *Rht8*, and Xifeng 20 are reported in {11096}. **matv:** *Xbarc118-6A* – 1.4 cM – *RHT18/TdGA2Ox-A9/S470865SSR4/Xbarc37-6A* – 0.4 cM – *IWA4371* – 0.4 cM –*Xgwm82.1-6A* {11295}. **c:** See *Rht24*.

Independent ‘overgrowth’ mutants isolated from Icaris contained changes in the *GA2oxA9* coding region; this gene is predicted to encode GA2-oxidase that metabolizes GA biosynthetic intermediates into inactive products thus reducing bioactive GA_1 {11301}.

RHT19

Rht19 {718}. **tv:** Vic M1 {718}.

RHT20

Rht20 {718}. **v:** Burt M860 {718}.

RHT21

Rht21 {0230}. The existence of this gene was not confirmed {0231}.

RHT22

Rht22 {10857}. 7AS {10857}. **tv:** Aiganfanmai {10857}. Ailanmai {11587}. **ma:** *Xgwm471-7A* – 29.5 cM – *Rht22* – 20.1 cM – *Xgwm350-7A* {10857}.

RHT23

Rht23 {11077}. 5DL {11077}. **v:** NAUH164 {11077}. **ma:** *Xgdm63-5D* – 4.7 cM – *Rht23* – 11.1 cM – *Xbarc110-5D* {11077}.
NAUH164 is an EMS-derived mutant of Sumai 3 {11077}.

RHT24**.** **c:** Encodes *TaGA2ox-A9* which is more highly expressed by the *Rht24b* allele {11623}. Same locus as *Rht14*, *Rht16*, and *Rht18*.

Rht24a**.** *Rht24* {11185}. [*QTL_height_6A_1* {11183}, *QPH.caas-6A* {11184}, *Rht24b* {11293, 11294}.]. 6AL {11185}. **v:** Aikang 58 {11185}; Solotar {11294}. **ma:** *Xwmc256-6A* – 2.71 cM – *TaGa3* – 7.05 cM – *TaAP2* – 0.24 cM – *Rht24* – 1.61 cM – *TaFAR* – 13.87 cM – *Xbarc103-6A* {11185}. Excalibur_rep_c69275-346 {11294}.
Rht24 was identified in many Chinese cultivars and a low number of European wheats based on flanking markers designed from *TaAP2* and *TaFAR* {11185}. *Rht24* occurs at relatively high frequency in European and Chinese wheat cultivars, and maps in the same region as *Rht14, Rht16* and *Rht18* {11293}.

Rht24b**.** **v:** Chuanmai 107 {11623}; Fan 6 {11623}; Jinan 2 {11623}; Jing 411 {11623}; Taishan 1 {11623}; Yannong 5 {11623}, Zhongmai 175 {11623}. **tv:** Also identified in wild and cultivated emmer and durum accessions {11623}.

RHT25 *TraesCS6A02G156600*

Significant differences in *RHT25* haplotypes were reported in {11659}.

Rht25a**.** *Platz*-A1. **c:** Encodes a PLATZ transcription factor that interacts with DELLA (RHT1) {11659}.

Rht25b {11300}. *QHt.ucw-6AS* {11300}. 6AS {11300}. **v:** Patwin-515HP {11659}; **U**C1110 *Rht-D1b* {11300}. **ma:** *QHt.ucw-6AS* was located in a 0.2 cM interval flanked by *6A13699/6A13791/6A14397* and *6A14825* {11300}.

RHT26
Rht26a {11739}. **v2:** Lunxuan 987 *RhtB1b* {11739.

Rht26b**.** 3DL {11739}. **v:** Jing 411 {11739}. **v2:** Zhongmai 175 *Rht-B1a* {11739}. **ma:** Delimited to a 1.4 Mb interval (517.1 – 518.5 CSRefSeqv.1) flanked by markers *KASP517* and *KASP518* {11739}.

RHT27**.** GA sensitive. 3AL {11740}.

Rht27 {11740}. **dv:** *T. urartu* G1812 {11740}. **ma:** Flanked by *3T-387* and *3T-306* {11740}. Delimited to a 1.55 Mb region (517.5 – 528.6 Mb, CS RefSeq v1.0) containing 20 genes, 2 of which, or homoeologs of which, coded genes affecting plant height {11740}.

rht27 {11740}. **dv:** Reduced Height 27 {11740}.
The height of the mutant was 27% of the wild type {11740}.

1.42.3. Reduced height: temporary designations

Rht_NM9 {11273}. 2A {11273}. **v:** Induced mutant NM9 {11273}. **ma:** *Xgwm122-2A* – 1.7 cM – *SNP34* – 1.9 cM – *Rht_NM9* – 1.9 cM – *SNP41* – 14 .0 cM – *Xwmc261-2A* {11273}.

1.42.4. Reduced height : QTL

QHt.fcu-4BL {10256}. **ma:** Associated with *Xbarc125-4B* ($R^2 = 0.57$) {10256}.
Reduced height allele in Grandin {10256}.

QHt.fcu-6AS {10256}. **ma:** Associated with *Xbarc23-6A - Xcp201-6A* ($R^2 = 0.07$) {10256}.
Reduced height allele in BR34 {10256}.

In **RL4452 / AC Domain:**

QHt.crc-2D {10287}. 2D {10287}. **ma:** Linked to BE497718-260 (LOD 4.2).

QHt.crc-4B {10287}. 4B {10287}. **ma:** Linked to *Rht-B1* (LOD 7.7) {10287}.
Associated with QTLs for lodging and 1000-grain weight.

QHt.crc-4D{10287}. 4D {10287}. **ma:** Linked to *Rht-D1* (LOD 30.9) {10287}.
Associated with QTLs for lodging 1000-grain weight, yield, height, and test weight.

QHt.crc-5B {10287}. 5B {10287}. **ma:** Linked to *Xwmc640-5B* (LOD 6.1) {10287}.

QHt.crc-7A{10287}. 7A{10287}. **ma:** Linked to *Xwmc139-7A* (LOD 3.3) {10287}.

QHt.crc-7B{10287}. 7B{10287}. **ma:** Linked to *Xgwm333-7B* (LOD 3.3) {10287}.

In **Courtot / CS:**

QHt.fra-1A {9957}. **ma:** Linkage with *Xfba393-1A* {9957}.

QHt.fra-1B {9957}. **ma:** Linkage with *Xcdo1188-1B.2* {9957}.

QHt.fra-4B {9957}. **ma:** Linkage with *Xglk556-4B* {9957}.

QHt.fra-7A {9957}. **ma:** Linkage with *Xglk478-7A* {9957}.

QHt.fra-7B {9957}. **ma:** Linkage with *XksuD2-7B* {9957}.

In Renan / Recital:

QHt.inra-2B {10069}. **ma:** Associated with *Xgwm249-2B* (LOD=5.8, R^2=15.4%) {10069}.

QHt.inra-4A {10069}. **ma:** Associated with *Xfba243-4A* (LOD=6.5, R^2=15.0%) {10069}.

QHt.inra-5A {10069}. **ma:** Associated with *Xgwm639b-5A* (LOD=5.7, R^2=10.8% {10069}.

QHt.inra-6D {10069}. **ma:** Associated with *Xcfd76-6D* (LOD=3.7, R^2=8.1% {10069}.

QHt.inra-7A {10069}. **ma:** Associated with *Xcdo545-7A* (LOD=3.2, R^2=7.7%) {10069}.

In **Opata 85 / W-7984 (ITMI)** RIL mapping population:

QHt.ipk-4A {0255}. 4AL{0255}. Tall allele contributed by Opata 85 {0255}. **ma:** Associated with *Xmwg549-4A, Xabg390-4A* and *Xbcd1670-4A* {0255}.
QHt.ipk-4A coincided with QTLs for ear length (*QEl.ipk-4A*), grain number (*QGnu.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) {0255}.

QHt.ipk-6A {0255}. 6A {0255}. Tall allele contributed by W-7984 {0255}. **ma:** Associated with *Xcdo29-6A* and *Xfba234-6A*{0255}.
QHt.ipk-6A coincided with QTLs for peduncle length (*QPdl.ipk-6A*) and ear length (*QEl.ipk-6A*) {0255}.

In **CS / CS(Kanto107 4A)** mapping population:

QHt.ocs-4A.1 {0047}. 4AL {0047}. **ma:** Associated with *Xpsr119-4A* and *Wx-B1* {0047}.

QHt.ocs-4A.2 {0047}. 4AS {0047}. **ma:** Associated with *Xbcd1738-4A* and *Hd*{0047}.

In **CS(*T. spelta* 5A) / CS(Cappelle-Desprez 5A)** RI mapping population:

QHt.ocs-5A.1 {0068}. [*Qt.ocs-5A.1* {0068}]. 5AL {0068}. **ma:** Associated with the interval *Xcdo1088-5A* – *Xbcd9-5A*{0068}.
This QTL coincided with a QTL for culm length, *QCl.ocs-5A.1* {0068}.

In: **Sevannah / Senat** DH population:

QHt.riso-3A {10067}. **ma:** Mapped on the centromeric region between SSR markers *Xwmc505-3A* and *Xwmc264-3A* (LOD >6) {10067}.

QHt.nau-2D {11463}. Recessive. Gibberellin-sensitive. 2DS {11463}. **bin:** 2DS-0.47-1.00. **v:** EMS-Induced Dwarf Wangshuibai {11463}. **ma:** *Xbarc-2D* – 2.6 cM-*2D* – *QHt.nau-2D* – 0.3 cM-*2D* – *Xgpw361-2D* {11463}.

Two QTLs for plant height were assigned to chromosome 3A in RSLs from Cheyenne*7/ Wichita 3A substitution line {0025}.

Seven QTLs on chromosomes 1A, 1D, 2B, 2D and 4B affected plant height among RILs of **CS / *T. spelta duhamelianum***. Effects linked with the CS alleles of *Xbcd1160-1A*, *Xksu127-1D* and *XksuF11-2D* increased height whereas those CS alleles associated with *Xpsr131-2B*, *Xpsr125-2B*, *Xpsr934-2D* and *Xcs22.2-4B* reduced it {0196}.

For review and identification of 65 QTL-rich clusters associated with plant height see {11741}.

1.43. Herbicide Response

1.43.1. Difenzoquat insensitivity

DFQ1

Dfq1 {1396}. Insensitive. 2B {1396}. 2BL {789}. **v:** CS{1396}.

dfq1. Sensitive. **s:** CS*6/Ciano 67 2B {1396}; CS*7/Marquis 2B {789}; CS*/Sicco 2B {1396}. **v:** Ciano 67 {1396}; Sicco {1396}.

Busch *et al.* {153} reported a single dominant gene for tolerance of Era and Marshall compared with the susceptibility of Eureka and Waldron, but its relationship to *Dfq1* is unknown.

1.43.2. 2,4-D tolerance

Randhawa *et al.* {1190} reported a single dominant gene in each of WL711, CPAN1874 and CPAN1922 controlling tolerance. HD2009 and PBW94 were described as susceptible.

1.43.3. Chlortoluron insensitivity

SU1

Su1 {1402}. Insensitive. 6BS {799}. 6B {1402}. **v:** Cappelle-Desprez {1402}. **tv:** B-35 {735}.

su1. Sensitive. **v:** Chinese Spring {1402}; Poros {1402}. **tv:** B-7 {735}. **ma:** *Xpsr312-6B* – 5.3 cM – *Su1* – 6.8 cM – *Xpsr477(Pgk2)-6B* {736}. **ma,tv:** *Nor2* (6BS) – 2.7 cM – *Su1* {1401}; *Su1* – 5.2 cM – *Xpsr371-6B* (6BL) {735}.
Su1 also controls insensitivity to metoxuron {1402}.

A single dominant gene for tolerance to isoproturon was found in tetraploid wheats derived from a tolerant *T. monococcum* source {1044}. This gene is presumably different from *Su1*.

1.43.4. Imidazolinone resistance

Resistance alleles found in mutagenized populations were incompletely dominant and additive in effect {10099}. Resistance is due to single base pair changes in acetohydroxyacid synthase.

IMI1

Imi1 {10099}. [*Fs-4* {10100}, *AhasL-D1* {10101}]. 6DL {10101}. **v:** BW755 = Grandin*3/Fidel-FS-4 {10099}; CDS Teal IMI 1A {10099}; CDC Teal IMI 9A {10099}; CDC Teal IMI 10A = Fidel-FS-2 {10099}; Clearfield WHS Janz = Janz*4/Fidel-FS-2; Clearfield WHS Stiletto = Stiletto*3//Spear/Fidel-FS-3; Fidel-FS-2 = ATCC40997 {10100}. **v2:** CDC Teal IMI 15A = PTA 3955 *Imi3* {10099}.

IMI2

Imi2 {10099}. [*AhasL-B1* {10101}]. 6BL {10101}. **v:** CDC Teal IMI 11A = PTA 3953 {10099}.

IMI3

Imi3 {10099}. [*AhasL-A1* {10101}]. 6AL {10101}. **v2:** CDC Teal IMI 15A *Imi3* {10099}. **dv:** *T. monococcum* mutant EM2 (mutant of susceptible line TM23 {10102}).

Mutant EM2 has a serine to asparagine substitution near the carboxyl end of the enzyme. The same change led to imidazolinone resistance in hexaploid wheat, rice and *Arabidopsis* {10102}.

1.44. Hybrid Weakness

1.44.1. Hybrid necrosis

[Progressive lethal necrosis {155}; Firing {971}].
Complementary dominant genes. Descriptive alleles *w* (weak), *m* (medium) and *s* (strong) were allocated by Hermsen {532}. Phenotype is affected by modifying genes (and/or genetic background) and environment {566}. According to Dhaliwal *et al.* {257} progressive necrosis is suppressed at 28C.

NE1

Ne1 {530}. [*Le* {550}, {155}, *F*{971}, *Le1* {1491}]. 5B {1491}. 5BL {1636}. **ma:** *Xbarc216-5B* – 8.3 cM – *Ne1* – 2 cM – *Xbarc74-5B* {10334}. *Ne1* – 11 cM – *Xgwm639-5B* {11343}. Mapped to a 4.06 Mb region (383.03 – 3.87.10 Mb) that was deleted in all tested non-*Ne1* carriers {11517}. Co-segregation with the null allele of indel marker *5B-InDel385* {11517}; Mapped to a 4.45 Mb interval represented by *Xwgrc3074-5B* – 0.07 cM – *NE1/5markers* – 0.12 cM – *Xwgrc3009-5B* {11518}. *Xbarc216-5B* – 3.8 cM – *Xwgrc3030* – 0.3 cM – *NE1/Xwgrc1426/*3009 – 4.8 cM – *Xbarc74-5B* {11537}; *Xgwrc3030* – 1.4 cM – *Ne1/Xwgrc3146/3147/3150/Xmag1426* – 0.12 cM – *Xwgrc3150* {11537}; markers *Xwgrc3146, Xwgrc3147* and *Xwgrc3150* were dominant {11537}. *Nwu_5B-4137* – 0.2 cM – *NE1* – 0.3 cM – *Nwu_5B_4114* at 383.30 – 388.01 Mb in CS RefSeq 1.0 {11594}.

Ne1s {530}. **v:** Big Club {550}, {532}, {155}; C306 {1475}; Felix {531}; Gaza 141 PI 220429 {532}; Luteseens 1163 {1264}; Marquillo {550}, {115}, {532}; Ponca {532}; Spica {939}; Synthetics TA4152-19, TA4152-37, TA4152-44, TA4152-60 {10334}. **tv:** Gaza 1E PI 133460; Gaza PI 189262 {532}; Iumillo {532}; Kubanka {532}; PI 94587 {532, 155}; Quanah {532}.

Ne1s is common in tetraploid wheats {1080}.

Ne1w {530}. **v:** Bobin group {532}: Kenya Farmer {532}; The Bobin selection used in breeding Gabo {532} and its sister selection, Timstein {532, 1556} was in fact Gular. Hence Gular, not Steinwedel, is the presumed source. The Sydney University accession Bobin W39 was the parent of Gabo and Timstein, whereas "true" Bobin carried the accession number W360. The particular accession tested by Hermsen is not clear. According to Metgzer {1000} Steinwedel is a non-carrier; Federation group {532}; Cadia {532}; Cleveland {971}; Minister group {532}; Rieti group {532}: Mentana {532}; Mara {532}.

Ne1m {530}. **i:** S-615[*]11/Prelude {1500}. **v:** Carpo {532}; Eskisehir 220-39 {532}; Garnet {532}; Klein Aniversario {532}; Koga {532}; Mus XII/80/22 {532}; Prelude {1491, 532}.

Unknown ***Ne1*** alleles. **tv:** HW75 {697}; HW178 {697}.

Chinese Spring carries the weakest allele {532} and its effect can be observed in CS*7/Atlas 66 2B {939} relative to CS.

NE2 *TraesCS2B01G182800* {11530, 11531, 11532}; also predicted in {11529}.

Ne2. [*F* {971}, *Le2* {1491}, {550}, {155}]. 2B {1491}. 2BS {1085}. **ma:** *Xgwm148-2B* – 6.7 cM – *Ne2* – 3.2 cM – *Xbarc55-2B* {10334}. *Xbarc7-2B* – 3 cM – *Ne2* – 6 cM – *Xwmc344-2B* {11343}. *Xgwm148-2B* – 5.2 cM – *Xwgrc1713/Xwgrc1736-2B* – 1.3 cM – *NE2/*3 markers {11518}; *Xgwm148-2B* – 5.4 cM – *Ne2/Xwrgc1774/1775/1739* – 3.0 cM – *Xwmc474-2B* {11537}.

Ne2s {530}. **i:** S-615[*]11/Kharkov {1500}. **v:** Crimean group {532}: Blackhull {550}; Chiefkan {550}; Clarkan {550}; Kharkov {1491}; Liaochun 10 {11530}; Zhoumai 22 {11531}; Michigan Amber {532}; Minhardi {155}; Red Chief {550}; Stepnaja 135 {1264}; Turkey {532}. **c:** Encodes a CC-NBS-LRR protein {11531; 11532; 11533}. One of two *Ne2m* haplotypes is *Lr13* {11531}. GenBank MW756036 {11532}. **c:** Add: *N22m* is an allele of the *YR27/LR13* locus {M22053}.

Ne2m? {530}. **v:** Barleta group {532}: South American wheats, e.g. Klein Titan {532}; La Prevision 25 {532}; Lin Calel {532}.

Ne2ms {530}. **v:** Mediterranean group {532}: Dawson {550}, {155}; Fultz {550}; Fulcaster {550}; Fulhard {550}; Honor {550}; Jones Fife {1491}; Shepherd {550}, {971}; Trumbull {155}; Vermillion {530}; Wabash {155}. (Although placed in this group on basis of pedigree, the last three stocks, as well as Fultz selection of CI 19293, appear to have the stronger allele of the Crimean group {532}; Mironovskaya {10630}; Noe group {532}: Vilmorin 27 {532}

Ne2m {530}. **v:** Alsen {10334}; Squarehead group {532}: European wheats {532}; Fronteira group {532}: Sonalika {1475}; South American wheats and derivatives, e.g. Atlas 40 {532}: Wheats possessing *Lr13* {939}, e.g. Manitou {939}; HD2329 {10985}. **ma:** *Xbarc55-2B* – 1.1 cM – *Xkwh37* – 4.9 cM – *Lr13/Ne2* – 5.8 cM; *Xgpw1109* – 3.7 cM – *Xbarc18-2B* {11068}.

Ne2w {530}. **v:** Vakka {532}; Varma {532}.

Unknown ***Ne2*** allele {532}; **v:** Harvest Queen {532}. **tv:** Acme {532}; Arnautka {532}; Carleton {532}; Langdon {1498}; Mindum {532}; Stewart {532}.
However, *Ne2* was stated to be absent or rare in tetraploid wheats {1080}.
The Chinese Spring 2BS telosome carries an *Ne2* allele that is not present in Chinese Spring {1085}.

ne1 ne2. **v:** Chancellor {531}; Elgin {1491}; Gladden {155}; Leap {155}; Purkof {155}; Red Bobs {1491}; Red Egyptian {1491}; Steinwedel {1000}; S-615 {1491}; Wichita {531}.

Genotype lists in {531}, {532}, {535}, {640}, {696}, {698}, {1093}, {1135}, {1264}, {1381}, {1473}, 1474, 1475, 1492, 1496, 1497, 1502, 1503, 1512, 1505, 1506, 1507, 1508, 1509, 1510, 1630, 1631, 1632, 1633, 1637, 1638, 1639, 0112, 10985}.

The incompletely dominant *Els2* mutant found in an EMS-treated M_2 population of H261 was likely *ne2* {11472}; A similar situation was described in {11423} where a claimed a putatively novel gene was designated as *yglw-1*.

Rye line 1R136-2 carries *Ner1* {1210} that complements wheat gene *Ne2* {1289, 1210} and rye gene *Ne2* {1210} to produce necrosis. Rye lines L155 and L256 carry *Ne2* {1210} that complements *Ne1* {630,} {1210} and *Ne1* {1210}.

Ner1 {1210}. 5RL {1211}. **al:** *S. cereale* 1R136-2 {1210}.

Ner2 {1210}. 7RL {1211}. **al:** *S. cereale* L155, L256 {1210}.

1.44.2. Hybrid chlorosis type 1

CH1

Ch1 {535}. [m^a {1245}]. 2A {939}, {538}. **i:** Steinwedel*2/Khapli {939}; *T. macha* var. *colchicum* {535}. **v:** *T. macha* var. *subletschumicum* {1493, 1245}. **tv:** Khapli {1549, 1080}; *T. dicoccoides* var. *kotschyanum* {535}; *T. dicoccoides* var. *straussianum* {535}.
36 group dicoccon wheats are listed in {697}.

CH2

Ch2 {535}. [*Ne3* {1504}, m^b {1245}]. 3DL {692}, {939}. 3D {1504, 1495}. **v:** Chinese Spring {1504}, {535}; *T. vavilovi*.
Extremely widespread, very few wheats lack this gene.
Allelic variation at the *Ch2* locus was suggested {537}, {1000}. Prelude, Reward and Red Bobs were exceptional in producing severe symptoms and death at an early stage. Konosu 25 may carry a weak allele {1000}. Different alleles in C306 (strong) and Sonalika (medium) were suggested in {697}.

ch1 ch2. **v:** Albit {1509, 1000}; Burt {1509, 1000}; Chancellor {1000}; Garra {1549}; Kharkof {535}; Steinwedel {1549}. **su:** TAP 67 (= Pawnee 3Ag(3D)) {1644}.

Lists in {535}, {697}, 1381, 1473, 1474, 1475, 1496, 1497, 1502, 1503, 1512, 1505, 1506, 1507, 1508, 1509, 1510}.

A gene, *Chr1*, in rye produces chlorosis symptoms in hybrids with wheats such as C306, HD2939 and NI5439 possessing *Ch2* {1472}. Evidence for multiple alleles of *Chr1* was also presented {1472}.

Chr1 {1472}. **dv:** Cereal rye lines, EC179188 = WSP527A {1472}; EC143825 = WSP506A {1472}; EC338685 = Blanco {1472}; others {1472}.

chr1 {1472}. **dv:** EC179178 {1472}; EC179185 = SAR/SWPY5 {1472}.

1.44.3. Hybrid chlorosis type 2

CS1

Cs1 {1511}. [*Chl*^{1}]. 5A {1498}. **v:** *T. dicoccum* cv. Hokudai {1511}.
Occurs at high frequency in the *T. paleocolchicum* group of emmers.

CS2

Cs2 {1511}. [*Chl*^{2} {1501}]. 4G {1498}. **tv:** Many accessions of *T. timopheevii* and *T. araraticum* {1511},{637}.
Multiple allelism at the *Cs2* locus is discussed in {637}.

A gene named *NetJingW176* (after *Ae. tauschii* accession Jing Y176) was located in chromosome 2DS: *Xgwm-102*-2D – 4.5 cM – *Nec2* – 3.8 cM – *Xgwm515-2D* {11307}.

1.44.4. Apical lethality

Apical lethality is caused by complementary recessive genes and is characterized by stunting and tiller death at the 4-5 leaf stage. The lethal genotype was designated *apd1 apd1 apd2 apd2* {10492}.

Apd1{10492}. **v:** WR95 = Kalyansona/Gigas//HD1999/Sonalika/3/*T. carthlicum* {10492}.

Apd2{10492}. **v:** HD2009 {10492}; HW2041 {10492}; Lok-1 {10492}; others {10492}.

Apd1 Apd2. **v:** Atila {10492}; Kalyansona {10492}; others {10492}.

apd1 apd2. Lethal genotype.
Uniculm plants occured as heterozygous segregates among progenies, but homozygous uniculm lines could not be established {10492}.

1.44.5. Hybrid necrosis type 3

NEC1

Nec1 {11158}. 7DS {11158}. **v:** (*T. durum* cv. Langdon x *Ae. tauschii* KU-2828) amphiploid {11158}. **al:** *Ae. tauschii* KU-2828 {11158}. **ma:** *Xbarac352-7D* – 5.3 cM – *Lr34* – *Xgwm295-7D* – 4.0 cM – *Xbarc154-7D* – 1.7 cM – *Nec1* – 13.2 cM – *Xcfd-7D* {11158}.
Although this form of hybrid necrosis is caused by complementary genes, mapping of *Nec1* was based on a cross of necrotic and non-necrotic Langdon x *Ae. tauschii* amphiploids. Consequently only *Nec1* was mapped {11158}.

1.45. Iron deficiency

Fe1 {921}. 7DL {927}. **v:** Saratovskaya 29 {921}.

Fe2 {921}. 7BS {927}. **v:** CS {927}.

1.46. Lack of ligules

The liguleless character is controlled by complementary recessive genes in hexaploid wheat {077}, {738}, {942} and by a single recessive in tetraploid wheat {047}, {050}, {939}, {10133}. One gene at the tetraploid level is allelic with one of those in the hexaploid {939}, {10133}. Evidence for orthology of *lg1* and *lg2* with *lg* of rice {170}, *lg1* of maize {004}, *li* of barley {1155} and *al* of rye was presented in {725}. An Imperial rye chromosome 2R addition restored the liguled condition to a liguleless CS derivative {939}. An erect leaf mutant involving *TaSPL8* (SQUAMOSA promoter-binding protein-like transcription factor), a homolog of *LG1* in maize and rice and was located in chromosome 2D. Knockout mutants of *TaSPL8* orthologs led to a fully liguleless phenotype. The gene in 2D was identified as *TraesCS2D01G502900. TaSPL8* transcript was highly expressed in the laminar joint region and young spike. *TaSPL8*-2D transcript was produced at much higher levels than *TaAPL-2B* whereas *TaSPL-2A* was produced at a minimal level {11401}.

LG1

lg1 {47}. 2B {942}. 2BS {10767}. **i:** ANK33 = Novosibirskaya 67*10/K59990 {10061}. **v:** Eligulate W1342 *lg2 lg3* {942}, {10133}; K31289 {10133}; K59990 {10061}; K53660 {10133}; Liguleless partial backcross derivative of CS {939}; Partial backcross derivative of CS {939}. **tv:** K17769 {10133}; K17784 {10133}.

LG2 *TraesCS2D01G502900*. **bin:** C-2DL3-0.49. **ma:** *Xbarc228-2D* – 12.7 cM – *LG2/G3489_1DL12del/G3489_2DL11del* – 3.3 cM – *Xgdm6-2A* – 47.8 cM – *Xgwm301-2D* {11220}.

lg2. 2D {942}. **i:** ANK33 = Novosibirskaya 67*10/K59990. **v:** Eligulate W1342 *lg1 lg3*; Liguleless partial backcross derivative of CS {939}.
A dominant mutant allele for liguleless phenotype is reported in *Ae. tauschii* – this locus is located in chromosome 2DL but is independent of *LG2*.

LG3

lg3 {10133}. 2A {10133}. **i:** ANK33 = Novosibirskaya 67*10/K59990 {10061}. **v:** Present in all hexaploid cultivars.

LG^{t} [{11220}]. **bin:** C-2DL9-0.75. **ma:** *Xgwm301-2DL*……… *Xbarc159-2D* – 9.3 cM – *LG*^{t} {11220}.

Lg2^{t} {11220}. **dv:** Liguleless mutants of *Ae. tauschii* accession KU20-9 {11220}.

Genotypes of selected tetraploid wheat {10133}:
Lg1Lg1 Lg3 Lg3: *T. turgidum* var. *durum* Ldn - dic DS 2A: *T. turgidum* var. *dicoccum*
Khapli and Vernal; *T. turgidum* var. *dicoccoides* Israel A; MG4343.
Lg1Lg1 lg3 lg3: *T. turgidum* var. *durum*: Altaiskaya Niva; Castelpoziano; Langdon; Ldn-GB DS 2B; Golden Ball; Modoc; PI349056.
lg1lg1 Lg3Lg3: None identified.

1.47. Leaf characteristics

1.47.1. Leaf erectness

QLer.ipk-2A {0255}. 2AS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}; The erect leaf phenotype was contributed by Opata {0255}. **ma:** Associated with *Xbcd348-2A* {0255}.
Mutants lacking ligules are known to have erect leaves. However, the QTL for leaf erectness reported here is not related to liguleless mutants {0255}.

1.47.2. Leaf tip necrosis

LTN1

Ltn1{10281}. [*Ltn* {1361}]. 7D {1361}. v: Wheats with *Lr34/Yr18* {301}, {1361}; **v2:** Parula *Ltn2* {10281}. **ma:** Associated with *Xgwm295-7D* and *Xgwm130-7D*{10281}. **c:** Putative ABC transporter {10862}.
This gene is identical to *Lr34, Sr57, Yr18, Pm38*. *Ltn1* reportedly has effects on response to other diseases and pathogens including BYDV and *Biploaris sorokiniana*.

LTN2

Ltn2 {10281}. 1B {10281}. **v:** Wheats with *Yr29/Lr46* {10281}; See *Yr29, Yr46*. **v2:** Parula *Ltn1* {10281}. **ma:** *Xwmc44-1B* – 1.4 cM – *Xbac24prot* – 9.5 cM – *Ltn2* – 2.9 cM – *Xbac17R*........*Xgwm140-1B* {10281}; *Xgwm44-1B* – 3.6 cM – *Ltn2* – 2.1 cM – *XtG818/XBac17R*.....*Xgwm140-1B* {10281}.

According to Messmer et al. {0031} LTN may be caused by several QTLs and is affected by genetic background and environment.

LTN3

Ltn3 {11070}. **i:** RL6077 {11070}. **v:** Chapingo 48 {11070}. **c:** This multiple disease resistance/necrosis locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

QTL

QLtn.sfr-1B {0050}. 1BS {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xgwm18-1B* and *Xglk483-1B* {0050}.

QLtn.sfr-3A {0050}. 3A {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr570-3A* and *Xpsr543-3A* {0050}.

QLtn.sfr-4B.1 {0050}. 4B00 {50}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr921-4B* and *Xpsr593-4B* {0050}.

QLtn.sfr-4B.2 {0050}. 4B {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr593-4B* and *Xpsr112-4B* {0050}.

QLtn.sfr-4D {0050}. 4DL {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr302-4D* and *Xpsr1101-4D*{0050}.

QLtn.sfr-5A {0050}. 5A {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr549-5A* and *Xglk163-5A* {0050}.

QLtn.sfr-6A {0050}. 6A {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr563-6A* and *Xpsr966-6A* {0050}.

QLtn.sfr-7B.1 {0050}. 7B {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr350* and *Xbzh232(Tha)-7B* {0050}.

QLtn.sfr-7B.2 {0050}. 7B {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xglk750-7B* and *Xmwg710-7B* {0050}.

QLtn.sfr-7D {0050}. 7DS {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0050}. **ma:** Associated with *Xpsr160-7D* and *Xgwm44-7D* {0050}.

1.47.3. Seedling leaf chlorosis

SC

Sc {149}. 3BS {149}. **s:** CS*/Hope3B {149}. **v:** Hartog {149}; Suneca {149}; wheats with *Sr2* {149}.
Leaf chlorosis is affected by temperature and light and is enhanced by infection with pathogens. The *sc* allele is completely linked with *Pbc* (pseudo-black chaff) and *Sr2* (reaction to *Puccinia graminis*).

1.47.4. Early leaf senescence

ELS1

els1 {11326}. 2BS {11326}. **v:** ZK331 / Xiangmai 99171 // 2*Lumai 30 Line 114 {11326}. **ma:** *WGGB305* – 0.3 cM – *els1/WGGB302* – 1.2 cM – *WGGB303/WGGB304/WGGB306* – 0.6 cM – *Xbarc92-2B* {11326}.

The *els1* 'mutant' was detected in an F_4 population. Since the parents had normal phenotype complementary genes were likely involved. The similar location of *ELS1* to the *NE1* locus in chromosome 2BS and similar phenotype suggests that this gene may be *Ne2*. See 49, Hybrid Weakness; 49.1, Hybrid necrosis

ELS2

Els2 {11472}. 2BL {11472}. **v:** LF2099 {11472 }. **ma:** *Xgpw4043-2B* – 8.87 cM – *Els2* – 22.27 cM *Xwmc149-2B* {11472}.
The incompletely dominant *Els2* mutant was found in an EMS-treated M_2 population of H261 {11472}.

***ELS3*.** Candidate gene *CS2D02G332700.* **ma:** Located in a 2.52 Mb interval – *AX-109501942* – 2.0 cM – *Els3* – 1.4 cM – *AX109998182* {11772}.

Els3 {11772}. **v:** Yanzhan 4110 {11772}. **c:** The candidate encodes an LRR-RLK -like gene located on the cell membrane {11772}.

***els3*.** **v:** els3 mutant {11772}.

The mutant was identified in an EMS-mutagenized population of Yanzhan 4110 {11772}.

1.48. Lesion Mimicry

Add introductory sentence: Lesion mimic phenotypes are characterised by spontaneous hypersensitivity not unlike disease resistance. Lesions are often not produced when leaf sectors are protected from light, and disease levels on mutant individuals may be lower than on non-mutant sibs. Lesion mimics that resemble the response of plants to infection by pathogens occur in many species ({10743} for examples).

LM

lm {10743}. 1BL {10743}. **bin:** C1BL6-0.32 {10743}. **v:** Ning 7840 {10743}. **ma:** Proximal to *Xgwm264.1-1B* {10743}.
LM was positively associated with *QLr.pser.1BL* {10743}.

LM1* and *LM2

LM1 {11572}. 3BS {11572}. **ma:** *Xwmc674-3B* – 1.2 cM – *LM1* – 3.8 cM – *Xbarc133/Xbarc147-3B* {11572}.

lm1 {11572}. **v:** Zaosui 30 *Lm2* {11572}.

LM2 {11572}. 4BL {11572}. **ma:** *Xgwm513-4B* – 1.5 cM – *LM2* – 2.9 cM – *Xksum154-4B* {11572}.

lm2 {11572}. **v:** Yanzhan 1 *Lm1* {11572}.

LM3 {11573}. 3BL {11573}. **ma:** Mapped to a 3 cM proximal region of chromosome 3BL {11573}.

Lm3 {11573. Partially dominant. **v** Line Lm3 {11573}.
The mutant phenotype appeared in an F_1 plant of cross Line 3-1/Jing 411. The plant was then backcrossed 6 times with Line3-1 and the selected line was named Lm3.

LM4 {11577}. 2DS {11577}. **ma:** Fine mapped within a 8.06 cM interval flanked by *Xgwm210*-2D and *Xgwm455-2D* using specifically developed markers *m4_01_cib* and *lm4_02_cib* {11577}.

***Lm4*.** Wild type allele. Recessive.

lm4 {11577}. The allele named *lm4* and conferring the lesion phenotype was described as dominant {11577}.
This lesion mutant appeared in a Yanzhan 1/Neixiang 188 RIL population in which the segregation of mutant versus normal phenotype was 1:1.

***LM5*.** Semi-dominant. 2AL {11576}.

Lm5 {11576}. **v:** MC21, an EMS-induced mutant in Chuannong 16 {11576}. **ma:** *KASP-4211* (630.3 Mbp) – 0.6 cM – *Lm5* – 3.7 cM – *KASP5353* (703.53 Mbp) {11576}.

1.49. Lodging

QTL

QLd.crc-3D {10287}. 3D {10287}. **ma:** Linked to *Xgwm191-3D* (LOD 3.7) in RL4452/AC Domain {10287}.

QLd.sfr-1B {0052}. 1BS {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xpsr949-1B* and *Xgwm18-1B* {0052}.
This QTL coincided with QTL for reduced height, increased culm stiffness and broader leaf width {0052}.

QLd.sfr-2A {0052}. 2AS {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr958-2A* and *Xpsr566-2A* {0052}.
This QTL coincided with QTL for reduced height, increased culm stiffness, broader leaf width, more erect growth habit, later ear emergence and increased culm thickness {0052}.

QLd.sfr-2D {0052}. 2D {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xpsr933-2D* and *Xglk529-2D* {0052}.

QLd.sfr-3A {0052}. 3AS {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr598-3A* and *Xpsr570-3A* {0052}.
This QTL coincided with QTL for increased culm stiffness and reduced culm thickness {0052}.

QLd.sfr-4A {0052}. 4AS {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xgwm397-4A* and *Xglk315-4A* {0052}.
This QTL coincided with QTL for reduced height, increased culm stiffness and more erect growth habit {0052}.

QLd.sfr-5A {0052}. 5AL {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xpsr918-5A* and *Xpsr1201-5A* {0052}.
This QTL coincided with QTL for reduced height, increased culm stiffness, reduced leaf width, more erect growth habit, later ear emergence and increased culm thickness {0052}.

QLd.sfr-5B {0052}. 5BL {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xpsr370-5B* and *Xpsr580-5B* {0052}.
This QTL coincided with QTL for increased culm stiffness, broader leaf width and more erect growth habit {0052}.

QLd.sfr-6B {0052}. 6BL {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xpsr964-6B* and *Xpsr142-6B* {0052}.

QLd.sfr-7B {0052}. 7BL {0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population {0052}. **ma:** Associated with *Xpsr927-7B* and *Xpsr350-7B* {0052}.
This QTL coincided with QTL for reduced height and later ear emergence {0052}.

1.50. Male sterility

1.50.1. Chromosomal

Ms1376 {10814}. Sterility is dominant. **v:** TR1376A {10814}.
Male fertile counterpart: TR1376B {10814}.
Ms1376 was discovered among progenies of a transgenic family of Xinong 1376 containing leaf senescence-inhibiting gene P_{SAG12}-IPT {10814}.

MS1 4B {268}. 4BS {64}. *TraesCS4B02G017900.* **ma:** Located in a 0.05 cM region between *X27140346* and *X12360198* {11269}.

***Ms1*.** **c:** Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is essential for pollen exine production {11269}. GenBank KX447407. *Ms1* is a phospholipid-binding protein {11421}. Sequence: SRP113340. Encodes a 219 amino acid polypeptide with similarity to a large family of GPI-anchored lipid transfer proteins affecting exine development {11269}. *Ms-A1 = TraesCS4A02G295900*; *Ms-B1 = TraesCS4B02G017900.*

ms1. Recessive alleles for sterility

ms1a {268}. **v:** Briggle's Chancellor Derivative {268}; Pugsley's Male Sterile {268}. **c:** Terminal deletion {11422}.

ms1b {268}. **v:** Probus mutant {268}. **c** Interstitial deletion {11269}.

ms1c {64}. **v:** Cornerstone {64}. **c:** Terminal deletion {11269}.

ms1d {619}. **v:** Mutant FS2 {619}; Ningchen mutants *msd.1* and *msd.2* {11421}. **c:** G329A in exon 1 {11421, 11269}.

ms1e {619}. **v:** Mutant FS3 {619}. **c:** G1431A del1432 {11421}; C1435T + 16 bp del in exon 2 {11269}.

ms1f {619}. **v:** Mutant FS24 {619}. **c:** G155A in exon 1{11269}.

ms1g {10355, 11421}. 4BS {10354}. **v:** Lanzhou Mutant 257A {10355, 10354}; Male sterile line 257A{10546}. **c:** Deletion of entire sequence {11421}.

ms1h {11421}. **v:** Ningchun 4 mutant {11421}. **c:** C1762T {11421}.

ms1i {11421}. **v:** Ningchun 4 mutant {11421}. **c:** G1603A {11421}.

ms1j {11421}. **v:** Ningchun 4 mutant {11421}. **c:** C1775A {11421}.

ms1k {11421}. **v:** Ningchun 4 mutant {11421}. **c:** G1397A {11421}.

ms1l {11421}. **v:** Ningchun 4 mutant {11421}. **c:** C226T {11421}.

ms1m {11421}. **v:** Ningchun 4 mutant {11421}. **c:** C1472T {11421}.

ms1n {11421}. **v:** Ningchun 4 mutant {11421}. **c:** T164A {11421}.

ms1o {11421}. **v:** Ningchun 4 mutant {11421}. **c:** G281A {11421}.

ms1p {11421}. **v:** Ningchun 4 mutant {11421}. **c:** G155A {11421}.

ms1q {11421}. **v:** Ningchun 4 mutant {11421}. **c:** C148T {11421}.

ms1r {11269]. [*Ms1h* {11269}]. **v:** Tilling mutant in Qual2000 {11269}. **c:** G178A {11269}.

Ms1 orthologs in the A and D genomes are epigenetically silenced {11421}.

MS2

ms2 {806}. Dominant allele for sterility. [*Ta1* {240}]. 4DS {806}. **v:** Taigu = Line 223 {240}, {806}, {807}; *ms2* confers sterility when present in octaploid triticale {597}. **ma:** Mapped to a 0.05 cM region

flanked by *Xsauw27-4D* and *Xsdauw29-4D* {11388}. **c:** *Ms2* has a long terminal-repeat in miniature (TRIM) transposon at position -314 to -310 {11388}. Genbank KX585234 {11388}.
The TRIM element acts as an enhancer that activates anther-specific transcription of the *Ms2* allele {11388, 11389}. *Ms2* induced male sterility in barley and Brachypodium {11388} as well as triticale {597}, {11388}.

MS3

ms3 {872}. Dominant allele for sterility. 5AS {872}. **i:** Chris derivative {872}; KS87UP9 {219}. **ma:** *Xwg341-5A* – 0.8 cM – *ms3*.......cent {0289}; *Xcdo-677-5A* and *Xbcd1130-5A* also cosegregated with *Xwg341-5A* but were located in a different region in the physical map {0289}.

MS4

ms4 {293}. Dominant allele for sterility, distinguished from *ms2* on the basis of different degrees of recombination with the 4D centromere. 4DS {0293}. **v:** Konzak's male sterile.

MS5. *TraesCS3A02G217000*. 3A {619}, 3AL {11427}.

***Ms5*:** Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is required for pollen exine development {11427}. *TraesCS3A02G217000* {11427}. GenBank MK577897.

ms5 {619}. **v:** Mutant FS20 {619}; H45 {11427}.
Complete sterility conferred by *ms5* is dependent on the homoeologous *ms-D* genotype – Ecalibur, Gladius and RAC 875 have an *ms-D* allele that restores fertility to *ms5* genotypes {11427}.

Two non-functional *ms-B* alleles (Chinese Spring and Synthetic W7984 types) were identified {11427}.

1.50.2. Sterility in hybrids with wheat

Shw {331}. [1HL {331}]. **ad:** Additions of 1H and 1HL to wheat and certain translocation lines {331}. **ma:** Located in a 16.4 cM interval flanked by *Xmwg800-1H* and *Xmwg943-1H*. A possible relationship with *Ncc* genes is discussed {331}.

1.50.3. Photoperiod and/or temperature-sensitive male sterility (PTGMS)

tmsBS20T {11157}. 2BL {11157}. **v:** BS20-T {11157}. **ma:** *Xgwm403-2B* – 2.2 cM – *tmsBS20T* – 4.5 cM – *Xgwm374-2B* {11157}.

WTMS1

wtms1 {10332}. 2B {10332}. **v:** BNY-S {10332}. **ma:** E: AAG/M:CTA$_{163}$ – 6.9 cM – *wtms1* – 4.8 cM – *Xgwm374-2B* {10332}.
Described as a thermo-sensitive gene (TGMS), giving complete sterility at less than 10C, but fertile at higher temperatures {10332}.

WPTMS1

wptms1 {10333}. 5B {10333}. **v:** Line 337S *wptms2* {10333}. **ma:** *Xgwm335-5B* – 4.2 cM – *wptms1* – 24.4 cM – *Xgwm371-5B* {10333}.
wptms1 produces sterility only in the presence of *wptms2*.
Chromosome 5B was also implicated in spontaneous mutant line Xinong 291S: a second gene was not located {11143}.

WPTMS2

wptms2 {10333}. 2B {10333}. **v:** Line 337S *wptms1* {10333}. **ma:** *Xgwm374-2B* – 6.9 cM – *wptms2* – 20.9 cM – *Xgwm120-2B* {10333}.
wptms2 produces sterility only in the presence of *wptms1*. *wptms1* and *wptms2* were analysed and mapped under long photoperiod/high temperatures, but an earlier study indicated a single gene for male sterility under short photoperiod/low temperatures. Although mapping data are different a possible relationship between *wtms1* and *wptms2* needs to be resolved.

1.51. Manganese efficiency

QTL

Stojocri 2 (Mn efficient) / Hazar (MN inefficient): durum cross: Variation associated with *Xcdo583-4B* explained 42% of the variation in Mn efficiency {0320}.

1.52. Maturity time

RL4452 / AC Domain:

QMat.crc-3B {10287}. 3B {10287}. **ma:** Linked to *Xwmc231-3B* (LOD 3.0) {10287}.

QMat.crc-4A {10287}. 4A {10287}. **ma:** Linked to *Wx-B1* (LOD 6.1) {10287}.

QMat.crc-7D {10287}. 7D {10287}. **ma:** Linked to *Xgwm130-7D* (LOD 17.5) {10287}.

1.53. Megasporogenesis

1.53.1. Control of megasporogenesis

Msg {625}. 7AS {625}. **tv:** Langdon {625}.

54. Meiotic characters

1.54.1. Low-temperature pairing

LTP

Ltp {527}. **v:** Chinese Spring {527}.
Expressed in the absence of chromosomes 5D at 12ºC - 15ºC, but not at 20ºC. A contrasting allele, *Ltp*, for normal pairing at the lower temperature range was demonstrated in *T. dicoccum*.

1.54.2. Pairing homoeologous

PH1. Traes………

Ph1 {1537}. ***Ta-Zip4-B2*** {11765}. 5BL {1301}. **v:** Hexaploid wheat. **tv:** Tetraploid wheat. **ma:** PCR-based assays for presence and absence of *Ph1* were described {359}, {0217}, {9965}, {0214}; The *Ph1* factor(s) was restricted to a region flanked by *Xrgc846-5B* and *Xpsr150-5B* {0219}; *Ph1* was physically mapped in 5BL to fraction length 0.55, bracketed by deletions 5BL-1 and *ph1b* {446}.
A complex *Ph1* candidate structure comprising at least one 5B-specific member of the *cdc2* complex multigenic cluster (involved in chromosome condensation), a unique repeat structure with similarities to repeats on chromosome 3B, and a heterochromatic sub-telomeric insertion from chromosome 3AL was identified {10240}. *Ta-Zip4-B2* is embedded within this complex {11765}.

A set of homoeologous set of *Ta-Zip-1* genes (*Ta-Zip-A1*, *TaZip-B1* and *TaZip-D1* genes is present in Group 3 chromosomes but their expression levels are very low compared to *Ta-Zip-B2* {11765).

ph1a. - Not applicable - see *ph2b* {1303}.

ph1b {1301}. **v:** Sears' high pairing mutant {1301}. **ma:** A PCR-based detection system for *ph1b ph1b* individuals is described in {9965}. Dualplex marker *Xwgc2111* + *Xwgc2049* behaves like a co-dominant marker {11359}. The *Ph1b* deletion involves a region of at least 60,014,523 bp {11359}.

ph1c {593}. **tv:** Cappelli *ph1* mutant {593,449}; This mutant is deficient for a terminal portion of chromosome 5BL{449}. **ma:** Mutant lines with *ph1b* and *ph1c* carry deletions of the chromosome segment possessing *Ph1* in the respective parent lines {593, 447}.
Several *ph1* mutants are described in {0219}.

PH2 *TraesCS3D02G119400*.

Ph2 {1302}. 3DS {1302}. *TaMSH703D* {11527}.

ph2a {1302}. **v:** Sears' intermediate pairing mutant {1302, 1301}. **ma**: *ph2a* is a 120-125 Mb deletion {11526}.

ph2b {1304, 1303}. [*ph1a* {1537}]. **v:** Chinese Spring mutant 10/13 {1537}. **c:** Contains a G to A transition at position 74,359.312 in the TaMSH7-3D gene {11527}. *TaMSH7* is a plant-specific member of the DNA mismatch repair (MMR) family {11527}.
Wide cross hybrids involving *ph2* mutants have a 5.5-fold increase in homoeologous pairing {11516}.

1.54.3. Inhibitor of pairing homoeologous

Ph1^{I}. **al:** *Aegilops speltoides* {439}, {1218}.

1.54.4 Asynapsis/desynapsis

A putative gene for desynapsis designated *Ddes2* was placed between *Xwmc325-3B* and *wPt-8983* in deletion bin 3BL7-0.63-1.00 by mapping of deletion hybrids {11339}. There is no mutant stock to represent this gene first reported in CS nullisomic 3B by Sears {1293}.

TaASY1 {11766}. Encodes an axial-element-associated protein that is essential for synapsis and cross-over formation in Arabidopsis and rice {11766}. Mutants affect synapsis and distribution of chiasmata along the chromosome {11767}.

TaASY-A1 {11767}.

TaASY-B1 {11767}.

TaASY-D1 {11767}.

<u>QTL</u>

QTug.sau-3B {11471}. **bin:** 5BS5-0.07-0.03. **ma:** *Xgwm285-3B* – 1.0 cM – *Xcfp11012-3B* {11471}. Identified in *T. turgidum / Ae. tauschii* hybrids involving Langdon durum (high unreduced gamete formation) crossed with AS313 and AS2225 (low unreduced gamete formation) topcrossed with *Ae. tauschii* AS60. The QTL was located near *Ttam*, a homologue of the *TAM* (tardy asynchronous meiosis/CYCA1;2) cyclin gene from Arabidopsis {11471}.

1.55. Nitrate reductase activity

NRA

Nra {424}. **v:** UC44-111 {424}.

nra {424}. **v:** Anza {424}.

1.56. Nuclear-cytoplasmic compatability enhancers

SCS

Scs {869}. Derived from *T. timopheevii* {869}. [*scs*^{ti} {10878}]. 1AL {870}, {27}. **v:** *T. timopheevii* {869}. **ma:** A number of completely linked RAPD makers were identified {44}; *Xbcd1449.2-1A* – 0.6 cM – *SCS* – 2.3 cM – *Xbcd12-1A* {10878}.
Asakura *et al*. {44} used the symbol *Ncc* as a synonymn for *scs* pointing out that the effects of the gene are not limited to a single species.

1.57. Nucleolus organizer regions

1.57.1. 18S - 5.8S - 26S rRNA genes

NORs were observed as secondary constrictions associated with nucleoli on satellited chromosomes, e.g. {221}, and by *in situ* hybridization to chromosome spreads {39}, {294}, {1014} of 18S-5.8S-26S ribosomal-DNA probes {38}, {433}. Allelic variation in gene number was demonstrated at all wheat *Nor*

sites and at *Nor-R1* by filter {367} and *in situ* hybridization {1012}. Allelic variants of the *Nor* loci were detected by hybridization of rDNA probes to restriction endonuclease-treated DNA on Southern blots {37}, {288}, {917}, {1399}. Alleles *Nor-B2a* to *Nor-B2f* were identified using *Taq1* digests of genomic DNAs hybridized to derivatives of the plasmid pTa250 {433} containing spacer-DNA fragments pTa250.4 {367}, {917} and pTa250.15 {288}.
Other variants may have been isolated {1399} using *BamH1/EcoR1* double digests and pTa71 {433}. The variants may or may not be equivalent to those described below.

Nor1a and Nor2a. **v:** Maris Huntsman {1399}.

Nor1b and Nor2b. **v:** Bezostaya 1 {1399}.

Nor1c and Nor2c. **v:** Cappelle-Desprez, Maris Ranger {1399}.

NOR-A1

Nor-A1. 1AS {1012, 221, 367, 835}. **v:** *T. spelta* {1012, 221, 367, 835}. **dv:** *T. monococcum* {658}.

NOR-B1

Nor-B1. [*Nor1* {1120}]. 1BS {1041, 221, 367, 835}. 1B {288, 37}. **v:** CS {288}.
Deletion mapping divided the *Nor-B1* in a proximal subregion *Nor-B1p* (short repeat) and a distal subregion *Nor-B1d* (long repeat) {0275}

Nor-B1a {918}. **v:** Cheyenne, Chinese Spring, Hope, Kite, Oxley, Teal, Timstein{288}, {37}; Vasco, 8 others {288}.

Nor-B1a- {918}. **v:** A derivative allele of *Nor-B1a* with a significantly reduced amount of spacer. Condor 64-1{918}; Sonora 64-1{918}.

Nor-B1b. **v:** Olympic, Robin, Shortim {917}.

Nor-B1c {918}. **v:** Banks {917}; Corella {917}; Warigal {917}; 5 others {917}.

Nor-B1c- {918}. **v:** Rosella {918}.

Nor-B1d {918}. **v:** Maris Huntsman {918}.

Nor-Ag^{i}1 {374}. 1Ag^{i} {374}. **ad:** Vilmorin27/*Ag. Intermedium* {374}.

Nor-H1. [*Nor-I1* {794}]. 1HS {794}. **dv:** Sultan barley {794}.

Nor-R1. 1RS {39}. **ad:** CS/Imperial {39}.

Nor-S1. 1SS {294}. **al:** *Ae. speltoides* {294}.

Nor-U1. 1U {906}. **su:** CS/*Ae. Umbellulata* {906}.

Nor-V1 {241}. 1V {241}. **ad:** CS/*D. Villosum* {241}.

Nor-B2. [*Nor2* {1120}]. 6BS {1041}, {221}, {366}, {835}. **v:** CS.

Nor-B2a {918}. 6B {288}. **v:** CS {37}, {917}.

Nor-B2a- {918}. **v:** Blueboy {918}; Sonora 64-1 {918}.

Nor-B2b. T6B {288}. **v:** Banks, Oxley, Shortim, Timstein {37}; 12 others {917}.

Nor-B2c. **v:** Corella, Robin, Teal, 1 other {917}.

Nor-B2d {918}. *H6B* {288}. **v:** Hope {37}; Olympic {917}; Warigal {917}.

Nor-B2d- {918}. **v:** Harrier {918}; Kite {918, 917}.

Nor-B2e. **v:** Vasco {917}.

Nor-B2f. *Ch6B* {288}. **v:** Cheyenne {37, 917}.

Nor-B2g {918}. **v:** Falcon; Gluclub; La Prevision {918}.

Nor-B2h {918}. **v:** Yaktana {918}.

Nor-B2i {918}. **v:** Maris Huntsman; Thatcher {918}.

More detailed listings for allelic variation at *Nor-B1* and *Nor-B2* are given in {917}, {918}.

Nor-E2. 6ES {294}. **ad:** CS/*E. elongate* {294}.

Nor-G2. 6G {578}. **tv:** *T. timopheevii* IPSR (PBI) No. 1 {294}.

Nor-H2. [*Rnr1* {1248}]. 6H {1070}, {39}, {1248}. 6HS {794}. **al:** Clipper barley {39}; Sultan barley {794}.

Nor-S2. 6SS {294}. **al:** *Ae. speltoides* {294}.

Nor-A3. 5AS {658}, {1014}. **dv:** *T. monococcum, T. urartu* IPSR (PBI) Acc. A.

NOR-D3

Nor-D3. 5DS {221}, {835}. **v:** CS; most wheats {288}, {37}, {917}.

Nor-Ag^{i}3. 5Ag^{i} {374}. **ad:** CS/*Ag. intermedium* {374}.

Nor-E3. 5ES {294}. **ad:** CS/*E. elongate* {294}.

Nor-H3. [*Rnr2* {1248}]. 5HS {794}. 5H {1070}, {39}, {1248}. **al:** Clipper barley {39}; Sultan barley {794}.

Nor-U3. 5U {906}. **ad,su:** CS/*Ae umbellulata* {906}.

NOR-D4

Nor-D4 {1042}. 7DL {1042}. **v:** CS {1042}. **dv:** *Ae squarrosa* {1042}.

Nor-H4. [*Nor-I4* {794}]. 7HS {793, 794}. **al:** Sultan barley {794}.

Nor-H5. [*Nor-I5* {794}]. 2HS {793, 794}. **al:** Sultan barley {794}.

NOR-B6

Nor-B6 {601}. 1BL {601}. **v:** CS; Cheyenne, Wichita {601}. **tv:** Langdon {601}.

NOR-A7

Nor-A7 {601}. 5AL {601}. **v:** CS; Cheyenne, Wichita {601}. **tv:** Langdon {601}.

NOR-D8

Nor-D8 {601}. 3DS {601}. **v:** Witchita {601}.

NOR-A9

Nor-A9 {120}. [*Nor-A1* {1012}, {221}, {367}, {835}]. 1AS {276}, {282}. **v:** *T. spelta* {1012}, {221}, {367}, {835}.

NOR-A10

Nor-A10 {120}. [*Nor-A3* {658}, {1014}]. 5AS {276}, {282}. **dv:** *T. monococcum* {276}, {282}; *T. urartu* IPSR (PBI) Acc. A.

Two sites designated temporarily as *Nor-Ax* and *Nor-Ay* were identified in *T. monococcum* ssp. *boeoticum*, but were absent in ssp. *urartu*.

1.58. Osmoregulation

Osmoregulation is a specific form of solute accumulation regulating turgor pressure and hydration during periods of stress with positive effects on growth. Wheat lines selected for higher osmoregulation in the greenhouse have greater growth and seed yields under water-limited conditions in the field.

OR

Or {1030}. Low osmoregulation. **s:** CS (Red Egyptian 7A). **v:** Cappelle Desprez; Condor*4/3Ag14 {1030}; Red Egyptian. **ma:** *Or* (proximal in 7AS) – 13 cM – *Xpsr119-7A* {1031}.

Or {1030}. High osmoregulation. 7AS {1031}. 7A {1030}. **v:** CS, Condor, Songlen, Takari {1030}.

1.59. Phenol colour reaction of kernels

Wheat genotypes vary in response when caryopses are treated with weak solutions of phenol, a dark colour response being indicative of a positive response. This response is believed to be related to the action of tyrosinase. There seems to a genetic relationship with polyphenol oxidase activity which causes a darkening of flour, pasta and noodle products (see also Polyphenol Oxidase (PPO) activity).

TC

Tc1 {10130}. 2AL {10130, 10131}. **su:** Various substitutions of chromosomes 2A into CS {10131}. **sutv:** Langdon*/dicoccoides 2A {10130}. **tv:** Golden Ball {10130}.

Tc2 {10130}. 2BL {10130}. **sutv:** Langdon*/Golden Ball 2B {10130}. **tv:** Golden Ball {10130}.

Tc3 {10131}. [*Tc* {10131}]. 2DL {10130}. **v:** Chinese Spring (intermediate response) {10130}. **v2:** Timstein *Tc1* {10131}. **su:** CS/*Timstein 2D {10131}. **tv:** Cocorit 71 {10130}; Langdon {10130}. **sutv:** Langdon*/CS 2D(2A); Langdon*/CS 2B(2D) {10130}; *T. dicoccoides* Israel A {10130}. Lines with a negative phenol colour reaction.

1.60. Pollen killer

KI

Ki {1306}. Killing allele is dominant. 6BL {1306}. **v:** Chinese Spring{1306}; Mentana {929}.

ki. **v:** Probably the majority of wheats including Timstein, Gabo and Yalta {1306}.
Modifiers also appear to be involved as Luig {840, and unpublished} found variation among *kiki* parents. Some F_2 and F_3 *Sr11sr11* plants from Yalta/Chinese Spring crosses segregated with less than 50% *Sr11*-phenotypes among the progeny indicating that killing extended to eggs as well as pollen. See also, Gametocidal Activity.

Kato & Maeda {10164} reported both partial pollen and seed sterility in crosses involving certain landraces and Chinese Spring. They attributed sterility to recessive alleles of three complementary genes. The genes were designated *Ki2, Ki3* and *Ki4* {10164}, but the relationship of *Ki3* to the earlier designated *Ki* was not established. Some genotypes:
Ki2 Ki3 Ki4: **v:** Aka Kawa Aka {10165}; Hope {10165}; Marquis {10165}; Red Russian {10165}
ki2 Ki3 Ki4: **v:** Akadaruma {10165}; Canthatch {10165}; Norin 61{10165}; Pakistani Landrace IL159 {10164}
Ki2 ki3 Ki4: **v:** Gabo {10165}; Thatcher {10165}; Timstein {10165}; Zlatiborka {10165}
Ki2 Ki3 ki4: **v:** Kagoshima {10165}; Komugi Jingoro {10165}; Sakobore {10165}
ki2 ki3 Ki4: **v:** Finnish Landrace WAG4339 {10165}; Hungarian Landrace WAG4458 {10165}; Novosadska Jara {10165}
ki2 Ki3 ki4: **v:** Chinese Spring {10165}; Eshima Shinriki {10165}; Ethiopian Landrace IL70 {10164}; Norin 26 {10165}
Ki2 ki3 ki4: **v:** Cadet {10165}; Iraqi Landrace IL171 {10165}; Rex {10165}
See Segregation distortion.

1.61. Polyphenol oxidase (PPO) activity

3,4 dihydroxyphenylalanine (L-DOPA) was used as a substrate in a non-destructive test of polyphenol oxidase activity in seeds. Chromosome 2D was shown to carry PPO gene(s) based on Langdon / Chinese Spring (2D) substitution lines and nullisomic-tetrasomic analysis {0342}. An orthologous series of genes affecting PPO activity in both common wheat and durum was proposed in {10149}. See also, Phenol colour reaction of kernels

QTL

Chara (mod high) / WW2449 (low): DH population: PPO activity Associated with *Xgwm294b-2A* (R^2=0.82), *Xwmc170-2A*, *Xgwm312-2A* and *Xwmc178-2A* (R^2>0.7) {10410}.

Chara (medium high PPO) / WW2449 (low PPO): one QTL was located on chromosome 2A. Two markers (one SNP, one CAPS) based on BQ161439 were polymorphic between the parents and showed linkage or allelism with PPO loci *Xtc1* and *XPPO-LDOPA*. – 0.6 cM – *XPPO-LDOPA/XPPO18/BQ161439* {10484}.

M6 (high activity)/ Opata 85 (low activity): A QTL on 2D, associated with *Xfba314-2D* was identified using the L-DOPA assay {0344}.

NY18 / Clark's Cream: Markers significantly associated with PPO activity were also detected on chromosomes 2A, 2B, 3B, 3D and 6B in the population {0344}. A multiplex of markers *PPO33* and *PPO16* was reliable for selecting genotypes with low PPO activity {10418}.

Zhongyou 9507 / CA9632: PPO18 explained 28-43% of the variation in PPO activity {10290}.

Tetraploid wheat
Jennah Khetifa (high) / Cham 1 (low): Associated with *Xgwm312-2AL* {10411}. STS marker PPO18 based on a polyphenol oxidase (*PPO*) gene (GenBank AY596268) was closely linked to SSR markers *Xgwm312-2AL* and *Xgwm294-2AL.*

Messopia / *T. dicoccoides*: RIL population: Associated with RFLP *Xutv1427-2A* {10411}.

1.62. Red grain colour

1.62.1 Red grain colour

Red colour is probably due to the polyphenol compounds phlobaphene or proanthocyanidin, synthesized through the flavanoid pathway. Himi & Noda {10107} provided evidence that the R genes were wheat forms of R2R3-type Myb-type transcription factors (*Tamyb10-3A, Tamyb10-3B, Tamyb10-3D*). Genetic evidence is provided in {10838}.
Red colour is dominant to white. At each locus, the white allele is assigned *a* and the red allele, *b*. White-grained *T. aestivum* and amber-grained *T. durum* wheats carry recessive *a* alleles at each locus. White-grained CS*7/Kenya Farmer and CS*6/Timstein are considered near-isogenic to CS with *R-D1b*.

R-1

R-A1 {548}. [*R2* {548}]. 3AL {1003}, {957}. **v:** Rio Blanco {10839}. **ma:** (Proximal) *Xpsr483(Cxp1)-3A* – 28 cM – *R-A1* – *Xpsr904-3A* {370} (distal); *Xwmc559-3A* – 16.3 cM – *R-A1/Xgwm155-3A* – 4.5 cM – *Xwmc153-3*^{a} {10839}.

R-A1a. **ma:** Based on *Tamyb10-A1* sequences this allele in CS lacks the ability to bind DNA due to deletion of the first half of the R2 repeat of the MYB domain {10838}; the *R-A1a* allele in Norin 17 has a 2.2 bp insertion in the second intron that appears to prevent transcription {10838}.

R-A1b. [*R2*]. *Tamyb10-A1* {10107}. **i:** Novosibirskaya 67*9/Solo {730}. **v:** Baron {370}; Diamant 2 {14}; Hustler {370}; Norin 10- Brevor, 14 {17}; Maris Widgeon {370}; Mercia; {370}; Motto {370}; Red Bobs {1003}; Sapphire {370}; Slejpner {370}; Talent {370}; Wembley {370}. **c:** GenBank AB191458.

R-B1 {548}. [*R3* {548}]. 3BL {1003}, {370}. **ma:** *Xbcd131-3B* – 5 cM – *R-B1* – 5 cM – *Xabc174-3B* {410}; *Xwmc29-3B* – 5 cM – *R-B1* – 5 cM – *Xbarc84-3B* {10280}; *Xgwm4010-3B* – 1.6 cM – *R-B1* – 4.6 cM – *Xgwm980-3B* {10839}.

R-B1a. **ma:** Based on the *Tamyb10-B1* sequence this allele in CS has a 19 bp deletion of the CCG repeat region causing a frameshift mutation {10838}.

R-B1b. [*R3*], *Tamyb-10-B1* {10107}. **i:** Novosibirskaya 67*9/k-28536 {730}. **v:** Canon {370}; Dollar {370}; Grana {370}; Supreme {370}. **c:** GenBank AB191459.

R-D1 {549}. [*R1* {548}]. 3DL {1291, 1293}. **v:** CS. **ma:** *Xbcd131-3D/R-D1* – 15 cM – *Xabc174-3D*{410}; *Xgwm2-3D* –.4 cM – *R-D1* – 3.2 cM – *Xgwm4306-3D* {10839}.

R-D1b. [*R1*], *Tamyb10-D1* {10107}. **i:** Novosibirskaya 67*9/CS {730}. **v:** Alexandria {370}; Apollo {370}; Axona {370}; CS {1293}; Dwarf A {370}; Fortress {370}; Jerico {370}; Longbow {370}; Luna {370}; Mardler {370}; Maris Huntsman {370}; Minaret {370}; NFC 75/93/27A; Rapier {370}; Pawnee {549}; Voyage {370}; Vuka {370}. **c:** GenBank AB19160.

R-N1 {1018}. 3N {1018}. **su:** CS/*Ae. Uniaristata* {1018}.

R-R1 {1011}. 6RL {1011}. **ad:** Holdfast/King II {1011}.

R-V1 {1518}. 3VL {1518}. **ad:** Creso/*D. villosum* {1518}.
A *3Ag* chromosome from decaploid *Ag. elongatum* carries an allele for red grain colour which was transferred to Agent and the majority of Sears' 3D-3Ae#1 translocations {939}.
Other studies have identified wheats carrying either one or two, unidentified *R-1* alleles: {056, 437, 549, 631, 654, 659, 1078, 1148, 1333, 1349, 1454, 370}.
See also Variegated Red Grain Colour.

R-A1b R-B1b R-D1a. [*R3, R2*]. **v:** Red Chief {548}; Avalon {370}; Bersee; Cappelle Desprez; Feuvert; Mission; Parade; Rendezvous; Yuri {370}.

R-A1b R-B1a R-D1b. [*R1, R2*]. **v:** Bezostaya 1 {370}; Brigand {370}; Broom {370}; Brock {370}; Kronjuwel {370}.

R-A1a R-B1b R-D1b. [*R3, R1*]. **v:** Fenman {370}; Kharkov {1003}; Norman {370}; Pastiche {370}; Riband {370}; Sperber {370}; Squadron {370}; Urban {370}.

R-A1b R-B1b R-D1b. [*R2, R1, R3*]. **v:** Bowie; Frondoso {1148}; Frontiera {437}; Hope {206, 204}; Japanese Bearded {1548}; Kanred {1078, 1426}; Lin Calel {1078}.

Functional markers based on *Tamyb10* sequences are given in {10838}.
A fourth QTL for red seed colour in hexaploid wheat was detected on chromosome 1B in a GWAS of U.S winter genotypes {11409}.

R-N1 {1018}. 3N {1018}. **su:** CS/*Ae. Uniaristata* {1018}.

R-R1 {1011}. 6RL {1011}. **ad:** Holdfast/King II {1011}.

R-V1 {1518}. 3VL {1518}. **ad:** Creso/*D. villosum* {1518}.

A *3Ag* chromosome from decaploid *Ag. elongatum* carries an allele for red grain colour which was transferred to Agent and the majority of Sears' 3D-3Ae#1 translocations {939}.
Other studies identified wheats carrying either one or two, unidentified *R-1* alleles: {056}, {437}, {549}, {631}, {654}, {659}, {1078}, {1148}, {1333}, {1349}, {1454}, {370}.
See also Variegated red grain colour.

1.61.2. Variegated red grain colour

Vg {498}. **v:** Line 10859 {498}.
vgvg genotypes in Line 10859 are variegated. The *Vg/vg* locus was independent of the single red gene locus in Line 10859. In a cross to Selkirk (*R-A1b, R-B1b, R-D1b) vgvg* was expressed only in plants with one *R* gene {498}. Variegated red pericarp was also studied in crosses of cv. Supreme. In this case, two red colour genes were present {0136}.

1.62. Reaction to black-point of grain

Black-point, a common grain defect, is a dark discoloration of the embryo region of the kernels. Whereas black-point is often attributed to infection by a number of fungi, the presence of such fungi may be a consequence of saprophytic colonization of affected tissues rather than the cause (see {10148} for references). The condition may be triggered by high humidity {0845}.

<u>QTL</u>

Batavia / Pelsart (resistant): DH population: Associated with markers *Xgwm319-2B* and *Xgwm048-4AS* {10494}.

Cascades / AUS1408: DH population: QTL from Cascades located in chromosomes 2D (5 cM from *Xgwm484-2D*, 18% of phenotypic variation), 2A (13%), and 7AS (12%) {10148}.

Sunco / Tasman: DH populaion: QTL located in chromosomes 2B (15% of phenotypic variation), 3D, 4A (from Sunco) and 1D, 5A and 7AS (from Tasman {10148}. The 2B gene was associated with the presence of *Sr36* {10148}.

1.63. Response to photoperiod

One-gene {1169} and two-gene {638}, {1137}, {1170} differences were reported in inheritance studies. In Chinese Spring/Hope substitution lines for chromosomes 1A, 4B and 6B greater sensitivity to short photoperiod was found, whereas substitutions of 3B and 7D were less sensitive {487}.

'a' alleles are dominant.
There is an orthologous gene series on the short arms of homoeologous group 2. The "a" alleles confer the insensitive response {0063}, the contrasting allele may be referred to as "b".

PPD-A1

Ppd-A1 {63}, {10612}. [*Ppd3* {1141}]. 2AL {1268}. **v:** C591 {0057}. **tv:** GS100, Kofa (1027-bp deletion in the promoter) {10612}; GS105, Svevo (1117-bp deletion in the promoter) {10612}; A survey of *Ppd-A1* allele is reported in {10915}. **ma:** *Xwmc177-2A – Ppd-A1*, 2.2 and 2.8 cM in GS100/GS101 and GS105/GS104, respectively{10612}.
GS100 and GS105 had different deletions relative to GS101 and GS104, respectively, and both were consistently a few days earlier flowering than their near-isogenic counterparts with *Ppd-A1b* {10612}.

Ppd-A1a {10612}. **tv:** GS100 {10612}; GS105 {10612}.
Ppd-A1a was present in 39% of Chinese landraces and 97% of improved cultivars {10622}. GS100 and GS105 had different deletions relative to GS101 and GS104, respectively and both were consistently a few days earlier flowering than their near-isogenic counterparts with *Ppd-A1b* {10612}

Ppd-A1b {10612}. **tv:** GS101 {10612}; GS104 {10612}.

PPD-B1

Ppd-B1. 2BS. **ma:** *Xwhs2002-2B/Xgwm257-2B – PpdB1 – Xgwm148-2B*. Actual linkage value varied between crosses {10129}; *Xpsr666-2B* – 1.2 cM – *Xpsr109-2B* – 4.4 cM – *Ppd-B1* – 4.8 cM – *Xpsr804-2B* ...Cent {0062}.
According to {10611} the *Ppd-B1* allele from Japanese wheats has a stronger effect than the allele from CS.

Ppd-B1a {0063}. [*Ppd2* {1566}]. **i:** H(C) = Haruhikari*5 / Fukuwasekomugi {10611}; H(D) = Haruhikari*/5/ Fukuwasekomugi *Ppd-D1a* {10611}. **s:** Cappelle-Desprez*/CS 2B {0058}. **v:** CS {1268}; Spica {557}; Timstein {1269}. **v2:** Fukuwasekomugi *Ppd-D1a* {10611}; Sharbati Sonora *Ppd-A1a* {887}. **c:** Varieties with the photoperiod insensitive allele have more than one *Ppd-B1* copy per chromosome 2B: two copies in Recital, three copies in Sonora 64, Timstein and C591, and 4 copies in Chinese Spring {10881}.

Ppd-B1b {10611, 10881}. **v:** Beaver {10881}; Cappelle-Desprez {10881}; Cheyenne {10881}; Norstar {10881}; Paragon {10881}; Renan {10881}. **v2:** Haruhikari *Ppd-D1b*{10611}. **c:** Varieties with the photoperiod sensitive allele have a single *Ppd-B1* copy {10881}.

PPD-D1

Ppd-D1. 2DS {1268}. Comparative mapping showed that *Ppd-D1* was co-linear with barley *Ppd-H1* - a member of the pseudo-response regulator (PRR) gene family {10466}.
Jagger amplified the 414 bp band {10466} associated with daylength sensitivity whereas 2174 amplified the 288 bp band associated with insensitivity {10722}.

Ppd-D1a {0063}. [*Ppd1* {1566}]. **i:** H(C) = Haruhikari*5/Fukuwasekomugi {10611}; Haruhikari*5/Saitama 27 {10611}; H(D) Haruhikari*5/Fukuwasekomugi *Ppd-B1a* {10611}. **s:** Capelle Desprez*/Ciano 2D {1598}; Capelle-Desprez*/Mara 2D {1598}; CS*/Ciano 2D *Ppd-B1a* {1268}. **v:** Akakomugi {1604}; Bezostaya 1 {1604}; Festival {10466}; Kavkaz; Mara {1604}; Orqual {10466}; Recital {10466}; Saitama 27 {10466}; Sava {1604}; Sideral {10466}; Soissons {10466}; Sonora 64 {1566}; Talent {10466}; Texel {10466}. **v2:** Sharbati Sonora *Ppd-D1a* {887}; Fukuwasekomugi *Ppd-D1a* {10611}. **ma:** Stocks with *Ppd-D1a* had a 2,089-bp deletion upstream of the coding region leading to mis-expression of the 2D PRR gene {10466}.

Ppd-A1b Ppd-B1b Ppd-D1b. **v:** Cheyenne {1141}; Diamont 1 {887}; Lancer {638}; Saratovskaya 29 {887}; Warrier {638}.
Two genes controlled photoperiod response in *T. turgidum* {788}.
Gene *Ppd-H2* on barley chromosome 2HS may be a member of the *Ppd-1* orthologous series {766}.

PPD-B2

Ppd-B2 {10628}. 7BS {10628}. **su:** Favorit (F26-70 7B) {10628}. **v:** F26-70 {0093}. **ma:** *Xgwm255-7B* – 20.7 cM – *Ppd-B2* – 4.4 cM – *Xgwm537-7B* {10628}.
This gene confers earlier flowering under long photoperiod conditions {10628}.

QTL

QPpd.zafu-4AL {11443}. 4AL {11443}. **s:** CASL 4AL {11443}. **tv:** *T. dicoccoides* TTD140 {11443}. **ma:** Flanked by *M576* and *Xwmc468-4AL* in a 1.2 cM region {11443}.
Other publications reporting *Ppd* genes/QTL in the same region are reviewed in {11443}.

Trident (early)/Molineux (late): In addition to an effect associated with chromosome 2B, three QTLs were designated as: *QPpd.agt-1AL* (*Xwmc304* – *Xgwm497* region), *QPpd.agt-7AS* (*Xbarc154* – *Xbarc108*) and *QPpd.agt-7BS* (*Xgwm46* – *Xgwm333*) {10382}. The QTL in chromosome 1A was possibly orthologous to *Ppd-H2* in barley.

QTL A QTL was detected in chromosome 4BS in Courtot/CS {0132}.

CONSTANS

Wheat genes *CONSTANS1* and *CONSTANS2* interact with *PPD1* to regulate photoperiodic response {11495}.

CONSTANS 1

CO-A1 {11495}. 7A. **v:** Chinese Spring. **c:** *TraesCS7A02G211300* {11295}. **tv:** Kronos {11495}. **c** GenBank MT043302 {11495}.

CO-B1 {11495}. 7B. **v:** Chinese Spring. **c** *TraesCS7B02G118300* {11495}. **tv:** Kronos {11495}. **c:** GenBank MT043303 {11495}

CO-D1 {11495}. 7D. **v:** Chinese Spring. **c:** *TraesCS7D02G212900* {11495}.

CONSTANS 2

CO-A2 {11495}. 6A. **v:** Chinese Spring. **c:** *TraesCS6A02G289400* {11495}. **tv:** Kronos. **c:** GenBank MT043304{11495}.

CO-B2 {11495}. 6B. **v:** Chinese Spring. **c:** *TraesCS6B02G319500* {11495}. **tv:** Kronos. **c:** GenBank MT043305 {11495}.

CO-D2 {11495}. 6D. **v:** Chinese Spring. **c:** *TraesCS6D02G269500* {11495}.

Triticum turgidum ssp. *durum* cv. Kronos: accession numbers MT043302 (*CO-A2*) and MT043305 (*CO-B2*) (11495}.

1.65. Response to salinity

1.65.1. K+/Na+ discrimination

Variation in K+/Na+ discrimination ratios correlates with salt tolerance, high ratios being indicative of higher tolerance.

KNA1

Kna1 {290}. 4DL {290}. 4BS.4BL-4DL {283}. 4BS.4BL-4DL-4BL {849}. **v:** Hexaploid wheats {290}. **tv,su:** Langdon 4D(4B) {283}. **tv,tr:** Various lines {290}; Selection 3*5-4 {849}. **ma:** *Kna1* was completely linked with *Xabc305-4B*, *Xabc305-4D*, *Xbcd402-4B*, *Xbcd402-4D*, *Xpsr375-4D*, *Xpsr567-4B*, *Xpsr567-4D*, *Xwg199-4B* and *Xwg199-4D* in recombined *T. turgidum* 4B and *T. aestivum* 4D chromosomes {849}, {283}.

Lophopyrum elongatum chromosome arms 1ES, 7ES, and 7EL enhance K^+/Na^+ selectivity in wheat under

salt stress {0065}.
Kna1 is a possible orthologue of *Nax2* and is the Na+ transporter *TaHKT1;5-D* {10455}.

1.65.2. Salt tolerance

QTL

Opata 85 / 7984: 77 QTLs effective at different growth stages were mapped to 16 chromosomes {10384}.

1.65.3. Sodium exclusion

NAX1

Nax1 {10452}. 2AL {10452}. **itv:** Tamaroi*6/Line 149 = P06306 {10453}. **tv:** Line 149 *Nax2* = 126775b {10452}. **dv:** AUS 90382 *Nax2* = C68.101 {10455} = JIC *T. aegilopoides* no. 3. **ma:** *Nax1* was mapped as a QTL in the region *Xpsr102-2A* – 5.4 cM – *Xwmc170-2A* – 0.9 cM – *Xksud22-2A/Xksu16-2A* – 0.8 cM – *Xgwm312-2A* with R^2 = 0.38 in Tamaroi/Line 149 {10452}; *TmHKT7-A2* was identified as a putative candidate Na^+ transporter {10454}.
Nax1 promotes withdrawal of Na^+ from xylem in leaf bases and roots {10453}.

NAX2

Nax2 {10453}. 5AL {10455}. **itv:** Tamaroi*6/Line 149 = P05603 {10453}. **tv:** Line 149 *Nax1* = 126775b {10452, 10453}. **dv:** AUS 90382 *Nax1* = C68.101 {10455} = JIC *T. aegilopoides* no. 3. **ma:** Co-segregation with *Xgwm291-5A/Xgwm140-5A/Xgpw2181-5A* {10455}; *TmHKT1;5-A* was identified as a candidate for *Nax2* {10455}.
Nax2 is a likely orthologue of *Kna1* {10455}.

QTL

Berkut / Krichauff: QTL for Na^+ exclusion and seedling biomass under salt stress were detected in chromosomes 2A (*Nax1* region) and 6A (*Xcfd080-Xbarc171-6A*) {10917}.

1.66. Response to tissue culture

Qtcr.ipk-2B.1 {84}. [*Tcr-B1* {84}]. **ma:** Weakly associated with *Xpsr102-2B* {84}.

Qtcr.ipk-2B.2 {84}. [*Tcr-B2* {84}]. **ma:** Closely linked and distal to *Ppd-B1* {84}.

Qtcr:ipk-2B.3 {84}. [*Tcr-B3* {84}]. **ma:** Linked with*Yr7/Sr9g* {84}.

QGpp.kvl-2A {0253}. 2AL {0253}. **v: Ciano / Walter** DH mapping population. The green plant percentage was contributed by Ciano {0253}. **ma:** Associated with *Xpsp3045-2A* {0253}.

QGpp.kvl-2B.1 {0253}. 2BL {0253}. **v: Ciano / Walter** DH mapping population. The green plant percentage was contributed by Ciano {0253}. **ma:** Associated with *Xgwm388-2B* {0253}.

QGpp.kvl-2B.2 {253}. 2BL {0253}. **v: Ciano / Walter** DH mapping population. The green plant percentage was contributed by Ciano {0253}. **ma:** Associated with AFLP markers {0253}.

1.67. Response to vernalization

The requirement for vernalization is particularly important for winter cereals to avoid cold injury of the sensitive floral organs during the winter. In wheat, vernalization requirement is controlled by four major genes designated *VRN-1, VRN-2, VRN-3,* and *VRN-4*. The first three genes were identified using map based cloning aproaches {10014, 10299, 10421}. The *VRN-1* gene encodes a MADS-box transcription factor closely related to the Arabidopsis *AP1/FRUITFULL* family, responsible for the transition of the shoot apical meristem from the vegetative to reproductive stage in wheat {10014}.
Deletions in the promoter (*Vrn-A1a, Vrn-A1b*) {10198} or the first intron of this gene (*Vrn-A1c, Vrn-B1a, Vrn-D1a*) {10202} are the most common sources of spring growth habit among landraces and commercial cultivars of polyploid wheat worldwide {10617, 10695, 10709}. The *VRN-2* locus produces two linked and related proteins designated ZCCT1 and ZCCT2, characterized by the presence of a putative zinc finger and a CCT domain {10299}.
Deletions and mutations involving both the ZCCT1 and ZCCT2 genes are frequent in diploid wheat and are associated with recessive alleles for spring growth habit {10299}.
Among the cultivated tetraploid and hexaploid wheat species the *Vrn-B2* gene is generally functional whereas the *Vrn-A2* gene is not {10710}. At least one functional copy of *Vrn-2* combined with homozygous recessive alleles at all three *Vrn-1* loci is required to confer winter growth habit in hexaploid wheat. The *VRN-B3* locus (formerly known as *Vrn-5* or *Vrn-B4*) is homologous to the Arabidopsis *FT* gene {10421}. This dominant allele, found in the variety Hope, is associated with the insertion of a transposable element in the *Vrn-B3* promoter. Natural variation at the *VRN-A3* and *VRN-D3* loci has been also described in hexaploid wheat {10533}. *VRN-3* promotes the transcription of *Vrn-1* and accelerates flowering {10421}. The *Vrn-D4* allele for early flowering was originally identified in the Australian cultivar Gabo {671} and was backcrossed into Triple Dirk to develop the isogenic line TDF {1172}. This locus was mapped on the centromeric region of chromosome 5D between markers *Xcfd78* and *Xbarc205* {10711}. Natural variation for flowering time at the centrometric region of homoeologous group5 chromosomes has been found, so far, only in the D genome. Incorrect TDF seed stocks generated initial confusion about the existence of *Vrn-D4* but molecular markers are now available to separate the incorrect stocks {10711}. Using genetic analyses, Iwaki et al. {10003} found the *Vrn-D4* allele for spring growth habit occurred with a higher frequency in India and neighboring regions. The *VRN-D4* locus in TDF includes a duplication of a 290 kb region from chromosome arm 5AL inserted into the proximal region of chromosome arm 5DS. This translocated segment includes a functional copy of *VRN-A1* that carries distinctive mutations in its coding and regulatory regions {11123}.

VRN-1 {1398}. Synonymous with *TaVRT-1* {10019}
Orthologous series in long arms of chromosomes of homoeologous group 5. *VRN-1* is a MADS-box gene similar to Arabidopsis *APETALA1* {10014}. Spring types are associated with mutations in the promoter

or the first intron {10014, 10198, 10202, 10288}. Reduction of *VRN-1* transcripts in transgenic hexaploid spring wheat delays flowering {10300}.

VRN-A1

Dominant spring habit alleles at the *Vrn-A1* locus

Vrn-A1a {1398}. [*Vrn1* {1172}, *Sk* {2}]. 5AL {775}, {883}. **i:** Triple Dirk D (GenBank AY616458 & AY616459). **s:** Kharkov 22MC*/Rescue 5A {358}; Winalta*8/Rescue 5A {876}; Rescue*/Cadet 5A *Vrn-D1a Vrn-B1a* {1221}. **v:** Cadet {1221}; Conley {1171}; Diamant II {885}; Falcon {1172}; Koga II {1611}; Kolben {1, 1171, 1172}; Konosu 25 {460}; Marquis {1}; Reward {1171}; Saitama 27 {460}; Saratov 29 {883}; Saratovskaya 29 {885}; Saratovskaya 210 {883}; Shabati Sonora {885}; Thatcher {1171}; WW15 {1172}. **v2:** Shortandinka *Vrn-B1a* {885}; Takari *Vrn-B1a* {253}; Triple Dirk *Vrn-B1a* {1173}; Hope *Vrn-B4a* {1424}. **ma:** *Vrn-A1* – 7.5 cM – *Xwg644-5A* {726}; Located mid chromosome 5A cosegregating with *Xcdo504-5A*, *Xwg644-5A* and *Xpsr426-5A* {419}; *Vrn-A1* – 0.8 cM – *Xbcd450-5A/Xrz395-5A* – 4.2 cM – *Xpsr426-5A* {9903}. *Xgwm271-5A* – 6.5 cM – *Vrn-A1* – *Xbarc232-5A*{10880};
Cultivars possessing *Vrn-A1a* are insensitive to vernalisation. *Vrn-A1a* is epistatic to other genes. According to {1221}, *Vrn-A1a* is not always fully dominant and not always epistatic. Kuspira *et al.* {745} attributed single gene variation in *T. monococcum* to the *Vrn-A1a* locus. Multiple recessive alleles were suggested {745}. *Vrn-A*^{m}1 was mapped on the long arm of chromosome 5A^{m} closely linked to the same RFLP markers as *Vrn-A1* {279}. *Vrn-A*^{m}1 was mapped to the *Xcdo504-5A - Xpsr426-5A* region {0312}. In the opinion of the curators this location may not be correct
Multiple alleles also were reported in {9930}, and the dominant allele of Novosibirskaya 67 and the weaker dominant allele of Pirotrix 28 were designated *Vrn1a* and *Vrn1b*, respectively.

Vrn-A1b {10198}. **v:** Marquis PI94548 (GenBank AY616461) {10198}. **tv:** *T. turgidum* var. *durum* ST36 {10198}.

Vrn-A1c {10198}. This allele has a promoter similar to recessive *vrn-A1a* from Triple Dirk C {10198} and a large deletion in intron 1 {10202}. **v:** IL162 {10198}; IL369 {10198} has a 5.5 kb deletion in *Vrn-A1* intron 1 {10202}. **tv:** Aldura PI 486150 {10202}; Leeds CI 13796 {10202}; Mexicali 75 PI 433760 {10202}; Minos CI 15161 {10202}. Most durum genotypes have a 7.2 kb deletion in intron 1 {10202}.

Vrn-A1d {10198}. **tv:** *T. turgidum* var. *dicoccoides* Amrim 34 {10198}; FA15 (GenBank AY616462) {10198}; Iraq 8736 {10198}; Tabigha 15 {10198}.

Vrn-A1e {10198}. **tv:** *T. turgidum* var. *dicoccum* ST27 = Vernal (GenBank AY616463) {10198}.

vrn-A1. Copy number variation for *vrn-A1* was detected in IL369 (2 copies) {10202}, Malacca (2 copies) and Hereward (3 copies). Higher copy number was associated with later flowering or with increasing requirement for vernalization (i.e. longer exposure to cold is needed to achieve full vernalization) {10881}.

vrn-A1a{10198}. **v:** Claire {10880}; Triple Dirk C {10880}. **v2:** Chinese Spring *Vrn-D1a* {10880}. **c:** GenBank AY616455 {10198}.

vrn-A1b {10881}. **v:** IL369 {10202}; Malacca {10881}. **c:** GenBank JF965396 {10881}.
This allele has two copies of the gene, possibly arranged in tandem although the physical structure is unknown. Both copies are distinguished from Chinese Spring *vrn-A1a* by a SNP in exon 7 (T in Malacca, C in Chinese Spring). One copy also has a SNP in exon 4 (T in Malacca, C in Chinese Spring). Sequenced cDNAs from Malacca show that both copies are expressed {10881}.

vrn-A1c {10881}. **v:** Hereward {10881}. **c:** GenBank JF965397 {10881}.
A comparison of Claire (*vrn-A1a*), Malacca (*vrn-A1b)* and Hereward (*vrn-A1c*) indicated that increasing gene copy number is associated with lateness {10881}. Two winter alleles were identified based on an SNP in exon 4 {10656}.

vrn-A1v {10916}. **v:** Don Ernesto INTA {10916}; Jagger {10916}; Norin 61 {10916}; Opal {10916}.

vrn-A1w {10916}. **v:** Bezostaya {10916}; Bavicora M 92 {10916}; Kavkaz {10916}; Gennson 81 {10916}; Seri M 82 {10916}; Wichita {10916}.

A polymorphism between Jagger and 2174 was associated with *vrn-A1a*. A point mutation was present in exon 4 {10695}; 17 of 19 genotypes surveyed, including Jagalene, carried the 2174 mutation and only Jagger and Overley carried the Jagger allele {10695}.

All accessions of *T. aestivum* ssp. *petropavlovsky* shared the *Vrn-A1a* sequence (*Vrn-A1L*) of Langdon (7,222 bp deletion 391-7,612 bp) and some other tetraploid wheat accessions {11668}.

VRN-B1

Vrn-B1. **ma:** *Tsn1* – 14.8 cM – *Vrn-B1* – 0.7 cM – *Xwmc75-5B* {10880}.

vrn-B1. **c:** GenBank AY747604.1{10695}.

Vrn-B1a {1398}. [*Vrn2*a = *Vrn2* {920}, {921}, *Vrn2* {1172}, *Vrn4* {1173},*Vrn2b* = *Vrn2* {920} {921}, *Ss* {2}]. 5BL {885}. 5B {885}, {920}, {921}; 5BL or 7BL {635}, {282}. 5D {635}. **i:** Ank-18 {920}, {921}; Triple Dirk B {1172}. **s:** Diamant 1*8 / Mironovskaya 5A {920}; Diamant 1*8 / Skorospelka 35 5A {920}; Rescue* / Cadet 5A *Vrn-A1 Vrn-D1a* {885}; Saratovskaya 29*8 / Mironovskaya 808 5A {920}; Saratovskaya 29*8 / Odesskaya 51 5A {920}. **v:** Bersee {557}; Brown Schlanstedt {1}, {2}, {1171}, {1172}; Cadet {1221}; Festiguay {1172}; Magali; Mara {1611}; Milturum 321 {920} {885}; Milturum 885 {920, 885}; Noe {2}; Pyrothrix 28 {920}; Spica {557}; *T. spelta* var. *duhamelianum* KT19-1 {10057}; Ulyanovka 9 {920}. **v2:** Borsum *Vrn1-A1a* {1}; Dala *Vrn1-A1a* {1}; Diamant 1 *Vrn1* {1}, {920}; Gabo *Vrn4* {1172}; Halland *Vrn-A1a* {1}; Harukikari *Vrn-A1a* {883}; Rubin *Vrn-A1a* {1}; Saratovskaya 29 *Vrn-A1a* {920}; Shortandinka *Vrn-A1a* {1221}; Triple Dirk *Vrn-A1a* {1173}. **ma:** A dCAPS marker derived from *Xwg644-5B* was 1.7 cM from *Vrn-B1* {10006}; *Vrn-B1a* –

1.6 cM – *Xwg644-5B* – 2.5 cM – *Xgwm408-5B* {10004}; Closely linked to *Xgwm408-5B* in Diamant I*/Mironovskaya 808 5A // Bezostaya 1 {10007}; A close association of *Vrn-B1* with *Xcdo1326-5B* was reported in {10057}. When mapped as a QTL *Vrn-B1* showed closest association with *Xgwm408-5B* {10007}. **c:** GenBank AY74603.1 {10695}.
All common wheat genotypes carrying *Vrn-B1a* studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk B, Bersee, Festiguay, Mara, Milturum, Noe, Spica) {10202}.
Two variants of *Vrn-B1a* were distinguished in {920}, {921}. Carriers of an earlier designated *Vrn2b* (characterized by Diamant 1*8/Skorospelka 35 5A) showed accelerated flowering after 15 and 30 days of vernalization, whereas carriers of *Vrn-2a,* (characterized by Ank-18 and Saratovskaya 29*8 /Mironovskaya 808 5A) did not respond to these periods of vernalization. This distinction was not made in the above list.

Vrn-B1b {10695}. **v:** Alpowa {10695}; Ciano 67 {10991}; Polo {10991}; Yaktana 54 {10991}. **c:** GenBank FJ766015. Relative to *Vrn-B1a* (Triple Dirk B), *Vrn-b1b* has a G-C SNP at position 1656 and a 36 bp deletion at 1661-1696 {10695}.

Vrn-B1c {10880}. **tv:** *T. turgidum* ssp. *carthlicum* PI 94749 {10880}. Much more common in durum cultivars from Russia and Ukraine than from Europe {11771}. **c:** GenBank JN817430 contains a 5,463 retrotransposon insertion in the 5' UTR region {10880}.

Vrn-B1d [{11520}]. *Vrn-B1c* {11520}. **v:** Paragon and 24 others {11521}; Saratovskaya 29 and 5 others {11521}. **c:** Carries a 0.8 kb deletion and 0.4 kb duplication in intron 1 relative to *vrn-B1* {11520, 11521}.

Vrn-B1e [{11522}]. *Vrn-B1d* {11522}. **v:** Hongchunmai {11522} **c:** Differs from *vrn-B1* by 2 deletions, a SNP and TTTT to ACAA change in in intron 1 {11522}; GenBank HQ130482 {11523}; HQ593668 {11521}.

Vrn-B1f {11523}. **v:** Barta {11523}. **c:** Has a partially duplicated 837 bp sequence in intron 1 {11523}.

VRN-D1

Vrn-D1 {1398}. *Vrn3* {1172} 5DL {775, 883}.
Vrn-D1a, Vrn-d1b and *Vrn-D1* were present in 27.3, 20.6 and 52.1% of 689 Chinese wheat accessions {11072}.

Vrn-D1a. **i:** Triple Dirk E {1172}. **s:** Rescue* / Cadet 5A *Vrn-A1a* {1221}. **v:** Chinese Spring {1172}; Loro {1172}; Norin 61 {460}; Shinchunaga {460}; Shirasagi Komugi {460}; Ushio Komugi {460}. **v2:** Rescue *Vrn-B1a* {1221}.
All the common wheat genotypes carrying *Vrn-D1a* studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk E, Chinese Spring, Norin 61, Shinchunaga, Shirasagi Komugi, Ushio Komugi) {10202}.

Vrn-D1b. **v:** Additional Chinese germplasm{11072}.

A *Vrn-D1* variant named *Vrn-D1s* contained a 844 bp TE insertion in the first intron of the wild type *vrn-D1* allele {11628}. GenBank KF800714. Identified in three *T. spelta* and one *T. compactum* accessions. **v:** *T. aestivum* ssp. *spelta* PI 348700 {11628}.

Stock: Genotype: Vernalization Response
Triple Dirk, Kolben: *Vrn-A1a Vrn-B1b Vrn-D1b*: No
Triple Dirk B, Festiguay: *Vrn-A1b Vrn-B1a Vrn-D1b*: Yes
Gabo *Vrn-A1b Vrn-B1a Vrn-D1b*: Yes
Triple Dirk E, Chinese Spring:*Vrn-A1b Vrn-B1b Vrn-D1a*: Yes
Triple Dirk F, *Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5a:* Yes
Triple Dirk C, *Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5b*: Yes, winter type.

Vrn1 {10014}. Spring type. d**v:** G2528 {10014}.

vrn1 {10014}. Winter type. d**v:** DV92 {10014}; G1777 {10014}; G3116 {10014}. **c:** *Vrn1* was completely linked to MADS-box genes *AP1* and *AGLG1*. *AP1* was considered a better candidate than *AGLG1* and differences between winter and spring genotypes appeared to be related to differences in the promoter region of *AP1* {10014}; The involvement of *AP1* in vernalization response conditioned by *Vrn-1* was also reported in {10019}.

VRN-1 genotypes in Pacific Northwest USA wheats are listed in {10695}.

VRN-2 {1398}.

Orthologous series in chromosomes of homoeologous group 4. *Vrn-A*^{m}2 was located in *T. monococcum* {279} on chromosome 5A^{m} on the 4A^{m} translocated region. *Vrn-A*^{m}2 was mapped to the distally located *Xwg114-5A - Xwec87-5A* region {0312}. *Vrn-H2* (*sh*/*sgh1*) occurs in barley chromosome 4H {1455} and is probably orthologous to *Vrn-A*^{m}2 based on comparative maps {279, 767}. *Vrn-2* is a zinc-finger/CCT domain transcription factor (*ZCCT1*) {10299}, and repressor of flowering down-regulated by vernalization and short days {10301}. Reduction of *Vrn-2* transcripts in transgenic hexaploid winter wheat accelerates flowering {10299}. A triple *Vrn2* mutant (PI 676269), synthetic *vrn2-null*) is available in hexaploid wheat combining the non-functional *vrn-A2* allele present in most polyploid wheats with a *Vrn-B2* deletion from tetraploid wheat, and a non-functional *vrn-D2* allele from *Ae. tauschii* {11124}.

VRN-A2

Vrn-A2a{279}. Winter habit, dominant in diploid wheat {279}. **dv:** G1777 {279}; G3116 {279}.

Vrn-A2b {279}. Spring habit, recessive in diploid wheat. **dv:** DV92 {279}; PI 355517 {10299}; PI 345242 {10299}; PI 352475 {10299}; PI 277137 {10299}.
Contains a non-functional mutation in the CCT domain {10299}.

Vrn-A2c {10299}. Spring habit, recessive in diploid wheat. **dv:** PI 352484 {10299}; PI 323437 {10299}; PI 286068 {10299}; PI 591871 {10299}; PI 542474 {10299}; PI 428175 {10299}; PI 237659 {10299}; PI 221329 {10299}; PI 225164 {10299}; PI 377662 {10299}; PI 377648 {10299};

PI 362610 {10299}.
Complete deletion of the *ZCCT1* gene {10299}.

VRN-B2

Vrn-B2. 4BL {11163}. A study of winter wheats 2174 and Jagger showed that 2174 has a tandem repeat of *Vrn-B2* whereas Jagger has a deletion of this gene {11163}. Identical apparently functional sequences of *Vrn-B2* were found in contig sequences of Chinese Spring obtained from chromosomes 4BS, 2BS and 5DL {11163}.

Vrn-D2. 4DL{11163}.

VRN3 **[***Vrn3* {1398}]. Orthologous series in chromosomes of homoeologous group 1 predicted from orthology with *Vrn-H3* (*Sh3*) in barley chromosome 1H {1455,1316}. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization {773}.

In both wheat and barley *VRN-3* is completely linked with a flowering promoter gene homologous to Arabidopsis *FLOWERING LOCUS (FT)* {10421}. Polymorphisms in the A and D genome copies of *TaFT* are associated with variation of earliness components in hexaploid wheat {10533}.

Vrn-A3**.** 7AS.

An earlier variant of *T. dicoccum* line TN28 was caused by a novel allele. Line TN26 lacked a 7 bp insertion, including a cis-element GATA box, in the *Vrn-A3* promoter region {11370}.

VRN-B3

Vrn-B3 {10421}. [*Vrn-4B* {279}, *Vrn5, eHi* {769}, {779}, {771}]. 7BS {769}, {768}, {771}. **s:** CS(Hope 7B) *Vrn-D1a* {768}. **v2:** Hope *Vrn-A1a* {1424}. **tv:** Very common in durum cultivars from Russia and Ukraine {11771}. **ma:** *Vrn-B3* is completely linked to *TaFT* and 1 cM distal to *Xabc158-7B* on the region of 7BS proximal to the translocation with homoeologous group 5 {10421}.
The dominant *Vrn-B3* allele in Hope has a retrotransposon insertion in the *TaFT* promoter (GenBank DQ890165) {10421}. Transformation of winter wheat Jagger with the dominant *Vrn-B3* significantly accelerated flowering {10421}. Different Hope seed sources were heterogeneous for this insertion {10421}. The retrotransposon insertion in the *TaFT* promoter is present in the CS (Hope 7B) {10421}.

vrn-B3. **v:** Chinese Spring *Vrn-D1* (GenBank DQ890162) {10421}.
TaFT are associated with variation of earliness components in hexaploid wheat {10533}.

Vrn-H3 {10421}. [*Sh3*]. **ma:** Completely linked to *HvFT* and 1 cM distal to *Xabc158* on 7HS. Originally mapped incorrectly on 1H based on loose linkage {1455, 1316}.

VRN4

Vrn4 {279}. [*Vrn5* {769}, {771}, *Vrn-D5* {10004}]. 5DL {10004}. 5D {10002}. **i:** Triple Dirk F {10711}. **v:** **v2:** CS (Hope 7B) *VrnD1a* {768}; Gabo *Vrn-B1a* {1172}; IL47/*Vrn-A1a* {10005}; Common in *T. sphaerococcum* accessions {11123}. **bin:** Centromeric region. **ma:** *Xgdm3-5D* – 11.5 & 4.5 cM – *Vrn4* {10004}; Located in a 1.8 cM interval flanked by markers *Xcfd78-5D* and *Xbarc205-5D* {10711}. **c:** *Vrn4* is located in a translocated segment from chromosome 5A containing a modified copy of *Vrn-A1* {11123}.
Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn4*. Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D. References to additional studies are given in {1424}.
Vrn4 was mapped on the centromeric region of 5D. Incorrect TDF seed stocks generated confusion about *Vrn-D4* existence {10711}. Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn4*. Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D.

VRN5

VRN-D5

Vrn-D5a {10004}. [*Vrn4* {1172}, *Vrn-D5* {10004}]. 5D {10002}. 5DL {10004}. **i:** Triple Dirk F {1172}. **v2:** Gabo *Vrn-B1a* {1172}; IL47 *Vrn-A1a* {10005}. **ma:** *Xgdm3-5D* – 11.5 & 4.5 cM – *Vrn-D5a* {10004}.
Eight landraces with only *Vrn-D5a* were detected in {10003}; others combined *Vrn-D5a* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn-D5a*. Goncharov {10108} confirmed the existence of *Vrn-D5a* but failed to confirm its location on chromosome 5D. References to additional studies are given in {1424}.

Three genes up-regulated by vernalization were cloned from *T. monococcum* {10531}. These were VIN3-like genes similar to Arabidopsis VIN3.

Vil-1 {10531}. GenBank DQ886919 {10531}. **ma:** *T. monococcum* chromosome $5A^m$ {10531}.

Vil-2 {10531}. GenBank DQ886917 {10531}. **ma:** *T. monococcum* chromosome $6A^m$ {10531}.

Vil-3 {10531}. GenBank DQ886918 {10531}. **ma:** *T. monococcum* chromosome $1A^m$ {10531}.

A QTL analysis of **Courtot / CS** is reported in {0132}.

A QTL on chromosome 5BL was linked to *Xgwm604-5B* (this QTL explained 11% of the variance in flowering time) {10075}

Allelic variations at the *Vrn-1* and *Vrn-B3* loci in Chinese wheat cultivars are summarized in {10617}. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization {773}.

Stem-elongation in winter wheat: In regions where wheat is used as a dual purpose crop for grazing and grain production a relatively long vegetative phase is required to maximize the vegetative tissue and to delay the stem elongation phase. Variation in this attribute occurs among winter wheats such as Jagger (early stem elongation) and 2174 (late elongation).
In a **Jagger / 2174** RIL population, QTL for stem elongation included *Qste.ocs-5A* (associated with the *Vrn-A1* locus), *Qste.ocs-1BL, Qste.ocs-2D* (associated with the *Ppd-D1* locus) and *Qste.ocs-6A* {1010}. In 2007 the respective R^2 values were 0.289, 0.155, 0.067 and 0.058. Jagger alleles on chromosome 5A, 1B and 6A promoted stem elongation whereas the allele on chromosome 2D had a delaying effect {10722}.

1.68. Restorers for cytoplasmic male sterility

1.68.1. Restorers for *T. timopheevi* cytoplasm

RF1

Rf1 {823}. 1A {1619}, {873}, 1224}. 1AS {868}. **v:** L22 {868}; (*T. timopheevii / Aegilops squarrosa)* // 3*Dirk {1619}. **v2:** *T. timopheevii* / 3*Marquis *Rf2* {823}; R113 *Rf4* {873}.
The second gene referred to as *Rf4*{1619} in the last stock was located in chromosome 7D, but its relationship to *Rf2* in {823} was unknown.

RF2

Rf2 {823}. 7D {871}. **v:** *T. timopheevii* / 3*Marquis *Rf1* {823}.

RF3

Rf3 {1453}. 1BS. 1B {1453}. **v:** R18 {10222}; R9034 {10222}; *T. spelta* var. *duhamelianum* {1453}. **v2:** Primepi *Rf7* {11476}. **ma:** *Xcdo388-1B* – 1.2 cM – *Xabc156-1B*{9934}; RFLP markers *Xcdo442-1B* and *Xbcd249-1B* were found to be associated with *Rf3* on 1BS{860}; Mapped as a QTL in the region *Xbarc207-1BS – Xgwm131-1BL – Xbarc61-1BL* in crosses R18/ND36 and R9034/ND36 {10222}; *Xbarc128-1Bs* – 5.3 cM – *IWB14060* – 2.0 cM – *Rf3/IWB72107/IWB73447* – 14.5 cM – *Xwmc406-1B* {11476}.

RF4

Rf4 {1619}. [*Rf2* {1619}]. 1BS {868}. 6B {1619}, {873}. **v:** L3 {868}; (*T. timopheevii/Aegilops squarrosa*) / 3^*Canthatch *Rf5* {1619}; R113 *Rf1* {873}.

RH5

Rf5 {1619}. [*Rf3* {1619}]. 6D {1619}. **v:** (*T. timopheevii / Aegilops squarrosa*) / 3^*Canthatch *Rf4* {1619}.

RF6

Rf6 {865}, {859}. 6BS [T6BL.6BS-6U] {865}. 6AS [T6AL.6AS-6U] {865}. **tr:** Line 2114 {865}; Lines 040-5; 061-1 {865}; 061-4 {865}.
Genes *Rfc3* in chromosome 6RL and *Rfc4* in chromosome 4RL were reported in {225}. Novel *Rf* genes were identified on 5AL linked to *Xcdo786-5A* and *XksuH1-5A* {860}.

RF7

Rf7 {11473}. [*Rf6* {11473}]. 5DS {11473}. **v2:** Primepi *Rf3* {11474}.

RF8

Rf8 **{**11474}. 2DS {11474}. **v:** PWR4099 {11474}. **ma:** *Xwmc503-2D* – 3.3 cM – *Rf8* – 5.8 cM – *Xgwm296-2D* – 0.9 cM – *Xwmc112-2D* {11474}.

RF9

Rf9 {11475}. 6AS {11475}. **v:** Gerek 79 {11475}. **ma:** *IWB72413-6A* – 4.3 cM – *Rf9* – 4.7 cM – *IWB1550*-6A {11475}.

Minor restorer effects were associated with *Xbarc330-5A* in R18 and *Xgdm130-7D* in R9034 {10222}. The relationships of these QTL with previously located restorers in chromosomes 5A {860} and 7D (*Rf2*) are unknown.

1.68.2. Restorers for *Aegilops longissima* cytoplasm

Vi {867}. 1B {870}. 1BS {27}. **v:** *T. turgidum* {867}.
Probably derived from a cv. Selkirk (*T. aestivum*) line with *Ae. cylindrica* cytoplasm {867}.

1.68.3. Restorers for photoperiod-sensitive *Aegilops crassa* cytoplasm

Morai & Tsunewaki {1047} described photoperiod sensitive CMS caused by *Ae. crassa* cytoplasm in wheat cv. Norin 26. Almost complete sterility occurred when plants were grown in photoperiods of 15 h or longer.

Rfd1 {1047}. 7BL {1047}. **v:** Chinese Spring {1047}.
A different system of restoration occurs in cv. Norin 61 where at least four chromosomes, 4A, 1D, 3D and 5D, appear to be involved {1046}. Several Japanese wheats carry a similar or equally effective gene combination {0335}.

1.68.4. Restorers for temperature-sensitive *Aegilops kotchyi* cytoplasm

Two recessive genes for temperature-sensitive sterility as follows.

rfv $_1$ ^{sp} {11151}. 1BS {11151}. **v2:** MS line KTP116A *rfv* $_2$ {11151}. **ma:** *Xgwm413-1B* – 8.9 cM – *rfv* $_1$ ^{sp} – 12 cM – *Xgwm11-1B* {11151}.

rfv $_2$ {11151}. 2A {11151}. **v:** MS line KTP116A *rfv* $_1$ ^{sp} {11151}. **ma:** *Xwmc474-2A* – 23.9 cM – *rfv* $_2$ – 13.7 cM – *Xwmc644-2A* {11151}.

1.68.5. Restorers for multi-species cytoplasm

Restorer of *Ae. kotschyi*, *Ae. uniaristata* and *Ae. mutica* cytoplasmic male sterility.

Rf ^{multi} {11477}. 1BS {11477}. **v:** All common wheat genotypes except *T. spelta* var. *duhamelianum* {11477}. **ma:** All common wheat genotypes except *T. spelta* var. *duhamelianum* {11477}.

rf ^{multi}**.** **v:** *T. spelta* var. *duhamelianum* {11477}.

Sterility in the same plasmons is also found in lines with the 1BL.1RS translocation. Hohn & Lukaszewski {11478} produced a chromosome $1B_{1:6}$ translocation with a short rye insert replacing the *Rf* ^{multi} region (*rf* ^{multi} equivalent) causing partial sterility that can be restored by most common wheat genotypes.

1.69. Ribosomal RNA

The *5S-Rrna-1* loci were physically mapped in 1AS, 1BS, and 1DS and the *5S-Rrna-2* loci were physically mapped in 5AS, 5BS and 5DS of Chinese Spring using deletion lines {1043}.
Table 1 in {276} lists the chromosome or chromosome arm locations of rRNA loci in 12 Triticeae species.

5S rRNA genes

Within the Triticeae there are basically two sets of 5S rRNA loci. One set, identified by repetitive units 320-468 bp in length, is located on group 1 chromosomes. The other set, identified by repetitive units 469-500 bp in length, is on group 5 chromosomes. Within species the repetitive units at a locus are extremely uniform in size and sequence. They remain stable in foreign genetic backgrounds.

5S-Rrna-A1. [*5SDna-A1* {295}]. 1AS {658, 295}. **v:** CS {1043}.

5S-Rrna-B1. [*5SDna-B1* {295}]. 1BS {39}, {295}. **dv:** *T. monococcum*. **ma:** A PCR marker specific *5S-Rrna-B1* was developed {9974}.

5S-Rrna-D1. [*5SDna-D1* {295}]. 1DS {295}. 1D {295}, {758}. **v:** CS {295}, {758}. **dv:** *Ae. tauschii* {758}. **ma:** A PCR marker specific for *5S-Rrna-D1* was developed in {9974}.

5S-Rrna-E1. [*5SDna-E1* {960}]. 1E {1290}. **dv:** *L. elongatum*.

5S-Rrna-R1. [*5SDna-R1* {1206}]. 1RS {1206}, {39}. **al:** *S. cereale*. **ma:** A PCR marker specific for *5S-Rrna-R1* was developed in {9974}.

5S-Rrna-Sc1. [*5SDna-Sc1* {960}]. 1S^c {1290}. **al:** *Elymus ciliaris*.

5S-Rrna-S^{t}1. [*5SDna-S*^{t}*1* {960}]. 1S^t {1290}. **al:** *E. trachycaulus*.

5S-Rrna-Y1. [*5SDna-Y1* {960}]. 1^Y {1290}. **al:** *E. ciliaris*.

5S-Rrna-A2. [*5SDna-A2* {295}]. 5AS {658},{ 295}. **v:** CS {295}. **dv:** *T. monococcum* {658, 295}.

5S-Rrna-B2. [*5SDna-B2* {295}]. 5BS {295}. **v:** CS.

5S-Rrna-D2. [*5SDna-D2* {295}]. 5DS {758}. 5D {295}, {758}. **v:** CS {295}, {758}. **dv:** *Ae. Tauschii* {758}.

5S-Rrna-R2. [*5SDna-R2* {1206}]. 5RS {1206}. **al:** *S. cereale*.

5S-Rrna-H^{t}2. [*5SDna-H*^{t}*2* {960}]. 5H^t {1290}. **al:** *E. trachycaulus*.

5S-Rrna-U2. [*5SDna-U2* {295}]. 5U {295}. **al:** *Ae. umbellulata*.

5S-Rrna-V2. [*5SDna-V2* {960}]. 5V {1290}. **al:** *D. villosa*.

5S-Rrna-H3. [*5SDNA-H3*{793}]. 2H{710}. 2HL{793}. **al:** Betzes Barley; Sultan barley.

5S-Rrna-H4. [*5SDNA-H4*{793}]. 3HL{793}. **al:** Betzes barley; Sultan barley.

5S-Rrna-H5. [*5SDNA-H5* {793}]. 4HL {793}. **al:** Betzes barley; Sultan barley.

5S-Rrna-H6. [*5SDNA-H6* {793}]. 4HS {793}. **al:** Betzes barley; Sultan barley.

1.70. Segregation distortion

See also, Gametocidal Genes.

QSd.ksu-1D {9931}. 1DL {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xcmwg706-1D* {9931}.

QSd.ksu-3D {9931}. 3DS {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc TA1704 {9925}. **ma:** Association with *Xwg177-3D* {9931}.

QSd.ksu-4D {9931}. 4DS {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *XksuF8-4D* {9931}.

QSd.ksu-5D.1 {9931}. 5D {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xcdo677-5D* {9931}.

QSd.ksu-5D.2 {9931}. 5DL {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xglk614-5D* (synonym '*Xtag614-5D*') {9931}.

QSd.ksu-5D.3 {9931}. 5DL {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xwg1026-5D* {9931}.

QSd.ksu-7D {9931}. 7DS {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xglk439-7D* (synonym '*Xtag439-7D*') {9931}.

1.70. Short roots

A 'very short root' phenotype was produced by heterozygous genotypes from selected crosses between Chinese Spring and certain synthetics. The *Vsr1* locus was localized to a 3.8 cM interval on chromosome 5DL {11014}.

Vsr1 {11014}. 5DL {11014}. **ma:** *Xwmc765-5D* – 7.7 cM – *Vsr1* – 1.1 cM – *Xbarc144-5D*{11014}; *Xwmc765-5D* – 1.9 cM – *XWL938* – 3.3 cM – *XWL2506* – 3.3 cM – *Vsr1* – 0.5 cM – *XWL954* – 0.5 cM – *Xbarc144-5D* {11014}.

Vsr1a. **v:** Chinese Spring {11014}.

Vsr1b. **v:** TA4152-71 {11014}.

1.71. Soft glumes

SOG was considered to be an homologue of *TG1* and *TG2*. See Tenaceous glumes. The Soft Glume locus was not considered to be an orthologue of Tenacious Glumes {10769}.

SOG

Sog {10555}. **dv:** *T. monococcum* ssp. *boeoticum* ID49 {10555}; *T. monococcum* ssp. *aegilopoides* TA4342-96 {10769}.

sog {10555}. 2AS {10555}. **bin:** C-2AS5-0.78. **dv:** *T. monococcum* ssp. *monococcum* var. *sinskajae* (syn. *aegilopoides*) UD69 {10555}; Tm-9, a mutant of TA4342-96{10769}. **ma:** Co-segregation with AFLP loci *Xe4232041* and *Xe373311* {10555}; *Xgwm71-2A* – 3.3 cM – *sog* – 3.5 cM – *Xbcd120-2A* {10769}.

1.72. Sterol esterification in kernels - Synthesis of b-sitosterol esters

Two sterol-ester phenotypes, p-L (palmitate + linoleate) and L (linoleate) are inherited as alleles at a single locus.

Pln {428}. [*P-L* {428}]. 7DS {1476}. **v:** Aradi {428}; Aragon 03 {428}.

pln {428}. [*L* {428}]. **v:** Mara {428}; Pane 247 {428}.

1.73. Stem solidness

Solid stem, caused by increased pith in normally hollow stem regions, is associated with resistance to wheat stem sawfly, *Cephus cinctus*. Solid stem confers resistance to wheat stem sawfly. See also Reaction to *Cephus* spp.

Qsst.msub-3BL. 3BL {10206}. **bin:** 3BL11-0.81-1.00. **v:** Fortuna {11230}; Genou {11230}; Judee {11230}; Rampart PI 59388 {10206}; Rescue {11230}; S-615 {11230}; Vida {11230}. **ma:** Linked to microsatellite markers *Xgwm247-3B, Xgwm340-3B*, and *Xgwm547-3B*. These markers explained 76% of the total variation for stem solidness in Rampart/Jerry {10206}.

Haplotype analyses in a range of hexaploid and tetraploid accessions suggested the possibility of multiple alleles or loci in the QTL region {11230, 11239}. Conan with an intermediate level of stem solidness represents a different haplotype from other North American cultivars {11230}.
Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines {10730}.

Qsst.msub-3DL. [*Qss.msub-3DL* {10395}]. 3DL {10395}.
Associated with *Xgwm645-3DL* (R^2=0.31), *Xwmc656-3DL* (R^2=0.1), and *Xcfd9-3DL* (R^2=0.13) {10395}. This gene acted as an enhancer of *Qsst.msub-3BL* {10395}.

Qsf.spa-3B {10351}. **tv:** Kyle*2 / Biodur (solid stem) // Kofa (hollow) DH population: *Qsf.spa-3BL* was located to a 21.3cM interval flanked by *Xgwm247-3B* and *Xgwm114-3B* {10351}. Mapped as a single gene, *Xgwm247-3B* – 6.9cM – *Qsf.spa-3B* –.4cM – *Xgwm114-3B* {10351}. This location was confirmed in two other crosses involving G9580B-FE1C and Golden Ball as the solid stem parents {10351}.

1.74. Temperature-sensitive winter variegation

This phenotype involves reduced vigour and chlorotic patches on leaves of certain genotypes in *Ae. umbellulata* cytoplasm when grown at low temperatures {1596}.

Vgw. Variegation is dominant {1596}. [*Vg* {1021}]. 5BL {1021}. **v:** Bersee {1596}; Cappelle-Desprez {1596}; Hobbit Sib {1596}; Mara {1596}.

vgw {1021}. **v:** Besostaya I {1596}; CS {1596}; Poros {1596}; Sava {1596}; *T. spelta* {1596}.

1.75. Tenacious glumes

TG1

Tg1 {1240}. Derived from *Ae. tauschii*. Dominant. [*Tg* {1240}]. 2DS {1240}. **bin:** 2BS-3 1.00-0.84. **v:** Synthetic ABD wheats {652}. **ma:** Placed in a 12 cM interval between *Xwmc112-2D* and *Xbarc168-2D* {10497}.

TG2

Tg2 {0046}. Derived from *T. dicoccoides* 2BS {0046}. **v:** TA 3419 = *Tetra Canthatch / Ae. tauschii* ssp. *meyeri* TA1599{10769}. **ma:** *Tg2* is associated with *Xrsq805(Embp)-2B* and *Xpsr899-2B*{0046}; *Xgwm261/Xwmc503-2D* – 2.3 cM – *Tg2* – 5.9 cM – *Xfba88/Xfbc400-2D* {10769}.

Soft Glume locus is not an orthologue of Tenacious Glumes {10769}.
A QTL analysis of the relationship of glume tenacity (*Gt*) with threshability (*Ft*) and the size of the glume base scar (*Gba*) after glume detachment in two crosses, viz. the ITMI population and CS*/CS (*Ae. tauschii* 2D), was undertaken {10497}. In the first cross *QFt.orst-2D.1* and *QGt.orst-2D.1* were closely associated with *Xgwm261-2D*, and *XFt.orst-2D.2* and *XGt.orst-2D* were associated with *Xgwm455-2D*, in the second population only the first pair along with *Xba.orst-2D* were detected; these appeared to correspond with *Tg1* {10497}.

1.76. Tiller inhibition / Tiller number

TIN1

Tin1 [*Tin* {1212}]. 1A {10193}. 1AS {1212}.

tin1 {1212}. Restricted tiller number is recessive{1212} **v:** Israel Uniculm 494 {1212}; Banks + *tin* {10193}; Oligoculm 390 {10193}; Uniculm 492 {10193}. **ma:** *Xpsp2999(Glu3)-1A* – 3.9 cM – *tin1/Xgwm136-1A* – 2.4 cM – *Xwhs179-1A*{10193}; the 350 bp allele of *Xgwm136-1A* was diagnostic of *tin1*{10193}. **c:** A candidate gene identified by map-based cloning was predicted to encode a cellulose synthase-like (Csl) protein with homology to members of the CslA clade; allelic variation was attributed to dinucleotide repeat-length polymorphism in the 5′UTR region of the *Csl* gene {11657}.

A near recessive gene, *ftin*, was located proximal to the *TIN1* locus in putative *Agropyron cristatum* derivative Pubing3558{11462}: *Xgwm136-1A* – 4.3 cM – *Xpsp2999-1A* – 0.7 cM – *Xcfa2153-1A* – 1.0 cM – *FTIN* {11462}.

TIN2. 2A {9909}.

Tin2 Tiller-reducing affect of this allele was dominant {9909}.

tin2 {1212}. [*Tin* {9909}]. **v:** 88 F2 185 {9909}.

TIN3. $A^{m}L$ {10329}.

tin3 {10329}. **dv:** *T. monococcum* TA4443 = TA4342-96 mutant {10329}. **ma:** *Xbcd131/Xbcd1431-3A* – 9.6 cM – *tin3/Xpsr1205-3A* – 4.7 cM – *Xcfa2076-3A* {10329}.

TIN4. 2DL {11574, 11575}.

Tin4 {11575}. *QLtn.sicau-2D* {11574}. Low tillering. **i:** H461/Chuannong 16 NIL7A {11575}. **v:** H461 {11574, 11575}.

tin4. High tillering. **i:** H461/Chuannong 16 NIL7A {11575}. **v:** Chuannong 16 {11574, 11575}.

An EMS-derived, reduced tiller number mutant allele identified in YZ4110 was named *tn1* {11650}. The *TN1* allele in YZ4110 encoded a transmembrane ankyrin (ANK) repeat protein and the *TN1* locus was identified as *TraesCS6B02G013100* (CS REFSeq 1.0) {11650}. *Tn1* likely promoted tillering by inhibiting ABA biosynthesis and signalling {11650}.

QTL

Fukuho-Komugi / Oligoculm: DH population: A QTL of large effect on spike number per plant in a DH population of mapping to the *Hg* – *Xpsp2999(Glu3)-1A* region {10218} probably corresponds to *Tin1*.

Three QTL were located on chromosomes 2DL (*Qltn.siau-2D*), 2BL and 5AL in a RIL population from **H461 (low tillering) / CN16 (high tillering)**, but only the 2DL QTL was confirmed in **H461 / CM107** and **H461 / MM37** RIL populations {11465}.

1.77. Uniculm stunt

Stunting is favoured by a combination of long days and low night temperatures {581}. Caused by duplicate recessive genes, *us1* and *us2*, located in chromosomes 4A and 5B, respectively {200}.
Genotypes: Normal: **v**: *Us1 us2*: Alfa {581}; Jaral {581}.
Normal: **v**: *us1 Us2*: Mabruk {581}.
Stunted: **v**: *us1 us2*: Line 492 {581}.

1.78. Yield and yield components

1.78.1. Grain number per spike

QGnu.ipk-4A {0255}. 4AL {0255} **v: Opata / W-7984** (ITMI) RI mapping population {0255}; Higher grain number was contributed by Opata {0255}. **ma:** Associated with *Xmwg549-4A, Xabg390-4A* and *Xbcd1670-4A* {255}.
QGnu.ipk-4A coincides with QTL for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) {0255}.

QKps.unl-3A.1 {10044}. 3AS {10044}. **v: Cheyenne / Cheyenne(Wichita 3A)** RI mapping population{10044}; a higher kernel number of 0.3 kernels was contributed by Wichita and the QTL explained 15.5% of the phenotypic variation {10044}; The QTL coincided with QTLs for grain yield, kernel number per square metre and 1000-kernel weight {10044}. **ma:** Associated with *Xbarc12-3A* {10044}.

Qkps.unl-3A.2 {10044}. **v: Cheyenne / Cheyenne(Wichita 3A)** RI mapping population {10044}; a higher kernel number of 0.3 kernels was contributed by Cheyenne and the QTL explained 9.5% of the phenotypic variation{10044}. **ma:** Associated with *Xbcd141-3A* {10044}.

Three QTL for kernel number per spike were assigned to chromosome 3A in RSLs from **Cheyene*7/Wichita** {0025}.

1.78.2. Grain volume weight

QGvwt.unl-3A.1 {10044}. 3A {10044}. **v: Cheyenne / Cheyenne(Wichita 3A)** RI mapping population {10044}; higher grain volume weight (+23 kg/hL) was contributed by Wichita and the QTL explained 43.1% of the phenotypic variataion {10044}; the QTL coincided with a QTL for spikes per square metre {10044}. **ma:** Associated with *Xbcd1380-3A* {10044}.

1.78.3. Grain weight

50-grain weight

QFgw.ocs-4A.1 {0047}. 4A {0047}. **v: CS / CS(Kanto107 4A)** mapping population{0047}. **ma:** Associated with *Xbcd265-4A* and *Xbcd1738-4A* {0047}.

1000-grain weight

TaGW2-A1 6AS, a homolog of *OsGw2* {11690}.

gw-A1. A TILLING mutation (mutant T4-2235; G2373A) in **tv:** Kronos backcrossed to Kronos and **v:** Paragon caused increased TGW, grain length and grain width; the increased grain size was attributed to larger carpel size {11690}.QTL

TaCKX6-D1 {11407}. 3D {11407}. Encodes a cytokinin oxidase/dehydrogenase. **v:** Hap a associated with high TKW has an 18 bp deletion relative to hap b: Wenmai 6, Yanzhan 1, Lumai 14 {11407}; Hap b: Bainong 321, Chinese Spring, Hanxuan 10, Neixiang 188 {11407}. **ma:** *Xcfd70-3D* – 3.7 cM – *TaCKX6-D1* – 2.0 cm – *Xwmc533-3D* {11407}.

TaCwi-A1 {10812}. **ma:** *Xbarc15-2A* – 10.9 cM – *TaCwi-A1* – STS markers *Cwi21* and *Cwi22* – 17.6 cM – *Xgwm71-2AL* {10812}.
TaCwi-A1 was cloned based on the rice *GIF1* gene encoding a cell wall invertase (GenBank accession EU095553), and STS markers *Cwi21* and *Cwi22* were developed from the polymorphisms between two allelic variants. On average, *TaCwi-A1a* had 1,000 grain weights 2.4 g higher than *TaCwi-A1b* {10812}.

TaGW2-6A {10781}. **ma:** *Xcfd80-6AS.2* – 0.6 cM – *TaGW2-CAPS* – 0.5 cM – *Xbarc146-6A.1/Xwms132.4-6A* {10781}.
Based on its *OsGW2* orthologue in rice this gene was characterized and mapped as a CAPS marker in wheat {10781}. SNPs in the promoter region allowed distinction of two haplotypes. Hap-6A-A was mainly present in southern Chinese wheats; Hap6A-G was present in varieties from central and eastern Europe. On average Hap-6A-A had 1,000 grain weights more than 3g higher than Hap-6A-G {10781}. Encodes an E3 RING ligase {11122}.

QTL

Cheyenne / Cheyenne(Wichita 3A): RI mapping population: ***QTkwt.unl-3A.1***{10044}. 3AS {10044}. Higher kernel weight of 0.27% was contributed by Cheyenne and the QTL explained 12.7% of the phenotypic variation {10044}; The QTL coincided with QTLs for grain yield, kernel number per square metre and kernels per spike {10044}. **ma:** Associated with *Xbarc12-3A* and *Xtam55-3A* {10044}.

Cheyenne[*]7 / Wichita 3A: RSL population: Two QTL for 1,000-kernel weight were assigned to chromosome 3A {0025}.

Forno / Oberkulmer spelt: Eight QTLs for 1,000-kernel weight accounted for 54% of the variatio) were mapped in {0280}.

Opata / W-7984 (ITMI): RI mapping population: ***QTgw.ipk-5A*** {255}. 5AL {255}. **v:** }; The higher yielding allele was contributed by W-7984 {255}. **ma:** Associated with *Xfba351-5A* and *Xcdo1312-5A* {255}.

RS111 / CS: mapping population: ***QGw1.ccsu-1A*** {0165}. 1AS {0165}. **ma:** Associated with *Xwmc333-1A* {0165}.

RS111/CS: RIL population {0236}: QTLs for grain size were identified on chromosome arms 1DS, 2DL and 6BL.

RL4452 / AC Domain: *QGwt.crc-3D* {10287}. 3D {10287}. **ma:** Flanked by *Xgwm341-3D* – *Xwmc552-3D* (LOD 4.3) {10287}; ***QGwt.crc-4A*** {10287}. 4A {10287}. **ma:** Flanked by *Xgwm494-4A* – *Xgwm162-4A* (LOD 6.7) {10287}; ***QGwt.crc-6D*** {10287}. 6D {10287}. **ma:** Flanked by *Xgwm325-6D* – *Xgwm55-6D* (LOD 3.9) {10287}.

1.78.4 Test weight

QTL

In **RL4452 / AC Domain**{10287}.

QTwt.crc-1B {10287}. 1B {10287}. **ma:** Linked to *Xgwm374.1-1B* (LOD 3.9) {10287}.

QTwt.crc-1D {10287}. 1D {10287}. **ma:** Linked to *Xgdm126-1D* (LOD 5.8) {10287}.

QTwt.crc-2D {10287}. 2D {10287}. **ma:** Linked to *Xgwm349-2D – Xbarc59-2D* (LOD 5.2) {10287}.

QTwt.crc-3B {10287}. 3B {10287}. **ma:** Linked to *Xwmc625-3B – Xbarc164-3B* (LOD 15.4) {10287}.

QTwt.crc-3D {10287}. 3D {10287}. **ma:** Linked to *Xbarc71-3D* (LOD 5.2) {10287}.

QTwt.crc-5D {10287}. 5D {10287}. **ma:** Linked to *Xgdm63-5D – Xwmc765-5D* (LOD 5.3) {10287}.

1.78.5. Grain weight/ear

QTL

CS / CS(Kanto107 4A): mapping population: ***QGwe.ocs-4A.1*** {0047}. 4AS{0047}. **ma:** Associated with *Xbcd1738-4A* {0047}.

In **Opata / W-7984** (ITMI): RI mapping population:

QGwe.ipk-2D {0255}. 2DS {0255}. Higher grain weight was contributed by Opata {0255}. **ma:** Associated with *Xcdo1379-2D* and *Xbcd1970-2D* {0255}.

QGwe.ipk-4A {0255}. 4AL {0255}. Higher grain weight was contributed by Opata {0255}. **ma:** Associated with *Xmwg549-4A, Xabg390-4A* and *Xbcd1670-4A* {0255}.
QGwe.ipk-4A coincided with QTLs for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain number (*QGnu.ipk-4A*) {0255}.

1.78.6. Grain yield

CS / CS(Kanto107 4A): mapping population: ***QYld.ocs-4A.1*** {0047}. 4AS {0047}. **ma:** Associated with *Xbcd1738-4A* {0047}.

Cheyenne / Cheyenne(Wichita 3A): RI mapping population: ***QGyld.unl-3A.1*** {10044}. 3AS {10044}. Higher grain yield of 32 kg/ha was contributed by Wichita and the QTL explained 6.6% of the phenotypic variation {10044}; The QTL coincided with QTLs for kernel number per square metre, 1000-kernel weight and kernels per spike {10044}; ***QGyld.unl-3A.2*** {10044}. 3A {10044}. Higher grain yield of 82 kg/ha was contributed by Wichita and the QTL explained 28.1% of the phenotypic variation {10044}; The QTL coincided with a QTL for kernel number per square metre {10044}. **ma:** Associated with *Xbarc67-3A* and *Xbcd366-3A* {10044}.

Renan / Recital: ***QYld.inra-7D*** {10071}. **ma:** *Xcdf69-7D* (R^2=3.7-15.7%) {10071}.

RL4452 / AC Domain: ***QYld.crc-2A*** {10287}. **ma:** Linked to *Xgwm339-2A* (LOD 3.0) {10287}. ***QYld.crc-2B*** {10287}. **ma:** Linked to *Xgwm257-2B* (LOD 9.4) {10287}. ***QYld.crc-4A*** {10287}. **ma:** Linked to *Xgwm130-4A* (LOD 4.4) {10287}.

Shamrock / Shango: DH population: Non-glaucous (virescent) lines had higher yields than glaucous sibs {10543}; see Glaucousness, subsection Epistatic inhibitors of glaucousness.

Tetrapoloid wheat

Langdon(DIC5B) / Langdon: ***QYld.ndsu-5B*** {10161}. [*QGy.ndsu-5B* {10161}]. Higher yield contributed by contributed by Langdon {10161}. **ma:** Mapped to the *Xbcd1030-5B* - *Xgwm604-5B* interval {10161}.

Grain yield under drought stress

Dharwar Dry (drought tolerant)/Sitta: SSR locus *Xwmc89-4AL* was the most closely associated marker with a QTL for grain yield, grain fill rate, spike density, grains/m^2, biomass and drought susceptibility index covering a genetic distance of 7.7 cM {10488}.

1.78.7. Kernel number per square metre

QTL

Cheyenne / Cheyenne(Wichita 3A): RI mapping population: ***QKpsm.unl-3A.1*** {10044}. 3AS{10044}. Higher kernel number (170 kernels) was contributed by Wichita and the QTL explained 14.6% of the phenotypic variation {10044}; The QTL coincided with a QTL for grain yield{10044}. **ma:** Associated with *Xbarc12-3A* {10044}; ***QKpsm.unl-3A.2*** {10044}. 3A{10044}. **ma:** Associated with *Xbarc67-3A*{10044}.

1.78.8. Spikelet number/spike

***NO FUL1* - CHECK**

FUL2

FUL2

Ful2 {11384}. Loss of function mutation in gene *FUL-A2* (Kronos mutant T4-837) and *FUL-B2* (Kronos mutant T4-2911) resulted in significant increases in spikelet number {11384}.

Flowering Locus *T2*

FT2

Loss-of-function mutations in *FT2* increased spikelet number per spike but reduced but reduced fertility {11604}.

FT-A2. *TraesCS3A02G143100*. 3AL {11605}.
A natural mutation causing an aspartic acid (**v:** Pavon; **tv:** Kronos**)** to alanine (**v:** Chinese Spring; Berkut) change at position 10 (D10A) in FT-A2 was associated with significant increases in SNS and grain number per spike with no negative effect on fertility {11605}.

WAPO-1 Aberrant Panicle Organization 1 **(**Wheat ortholog of rice *APO1* and Arabidopsis *UFO*).

WAPO-A1. *TraesCS7A02G481600* {11383}. 7AL {11383}.
WAPO-A1 is the causal gene for *QSNS.ucw-7A* {11383} that also affects grain number per spike and spike yield {11603}.

WAPO-A1a {11383}. Associated with low SNS; has a 115-bp promoter deletion and a D384N amino acid change {11383}. **v:** RAC875, Clark, Lancer, CDC Lanmark, Julius, Arina, Jagger, Cadenza, Robigus, and SY_Mattis {11383}. **tv:** _Kronos, Ben {11383}. Most frequent allele in durum {11383}.

WAPO-A1b {11383}. Associated with high SNS; has a C47F amino acid change and no promoter deletion {11383}. **v:** Berkut, Ning7840, PI 41025, MPV57, Platte {11383}. Most frequent allele in *T. aestivum*. **tv:** Rare in durum {11383}.

WAPO-A1c {11383}. Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion {11383}. **v:** *T. dicoccoides* PI 471033 and PI 355455; *T. dicoccum* CItr 14135, PI 94638, and PI 298586; *T. durum* PI 286539 {11383}.

WAPO-A1d {11383}**.** Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion but differs from *WAPO-A1c* by a C667 and G764A DNA changes {11383}. **tv**: *T. durum* Rusty and Lang; *T. dicoccum* CItr14919, PI 193877, PI 193882, PI 217640, PI 221400, PI 225332, PI 273980, and PI 94657 {11383}.

SVP1 and ***VRT2***
Loss-of-function mutations of both homoeologs in *SVP1* (TraesCS6A02G313800 and TraesCS6B02G343900) and *VRT2* (TraesCS7A02G175200 and TraesCS7B02G080300) in tetraploid wheat increase number of spikelets per spike, delay heading time and reduce plant height {11607}.

QTL

QSns.sau-2DS {11424}. 2DS {11424}. **v:** RIL populations from **Line 20828 / Chuanong 16**, **Line 20828 / Shumai 51** and **Line 20828 / Sy95-71**; LOD score 3.47 – 38.24, PV 10 – 46% in 8 environments. Located in a 2 cM interval flanked by *Ax-109836946* (32.8 Mb) and *AX-111956072* (34.43 Mb) {11424}.

QSns.ucw-7AL {11496}. 7AL {11383}. **v:** Underlying gene: *WAPO1*.

CS / CS(Kanto107 4A): mapping population: ***QSpn.ocs-4A.1*** {0047}. 4AS {0047}. **v:** {0047}. **ma:** Associated with *Xbcd1738-4A* {0047}.

1.78.8. Spike number per plant

Line 05210/Laizhou 953: *QSn.sdau-4BL* {10784}. **ma:** *Xwmc657-4B* – 4.6 cM – *QSn.sdau-4B* – 1.6 cM – *Xgwm495-4B* {10784}.
QSn.sdau-4BL was resolved as a single gene in {10784}. It was associated with decreased spike length and grain number per spike.

1.78.9 Spike number per square metre

QTL

Cheyenne*7 / Wichita 3A: RSL: A QTL for spike number per square metre was assigned to chromosome 3A {0025}.

1.78.10. Spike length

QTL

Courtot / Chinese Spring: Five QTL for spike length were detected in {0114} but only one on chromosome arm 5AL was consistent for at least two years.

Opata / W-7984: (ITMI) RI mapping population: ***QEl.ipk-1B*** {0255}. 1BL {0255}. Longer ear was contributed by Opata {0255}. **ma:** Associated with *Xbcd388-1B* and *Xwg605-1B* {0255}. ***QEl.ipk-4A*** {0255}. 4AL {0255} Longer ear was contributed by Opata{0255}. **ma:** Associated with *Xmwg549-4A, Xabg390-4A* and *Xbcd1670-4A* {0255}. This QTL is likely to be a pleiotropic effect of the gene underlying the height QTL, *QHt.ipk-4A* {0255}; ***QEl.ipk-5A*** {0255}. 5AL{0255}. Longer ear was contributed by W-7984 {0255}. **ma:** Associated with *Xmwg522-5A* {0255}.

1.78.11. Tiller number/plant

CS / CS(Kanto107 4A): mapping population: ***QTn.ocs-4A.1*** {0047}. 4AS {0047}. **ma:** Associated with *Xpsr163-4A* {0047}.

1.79. Yellow berry tolerance

QTL

RS111 / CS: A QTL for yellow berry tolerance, contributed by RS111, was associated with *Xgwm190-5D* and *Xgwm174-5D* in a RIL population from {0237}. A tolerance QTL contributed by CS, the susceptible parent, was detected on 6B {0237}.

Wheat Gene Catalogue – 2. Proteins

2.1. Grain protein content

Thirteen QTLs for grain protein content were identified in a RI population from the cross WL711 (low protein content)/PH132 (high grain content) {10055}. The QTLs that were identified using more than one method or in more than one environment are listed below. Also listed is a QTL that was identified in the mean over the four environments and was therefore deemed important {10055}. QTLs for grain protein content were detected on chromosome arms 6AS (associated AFLP marker, *XE38M90v200v*) and 1BL (associated RFLP marker, *Xcdo1188*) in Courtot/Chinese Spring' {0141}.

QGpc.ndsu-6Ba {623}. 6B. **tv:** Langdon {623}.

QGpc.ndsu-6Bb {10071}, {623}. 6B. **tv:** Langdon-*T. dicoccoides* 6B {623}. **v:** Glupro {0179}. **ma:** *QGpc.ndsu-6B* was associated (LOD score = 18.9) with the interval *Xmwg79-6B* - *Xabg387-6B*. These loci were mapped in 6BS: *Xmwg79-6B* – 5.9 cM – *Xabg387-6B* – 9.0 cM – centromere {623}; Located in the 4 cM interval flanked by *Xmwg79-6B* and *Xcdo365-6B* {0244}; Flanking microsatellite markers and PCR-specific markers for Glupro are available {0179}.

GPC-B1

Gpc-B1a. [*QGpc.ndsu-6Ba* {623}].
This allele, fixed in cultivated durum, is a non-functional frame-shift mutation {10438}. A similar non-functional allele, or a complete deletion of *GPC-B1*, is fixed in hexaploid wheat {10438}.

Gpc-B1b {10296}. [*QGpc.ndsu-6Bb* {10071}, {623}, *Gpc-6B1* {10299}, *NAM-B1* {10995}]. 6BS. **i:** Yecora Rojo NIL PI 638740 {10138}. **v:** As II {10995}; Burnside {11044}; Diamant {10995}; Glencross {11044}; Glupro {10138}; Lilian {11044}; Prins {10995}; Somerset {11044}; Stanley {10995}; *T. spelta* Altgold {10995}. **tv:** *T. dicoccoides* FA-15 {10138}. **ma:** Mapped to a 0.3 cM interval flanked by *Xucw79-6B* and *Xucw71-6B* {10229}; *Xcdo365-6B* – 1.5 cM – *Gpc-B1* – 1.2 cM – *Xucw67-6B* {10296. A high-throughput codominant marker, *Xuhw89-6B*, was then mapped less than 0.1 cM from *Gpc-B1* {10297}.
Gpc-B1b, the functional allele {10438} in *T. dicoccoides*, affects senescence and maturity in addition to grain protein content, accelerating senescence and maturity {10298}. *Gpc-B1* is a NAC transcription factor designated *Nam-B1* {10438}. A paralogous copy of this gene is present in homologous group 2 (*Nam2*).
This allele was relatively frequent in Scandinavian and Finnish common wheats, landraces and spelts {10995}.

PRO1 {777}. 5DL {777}. **s:** CS*6/Hope 5D {777}.
May be identical to *VRN-D1*.

PRO2 {777}. 5DS {777}. **s:** CS*6/Hope 5D {777}.
QGpc.ccsu-2B.1 {10055}. 2BL {10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 13.4% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm1249-2B* {10055}.

QGpc.ccsu-2D.1 {0015, 10055}. 2DL {0015, 10055}. **v:** WL711/PH132 RI mapping population {10055, 0015}; higher protein was contributed by PH132 and the QTL explained 19% {0015} and 14% {10055} of the phenotypic variation. **ma:** Associated with *Xgwm1264-2D* {10055}.

QGpc.ccsu-3D.1 {10055}. 3DS {10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 16.3% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm456-3D* {10055}.

QGpc.ccsu-3D.2 {10055}. 3DS {10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 14% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm892-3D* {10055}.

QGpc.ccsu-7A.1 {10055}. 7AS {10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 32.4% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm1171-7A* {10055}.

QGpc.ipk.7B {10628}. **v:** F26-70 {10628}; Closely associated with *Ppd-B2* {10628}. **su:** Favorit (F26-70 7B) {10628}.
See Response to Photoperiod.

QGpc.ndsu-5B.1 {10161}. 5B {10161}. **v:** LDN (DIC5B)/LDN, contributed by DIC5B {10161}. **ma:** Nearest marker, *Xgwm604-5B* {10161}.

QGpc.ndsu-5B.2 {10161}. 5B {10161}. **v:** LDN (DIC5B)/LDN, contributed by DIC5B {10161}. **ma:** Nearest marker, *Xabc310-5B* {10161}.

QGpc.ndsu-5B.3 {10161}. 5B {10161}. **v:** LDN (DIC5B)/LDN, contributed by DIC5B {10161}. **ma:** Nearest marker, *Xwg909-5B* {10161}.

QGpc.ndsu-6B {623}. 6BS {623}. **tv:** Langdon {623}.

QPro.inra-2A {10071}. 2A {10071}. **v:** Renan/Recital {10071}. **ma:** *XksuD18-2A – Xgwm614-2A* (R^2 = 4.4-8.9%) {10071}.

QPro.inra-3A {10071}. 3A {10071}. **v:** Renan/Recital {10071}. **ma:** *Xcfd79-3A – Xfbb250-3A* (R^2 = 4.1-8.3%) {10071}.

QPro.inra-4D {10071}. 4D {10071}. **v:** Renan/Recital {10071}. **ma:** Linked to *Xcfd71-4D* (R^2 = 4.6-10.3%) {10071}.

QPro.inra-7D {10071}. 7D {10071}. **v:** Renan/Recital {10071}. **ma:** *Xcfd69-7D – Pch1* (R^2=6.4-10.4%) {10071}.

QPro.mgb-4B. Associated with *Gai1* and *Xpsr622-4B* {110}[2].

QPro.mgb-5A. Associated with *Xpsr911-5A* {110}[2] and *Xcdo412-5A* {0343}[*].

QPro.mgb-6A.1. Associated with *Xpsr167-6A* and *XksuG8-6A* {110}[2].

QPro.mgb-6A.2. Associated with *Xmgb56-6A* {110}[2] and *Xpsr627-6A* {0343}[*].

QPro.mgb-6B. Associated with *Gli-B2-6B* {110}^{2} and *Nor-2* {0343}*. **ma:** *QGpc.ndsu-6B* was associated (LOD score =18.9) with the interval *Xmwg79-6B* – *Xabg387-6B*. These loci were mapped in 6BS: *Xmwg79-6B* – 5.9 cM – *Xabg387-6B* – 9.0 cM – centromere {623}.

Qpro.mgb-7A. Associated at P<=0.01 with *Pan2* {0343}*.

QPro.mgb-7B. Associated with *Xpsr490(Ss1)-7B*, *Pc* {110}^{2} and *Xutv913-7B* {0343}*.
QTLs for grain protein content were detected on chromosome arms 6AS (associated AFLP marker, *XE38M60*$_{200}$) and 1BL (associated RFLP marker, *Xcdo1188-1B*) in Courtot/Chinese Spring {0141}.

Forno / Oberkulmer spelt: Nine QTLs (51% of the variation) were mapped in cross {0280}.

Cheyenne (high quality wheat) / CS (low quality wheat): RSL population: A QTL for grain and flour protein content, contributed by CS, was associated with *XTri-1D*/Centromere {0251}.

Renan / Recital: Four QTL conferring grain protein content {10071}; only QTL stable over at least 4 of 6 locations were presented. Renan contributed the four alleles for high grain protein content.

Ning 7840 / Clark: RIL population: QTL from Ning 7840 were detected on chromosomes 3AS (*Xwmc749-3AS* – *Xgwm369-3AS*; R^2 = 0.09-0.11) and 4B (*Xgwm368-4B* – *Xwmc617-4B*, R^2 = 0.08-0.11) {10702}.

Tetraploid wheat

T. dicoccoides **/ Latino:** In line 3BIL-85 high grain protein was detected in chromosomes 2AS (associated with *Xcfa2164-2A*, R^2 = 17%), 6AS (*Xp39M37*$_{250}$-6A, R^2 = 17%) and 7BL (*Xgwm577-7B*, R^2 = 9%) {10338}.

2.2. Enzymes

2.2.1. Acid phosphatase

ACPH-1

Acph-A1 {504}. [*Acph-B1* {936}, *Acph3* {516}, *Acph2* {516}]. 4AS {504, 516}. **v:** CS.

Acph-B1 {504}. [*Acph8* {516}, *Acph4* {516}, *Acph-A1* {936}]. 4BL {504}, {516}. **v:** CS.

Acph-D1 {504}. [*Acph5* {516}, *Acph6* {516}]. 4DL {504}, {516}. **v:** CS.

Acph-H1 {1153}. 4H {1153}. **ad:** CS/Betzes.
Acph-M^{v}1 {237}. [*Acph-M*^{v}*1* {985}, *Aph-v* {237}]. 4M^{v} {237}. **tr:** H-93-33 {984}.
Acph-R1. 7R {1457}. 7RS {506}. **ad:** CS/Imperial.
Acph-S^{s}1 {1140}. 4S^{s} {1140}. **ad:** CS/*T. searsii*.

ACPH-2

Acph-D2 {10407, 10309}. [*Acph1* {10309}]. 2DL {10309}. **dv:** *Acph-D2*$_{100}$ and *Acph-D2*$_{95}$ alleles distinguished accessions of *Ae. tauschii* ssp. *tauschii* and *strangulata*, respectively {1030}. **tv:** *Ae. tauschii* {10407}. **ma:** Cent ... *Acph-D2* – 4 cM – *Xgwm157- 2D* {10309}.

Acid phosphatase gene loci were reported for 7RL in *S. cereale* {1251}, chromosomes L1 (= 7Ag^i) and L4 (= 4Ag^i) of *Thin. intermedium* {361}, and chromosome E of *Ae. umbellulata* {0069}. Two loci on 7R were separated by 25 +or- 5.2 cM {1534}. Wehling {1559} identified four acid phosphatase loci in *S. cereale*, three of which were in 7R.

2.2.2. Alcohol dehydrogenase (Aliphatic)

ADH-1

ADH-A1 {502}. [*Adh-B1* {504}, *Adh*$_B$ {502}]. 4A {502}. 4AL {504}, {516}. **v:** CS.

ADH-B1 {501}, {502}. [Adh$_1$ {501}, Adh$_A$ {502}, Adh-A1 {504}]. 4B {502}. 4BS {504},{516}. **v:** CS.
Adh-B1a {1442}. [*Adh*$_{11}$ {501}, *Adh-A1a* {1442}]. **v:** CS. **tv:** PI 226951 {501}; Malavika {1442}.
Adh-B1b {1442}. [*Adh*$_{12}$ {501}, *Adh-A1b* {1442}]. **v:** Rageni derivative {1443}. **tv:** CI 4013 {501}; Bijaga Yellow {1442}.
Adh-B1b was the only variant *ADH-1* allele detected in study of a large number of *T. aestivum* and *T. turgidum* accessions {503}.

ADH-D1 {504}. [*Adh*$_D$ {502}]. 4D {502}. 4DS {504, 516}. **v:** CS. **ma:** *Adh-D1* [*Adh1, Adh2*] was mapped 4 cM distal to *Xpsr163-4D* and closely proximal to *Xcsiha114-4D.1*. [*XcsIHA114-1a*'] {757}.

ADH-C1 {1278}. [*G* {1278}]. **ad:** *T. aestivum* cv. Alcedo/*Ae. caudata* line G.
ADH-Ag^{i}1 {560}, {374}. [*Adh-X1* {361}]. 4Ag^i {560}. **ad:** Vilmorin 27/*Th. intermedium*; Caribo/*Th. intermedium*.
ADH-E1 {518}. 4ES {518}. **ad:** CS/*E. elongata*.
ADHG-H1 {520}. 4H {520}. **ad:** CS/Betzes.
***ADH-M^v*1** {984}. [*ADHmu* {984}, *Adh-M^{v}1* {985}]. 4M^v {984}. **v:** H-93-33.
ADH-R1{1457}. [*AdhR2* {582}]. 4R {1457, 582}. 4RS {506}. **ad:** CS/Imperial {1457, 506}; FEC28/Petkus {43}; Holdfast/King II {582}.
ADH-V1 {1026}, {242}. 4V {1026}. **ad:** CS/*D. villosum*.

Three *Adh* genes were identified in *Hordeum vulgare* and *H. spontaneum* {144}, {490}, {493}, {520}. Two of these were tightly linked at the *Adh-H1* locus {144}. The third gene was tentatively located in 5H {490}.
A low-level of aliphatic alcohol dehydrogenase activity is commonly observed on zymograms in the absence of added substrate {513}; this may account for the observation of wheat lactate dehydrogenase that was reported in {1465}.
The gene series formerly designated *Adh-2* and *Adh-3* appear under Aromatic Alcohol Dehydrogenase

2.2.3. Aminopeptidase

AMP-1

AMP-A1 {504}. 6AS {504}, {516}. **v:** CS.
Amp-A1a. **v:** CS {1533}.
Amp-A1b. **v:** Vitka {1533}.

AMP-B1 {504}. 6BS {504}, {516}. **v:** CS.
Amp-B1a. **v:** CS {1533}.
Amp-B1b. **v:** Iskra {1533}.
Amp-B1c {703}, {1244}. Null allele. **v:** *T. spelta* IPSR 1220017 {703}; Sinvalocho M.A {1244}.

AMP-D1 {504}. 6DS {504}, {516}. **v:** CS.
Amp-D1a {703}. **v:** CS.
Amp-D1b {703}. **v:** Sears' Synthetic IPSR1190903.

AMP-Ag^{e}1 {1575}. 6Ag^{e} {1575}. **ad,su:** Rescue/*Th. elongatum*.
AMP-Ag^{i}1 {703}. 6Ag^{i} {703}. **ad:** Vilmorin 27/*Th. intermedium*.
AMP-C1 {1278}. 6D {1278}. **ad:** Alcedo/*Ae. caudata* line D.
AMP-E1 {518}. 6E {518}. **ad:** CS/*E. elongata*.
AMP-H1 {520}. 6H {520}. **ad:** CS/Betzes.
AMPp-R1 {1457}. 6R {1457, 1280}. **ad:** CS/Imperial {1457}; Holdfast/King II {1280}.

AMP-2

AMP-A2 {703}. 4AL {703}. **v:** CS.
Amp-A2a {703}. **v:** CS.
Amp-A2b {703}. **v:** *T. spelta* IPSR 1220017.

AMP-B2 {703}. 4BS {703}. **v:** CS
Amp-B2a {703}. **v:** CS.
Amp-B2b {703}. **v:** Timstein.
Amp-B2c {703}. **v:** Hope.

AMP-D2 {703}. 4DS {703}. **v:** CS.
Amp-D2a {703}. **v:** CS.
Amp-D2b {703}. **v:** Sears' Synthetic IPSR 1190903.
Amp-D2c {703}. **v:** Bersee.

AMP-Ag^{i}2 {703}. 4Ag^{i} {703}. **ad:** Vilmorin27/*Th. intermedium*.
AMP-E2 {703}. 4E {703}. **ad:** CS/*E. elongata*.
AMP-H2 {703}. 4H {703}. **ad:** CS/Betzes.
AMP-H^{ch}2 {703}. 4H^{ch} {703}. **ad:** CS/*H. chilense*.
AMP-J2 {703}. 4J {703}. **ad:** CS/*Th. junceum*.
AMP-M^{v}2 {235}. 4M^{v} {235}. **su:** H-93-33 {235}.
AMP-R2 {703}. 4RS {702}, {93}. 4R {703}. **ad:** CS/Imperial.
AMP-S^{l}2 {703}. 4S^{l}L {703}. **ad:** CS/*Ae. sharonensis* {180}. **tr:** 4DS.4DL-4S^{l}L {660}.
AMP-V2 {703}. 4V {703}. **ad:** CS/*D. villosum*.

AMP-3

AMP-A3 {703}. 7AS {703}. **v:** CS.
Amp-A3a {703}. **v:** CS.
Amp-A3b {703}. **v:** Timstein.

AMP-H3 {703}. 7H {703}. **ad:** CS/Betzes.

2.2.4. Alpha-amylase

a-AMY1

a-Amy1c {1083}. [*a-Amy-B4*]. **tv:** *T. durum* ssp. *georgicum*.

The presence of *a-Amy1* reported in {1084} was confirmed by tests of segregation in a CS/Jones Fife population and in a population derived from a tetraploid cross {1083}. Recombinations with *a-AmyB1* were 9.3% and 22.3%, respectively.

A further set of a-amylase genes, *Xa-Amy-5* [*a-Amy3*], was identified in 5A, 5B and 5D by cross-hybridization with *a-AMY-1* and *a-AMY-2* probes {80}. Only one gene copy appears to be present at each locus. In rye, evidence was obtained for three *a-Amy-1* genes, two or three *a-Amy-2* genes and three *a-Amy-3* genes {907}.

Synthesis of a-amylase isozymes controlled by *a-Amy-1* genes on chromosomes 6A and 6D is reduced in DT6BS compared to euploid CS. This result suggests the presence of a gene(s) on the long arm of chromosome 6B, which is (are) required for GA-induced alpha-amylase synthesis in the aleurone {0072}.

a-AMY-1

a-AMY-A1 {7}. [*Amy6*$_A$ {1082}]. 6AL {412}, {1082}. **v:** CS.
a-Amy1a {1083}. [*a-Amy-B1a*]. **v:** CS.
a-Amy1b {1083}. [*a-Amy-B1b*]. **v:** CS.

a-AMY-A1
a-Amy-A1a {7}. [*Amy 6A1* {1084}]. **v:** CS.
a-Amy-A1b^5 {7}. **v:** Bezostaya 1; Kavkaz.
a-Amy-A1c^5. [*Amy 6A1*^{m} {1084}]. **v:** Aka.

a-AMY-B1
a-Amy-B1a {7}. [*Amy 4* {1084}, *Amy 6B2*^{o} {1084}, *Amy 6B1* {1084}]. **v:** CS {7}; Rare.
a-Amy-B1b {7}. [*Amy 4*^{m} {1084}, *Amy 6B1*^{o} {1084}, *Amy 6B2* {1084}]. **v:** Mara {7}.
a-Amy-B1c {7}. [*Amy 6B1* {1084}, *Amy 6B2* {1084}, *Amy 4* {1084}]. **v:** Sava {7}; Rare.
a-Amy-B1d {7}. [*Amy 4*^{m} {1084}, *Amy6B2*^{o} {1084}, *Amy 6B1*^{o} {1084}]. **v:** Sicco {7}; Rare.
a-Amy-B1e {7}. [*Amy 6B2*^{o} {1084}, *Amy 6B1*$^{4'}$ {1084}, *Amy 4*^{m} {1084}]. **v:** Cappelle-Desprez {7}.
a-Amy-B1f {7}. [*Amy 6B1*^{4} {1084}, *Amy 6B2*^{o} {1084}, *Amy4*^{m} {1084}]. **v:** Sappo {7}.
a-Amy-B1g {7}. [*Amy 4* {1084}, *Amy 6B2*^{o} {1084}, *Amy 6B1*^{4} {1084}]. **v:** Cheyenne {7}.
a-Amy-B1h {7}. [*Amy 6B2*^{o} {1084}, *Amy 6B1*^{o} {1084}, *Amy 4* {1084}]. **v:** *T. macha* Line 1 {7}; Rare.

a-AMY-D1 {7}. [*Amy6D* {1082}]. 6DL {412, 1082}. **v:** CS.
a-Amy-D1a {7}. [*Amy6D1* {1084}, *Amy 6D2* {1084}]. **v:** CS.
a-Amy-D1b {7}. [*Amy 6D2* {1084}, *Amy6D1* {1084}]. **v:** Prelude {1082}; Cappelle-Desprez {7}.
a-Amy-D1c. [*Amy6D1*^{m} {1084}, *Amy 6D2* {1084}]. **v:** *T. spelta* var. *duhamelianum*.

a-AMY-Ag^{i}1 {374}. 6Ag^{i} {374}. **ad:** Vilmorin 27/*Th. intermedium*.
a-AMY-E1 {13}. 6E {13}. **ad:** CS/*E. elongata*.
a-AMY-H1. [*a-Amy1* {146}]. 6H {146,1 051}. **ad:** CS/Betzes.
a-AMY-R1 {13}. 6RL {13}. **su,ad:** CS/Imperial; CS/King II; Holdfast/King II.
a-AMY-R^{m}1 {13}. 6R^{m}L {13}. **ad:** CS/*S. montanum*.
a-AMY-S1 {598}. 6SS {598}. **v:** Wembley derivative 31. **al:** *Ae. speltoides*.

Two types of nomenclature were assigned to the genes encoding the a-AMY-1 isozymes. In one, allelic states were defined for individual isozymes {1084} whereas in the other, several isozymes were considered the products of compound loci {7, 412}. This listing shows the 'alleles' described in {1084} which are assumed in {7} to be synonymous with the a-*Amy-B1a* through *a-Amy-B1h* nomenclature. *Amy*

4 and *Amy 4*^{1} are unmapped alternatives {1084} which appear to be identical to zymogram bands [bands 9 and 9b {7}] forming part of the *a-AMY-B1* phenotype. *Amy 6B1*°, [with forms *Amy 6B1*°, and *Amy 6B1*$^{4'}$, considered to be mutually exclusive {1084}] and *Amy 6B2* [with forms *Amy 62* and *Amy 6B2*° {1084}] describe further aspects of *a-AMY-B1* {7}. See *a-Amy1* below for further consideration of *Amy 6B2* {1084}.

a-AMY-2
a-AMY-A2 {7}. [*Amy*$_{7A}$ {1082}]. 7AL {412, 1082}.

a-AMY-B2 {7}. [*Amy*$_{7B}$ {1082}]. 7BL {412}, {1082}. **v:** CS. **v:** CS.
a-Amy-B2a {412}. [*Amy 7B 1* {1084}, Amy 7B2 {1084}]. **v:** CS.
a-Amy-B2b {412}. [*Amy 7B1* {1084}, *Amy 7B2*^{m} {1084}]. **v:** Hope.
The alternative states of *Amy 7B2*, namely, *Amy 7B2* and *Amy 7B2*^{m} {1084}, are identical to the variation in band 2 {412}. The complete description of the *a-Amy-B2* variation also includes variation in band 11 {412}.

a-AMY-D2. [*Amy*$_{7D}$ {1082}]. 7DL {412, 1082}. **v:** CS.
a-Amy-D2a {412}. [*Amy 7D1* {1084}]. **v:** CS.
a-Amy-D2b {417}. [*Amy 7D1*^{o} {1084}]. **v:** Largo {7}; Sears' Synthetic {7}; VPM1 {417}.
It was estimated {902} that there are two *a-Amy-1* genes in chromosome 6A and five or six in both 6B and 6D, and three or four *a-Amy-2* genes at each of the 7A, 7B, and 7D loci.

a-AMY-Ag^{i}2 {374}. 7Ag^{i} {374}. **ad:** Vilmorin 27/*Th. intermedium*.
a-AMY-E2 {13}. 7EL {13}. **ad:** CS/*E. elongata*.
a-AMY-H2. [*a-Amy2* {146}]. 7HL {146, 1051, 793}. **ad:** CS/Betzes.
a-AMY-H^{ch}2 {1015}. 7H^{ch}beta {1015}. **su,ad:** CS/*H. chilense*.
a-AMY-R2 {13}. 7RL {13}. **su,ad:** CS/Imperial; CS/King II; Holdfast/King II.
a-AMY-S^{b}2 {13}. 7S^{b} {13}. **ad:** Holdfast/*Ae. bicornis*.
a-AMY-U2 {13}. 7U {13}. **ad:** CS/*Ae. umbellulata*.
Three other *a-Amy2* loci, namely, *Amy 6B2, Amy 6D2, and Amy 7B2*, were reported {1084}. No variation was observed for the products of *Amy 6D2 and Amy 7B2*, although nullisomic analysis located the genes in 6DL and 7B, respectively. In accordance with the Guidelines, these genes are assumed to be part of the *a-Amy-D1* and *a-Amy-B2* loci, respectively. *Amy 6B2* was observed to produce alternative phenotypes {1084}. In a test of the segregation of these phenotypes relative to two alternative products of *Amy 6B1*, the two loci were found to be linked with a recombination frequency of 20.6% {1084}. However, an attempt to confirm the presence of more than one *a-Amy* locus in 6BL was unsuccessful {7}.

a-Amy1 {1084, 1083}. [*Amy 6B2* {1084}, *Amy-B2* {1083}]. 6BL {1084, 1083}. **v:** CS.
a-Amy1a {1083}. [*a-Amy-B1a*]. **v:** CS.
a-Amy1b {1083}. [*a-Amy-B1b*]. **v:** CS.

2.2.5. *b*-amylase

b-AMY-1

b-AMY-A1 {227}, {8}. [*b-Amy-A2* {8}, *b-Amy-B1* {1331}]. 5AL {227}, {8}. **v:** CS {8}. **s:** CS/Federation {227}.
b-Amy-A1a {8}. [*b-Amy-A2a* {8}, *b-B1a* {936}]. **v:** CS.
b-Amy-A1b {8}. [*b-B1b* {936}, *b-Amy-A2b* {8}]. **v:** Koga II..
b-Amy-A1c {8}. [*b-B1c* {936}, *b-Amy-A2c* {8}]. **v:** *T. macha* IPSR 1240005.

b-Amy-A1d {8}. [*b-Amy-A2d* {8}, *b-B1d* {936}]. **v:** Holdfast.
b-Amy-A1e {8}. *[b-Amy-A2e* {8}, *b-B1e* {936}]. **v:** Bezostaya I.

b-AMY-B1 {628}. [*b-Amy-A1* {8}]. 4BL {628, {8}. **v:** CS.
b-Amy-B1a {1330}. [*b-Amy-A1a* {1330}}, {8}]. **v:** CS.
b-Amy-B1b {1330}. [*b-Amy-A1b* {1330}, {8}]. **v:** Sears' Synthetic IPSR 1190903.
b-Amy-B1c {1330}. [*b-Amy-A1c* {1330}, *b-Amy-A1b* {8}]. **v:** Ciano 67.
Amy-B1d {1330}. [*b-Amy-A1c* {1330}, {400}]. **v:** Manella.

b-AMY-D1 {8}. 4DL {628, 8}. **v:** CS.
b-Amy-D1a {8}. **v:** CS.
b-Amy-D1b {8}. **v:** Bersee.
b-Amy-D1c {8}. **v:** Sears' Synthetic. Rare.
Previously listed alleles *b-Amy-D1d* and *-D1e* were found to be *b-Amy-B1* alleles {400}.
Two *b-Amy-D*^{t}1 alleles were predominant in 60 accessions of *T. tauschii* {1578}.

b-AMY-Ag^{i}1 {168}, {13}. 4Ag^{i} {168}. **ad:** Vilmorin27/*Th. intermedium*.
b-AMY-C1 {1278}. *B* {1278}. **ad:** *Aestivum* cv. Alcedo /*Ae. caudata* line B.
b-AMY-E^{b}***1*** {661}. 5E^{b}L {661}. **tr:** 5AS.5E^{b}L.
b-AMY-H1. 4H {1153}. **ad:** CS/Betzes.
b-AMY-H^{ch}***1*** {13}. 4H^{ch} {13}. **ad:** CS/*H. chilense*.
b-AMY-R1. [*b-AmyR1* {43}, *b-Amy-R2* {13}]. 5R {1280, 103}. 5RL {43}. **ad:** FEC 28/Petkus {43}; Holdfast/King II {43}, {1280}. **tr:** CS/Imperial 5BL-5RL {43}.
b-AMY-S^{l}***1*** {13}. *D* {13}. 4S^{l} {13}. **ad:** CS/*Ae. sharonensis* D {13}. **su:** CS/*Ae. sharonensis*. **ad:** CS/*Ae. longissima*.
b-AMY-U1 {13}. [*b-Amy-U2* {13}]. 5U {13}. **su:** CS/*Ae. umbellulata*.

A second set of loci with homology to *b-Amy-1* genes was identified in 2AS, 2BS and 2DS and designated the *Xb-Amy-2* [*b-Amy-2* {1331}] set. Evidence for these genes derived from cross-hybridization with a *b-AMY-H1* cDNA probe {1331}. Further members of the same set were identified in 2H {732}, and 2R and 2U {1331}.

2.2.6. Endopeptidase

EP-1

EP-A1 {516}. 7AL {516}. **v:** CS.
Ep-A1a {516}, {708}. **v:** CS.
An EP isozyme encoded by *Ep-A1a* of CS is visible on zymograms following starch gel electrophoresis {516}. The product of this allele is not observable, however, on zymograms following isoelectric focusing {708}.
Ep-A1b {708}. **v:** Cappelle-Desprez {708}; Hobbit {704}; Rendezvous {1603}.
Ep-A1c {708}. **v:** Sears' Synthetic.
Ep-A1d {894}. Isozyme 6. **v:** PI 294994 {894}.

EP-B1 {516}. [*Ep1* {516}]. 7BL {516}. **v:** CS.
Ep-B1a {708}. **v:** CS.
Ep-B1b {708}. **v:** Cappelle-Desprez.
Ep-B1c {708}. **v:** Ciano 67.
Ep-B1d {708}. **v:** Bersee.
Ep-B1e {708}. **v:** Sears' Synthetic.

EP-D1 {516}. 7DL {516}. **v:** CS.
Ep-D1a {708}. **v:** CS.
Ep-D1b. [*EP-V1* {973}]. **v:** 5L 219 {1521}; H-93-70 {1521}; Hyak {21}; Madsen {20}; Rendezvous {708}; VPM1 {973}.
Assuming that *Ep-D1* encoded an oligopeptidase G, comparative genetics were applied to develop a STS marker for identifying resistance gene *Pch1* {10513} (see Reaction to *Tapesia yallundae*.
Ep-D1c {708}. **v:** Sears' Synthetic.
Ep-D1d {1587}. Null allele. **v:** Wheats with *Lr19* {1587}.
Ep-D1e {894}. Isozyme 5. **v:** PI 294994 {894}.

EP-E1 {518}. 7EL {518}. **al:** CS/*E. elongata*.
EP-H1 {520}. 7HL {520}. **al:** CS/Betzes.
EP-H^{ch}1 {708}. 7H^{ch} {708}. **su:** CS/*H. chilense*.
EP-H^{t}1 {1037}. 7H^{t}S {1037}. **ad:** CS/*E. trachycaulus*.
EP-M^{v}1 {985}. [*Ep-M^{v}1* {985}]. 7M^{v}L. **su:** 7M^{v}.
EP-R1 {92}, {708}, {266}. 6RL {92}. **ad:** CS/Imperial.
EP-S^{b}1 {708}. 7S^{b} {708}. **su:** Holdfast/*Ae. bicornis*.
EP-S^{l}1 {517}. 4S^{l} {517}. **ad:** CS/*Ae. longissima*.
EP-S^{s}1 {1140}. 7S^{s} {1140}. **ad:** CS/*T. searsii*.
EP-U1 {708}. 7U {708}. **su:** CS/*Ae. umbellulata*.
EP-V1 {708}. 7V {708}. **ad:** CS/*D. villosum*.

EP-2
EP-B2 {599}. 6BS {599}.

An *Ep* locus was located in 4RS in King II rye {1280}, using Holdfast/King II addition lines and in 4R in Imperial {266} using Chinese Spring/Imperial addition lines.

2.2.7. Esterase

Genetic control of esterases [carboxylic ester hydrolases (E.C.3.1.1.1)] was the subject of a comparative study {814}.
EST-2, EST-5 and EST-8 are controlled by genes on 3L and where a recombination test was possible between *EST-D5* and *EST-D8*, no segregation was observed. The different gene symbols were retained because of the different tissue specificities and polymerisation profiles of the enzymes. The same arguments surround the *EST-1* and *EST-6* genes located in the 3S arms {814}.
The *EST-6* gene of rye was mapped {249}. The *EST-6* genes of wheat were mapped comparatively in the proximal regions of chromosomes 2S {256}. The *EST-2, EST-5* and *EST-8* were mapped to the extreme distal regions in the 3L arms {247}.

EST-1

EST-1 is a dimeric enzyme that electrofocuses around pH4.0 and is expressed in all tissues except endosperm {814}.
EST-A1. [*Est$_{A}$* {61}]. 3AS {60}. **v:** CS.

EST-B1. [*Est$_{B}$* {61}]. 3BS {100}. 3B {60}. **v:** CS.

EST-D1. [*Est$_{D}$* {61}]. 3D {60}. 3DS {100}. **v:** CS.

Each of 208 hexaploid accessions carried the same *Est-1* allele except accessions of *T. compactum* var. *rubriceps*, each of which carried an *Est-B1* or *Est-D1* electrophoretic mobility variant {585}.

EST-E1 {518}. 3ES {518}. **ad:** CS/*E. elongata*.
EST-H1 {814}. 3H {814}. **ad:** CS/Betzes.
EST-R1. [*Est*$_R$ {61}]. 3R {1254,60}. **ad:** CS/Imperial {60}; Holdfast/King II {100}; Kharkov/Dakold {100}.
EST-S^1***1*** {814}. 3S^1 {814}. **ad:** CS/*Ae. longissima*.

EST-2
EST-2 is a coleoptile-specific monomeric enzyme that electrofocuses at low pI.
EST-A2. [*Est-2*$_A$ {585}]. 3A {585}. **v:** CS.

EST-B2. [*Est-2*$_B$ {585}]. 3BL {585}. **v:** CS.
Among 208 hexaploid accessions, an apparent *Est-B2* null allele occurred frequently in accessions of *T. macha* and *T. sphaerococcum* and occasionally in accessions of *T. compactum*. The allele was not observed in *T. aestivum* and *T. spelta* accessions {585}.
EST-D2. [*Est-2*$_D$ {585}]. 3DL {585}. **v:** CS.

EST-3
EST-3 is a monomeric enzyme that is expressed in young seedlings (this enzyme was not observed in {814}).

EST-B3. [*Est-3*$_B$ {585}]. 7BS {585}. **v:** CS.

EST-D3. [*Est-3*$_D$ {585}]. 7DS {585}. **v:** CS.

EST-H3 {520}. 7H {520}. **ad:** CS/Betzes.
One accession carrying an apparent *Est-B3* null allele and one carrying an apparent *Est-D3* null allele were found among 208 hexaploid accessions {585}.
A 7AS locus encodes three esterase isozymes in immature grains {009}.

***EST*-4**
EST-4 is a monomeric, leaf-specific enzyme that electrofocuses around pH 4.5.

EST-A4. [*Est-4*$_A$ {585}]. 6AL {585, 919}. **v:** CS.

EST-B4. [*Est-4*$_B$ {585}]. 6BL {585, 919}. **v:** CS.

EST-D4. [*Est-4*$_D$ {585}]. 6DL {585, 919}. **v:** CS.

Probable *Est-A4* and *Est-D4* null alleles were detected in several accessions of *T. compactum* var. *rubriceps* {585}; otherwise, no *Est-4* variant occurred among 208 hexaploid accessions {585}.

An esterase gene was located in chromosome L7 (= 6Ag^i) of *Th. intermedium* {361}.

EST-5 {9}.

EST-5 consists of 20 or more monomeric, grain-specific isozymes that electrofocus between pH 5.6 and 7.0.

EST-A5 {9}.
Est-A5a {9}. 3AL {9}. **v:** CS.
Est-A5b {9}. **v:** Kalyansona{9}; *T. compactum* AUS12084{756}.

EST-B5 {9}. 3BL {9}. **v:** CS.
Est-B5a {9}. **v:** CS.
Est-B5b {9}. **v:** Big Club.
Est-B5c {9}. **v:** Timstein.
Est-B5d {9}. **v:** Sears' Synthetic.

EST-D5 {9}. 3DL{9}. **v:** CS.
Est-D5a {9}. **v:** CS
Est-D5b {9}. **v:** *T. macha*.
Est-D5c {9}. **v:** Hobbit 'S'.
Est-D5d {9}. **v:** *T. macha* Line 1.
Est-D5e {756}. **v:** *T. macha* WJR 38548.
Sixty *Ae. tauschii* lines revealed six *Est-D*^{t}5 alleles {1578}.

Encoding of the endosperm esterases of hexaploid wheat by 12-15 genes in five compound loci located in 3AL, 3BL, 3DL, 3AS and 3DS was postulated in {1204}.
Three and six alleles at *Est-D*^{t}5 (in *Ae. tauschii*) were reported in {756} and {1578}, respectively.

In *S. cereale*, in addition to *EST-R1*, genes encoding leaf esterases were located in three chromosomes {1561}. These included a gene designated *EST8* in 6R in cvs. Imperial and King II, a gene designated *EST2* and two genes, designated *EST6* and *EST7*, which are part of a separate compound locus {1560}, in 5RL in Imperial, and a gene desigaged *EST10* in 4R of King II and 4RL of Imperial. In *Hordeum vulgare*, genes encoding leaf esterases were in 3H {1071; see also, 520,580} and 7H {520}.

EST-Ag^{i}***5*** {374}. 3Ag^{i} {374}. **ad:** Vilmorin 27/*Th. intermedium*.
EST-H5 {10}. 3H {10}. **ad:** CS/Betzes.
EST-H^{ch}***5*** {10}. 3H^{ch} {10}. **ad:** CS/*H. chilense*.
EST-R5 {10}. [*EstA* {737}]. 6R {43}, {1280}. **ad:** CS/Imperial {10, 43}; Kharkov/ Dakold 6RL {10}, {1280}; CS/King II {10}; Holdfast/King II {43}, {1280}.
A second *S. cereale* gene encoding grain esterases, designated *EstB*, was located in 4RL in King II and Petkus and in 7RS in Imperial {737}.
EST-R^{m}***5*** {10}. [*EstB* {737}]. 6R^{m}L {737}. 6R^{m} {10}. **ad:** CS/*S. montanum*.
EST-S^{b}***5*** {10}. 3S^{b} {10}. **su,ad:** CS/*Ae. bicornis*.
EST-S^{l}***5*** {10}. 3S^{l} {10}. **ad:** CS/*Ae. longissima*.

EST-6
EST-6 is a dimeric enzyme that electrofocuses around pH 7.6 and is specific to endosperm.
EST-A6 {1130}. 2AS {1130}. **v:** CS.
Est-A6a {1130}. **v:** CS.
Est-A6b {1130}. **v:** Ceska Previvka.

EST-B6 {1130}. 2BS {1130}. **v:** CS.

Est-B6a {1130}. **v:** CS.
Est-B6b {1130}. **v:** Hope.

EST-D6 {1130}. 2DS {1130}. **v:** CS.
Est-D6a {1130}. **v:** CS.
Est-D6b {1130}. **v:** Sears' Synthetic IPSR 1190903.

EST-M6 {1130}. 2MS {1130}. **su:** CS/*Ae. comosa*.
EST-R6 {370}. 2RS {370}. **al:** DS2 x RxL10 rye popn.

A group of leaf esterase isozymes controlled by the long arms of the homoeologous group 3 chromosomes were reported {919}. The relationship of these esterases to EST-2 and to the leaf esterase designed EST-6 reported in {629} was not determined.

EST-7

EST-7 is a monomeric enzyme that electrofocuses in the same region as EST-6 but is specific to green tissues.

EST-A7 {812}. 2AL {812}. **v:** CS.

EST-B7 {812}. 2BL {812}. **v:** CS.

EST-D7 {812}. 2DL {812}. **v:** CS.
Est-D7a {812}. **v:** CS.
Est-D7b {812}. **v:** Synthetic {IPSR 1190903}.

EST-E7 {812}. 2^E {812}. **ad:** CS/*E. elongata*.
EST-H7 {812}. 2HL {812}. **ad:** CS/Betzes.
EST-R7 {812}. 2RL {812}. **ad:** CS/Imperial. **su:** Holdfast/KingII.
EST-R^{m}7 {812}. 2R^{m}alpha {812}. **ad:** CS/*S. montanum*.
EST-U7 {812}. 2U {812}. **ad:** CS/*Ae. umbellulata*.
EST-V7 {812}. 2V {812}. **ad:** CS/*D. villosum*.

EST-8

EST-8 consists of about 10 isozymes that electrofocus between pH 4.5 and 6.5 and are expressed only in vegetative tissues. EST-8 is likely to be the enzyme previously described in {919} and {629}.
EST-A8 {629}, {814}. [*Est-A6* {629}]. 3AL {629}. **v:** CS.

EST-B8 {613}, {814}. [*Est-B6* {629}]. 3BL {629}. **v:** CS.

EST-D8 {629}, {814}. [*Est-D6* {629}]. 3DL {629}. **v:** CS.

EST-R8 {613}, {814}. 6RL {629}. **ad:** CS/Imperial, CS/King II.

EST-9

EST-9 is a monomeric enzyme that electrofocuses around pH 5.0 and is expressed only in embryos.
EST-A9 {814}. 3AS {814}. **v:** CS.

EST-B9 {814}. 3BS {814}. **v:** CS.

EST-D9 {814}. 3DS {814}. **v:** CS.

2.2.8. Glucosephosphate isomerase

Varietal differences in GPI zymograms were noted in {1127}.
GPI zymogram phenotypes observed in *Triticum* and *Aegilops* species are reported in {456, 457}.
GPI-1
GPI-A1 {507}. 1AS {507, 195}. **v:** CS.

GPI-B1 {507}. 1BS {507, 195}. **v:** CS.

GPI-D1 {507}. 1DS {507, 195}. **v:** CS.
Gpi-D1a {195}. **v:** CS.
Gpi-D1b {195}. **v:** CS variant and certain CS aneuploids. Rare.
No allelic variation at *Gpi-D*^{t}1 was found in 60 accessions of *Ae. tauschii* {1578}.

GPI-Ag^{i}***1***. [*Gpi-X1* {361}]. 1Ag^{i} {361}. **ad:** Vilmorin 27/*Th. intermedium*.
GPI-E1 {518}. 1ES {518}. **ad:** CS/*E. elongata*.
GPI-H1 {1153}. 1HS {1153}. **ad:** CS/Betzes.
GPI-H^{ch}***1*** {195}. 1H^{ch} {195}. **ad:** CS/*H. chilense*.
GPI-R1 {195}. 1R {195}.1RS {779}. **ad:** CS/King II {195}. **al:** 2a, 2b, and R14 {779}.
GPI-R^{m}***1*** {195}. 1R {195}. **ad:** CS/*S. montanum*.
GPI-S^{l}***1*** {1228}. 1S^{1}S {1228}.1S^{1} {517}. **ma:** In *Ae. longissima 2 x Ae. longissima 10, GPI-S*^{l}*1*, two glutenin loci, and three gliadin loci were mapped relative to one another as follows: *GLU-S*^{l}*1* – 15.9 cM – *GPI-S*^{l}*1* – 38 cM – *GLI-S*^{l}*4* – 7.1 cM – *GLU-S*^{l}*3* – 0.9 cM – *GLU-S*^{l}*1* – 5.6 cM – *GLI-S*^{l}*5*{1228}; *GLU-S*^{l}*1* is located in 1S^{l}L and the other loci are in 1S^{l}S.
GPI-S^{s}***1*** {1140}. 1S^{s} {1140}. **ad:** CS/*Ae. searsii*.
GPI-U1 {195}. 1U {195}. **ad:** CS/*Ae. umbellulata*.
GPI-V1 {1026}. 1V {241, 1026}. **ad:** CS/*D. villosum*.

2.2.9. Glutamic oxaloacetic transaminase

GOT-1
GOT-A1 {505}. 6AS {505}. **v:** CS.

GOT-B1 {505}. 6BS {505}. **v:** CS.

GOT-D1 {505}. 6DS {505}. **v:** CS.

Wehling {1559} identified a GOT locus designated *Got1* in 4RL of *S. cereale*

GOT-2
GOT-A2 {505}. 6AL {505}. **v:** CS.

GOT-B2 {505}. 6BL {505}. **v:** CS.

GOT-D2 {505}. 6DL {505}. **v:** CS. **ma:** Cent – *Got-D2* – 2 cM – *Xpsr154-6D* {757}.

GOT-Ag^{e}***2*** {1575}. 6Ag^{e} {1575}. **ad,su:** Rescue/*Th. elongatum*.

GOT-E2 {518}. 6EBeta {518}. **ad:** CS/*E. elongata*.
GOT-H2 {520}. 6H {520}. **ad:** CS/Betzes.
GOT-H^{t}2 {1037}. 6H^{t} {1037}. **ad:** CS/*E. trachycaulus*.
GOT-R2 {1457}. [Got3 {1559}]. 6R {1457}; 6RL {1280}. **ad:** CS/Imperial 6R {1457}; Holdfast/King II 6RL {1280}.
GOT-V2 {1026}, {242}. 6V {1026}. **ad:** Creso/*D. villosum*.

GOT-3
GOT-A3 {505}. 3AL {505}. **v:** CS.

GOT-B3 {505}. 3BL {505}. **v:** CS.

GOT-D3 {505}. 3DL {505}. **v:** CS.

GOT-Ag^{e}3 {521}. 3Ag^{e}L {521}. **ad:** CS/TAP 67. **su:** CS/TAP 67. **tr:** Certain CS 3D/Ag lines.
GOT-C3 {1278}. *F* {1278}. **ad:** *T. aestivum* cv. Alcedo /*Ae. caudata* line C. ***Got-E3*** {518}. 3EL {518}. **ad:** CS/*E. elongata*.
GOT-H3. [*Got-b3* {90}]. 3H {90}. **ad:** CS/Betzes.
GOT-H^{ch}3 {351}. 3H^{ch} {351}. **ad:** MA/*H. chilense*.
GOT-R3 {1457}. [Got3 {1559}]. 3R {1457}. **ad:** CS/Imperial {1457}; Holdfast/ King II {1253}; Kharkov/Dakold {1253}.
GOT-S^{s}3 {1140}. 3S^{s} {1140}. **ad:** CS/*Ae. searsii*.
GOT-V3 {1518}, {242}. 3VL {1518}. **ad:** Creso/*D. villosum*.

GOT-4

GOT-R4. [*Got1/7R* {1203}, *Got2* {1559}]. 7RL {1203}. **al:** *S. cereale*.

2.2.10. Hexokinase

HK-1

HK-B1 {6}. 1BS {6}. **v:** CS.

HK-D1 {6}. 1DS {6}. **v:** CS.

HK-2
Allelic variation was observed in three of 55 hexaploid wheat accessions {6}.

HK-A2 {810}. 3A {810}. **v:** CS.
Hk-A2a {810}. **v:** CS.
Hk-A2b {810}. **s:** CS*/Sears' Synthetic 3A. **v:** Sears' Synthetic IPSR 1190903.

HK-B2 {6}. 3BS {810,6}. **v:** CS.

HK-D2 {810}. 3DS {810}. **v:** CS.
Hk-D2a {810}. **v:** CS.
Hk-D2b {810}. **v:** Sears' Synthetic IPSR 1190903.

HK-E2 {6}. 3ES {6}. **ad:** CS/*E. elongata*.

2.2.11. Lipoxygenase

The *LPX-1* gene in wheat corresponds to barley *LoxA* (GenBank L35931). The *LPX-B1* locus is duplicated, with the *LPX-B1.1* and *LPX-B1.2* loci corresponding to GenBank sequences DQ474240 and DQ474241, respectively. The *Lpx-B1b* allele corresponds to a deletion associated with a 4.5-fold reduction in lipoxygenase activity. The *LPX-2* gene in wheat corresponds to the barley *LoxC* gene (GenBank L37358) whereas the *LPX-3* gene in wheat corresponds to the barley *LoxB* gene (GenBank L37359).

LPX-1

LPX-A1 {516}. [*Lpx-B1* {516}]. 4AL {516}. **v:** CS {516}. **ma:** *Xksu919(Lpx-1)-4A* {0091}.

LPX-B1 {516}. [*Lpx-A1* {516}]. 4BS {516}. **v:** CS {516}. **ma:** *Xcn110(Lpx-1)-4B* {0367, 0269}.
Lpx-B1a {1533}. [*Lpx-A1a* {936}]. **v:** CS.
Lpx-B1b {1533}. [*Lpx-A1b* {936}]. **v:** Bosanka {1533}.

LPX-B1.1 {10303}. 4BS {10303}. **ma:** *Xksm62-4B* – 8 cM – *LpxB1.1* – 13 cM – *Xwmc617b-4B* {10303}.
Lpx-B1.1a {10303}. **tv:** UC1113 {10303}.
Lpx-B1.1b {10303}. **tv:** Kofa, deletion {10303}.

LPX-B1.2 {10303}. 4B {10303}. **v:** CS.

LPX-D1 {516}. 4DS {516}. **v:** CS.

LPX-E1 {518}. 4ES {518}. **ad:** CS/*E. elongata*.
LPX-H1 {716}. 4H {716}. **ad:** CS/Betzes.

LPX-2

LPX-A2 {516}. 5AL {516},{10303}. **v:** CS. **ma:** *Xksu919(Lpx-2)-5A* {91}.

LPX-B2 {516}. 5BL {516},{10303}. **v:** CS. **ma:** *Xksu919(Lpx-2)-5B* {91}; *Xcn111(Lpx-2)-5B* {269}.

LPX-D2 {516}. 5DL {516}. **v:** CS.

LPX-E2 {518}. 5EL {518}. **ad:** CS/*E. elongata*.
LPX-H2 {716}. 5H {716}. **ad:** CS/Betzes.
LPX-*S^s*2 {1140}. 5S^s {1140}. **ad:** CS/*Ae. searsii*.
LPX-V2 {242}. 5V. **ad:** CS/*D. villosum*.

LPX-3

LPX-A3 {10303}. 4AL {10303}. **tv:** UC1113 (GenBank DQ474244) and Kofa (GenBank DQ474242) {10303}. **ma:** *Xwmc617a-4A* – 10 cM – *Lpx-A3* – 15 cM – *Xgwm192b-4A* {10303}.

LPX-B3 {10303}. 4B {10303}. **tv:** UC1113 and Kofa (GenBank DQ474243) {10303}.

2.2.12. Malate dehydrogenase

MDH-1

MDH-A1. [*Mdh2A* {87}]. 1AL {87}. **v:** CS.
Mdh-A3a {811}. **v:** CS.

Mdh-A3b {811}. **v:** Bersee.

MDH-B1. [*Mdh2B* {87}]. 1BL {101, 87}. **v:** CS.
Mdh-B3a {811}. **v:** CS.
Mdh-B3b {811}. **v:** Hope.

MDH-D1. [*Mdh2D* {87}]. 1DL {87}. **v:** CS.

MDH-H1 {1153}. 1HL {1153}. **ad:** CS/Betzes.
MDH-H^{ch}***1*** {352}. 1H^{ch} {352}. **ad:** MA/*H. chilense*.
MDH-R1. [*Mdh2-1* {1252}]. 1RL {1252}. **ad:** CS/Imperial 1R; Kharkov/Dakold 1R; Holdfast/King II 1RL.
MDH-S^{s}***1*** {1140}. 1S^{s} {1140}. **ad:** CS/*T. searsii*.

MDH-2

MDH-H2. [*Mdh2-b2* {90}]. 3H {90}.
MDH-R2. [*Mdh2-2* {1252}]. 3R {1252}. **ad:** CS/Imperial.

A third set of dimeric MDH isozymes identified in mature grain was separable from MDH-1 and MDH-2 by their higher pI's in IEF {811}.
MDH-3
MDH-A3 {811}. 5AS. **v:** CS.
Mdh-D3a {811}. **v:** CS.
Mdh-D3b {811}. **v:** Sears' Synthetic.

MDH-B3 {811}. 5BS. **v:** CS.

MDH-D3 {811}. 5DS. **v:** CS.

MDH-E3 {811}. 5ES. **ad:** CS/*E. elongata*.
MDH-H3 {811}. 5H. **ad:** CS/Betzes.
MDH-U3 {811}. 5U. **ad:** CS/*Ae. umbellulata*.
MDH-R4 {360}. 1RL {360}. **v:** Various crosses.

2.2.13. Peroxidase

Peroxidase (EC1.11.1.7) isozymes have high tissue specificity. Staining and electrophoretic systems are reviewed in {118}. PER-1, -2, -3, -4 and -5 are all reported in {816}.
PER-1. PER-1 is expressed in leaf {12} and coleoptile {816} tissues.

PER-B1 {12}. 1BS {919, 12}. **v:** CS.

PER-D1 {12}. 1DS {919, 12}. **v:** CS.
Per-D1a {12}. **v:** CS.
Per-D1b {12}. **v:** Sears' Synthetic.

PER-H^{ch}***1*** {12}. 1H^{ch} {12}. **ad:** CS/*H. chilense*.
PER-R1 {12}. [*Prx* {1561}]. 1RS {1561, 12}. **ad:** CS/King II {12}; Holdfast/King II {1561}. **tr:** Veery 'S' {12}.

PER-V1 {241}. 1V {241}. **ad:** Creso/*D. villosum*.

PER-2. PER-2 is expressed in young leaf {118}, coleoptile and root {816} tissues.
PER-A2. 2AS. **v:** CS.
Per-A2a {816}. **v:** CS.
Per-A2b {816}. **v:** Timstein.

PER-B2 {118}. 2BS {118}. **v:** CS.
Per-B2a {816}. **v:** CS.
Per-B2b {816}. **v:** Sears' Synthetic IPSR1190903.

PER-D2 {118}. 2DS {118}. **v:** CS.

PER-H2 {118}. [Per-5 {95}]. 2H {118}. **ad:** CS/Betzes.
PER-R2 {118}. 2RS {118}. **ad:** CS/Imperial; Kharkov/Dakold.

PER-3. PER-3 is expressed in embryo {119, 816} and scuteller {119} tissues.
PER-A3 {119}. 3AL {119}. **v:** CS.
Per-A3a {816}. **v:** CS.
Per-A3b {816}. **v:** Timstein.
Per-A3c {816}. **v:** Hobbit 'S'.

PER-B3. [*Per4* {961}]. 3BL {86, 119}. **v:** CS.
Per-B3a {816}. **v:** CS.
Per-B3b {816}. **v:** Hope.
Per-B3c {816}. **v:** *T. macha* IPSR1240005.
Per-B3d {816}. **v:** Timstein.
Per-B3e {816}. **v:** Sears' Synthetic IPSR1190903.

PER-D3. [*Per5* {961}]. 3DL {86, 119}. **v:** CS.
Per-D3a {816}. **v:** CS.
Per-D3b {816}. **v:** Hope.
Per-D3c {816}. **v:** Timstein.
Per-D3d {816}. **v:** *T. macha* IPSR 142005.
Per-D3e {816}. **v:** Sava.
Per-D3f {816}. **v:** Cheyenne.
Per-D3g {816}. **v:** Sears' Synthetic IPSR 1190903.

Varietal variation for *PER-3* was reported in {94}.

PER-4. PER-4 is expressed in endosperm tissue {86, 119}.
PER-A4. [*Per3* {961}]. 7A {695}. 7AS {694, 086, 119}. **v:** CS.
Per-A4a {816}. **v:** CS.
Per-A4b {816}. **v:** Hope.
Per-A4c {816}. **v:** Sicco

PER-B4. [*Per2* {961}]. 4A {695}. 4AL {694, 86, 119}. **v:** CS.
Per-B4a {816}. **v:** CS.
Per-B4b {816}. **v:** Hope.

Per-B4c {816}. **v:** Thatcher.

PER-D4. [*Per1* {961}]. 7D {695},7DS {694, 86, 119}. **v:** CS.
Per-D4a {816}. **v:** CS.
Per-D4b {816}. **v:** Thatcher.

PER-Ag^{e}4. 7Ag^{e}S {694}. **tr:** Certain CS 7D/*Ag*^{e} lines.
PER-Ag^{i}4. [*Per-Ag^{i}3* {374}]. 7Ag^{i} {168}. **ad:** Vilmorin 27/*Th. intermedium*.
Cultivar variation for *Per-4* was reported in {94}.

PER-5. PER-5 is expressed in roots {816}.

PER-D5 {816}. 2DS {816}. **v:** CS.

PER-S^{l}5 {816}. 2S^{l} {816}. **ad:** CS/*Ae. longissima.*

3.2.14. Phosphodiesterase
PDE-A1. [*Pde-A3* {1590}]. 3AS {1589}.3A {1590}. **v:** CS.

PDE-B1. [*Pde-B3* {1590}]. 3BS {1589}.3B {1590}. **v:** CS.

PDE-D1. [*Pde-D3* {1590}]. 3DS {1590}. **v:** CS.

PDE-S^{l}1. 3S^{l}S {172}. **ad:** CS/*Ae. longissima.*
PDE-V1 {1518}. 3VS {1518}. **ad:** CS/*D. villosum.*

2.2.15. Phosphogluconate dehydrogenase
PGD1 {282}. [*Pgd-A3* {963}, *Pgd3* {282}]. 7A^{m}S {282}. **v:** *T. monococcum* {664}.

PGDR1. 4RL {1191}. **ad:** CS/Imperial; Holdfast/King II.

PGDR2. 6RL {1191}. **ad:** CS/Imperial; Holdfast/King II.

Loci were also identified in 6B {1435}, 1EL {1435}, 1HL {147}, {1072}, 1H^{ch} {352} and 1RL {779}.

2.2.16. Phosphoglucomutase
PGM-A1 {88}. [*Pgm-B1* {88}]. 4AL {88}. **v:** CS.

PGM-D1 {88}. 4DS {88}. **v:** CS.

PGM-Ag^{i}1. [*Pgm-X1* {361}]. 4Ag^{i} {361}. **ad:** Vilmorin 27/*Th. intermedium.*
PGM-H1. [*Pgm-b1* {90}]. 4H {90}. **ad:** CS/ Betzes.
PGM-H^{ch}1 {351}. 4H^{ch} {351}. **ad:** MA/*H. chilense.*
PGM-R1. 4RS {1561, 1253}. **ad:** CS/Imperial 4RS {1561, 1253}; Kharkov/Dakold 4R {1253}; Holdfast/King II 4RS{1561, 1253}.

2.2.17. Shikimate dehydrogenase
SKDH-1

SKDH-A1 {1065}, {706}. 5AS {1065}, {706}. **v:** CS.

SKDH-B1 {1065}, {706}. 5BS {1065}, {706}. **v:** CS.

KDH-D1 {1065}, {706}. 5DS {1065}, {706}. **v:** CS.

SKDH-H1 {85}. 5H {85}. **ad:** CS/Betzes.
SKDH-H^{t}1 {1037}. 5H^{t} {1037}. **ad:** CS/*E. trachycaulus*.
SKDH-M^{v}1 {985}. [*Skdh-M^{v}1* {985}]. 5M^{v}. **su:** 5M^{v}(5A), 5M^{v}(5D).
SKDH-R1 {706}. 5RS {706}. 5R {85}. **ad:** CS/King II {85}; CS/Imperial {706}; Kharkov/Dakold {85}. **tr:** CS 4AS-5RL; CS 5BL-5RL.
SKDH-S^{l}1 {85}. 5S^{l}S {85}. **ad:** CS/ *Ae. longissima*.
SKDH-S^{s}1 {1140}. 5S^{s} {1140}. **ad:** CS/*Ae. searsii*.
SKDH-U1. 5U {706}. **ad,su:** CS/*Ae. umbellulata*.
SKDH-V1 {85}. 5V {85}. **ad:** CS/*D. villosum*.

2.2.18. Superoxide dismutase

SOD-1
SOD-A1 {1066}. 2AL {1066}. **v:** CS.

SOD-B1 {1066}. 2BL {1066}. **v:** CS.

SOD-D1 {1066}. 2DL {1066}. **v:** CS.

SOD-E1 {808}. VI E {808}. **ad:** CS/*E. elongata*.
SOD-H1 {716}. 2H {716}. **ad:** CS/Betzes.
SOD-R1 {1066}. [*Sod-3* {586}]. 2R {1066}. **ad:** CS/Imperial.
SOD-S^{s}1 {1140}. 2S^{s} {1140}. **ad:** CS/*Ae. searsii*.
SOD-VI {1026}. 7V {1026}. **ad:** CS/*D. villosum*.

2.2.19. Triosephosphate isomerase

TPI-1
TPI-A1 {1139}. 3AS {1139}. **v:** CS.

TPI-B1 {1139}. 3BS {1139}. **v:** CS.

TPI-D1 {1139}. 3DS {1139}. **v:** CS.

TPI-E1 {1139}. 3E {1139}. **ad:** CS/*E. elongata*.
TPI-H1 {1139}. 3H {1139}. **ad:** CS/Betzes.
TPI-R1 {1139}. 3R {1139}. **ad:** CS/Imperial; Kharkov/Dakold.
TPI-S^{l}1 {1139}. 3S^{l} {1139}. **ad:** CS/ *Ae. longissima*.

TPI-2
TPI-A2 {1139}. 5AL {1139}. **v:** CS.

TPI-B2 {1139}. 5BL {1139}. **v:** CS.

TPI-D2 {1139}. 5DL {1139}. **v:** CS.

TPI-Ag^{i}2 {374}. 5Ag^{i} {374}. **ad:** Vilmorin 27/*Th. intermedium*.
TPI-H2 {1139}. 5H {1139}. **ad:** CS/Betzes.
TPI-R2 {1139}. 5R {1139}. **ad:** CS/Imperial; Kharkov/Dakold.
TPI-S^{l}2 {1139}. 5S^{l} {1139}. **ad:** CS/*Ae. longissima*.
TPI-U2 {1139}. 5U {1139}. **ad:** CS/*Ae. umbellulata*.

2.2.20. Aromatic alcohol dehydrogenase

AADH-1
AADH-A1. [*Adh-A2* {584}]. 5AL {584}. **v:** CS. **ma:** *XksuG44-5A*(proximal) - 6.9 cM - *AADH-A1* - 24.7 cM - *Xcdo412-5* (distal) {9959}.
Aadh-A1a. **v:** CS; 133 other accessions {584}.
Aadh-A1b. **v:** *T. spelta*; K-24696; other accessions {584}.

AADH-B1. [*Adh-B2* {584}]. 5BL {584}. **v:** CS.
Aadh-B1a. **v:** CS {1533}.
Aadh-B1b. **v:** Drina {1533}.

AADH-D1. [*Adh-D2* {584}]. 5DL {584}. **v:** CS.

AADH-C1 {1278}. *C* {1278}. **ad:** Alcedo/*Ae. caudata* line C.
AADH-E1. [*Adh-E2* {518}]. 5EL {518}. **ad:** CS/*E. elongata*.
AADH-R1. 5RL {1280}. **ad:** Holdfast/King II.

AADH-2
AADH-A2. [*Adh-A3* {508}]. 6A {1279}.6AL {513}, {587}. **v:** CS {513}; Carola {1279}.

AADH-B2. [*Adh-B3* {508}]. 6B {1279}.6BL {513}. **v:** CS {513}; Carola {1279}.

AADH-D2. [*Adh-D3* {508}]. 6DL {513}.6D {1279}. **v:** CS {513}; Carola {1279}.

AADH-Ag^{e}2 {1575}. 6Ag^{e} {1575}. **ad,su:** Rescue/*Th. elongatum*.
AADH-E2. [*Adh-E3* {518}]. 6EBeta {518}. **ad:** CS/*E. elongata*.
AADH-R2. 6RL {1280}. **ad:** Holdfast/King II.
AADH-V2 {241}. 6V {241}. **ad:** CS/*D. villosum*.

The *AADH-1* and *AADH-2* loci were designated with the synonyms *Adh-2* and *Adh-3*, respectively, in some publications in addition to {508}, {518}, {584}. These include: {510}, {509}, {511}, {519}, {517}, {587}, 1066, 1139}.

2.2.21. Aconitase

ACO-1
ACO-A1 {189}. 6AL {189}. **v:** CS.
Aco-A1a. **v:** CS {1533}.
Aco-A1b. **v:** Dubravka {1533}.

ACO-B1 {189}. 6BL {189}. **v:** CS.
Aco-B1a. **v:** CS {1533}.

Aco-B1b. **v:** Dubravka {1533}.
Aco-B1c. **v:** Slavonka {1533}.

ACO-Ag^{e}1 {1575}. 6Ag^{e} {1575}. **ad,su:** Rescue/*Th. elongatum*.
ACO-E1 {189}. 6Ebeta {189}. **ad:** CS/*E. elongata*.
ACO-H1. [*Aco-1* {147}]. 6HL {189}.6H {147}. **ad:** CS/Betzes.
ACO-R1 {189}. 6RL {189}. **ad:** Sturdy/PI 252003.
ACO-S^{l}1 {189}. 6S^{l} {189}. **ad:** CS/*Ae. longissima*.
ACO-S^{s}1 {1140}. 6S^{s} {1140}. **ad:** CS/*Ae. searsii*.
ACO-U1 {189}. CSU-31 {189}. **ad:** CS/*Ae. umbellulata*.

ACO-2
ACO-B2
Aco-B2a {1513}. **v:** CS.
Aco-B2b {1513}. **v:** PI 278437.
Aco-B2c {1513}. **v:** PI 182575.
Aco-B2d {1513}. **v:** PI 157589.

ACO-D1 {189}. 6DL {189}. **v:** CS.

Further alleles at *Aco-A1* and *Aco-B1* are listed in {1127}; these have not been tested against those found in {1533}.

ACO-A2 {189}. 5AL {189}. **v:** CS.

ACO-B2 {189}. 4BL {1513}. **v:** CS.

ACO-D2 {189}. 4DL {1513}. **v:** CS.

ACO-E2 {189}. 4EL {189}. **ad:** CS/*E. elongata*.
ACO-M^{v}2 {1341}. [*Aco-M^{v}2* {985}]. 5M^{v}. **ad:** 5M^{v}(5A),5M^{v}(5D).
ACO-R2 {189}. 5RL {189}. **ad:** CS/King II 5R; Holdfast/ King II 5RL.
ACO-S^{s}2 {1140}. 4S^{s} {1140}. **ad:** CS/*Ae. searsii*.

2.2.22. NADH dehydrogenase

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *NDH1* (NADH dehydrogenase) and *DIA3* (diaphorase) represent the same locus {0356}.

NDH-1
NDH-A1. [*Ndh-B1* {513}]. 4AL {513}. **v:** CS.
Ndh-A1a {1533}. [*Ndh-B1a* {936}]. **v:** CS.
Ndh-A1b {1533}. [*Ndh-B1b* {936}]. **v:** Sutjeska.
Ndh-A1c {1533}. [*Ndh-B1c* {936}]. **v:** Fruskogorka.
Ndh-A1d {1037}. [*Ndh-A1b* {1037}]. **v:** Hope, Timgalen.

NDH-B1 {513}. [*Ndh-A1* {513}]. 4BS {513}. **v:** CS.

NDH-D1 {513}. 4DS {513}. **v:** CS.

NDH-E1 {362}. 4E {362}. **ad:** CS/*E. elongata*.
NDH-H1. [*Nadhd-1* {147}]. 4H {147}.4HS {813}. **ad:** CS/Betzes.
NDH-H^{ch}***1*** {813}. 4H^{ch} {813}. **ad:** CS/*H. chilense*.
NDH-V1 {241}. 4V {241}. **ad:** CS/*D. villosum*.
NDH-R1 {813}. 4RS {813}.4R {362}. **ad:** CS/Imperial, CS/King II {813, 362}; CS/Dakold {362}.
NDH-S^{l}*1* {813}. 4S^{l} {813}. **ad:** CS/*Ae. longissima*.
NDH-U1 {362}. *A* {362}. **ad:** CS/*Ae. umbellulata*.

NDH-2
Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *NDH-2* (NADH dehydrogenase) and *DIA2* (diaphorase) represent the same locus {0356}.

NDH-A2 {813}. 7A {813}. **v:** Hope.

NDH-D2 {813}. 7DS {813}. **v:** CS.

NDH-R2 {813}. 7RS {813}. **ad:** CS/Imperial, CS/King II, Holdfast/King II (7R).

NDH-3
NDH-A3 {813}. 3AL {813}. **v:** CS.

NDH-B3 {813}. 3BL {813}. **v:** CS.
Ndh-B3a {813}. **v:** CS.
Ndh-B3b {813}. **v:** Carmen.

NDH-D3 {813}. 3DL {813}. **v:** CS.

A *NDH* locus, designated *NADHD2*, was mapped 27 cM from *Est-D10* in an *Ae. taushii* F$_2$ population derived from VIR-1954/VIR-1345 {10046}. This locus may be homologous to *NDH-D3*.

NDH-H3 {813}. 3HL {813}. **ad:** CS/Betzes.
NDH-R3 {813}. 6RL {813}. **ad:** Holdfast/King II, CS/Imperial (6R), CS/King II (6R).
NDH-S^{l}***3*** {813}. 3S^{l}L {813}. **ad:** CS/*Ae. longissima*; CS/*Ae. sharonesis* (3S^{l}).

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that *NDH-3* (NADH dehydrogenase), *DIA1* (diaphorase) and *MNR1* (menadione reductase) represent the same locus {0356}.

NDH-4
NDH-A4 {813}. 3AS {813}. **v:** CS.

NDH-B4 {813}. 3BS {813}. **v:** CS.

NDH-E4 {813}. 3ES {813}. **ad:** CS/*E. elongata*.
NDH-H4 {813}. 3HS {813}. **ad:** CS/Betzes.
NDH-R4 {813}. 3RS {813}. **ad:** CS/King II, CS/Imperial (3R).

2.2.23 Dipeptidase

DIP-1
DIP-A1. [*Pept-A1* {454}]. 6AL {700}, {454}. **v:** CS.
Dip-A1a {700}. **v:** CS.
Dip-A1b {700}. **v:** Cheyenne.

DIP-B1. [*Pept-B1* {1533}]. 6BL {700, 454}. **v:** CS.
Dip-B1a {700}. **v:** CS.
Dip-B1b {700}. **v:** Cappelle-Desprez.

DIP-D1 {700}. 6DL {700}. **v:** CS.

DIP-H1. [*Pept-1* {147}, *Dip 1* {145}]. 6H {145}, {147}, {700}. **ad:** CS/Betzes.
DIP-J1 {700}. 6J {700}. **ad:** CS/*Th. junceum*.
DIP-V1 {700}. 6V {700}. **ad:** CS/*D. villosum*.

2.2.24. Malic enzyme

A dimeric enzyme extractable from mature grains.
MAL-A1 {809}. 3AL. **v:** CS.
Mal-B1a {809}. **v:** CS.
Mal-B1b {809}. **v:** *T. spelta* IPSR line 1.
Mal-B1c {809}. **v:** Sears' Synthetic.

MAL-B1 {809}. 3BL. **v:** CS.

MAL-D1 {809}. 3DL. **v:** CS.

MAL-E1 {809}. 3E. **ad:** CS/*E. elongata*.
MAL-H1 {809}. 3H. **ad:** CS/Betzes.
MAL-R1 {809}. 3R. **ad:** CS/Imperial.

2.2.25. Adenylate kinase

ADK-1
ADK-A1 {91}. [*Adk-a* {91}]. 7AL {91}. **v:** CS.

ADK-B1 {91}. [*Adk-b* {91}]. 7BL {91}. **v:** CS.

ADK-D1 {91}. [*Adk-d* {91}]. 7DL {91}. **v:** CS.

ADK-E1 {91}. 7E {91}.7E {1435}. **ad:** CS/*E. elongata*.
ADK-H1 {91}. 7HS {1435}.7H {91}. **ad:** CS/Betzes.
ADK-M^{v}1 {985}. [*Adk-M^{v}1* {985}]. 7M^{v}L. **su:** 7M^{v}(7D).
ADK-R1 {91}. 7RL {91}. **ad:** CS/Imperial; Holdfast/King II.
ADK-U1 {91}. *E* {91}. **ad:** CS/*Ae. umbellulata*.
ADK-Ag^{i}1 {91}. 7Ag^{i} {91}. **ad:** CS/*Th. intermedium*.
ADK-H2. 6HL {1435}. **ad:** CS/Betzes.

2.2.26. Glutamate-pyruvate transaminase

GPT-1

GPT-A1 {1435}. 1AS {1435}. **v:** CS.

GPT-B1 {1435}. 1BS {1435}. **v:** CS.

GPT-D1 {1435}. 1DS {1435}. **v:** CS.

GPT-E1 {1435}. 1ES {1435}. **ad:** CS/*E. elongata* 1E.
GPT-H1 {1435}. 1H {1435}. **dv:** *H. vulgare* cv. Betzes.

2.2.26. Glutamate-pyruvate transaminase

CAT-1

CAT-B1 {1466}. [*Cat-A1* {1466}]. 4BL {1466}. **v:** CS.

A catalase locus, designated *CAT2*, was mapped 6 cM proximal to *ACO-D2* in an *Ae. tauschii* F_2 population derived from VIR-1954/VIR-1345 cross {10046}. This locus may be orthologous to *CAT-B1* {10046}.

2.2.28. Beta-glucosidase

b-GLS {282}. $2A^mL$ {282}. **dv:** DV92.
b-Glsa {282}. **dv:** DV92.
b-Glsb {282}. Null allele. **dv:** G3116.

2.2.29. Starch branching enzyme I

SBEI

SBEI1 {9937}. 1DL {9937}. **v:** CS {9937}.

SBEI2 {9937}. 7BL {9937}. **v:** CS {9937}.

2.2.30. Starch branching enzyme II

SBEII.

Suppression of SBEIIb expression alone had no effect on amylose contents; however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose {10534}. Combined loss-of-function mutations in *SbeIIa-A, SbeIIa-B, SbeIIb-A*, and *SbeIIb-B* (PI 670160) increased amylose content by 66% and resistant starch by 753% relative to the control in tetraploid wheat cv. Kronos {11125}. Combination of these four mutations with mutations of *SbeIIa-D* in hexaploid wheat (PI 670160) increased amylose content by 63% and resistant starch by 1,057% in field experiments relative to the control {11126}

2.2.31. Benzoxinones

The putative role of benzoxinones sets *BX-1* to *BX-5* is to catalyze the pathway Indole-3-glycerol phosphate to DIBOA. Primers designated from maize sequences were used to generate RT-PCR products utilised to screen a cDNA library from CS seedlings. Full-length cDNAs were heterologously expressed in yeast and the *Bx* gene products had enzymatic action. The *BX* genes located by Southern analysis of CS deletion stocks occurred as clustered groups in homoeologous groups 4 (*BX-1, BX-2*) and 5 (*BX-3.1, .2, BX-4, BX-5*) {10103}.

2.2.32. Acetohydroxyacid synthase (EC 4.1.3.18)

An orthologous series was mapped as the active target sites of imidazolinone herbicides. See section 1: Herbicide Response: Imidazolinone resistance.

AHASL_1

AHASL-A1 {10101}. [*Imi3* {10099}]. 6AL {10101}. **v2:** CDC Teal IMI 15A *Imi3* {10099}. **dv:** *T. monococcum* mutant EM2 (mutant of susceptible line TM23 {10102}.

AHASL-B1 {10101}. [*Imi2* {10099}]. 6BL {10101}. **v:** CDC Teal IMI 11A = PTA3953 {10099}.

AHASL-D1 {10101}. [*Imi1* {10099}]. 6DL {10101}. **v:** BW755 = Grandin*3/Fidel-Fs-4 {10099}.

2.2.33. Phytoene synthase (EC 2.5.1.32)

Phytoene synthase, which condenses two molecules of geranyl geranyl diphosphate to produce phytoene, is the first of the specific enzyme necessary for carotene biosysthesis in plants.
Homology with the same gene in rice (*Psy1*) {10230}.
Phytoene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Section 1: Flour colour and Grain quality parameters: Flour, semolina and pasta colour). Gene *Psy-A1* was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents {10501}. Most hexaploid wheat cultivars have a 676-bp insertion in intron four that is absent in Australian cultivars Dundee, Raven, and Aroona with high yellow pigment. The *Psy-B1b* allele from tetraploid wheat Kofa is the result of a B-A intergenomic conversion event that probably occurred in Cappelli *ph1c* mutant 1 {10530}. An EMS mutation in the *Psy-E1* gene is associated with whiter endosperm in lines carrying the *Th. elongatum* 7EL translocation.

PSY-1

PSY1-A1 {10230}. 7AL {10230}. **tv:** Kofa {10230}. **ma:** *Xwmc809-7A* – 5.8 cM – *Yp7A* {10501}.
Psy1-A1a. **tv:** Kofa {10230}. **ma:** *Xwmc809-7A* - 5.8 cM - *Yp7A* {10501}.
Psy1-A1b. **v:** Chinese common wheats with low yellow pigment content {10501}; PH82-2 {10501}; Shaan 9314 {10501}; Xinong 336 {10501}. **c:** GenBank EF600064 {10501}. 37-bp insertion in intron 2 (231 bp fragment for marker *Yp7A*) {10501}. 676-bp insertion in intron 4 {10530}.
Psy1-A1c {10530}. **v:** M564 {10650}. **c:** GenBank EU650391 {10650}; No 37-bp insertion in intron 2 and no 676-bp insertion in intron 4 {10530}; High yellow pigment cultivars: Aroona (PI 464647) {10530}; Dundee (PI 89424, PI 106125) {10530}; Raven (PI 303633, PI 330959) {10530}.
Psy1-A1d {10651}. **tv:** Langdon {10651}; *T. dicoccum* DM28 {10652}. **c:** GenBank EU263018 {10651}; FJ393515 {10652}.
Psy1-A1e {10651}. **v:** Sunco {10654}. **tv:** DR8 {10651}. **c:** EU649791 {10654}; EU263019 {10651}.
Psy1-A1f {10652}. **dv:** *T. urartu* PI 428326 {10652}. **c:** FJ393516 {10652}.
Psy1-A1g {10652}. **dv:** *T. urartu* UR1 {10652}. **c:** FJ393517{10652}.
Psy1-A1h {10652}. **dv:** *T. boeoticum* BO1 {10652}; *T. monococcum* MO5 {10652}. **c:** FJ393518 {10652}; FJ393519 {10652}.
Psy1-A1i {10652}. **dv:** *T. monococcum* MO1 {10652}. **c:** FJ393520 {10652}.
Psy1-A1j {10652}. **dv:** *T. monococcum* MO2 {10652}. **c:** FJ393521 {10652}.
Psy1-A1k {10652}. **v:** Spelt 167 {10652}. **tv:** *T. dicoccoides* DS3 {10652}; *T. dicoccum* DM37 {10652}. **c:** FJ293527 {10652}; FJ293522 {10652}; FJ293523 {10652}.
Psy1-A1l {10652}. **tv:** Kofa {10530, 10230}; Strongfield {10653}; *T. dicoccoides* DS6 {10652}. **c:** EU096090 {10530, 10230}; FJ393524 {10652}.
Psy1-A1m {10652}. **tv:** *T. dicoccum* DM26 {10652}. **c:** FJ393525 {10652}.

Psy1-A1n {10652}. **v:** Spelt SP9{10652}. **c:** FJ393526 {10652}.
Psy1-A1o {10653}. **tv:** Commander {10653}. **c:** FJ234424 {10653}.
Psy1-A1p {10654}. **v:** Tasman {10654}. **c:** EU649792 {10654}.
Psy1-A1q {10654}. **v:** Cranbrook {10654}. **c:** EU649793 {10654}.
Psy1-A1r {10654}. **v:** Halberd {10654}. **c:** EU649794 {10654}.
Psy1-A1s {10654}. **v:** Schomburgk {10654}. **c:** EU649795 {10654}.
Psy1-A1t {10920}. **v:** WAWHT2074 {10920}. **ma:** *Xwgm344-7A* - 3.9 cM - *Psy1-A1t* - 9.9 cM - *Ccfa2257a-7A* {10920}. **c:** GenBank HM006895 {10920}.

PSY1-B1 {10230}. 7BL {10230}. **tv:** Kofa{10230}. **ma:** *Xcfa2040-7B* – 12 cM – *PSY1-B1* – 5 cM – *Xgwm146-7B* {10230}.
Psy1-B1a {10650}. GenBank EU096093 {10530}. [{10530}]. **v:** Chinese Spring {10654, 10650, 10530}; Spelt SP9 {10652}. **tv:** *T. dicoccoides* DS4 {10652}. **c:** FJ393529 {10652}; FJ393528 {10652}; EU650392 {10650}; EU096094 {10530}; EU649789 {10654}.
Psy1-B1b {10650}. **v:** Neixiang 188 {10650}. **c:** EU650393 {10650}.
Psy1-B1c {10650}. **v:** CA 9648 {10650}. **c:** EU650394 {10650}.
Psy1-B1d {10650}. **v:** Ning 98084 {10650}. **c:** EU650395 {10650}.
Psy1-B1e {10650}. **v:** M484 {10650}. **tv:** DR8 {10650}; *T. dicoccum* DM28 {10652}. **c:** EU263021{10650}; FJ393541 {10652}.
Psy1-B1f {10651}. **tv:** Langdon {10651}. **c:** EU263020 {10651}.
Psy1-B1g {10651}. **tv:** DR1 {10651}; *T. dicoccoides* DS6 {10652}. **c:** EU650396 {10651}; FJ393530 {10652}.
Psy1-B1h {10652}. **tv:** *T. dicoccoides* DS3 {10652}. **c:** FJ393531 {10652}.
Psy1-B1i {10652}. **tv:** *T. dicoccoides* DS8 {10652}. **c:** FJ393532 {10652}.
Psy1-B1j {10652}. **tv:** *T. dicoccum* DM26 {10652}. **c:** FJ393533 {10652}.
Psy1-B1k {10652}. **tv:** *T. dicoccum* DM33 {10652}. **c:** FJ393534 {10652}.
Psy1-B1l {10652}. **tv:** *T. dicoccum* DM37 {10652}. **c:** FJ393535 {10652}.
Psy1-B1m {10652}. **v:** Spelt 167 {10652}. **tv:** *T. dicoccum* DM47 {10652}. **c:** FJ393540 {10652}; FJ393539 {10652}.
Psy1-B1n {10530}. Previously designated *Psy1-B1b* {10656}. **tv:** Kofa. **c:** EU096092 {10530}; DQ642439 {10230}.
Psy1-B1o {10530}. Previously designated *Psy1-B1a* {10656}. **tv:** UC1113 {10530}; W9262-260D3 {10230}. **c:** EU096093 {10530}; DQ642440 {10230}.

PSY1-D1 {10652}. 7DL {10652}.
Psy1-D1a {10652}. **v:** Chinese Spring {10652}. **c:** EU650397 {10652}; EU649790 {10654}.
Psy1-D1b {10652}. **dv:** *Ae. tauschii* Ae34 {10652}. **c:** FJ393542 {10652}.
Psy1-D1c {10652}. **dv:** *Ae. tauschii* Ae46 {10652}. **c:** FJ393543 {10652}.
Psy1-D1d {10652}. **dv:** *Ae. tauschii* Y99 {10652}. **c:** FJ393544 {10652}.
Psy1-D1e {10652}. **v:** Spelt SP9 {10652}. **c:** FJ393545 {10652}.
Psy1-D1f {10652}. **v:** Spelt 217 {10652}. **c:** FJ393546 {10652}.
Psy1-D1g {10652}. **v:** Zhonliang 88375 {10652}. **c:** FJ807498 {10652}.
Psy1-D1h {10652}. **dv:** *Ae. tauschii* Ae37 {10652}. **c:** FJ807499 {10652}.
Psy1-D1i {10652}. **dv:** *Ae. tauschii* Ae38 {10652}. **c:** FJ807500{10652}.
Psy1-D1j {10652}. **dv:** *Ae. tauschii* Ae42 {10652}. **c:** FJ807501 {10652}.
Psy1-D1k {10655}. **v:** Nongda 3291 {10655}. **c:** FJ807495 {10655}.
Psy1-D1l {10655}. **v:** E 86642 {10655}. **c:** FJ807496 {10655}.
Psy1-D1m {10655}. **v:** Ning 97-18 {10655}. **c:** FJ807497 {10655}.

PSY1-E1. [*Psy-E1*].
Psy1-E1a {10530}. GenBank EU096095 {10530}. [*Psy-E1a* {10530}]. **v:** Agatha (7EL translocation) {10530}.
Psy1-E1b {10530}. [*Psy-E1b* {10530}]. Similar to EU096095, but with P to L substitution at amino acid 422 {10530}. **v:** EMS mutant Agatha 28-4 {10530}; Wheatear {10530}.
PSY1-S1 {10652}. **al:** *Ae. speltoides* Ae48 {10652}.
Psy1-S1a {10652}. **al:** *Ae. speltoides* Ae48 {10652}. **c:** FJ393536 {10652}.
Psy1-S1b {10652}. **al:** *Ae. speltoides* Ae49 {10652}. **c:** FJ393537 {10652}.
Psy1-S1c {10652}. **al:** *Ae. speltoides* Y162 {10652}. **c:** FJ393538 {10652}.

PSY-2 Homology with the same gene in rice (*Psy2*) {10230}.

PSY2-A1 {10230}. 5A {10230}. **tv:** Kofa {10230}.

PSY2-B1 {10230}. 5B {10230}. **tv:** Kofa {10230}. **ma:** *Xgwm191-5B* – 17 cM – *PSY-B2* {10230}.

2.2.34. Polyphenol oxidase

High PPO activity in kernels and flour leads to a time-dependent discolouration of end products such as noodles, pasta and breads.
Primers different from those in {10386} were developed in {10504}, but their ability to distinguish phenotypic groupings (alleles) was similar. A null allele of *Ppo-D1* was identified for this locus using primer pair WP3-2 {10504}.
PPO-1
PPO-A1 {10386}. *PPO-2A* {10385}. 2AL {10385}. **ma:** Detected with STS markers PPO18 {10385} and PPO33 {10386}; *Xgwm321-2A* – 1.4 cM – *PPO-A1* – 5.8 cM – *Xgwm294-2* {10385}; *Xcfa2058-2A* – 0.4 cM – *PPO-A2* – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – *PPO-A1* – 11.0 cM – *Xwmc181-2* {10931}.
Ppo-A1a {10386}. *PPO-2Aa* {10385}. **v:** Nongda 139 {10386}; Zhongyou 9507 {10504,10385,10386}; others{10504,10386}. **c:** EF070147{10386}.
Wheats with this allele tend to have lower PPO activity {10385, 10386}.
Ppo-A1b {10386}. *PPO-2Ab* {10385}. **v:** Chinese Spring {10386}; CA 9632 {10385, 10386}; Nongda 183 {10504}; others {10504, 10386}. **tv:** *T. dicoccoides* DS4 {10386}. **c:** EF070148 {10386}.
Ppo-A1c {10657}. **dv:** *T. urartu* UR1 {10657}. **c:** EU371651 {10657}.
Ppo-A1d {10657}. **dv:** *T. boeoticum* BO1 {10657}. **c:** EU371652 {10657}.
Ppo-A1e {10657}. **tv:** DR8 {10657}. **dv:** *T. monococcum* MO1 {10657}. **c:** EU371653 {10657}.
Ppo-A1f {10657}. **v:** Penawawa {10931}. **tv:** *T. dicoccoides* DS3 {10657}. **c:** EU371654 {10657}.
Ppo-A1g {10657}. **tv:** Langdon {10657}. **c:** EU371655 {10657}.
Ppo-A1h {10931}. **v:** Louise {10931}. **c:** GenBank JN632506 {10931}.

PPO-B1 {10658}. **v:** Chinese Spring {10658}.
Ppo-B1a {10658}. **v:** Chinese Spring {10658}. **c:** GQ303713 {10658}.

PPO-D1 {10386}. **ma:** Detected with primers PPO16 and PPO29. *Xwmc41-2D* – 2.0 cM – *PPO-D1* {10386}; *Xcfd62-2D* – 0.2 cM – *PPO-D2* – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – *PPO-D1* – 0.9 cM – *Xbarc349-2D* {10931}.
Ppo-D1a {10386}. **v:** Chinese Spring {10386}; Louise {10931}; Zhonghou 9507 {10504, 10386}; others {10504, 10386}. **c:** EF070149 {10386}.
Wheats with this allele tend to have lower PPO activity {10386}.

Ppo-D1b {10386}. EF070150 {10386}. **v:** CA 9632 {10386}; CA 9719 {10386}; Nongda 183 {10504}; others {10504, 10386}. **c:** EF070150 {10386}.
Wheats with this allele tend to have higher PPO activity {10386}.
Ppo-D1c {10657}. **dv:** *Ae. tauschii* Ae38 {10657}. **c:** EU371656 {10657}.
Ppo-D1d {10657}. **dv:** *Ae. tauschii* Y59 {10657}. **c:** EU371657 {10657}.
Ppo-D1e {10504}. [*Ppo-D1null* {10504}, *Ppo-D1c* {10656}]. **v:** Gaiyuerui {10504}; Zm2851 {10504}; XM2855 {10504}; 9114 {10504}.
Wheats with this allele tend to have lower PPO activity {10504}.

PPO-2
PPO-A2 {10930}. [*PPO-A2* {10931}]. 2AL {10930}. **ma:** *Xcfa2058-2A* – 0.4 cM – *PPO-A2* – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – *PPO-A1* – 11.0 cM – *Xwmc181-2* {10931}.
Ppo-A2a {10930}. **v:** Alpowa {10930}. **c:** GenBank HQ228148 {10930}.
Ppo-A2b {10930}. **v:** Panawawa {10931}. **c:** GenBank HQ228149 {10930}.
Ppo-A2c {10931}. **v:** Louise {10931}. **c:** JN632507 {10931}.

PPO-B2 {10930}. [*PPO-B2* {10930}]. 2B {10930}. **ma:** *Xiwa175/Xiwa4866-2B* - 0.7 cM - *PPO-B2* - 2.3 cM - *Xiwa7593-2B* {10931}.
Ppo-B2a {10930}. **v:** Penawawa {10931}. **c:** GenBank HQ228150 {10930}.
Ppo-B2b {10930}. **v:** Alpowa {10930}. **c:** GenBank HQ228151 {10930}.
Ppo-B2c {10930}. **v:** Louise {1211}. **c:** GenBank JN632508 {10930}.

PPO-D2 {10930}. [*PPO-D2* {10930}]. 2DL {10930}. **ma:** *Xcfd62-2D* – 0.2 cM – *PPO-D2* – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – *PPO-D1* – 0.9 cM – *Xbarc349-2D* {10931}.
Ppo-D2a {10930}. **v:** Louise {10931}. **c:** GenBank HQ228152 {10931}.
Ppo-D2b {10930}. **v:** Penawawa {10930}. **c:** HQ228153 {10930}.
Wheats with this allele tend to have lower PPO activity {10385, 10386}.

2.2.35. Protein disulfide isomerase (EC 5.3.4.1)
PDI-1
PDI-A1 {10422}. 4AL {10422}. **v:** CS {10422}.

PDI-B1 {10422}. 4DS {10422}. **v:** CS {10422}.

PDI-D1 {10422}. 4BS {10422}. **v:** CS {10422}.
The genes for PDI and their promoters were sequenced in {10423}. A related sequence on 1BS was shown to be a partial, non-expressed copy in {10424}, but not detected in {10409}. PCR-RFLP markers for [*TaPDI-4A*] and [*TaPDI-4B*] were designated [*Xvut(PDI)-4A*] and [*Xvut(PDI)-4B*] in {10409}. These were also closely associated with Germin (oxalate oxidase {10441}) genes {10409}.

2.2.36. Isoamylase 1

ISO-1 {10295}. [*ISA-1* {10295}]. **dv:** *Ae. tauschii* {10295}.

2.2.37. Polygalacturonase-inhibiting proteins
PGIPs are leucine-rich repeat (LRR) proteins involved in plant defence.
PGIP-1

PGIP-A1 {10608}. *Tapgip3*, AM180658 {10608}. **dv:** *T. monococcum* PI 538722 {10608}.
Not expressed in *T. urartu* PI 428315 (AM884191) {10608} or in polyploid wheat because of inactivation by an inserted copia transposon in the fourth LRR {10608}.

PGIP-B1 {10608}. [*Tapgip1* {10610}]. 7BS {10608, 10610}. **ma:** *XS13M50-7B* - 5 cM - *PGIP-B1* - 11.7 cM - *Xmgb105s-7B* {10608}.
Pgip-B1a {10608}. *Tapgip1a* {10608}. **tv:** Messapia {10608}.
Pgip-B1b {10608}. *Tapgip1b*, AM884195 {10608}. **tv:** *T. turgidum* ssp. *dicoccoides* MG4343 {10608}.
This non-expressed allele produces a large amplicon in southern blots using the Pgip sequence as probe, due to an insertion of a Vacuna mutator element {10608}.

PGIP-D1 {10608}. [*Tapgip2* {10610}]. 7DS {10610}. **tv:** Langdon 7D(7A) {10610}; Langdon 7D(7B) {10610}.

Pgip1 {10390}. 7BS {10390}. **v:** CS ditelo 7BL {10390}. **v2:** Chinese Spring *Pgip2* {10390}. **tv:** Langdon {10390}.

Pgip2 {10390}. 7DS {10390}. **v:** CS ditelo 7DL {10390}. **v2:** Chinese Spring *Pgip1* {10390}.

2.2.38. Flavone 3-hydroxylase (EC 1.14.11.9)

F3H-1
F3H-A1 {10823}. 2AL {10823}. **v:** CS {10823}. **ma:** *Xgwm1067-2A* – 2.1 cM – *F3H-A1* – 11.4 cM – *Xgwm1070-2*^{a} {10823}.
ALLELIC VARIATION

F3H-B1 {10823}. 2BL {10823}. **v:** CS {10823}. **ma:** *F3H-B1/Xgwm1067-2B* – 11.4 cM – *Xgwm1070-2B* {10823}.
ALLELIC VARIATION

F3H-D1 {10823}. 2DL {10823}. **v:** CS {10823}. **ma:** *Xgwm877-2D* – 1.8 cM – *F3H-D1/Xgwm1264-2D* – 22.7 cM – *Xgwm301-2D* {10823}.
ALLELIC VARIATION

F3H-2
F3H-B2 {10823}. 2BL {10823}. **v:** CS {10823}. **ma:** *Xgwm1070-2B* – 30.1 cM – *F3H-B2* {10823}; Located in the terminal region near *Xgwm1027-2B* {10823}.
ALLELIC VARIATION

2.2.39. Zeta-carotene desaturase

ZDS-1
ZDS-A1 {10905}. 2A {10905}. **tv:** Langdon {10905}.

ZDS-B1 {10905}. 2B {10905}. **tv:** Langdon {10905}.

ZDS-D1 {10906}. 2DL {10906}. **v:** CS {10906}.
Zds-D1a {10906}. [*TaZDS-D1a* {10906}]. **v:** CA9632 {10906}; Many Chinese wheats and 80 CIMMYT lines {10906}.

Zds-D1b {10906}. [*TaZDS-D1b* {10906}]. **v:** Ning 99415-8 {10906}; Zhengzhou 9023 {10906}; Zhongyou 9507 {10906}; Zhoumai 13 {10906}.
Cv. Zhongyou 9507 has lower yellow flour pigment content, preferred for Chinese steamed bread and dry Chinese noodles. A QTL in the *Zds-D1a* region explained 18.4% of the variation in yellow pigment content in Zhongyou 9507/CA 9632 {10906}.

2.2.40. Carotenoid beta-hydroxylase (non-heme di-iron type)

HYD are non-heme di-iron b-hydroxilases that act primarily on b-carotene.
HYD-1
HYD-A1 {10913}. 2AL {10913}. **tv:** Kronos {10913}. **v:** UC1041 {10913}.

HYD-B1 {10913}. 2BL {10913}. **tv:** Kronos {10913}. **v:** UC1041 {10913}.

HYD-D1 {10913}. 2DL {10913}. **tv:** Kronos {10913}. **v:** UC1041 {10913}.

HYD-2
HYD-A2 {10913}. 5AL {10913}. **tv:** Kronos {10913}. **v:** UC1041 {10913}.

HYD-B2 {10913}. 4BL {10913}. **tv:** Kronos {10913}. **v:** UC1041 {10913}.

HYD-D2 {10913}. 4DL {10913}. **tv:** Kronos {10913}. **v:** UC1041 {10913}.

2.2.41. Lycopene-zeta-cyclase

Catalyzes the conversion of lycopene to zeta-carotene, a step in the lutein pathway that leads to yellow flour colour.
e-LCY-A1 [{10654}]. *E-LCY3A* {10654}. 3A {10654}.
eLCY-A1a {11713}. **v:** Chinese Spring (11713{; WAWHT2074 {11713}. GenBank EU649785.
eLCY-A1b {11713}. **v:** Ajana {11713}. GenBank JX288762.
Alleles *a* and *b* were distinguished by a CAPS marker based on a SNP at position 2,028 bp. This difference was associated with differences in b flour colour in some Australian accessions {11713}.

e-LCY-B1 [{10654}]. *E-LCY3B* {10654}. 3B {10654}. GenBank EU649786.

e-LCY-D1 [{10654}]. *E-LCY3A* {10654}. 3D {10654}. GenBank EU649787.

2.2.42 Dehydration-responsive element (DREB) proteins; Dehydration response factors (DRF)

DREB genes with an ER EBP/AP2 binding domain, nearby Ser/Thr-rich region and N-terminal nuclear localization signal are a large family of transcription factors induced by abiotic stress.
DREB-A1 [{11718}]. 3AL {11718}].

DREB-B1 [{11718}]. 3BL {11718}]. **ma:** *Xmwg818-3B* – 27.3 cM – *DREB-B1* – 11.2 cM – *Xfbb11-3B* {11718}.
Dreb-B1a [{11718}]. **v:** Opata 85 [{11718}].
Dreb-B1b [{11718}]. **v:** Synthetic W7984 [{11718}].

DREB-D1 [{11718}]. 3DL {11718}.

2.3. Endosperm storage proteins

2.3.1. Glutenins

These are heterogeneous mixtures of proteins comprising subunits linked by disulfide bonds. 'A' are high-molecular-weight (HMW) and 'B', 'C' and 'D' are low-molecular-weight (LMW) subunits.
Using proteomic analysis of 2D gels of seed storage proteins in 39 ditelocentric lines of cv. CS, 105 protein spots were resolved {03129}. Locations of structural genes controlling 26 spots were identified in 10 chromosomal arms (4 on 1BL, 5 on 1BS, 4 on 1DL, 4 on 1DS, 2 on 6AS, 3 on 6BS, 1 on 6DL, 1 on 6DS, 1 on 3BS and 1 on 3BL). Multiple regulators of the same protein located on various chromosome arms were observed. Two novel subunits, named 1Bz and 1Dz, were found to have very similar structures to HMW glutenin subunit 12 (encoded by *Glu-D1-2a* - see the relevant list below) and were located to chromosome arms 1BL and 1DL, respectively.
PCR amplification of genomic DNA was used to isolate three LMW glutenin genes in cultivar Chinese Spring, named LMWG-MB1, LMWG-MB2 and LMWG-MB3 {01101}. The deduced amino-acid sequences showed a high similarity between these ORFs and with those of other LMW glutenin genes. The authors state that the study provided direct evidence that insertions and/or deletions provide a mechanistic explanation for the allelic variation, and hence the resultant evolution, of prolamin genes, and comment on relationships with gamma-secalins and beta-hordein families. Single-base substitutions at identical sites generate premature stop codons in both LMWG-MB2 and LMWG-MB3, indicating that these clones are pseudogenes.

86.3.1.1. GLU-1

The *GLU-1* loci, all of which are compound, encode HMW glutenin subunits.
Each *GLU-1* locus in hexaploid wheat contains two genes, the products of which were described as 'x-type' and 'y-type' based on differences in molecular weight and isoelectric point {1118}.
Other evidence has shown that these gene products differ in electrophoretic fingerprint pattern {1124} and cysteine content {1028}, and the genes themselves differ in nucleotide sequence {1470, 1433, 373}. Although early evidence suggested up to 6 genes in total at each locus {1471}, {373], it appears likely that only a single copy of each gene is present at the 1AL, 1BL, and 1DL loci {495}.
No 'y-type' protein from the *GLU-A1* locus has been demonstrated in hexaploid wheat {1118}, although they are found in diploid wheats {1535}, {798}, and sequencing experiments have shown the presence of two stop codons in the transcribed portion of the gene {10088}. Definitive evidence that subunit 21* {602}, which has a mobility close to that of subunit 21, is a 'x-type' protein rather than a 'y-type' protein has not been obtained. The gene coding for 'x-type' proteins within *GLU-A1* is also often silent {1118}, {420}.
The symbols for the genes within the *GLU-1* loci coding for 'x-type' and 'y-type' proteins will be *GLU-1-1* and *GLU-1-2*, respectively, rather than *GLU-1x* and *GLU-1y* {1470}. The genes are closely linked but recombination has been observed between *GLU-B1-1* and *GLU-B1-2* with a frequency of 3 in 3,450 {1117}. The gene order, relative to the centromere, has not been ascertained.
The subunit nomenclature used is that devised in {1116}; however, an alternative system based upon molecular weight was proposed in {1068}. A system of naming the *GLU-A1-1*, *GLU-A1-2*, *GLU-B1-1* and *GLU-B1-2* alleles in *T. turgidum* var. *dicoccoides* is given in {796}.
In {00116}, a comparison between spelt wheats (*T. spelta*) and bread wheat was carried out for the glutenins using a nomenclature system described in {00117}.
The *GLU-1* loci may be recognised by the DNA probe pTag1290 {1471} and probes pWHE3 (Ax2*), γWHE4 (Ay), γWHE5 (Bx7), γWHE6 (By9), pWHE2 (Dx5) and pWHE1 (Dy10) {03144}. Individual *GLU-1-1* loci on 1A, 1B and 1D and the *GLU-1-2* loci may be recognised by specific primers {263}.
In {00105}, the evolution of the high molecular weight glutenin loci of the A, B, D and G genomes of wheat was explored; 30 partial allele sequences were compared, designated by Greek letters (alpha, beta, gamma, etc.) (5 of which were cited as Schlumbaum, pers. comm.; the remaining 25 were deposited as GenBank, accession nos. X98583-X98592, X98711-X98715 and Y12401-Y12410). These partial alleles derive from all six *GLU-1-1* and *GLU-1-2* loci in current-day samples taken from seven species of wheat,

as well as from DNA extracted from charred grain of two samples from archaeological excavations, dated 3000 and 5000 years old, respectively.
Following the first listing which considers the *GLU-1* set for hexaploid wheat as a single locus, there is a provisional listing based on x- and y- type glutenins. These are not referenced.

A nomenclature system for prolamin banding patterns of triticale was proposed in {03139}. Extensive allelic variation in triticale at *GLU-A1, GLU-B1, GLU-R1* and *GLI-R2* loci was reported in {03121}.

GLU-A1 {1125}, {780}. [*Glt-A1* {420}, *Glu 1A* {1415}, *Glt-A2* {420}]. 1AL {1125}, {781}. 1A {780}. **s:** CS*/Hope 1A {1125}. **v:** CS {781}, {780}; various {420}.
Primers were designated that enabled Ax2* to be distinguished from Ax1 or Ax-null {10641}.
Glu-A1a {1116}. 1 {1116}. **v:** Hope.
Glu-A1b {1116}. 2* {1116}. **v:** Bezostaya 1.
Glu-A1c {1116}. Null allele {1116}. **v:** CS.
Glu-A1d {1535}. **v:** V74, Spain {1115}.
Glu-A1e {1535}. **v:** 132c, Poland {1115}.
Glu-A1f {1535}. **v:** 112-29, Sudan {1115}.
Glu-A1g {1535}. **v:** Landrace 1600.
Glu-A1h {1527}. [*GLU-A1-I* {1527}]. **tv:** PI 94683, USSR, *T. dicoccum*.
Glu-A1i {1527}. [*GLU-A1-II* {1527}]. **tv:** CI 12213, India, *T. dicoccum*; Lambro {1523}.
Glu-A1j {1527}. [*GLU-A1-III* {1527}]. 1' {125}. **tv:** PI 352359, Germany, *T. dicoccum*.
Glu-A1k {478}. 26 {478}. **v:** BT-2288 {478}.
Glu-A1l {847}. **tv:** Chinook, Canada.
Glu-A1m {1069}. **tv:** Nugget Biotype 1, Canada, *T. durum*.
Glu-A1n {1526}. [*Glu-A1m* {959}, *Glu A1-IV* {1526}]. 1' {125}. **tv:** Corado, Portugal {1526}.
Glu-A1o {1526}, {125}. [*Glu A1-V* {1526}, {125}, *Glu-A1n* {959}]. 2** {125}. **tv:** Aric 581/1 {125}; PI 61189 {1525}; USSR.
Glu-A1p {1146}. 3* {1146}. **v:** David 1.
Glu-A1q {125}. [*Glu A1VI* {125}]. 2*** {125}. **tv:** Melianopus 1528.
Glu-A1r {1232}. 39+40 {1232}. **i:** *T. thaoudar* IPSR 1020006/6*Sicco.
Glu-A1s {1231}. 41+42 {1231}. **i:** *T. thaoudar* G3152/6*Sicco.
Glu-A1t {602}. 21* {602}. **v:** W29323, W3879, W31169.
Glu-A1u {02106}. 2^{*B} {02106}. **v:** Bankuti 1201.
The allele designated *Glu-A1u* and *Glu-A1-1u* in the appropriate list below encodes a high molecular weight glutenin subunit (denominated 2^{*B}) that is identical to subunit 2* apart from one amino acid difference involving the exchange of serine for cysteine (which itself is due to a C to G point mutation at the 1181 bp point of the coding region of 2*). The authors of {02106} suggest that the additional cysteine residue facilitates the formation of further disulphide bonds (cf. the 1Dx5 subunit) which might lead to an improvement in gluten quality characters.
Glu-A1v [{03137}]. [*Glu-A1-VII* {03137}]. VII {03137}. **v:** Emmer accession PI 308879 {03137}.
Glu-A1w {10327}. 2.1* {10327} **v:** KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-A1x {10327}. 2' {10327}. **v:** TRI14165/91 {10327}.
The alleles formerly designated *t* to *x* in {959} were renamed *x* to *ab* because allele *t* in {847} and alleles *u, v* and *w* in {1069} had precedence.
Glu-A1y {10535}. [2'' {10535}]. **v:** 211.12014 {10535}.
Glu-A1z {10805}. [*Glu-A1^{m}a* {10805}]. **dv:** PI 191146, *T. monococcum* ssp. *monococcum* {10805}.
Glu-A1aa {10805}. [*Glu-A1^{m}b* {10805}]. **dv:** PI 190946, *T. monococcum* L. ssp. *monococcum* {10805}.
Glu-A1ab {10805}. [*Glu-A1^{m}c* {10805}]. **dv:** PI 191098, *T. monococcum* ssp. *monococcum* {10805}.

Glu-A1ac {10806}. [*Glu-A^{u}1-I* {10806}]. **dv:** PI 428319 {10806}.
Glu-A1ad {10806}. [*Glu-A^{u}1-II* {10806}]. **dv:** PI 428232 {10806}.
Glu-A1ae {10806}. [*Glu-A^{u}1-III* {10806}]. **dv:** PI 428240 {10806}.
Glu-A1af {10806}. [*Glu-A^{u}1-IV* {10806}]. **dv:** PI 428335 {10806}.
Glu-A1ag {10806}. [*Glu-A^{u}1-V* {10806}]. **dv:** PI 538741 {10806}.
Glu-A1ah {10806}. [*Glu-A^{u}1-VI* {10806}]. **dv:** PI 428230 {10806}.
Glu-A1ai {10806}. [*Glu-A^{u}1-VII* {10806}]. **dv:** PI 428253 {10806}.
Glu-A1aj {10806}. [*Glu-A^{u}1-VIII* {10806}]. **dv:** PI 427328 {10806}.
Glu-A1ak {10806}. [*Glu-A^{u}1-IX* {10806}]. **dv:** PI 428327 {10806}.
Glu-A1al {10806}. [*Glu-A^{u}1-X* {10806}]. **dv:** PI 428256 {10806}.
Glu-A1am {10806}. [*Glu-A^{u}1-XI* {10806}]. **dv:** PI 428224 {10806}.
Glu-A1an {10806}. [*Glu-A^{u}1-XII* {10806}]. **dv:** PI 428228 {10806}.
Glu-A1ao {10806}. [*Glu-A^{u}1-XIII* {10806}]. **dv:** PI 538724 {10806}.
Glu-A1ap {10806}. [*Glu-A^{u}1-XIV* {10806}]. **dv:** TRI 6734 {10806}.
Glu-A1aq {10806}. [*Glu-A^{u}1-XV* {10806}]. **dv:** TRI 11494 {10806}.
Glu-A1ar {10806}. [*Glu-A^{u}1-XVI* {10806}]. **dv:** TRI 11495 {10806}.
Glu-A1as {10806}. [*Glu-A^{u}1-XVII* {10806}]. **dv:** PI 428217 {10806}.
Glu-A1at {10806}. [*Glu-A^{u}3-XVIII* {10806}]. **dv:** PI 428225 {10806}.
Glu-A1au {10806}. [*Glu-A^{u}3-XIX* {10806}]. **dv:** PI 538733 {10806}.
Glu-A1av {10806}. [*Glu-A^{u}3-XX* {10806}]. **dv:** PI 428196 {10806}.
Glu-A1aw {10806}. [*Glu-A^{u}3-XXI* {10806}]. **dv:** PI 538724 {10806}.
Glu-A1ax {10806}. [*Glu-A^{u}3-XXII* {10806}]. **dv:** PI 428191 {10806}.
Glu-A1ay {10806}. [*Glu-A^{u}3-XXIII* {10806}]. **dv:** TRI 6734 {10806}.
Glu-A1az {10806}. [*Glu-A^{u}3-XXIV* {10806}]. **dv:** TRI 11496 {10806}.
Glu-A1ba {11106}. [*Glu-A1g* {11106}]. 1.1 {11106}. **v:** Barbela 28 {11106}.

The sequence encoding subunit 1Ax1.1 shows high nucleotide identity with other *GLU-A1* alleles, with the main difference being an insertion of 36 amino acids in the central repetitive region. It is the largest and most acidic subunit currently known at this locus and has been implicated in high dough extensibility in some cv. Barbela wheat lines, although this contrasts with other data showing a similar effect to that of subunit 1Ax1 {11107}.

Glu-A1bb [{11540}]. **tv:** *T. turgidum* ssp. *turgidum* BGE019307 {11540}.

The importance of the HMW glutenin subunits for bread-making quality was first noted from observations in wheat cultivars of related pedigree on the effects of the presence of subunit 1 encoded by *Glu-A1a* {0197}, effects that have repeatedly been confirmed since (for example {0198, 0199, 01100}). There is a possibility that *GLU-A1* alleles *i, j* {1527} and *k* {478} correspond to alleles *d, e, f* or *g* {1535} that were published shortly earlier. *Glu-A1m* [{1526}] was changed to *n*, because the *m* allele in {1069} has precedence. Allele *n* [{1526}] was changed to *o*. An earlier reference to an allele designated *Glu-A1d* {1411} was withdrawn {1114}. There appears to be a minor band associated with subunit 2 encoded by *Glu-A1b* {1516}; this may be the same as a band named A5 in {420}.

Six combinations involving 5 HMW subunits [1A (u-z)] are listed in {420}, from a study of 109 genotypes including representatives of botanical varieties. Numerous alleles in *T. turgidum* var. *dicoccoides* populations, 12 at *GLU-A1-1* and 3 at *GLU-A1-2*, were described in {798}. In a further study using different germplasm of this species {205}, 14 alleles at *GLU-A1* were observed, including 12 not previously found; the 15 alleles included up to 15 alleles at *GLU-A1-1* (with up to 10 not previously observed), and 5 alleles at *GLU-A1-2* (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously.

In a study including emmer accessions (*T. dicoccum*) {00115}, new subunits named 1$^+$ and 2$^-$ were found in accessions MG4378/1 and MG5380/1, respectively, and provisionally assigned to *GLU-A1*. Until confirmed, they are not included in the *GLU-A1* list.

GLU-B1. [*Glt-B1* {420}, *Glu 1B* {1415}, *Glt-B3* {420}, *Glt-B2* {420}]. 1BL {1125}, {107}, {780}. **v:** CS.
Glu-B1a {1116}. 7 {1116}. **v:** Flinor.
Glu-B1b {1116}. 7+8 {1116}. **v:** CS.
Subunit 8 of *Glu-B1b* (7+8) is more acidic in isoelectric focusing than subunit 8 of *Glu-B1d* (6+8) {555}. Variation in the mobility of subunits designated 7 was observed {1118}, according with later observations {714}, {1069}. The subunit encoded by *Glu-B1v* {1069} has the same mobility as subunit 7 of *Glu-B1c* (7+9); it could be the same subunit as 7' encoded by *Glu-B1ai* [{714}]. Variation in the staining intensity of subunit 7 in different lines was observed {1069}; a duplication of the gene encoding subunit 7 probably occurred in cultivar 'Red River 68', as evidenced by increased intensity of the subunit in SDS-PAGE and by approximately doubled intensity of restriction fragments carrying the gene in Southern blotting {9989}.
Glu-B1c {1116}. 7+9 {1116}. **v:** Bezostaya 1.
Glu-B1d {1116}. 6+8 {1116}. **v:** Hope. **tv:** Kronos **{**11497**}**.
Simultaneous and individual truncation mutations were found in *Glu-B1x* and *Glu-B1y* subunits in Kronos mutant lines {11497}. Germplasm was accessioned as PI 692251 (T4-0865, *Bx6* single mutant), PI 692253 (T4-2197, *By8* single mutant) and PI 692252 (T4-1280, *Bx6* + *By8* combined mutant).
Glu-B1e {1116}. 20 {1116}.20x+20y {03133}. **v:** Federation.
Glu-B1f {1116}. 13+16 {1116}. **v:** Lancota (rare).
Primers were designed to distinguish subunit By8 from By8*, for distinguishing subunit By9-containing alleles from non-By9 alleles, and for diagnosing the presence of *Glu-B1f*.
Glu-B1g {1116}. 13+19 {1116}. **v:** NS 335 (rare).
Glu-B1h {1116}. 14+15 {1116}. **v:** Sappo (rare).
Glu-B1i {1116}. 17+18 {1116}. **v:** Gabo.
Although alleles *Glu-B1i* encoding subunits 17+18, and *Glu-B1bc* encoding subunit 6+17, apparently share a common subunit (Ax17 and By17, respectively) it is not clear that this is in fact true.
Glu-B1j {1116}. 21 {1116}.21x+21y {3116}. **v:** Dunav (rare); Foison {03116}.
Glu-B1k {1116}. 22 {1116}. **v:** Serbian (rare).
Glu-B1l {778}. 23+24 {778}. **v:** Spica D.
Glu-B1m {1527}. [*GLU-B1-I* {1527}]. **tv:** PI 94640, Iran, *T. dicoccum*.
Glu-B1n {1527}. [*GLU-B1-II* {1527}]. **tv:** PI 355505, Germany, *T. dicoccum*.
Glu-B1o {1527}. [*GLU-B1-III* {1527}]. **tv:** PI 352354, Ethiopia, *T. dicoccum*.
Glu-B1p {1527}. [*GLU-B1-IV* {1527}]. 23+18 {125}. **tv:** Dritto {1523}; Ethiopia, PI 94655, *T. dicoccum*{1527}.
Subunit 23 of *Glu-B1p* (23+18) and *Glu-B1ad* (23+22) {125} may not be the same subunit as that numbered 23 of *Glu-B1l* (23+24) {778}.
Glu-B1q {1527}. [*GLU-B1-V* {1527}]. **tv:** PI 94633, Morocco, *T. dicoccum*.
Glu-B1r {1527}. [*GLU-B1-VI* {1527}]. 19 {125}. **tv:** PI 946669, Bulgaria, *T. dicoccum* {1527}; Lambro {1523}.
Glu-B1s {478}. 7+11 {478}. **v:** BT-2288.
Subunit 11 of *Glu-B1s* (7+11) was so numbered in {478} because its mobility is the same as one of the subunits encoded by a *GLU-D1* allele (2+11) described in {755}.
Glu-B1t {847}. **v:** Supreza, Canada.
Glu-B1u {1069}. 7^*+8 {1146}. **v:** Owens {1069}; Fiorello {1146}.
Glu-B1v {1069}. **v:** Mondor.
Glu-B1w {1069}. 6^*+8^* {1146}. **v:** Dawbull {1069}; Sieve {1146}.

Possible low gene expression at *Glu-B1* was noted for *Glu-B1w*, where subunits 6^*+8^* stain very faintly {1146}.

Glu-B1x {1526}. [*Glu-B1-VII* {1526}, *Glu-B1t* {959}]. **tv:** Canoco de Grao Escuro, Portugal, *T. turgidum*.

Glu-B1y {1526}. [*Glu-B1-VIII* {1526}, *Glu-B1u* {959}]. **tv:** Tremez Mollez, Portugal, *T. durum*.

Glu-B1z {1524}. [*Glu-B1-IX* {1524}, *Glu-B1v* {959}]. 7+15 {125}. **tv:** Roccia, Italy, *T. durum* {1523},{125}.

Glu-B1z carried by Roccia was numbered (7+15) and named *Glu-B1-XII* in {125}; however, the earlier name, *Glu-B1-IX* {1523}, has precedence; also, {1523} states that the *Glu-B1-IX* subunit of faster mobility is slightly slower than subunit 15.

Glu-B1aa {1524}. [*Glu-B1w* {959}, *Glu-B1-X* {1524}]. **tv:** Quaduro, Italy, *T. durum*.

Glu-B1ab {1523}. [*Glu-B1x* {959}, *Glu-B1-XI* {1523}]. **tv:** Athena, Italy, *T. durum*.

Glu-B1ac {125}. [*Glu B1XIII* {125}]. 6+16 {125}. **tv:** Espa l8914, *T. durum*.

Glu-B1ad {125}. [*Glu B1XIV* {125}]. 23+22 {125}. **tv:** Greece 20, *T. durum*.

Glu-B1ae {1146}. 18^* {1146}. **v:** David.

Glu-B1af {1146}. 26+27 {1146}. **v:** Cologna 1.

One of the *Glu-B1af* subunits was numbered 26 in {1146}; 26 was previously used to number the subunit encoded by *Glu-A1k* {478}.

Glu-B1ag {1146}. 28+29 {1146}. **v:** Forlani.

Subunit 28 of *Glu-B1ag* (28+29) {1146} is referred to as subunit 19^* in {1068}.

Glu-B1ah {782}. Null allele {782}. **v:** Olympic mutant.

Glu-B1ai {714}. 7' {714}. **v:** Adonis.

Glu-B1aj {759}. 8 {759}. **v:** AUS 14444, Afghanistan.

Glu-B1ak {899}. 7^*+8^* {899}. **v:** Norstar.

Glu-B1al {899}. 7^{OE}+7^{OE}+8^* {899}. **v:** Benkuti 1201; Glenlea {899}; Klein Universal II {10196}; Tezanos Pintos Precoz {10196}; Tobari 66 {10196}.

Other genotypes are listed in {10196}.

Many of the cultivars carrying the over-expressed subunit 7 encoded by *Glu-B1al* show %UPP values that transcend the normal range observed for cultivars that lack this subunit {10089}, which presumably is associated in some way with its unusually high amount in the grain. The underlying cause of the increased amount may be due to an increased transcriptional rate compared to other alleles, for which a known difference in promoter sequence compared to other alleles expressing normal levels of this subunit {10090} may be responsible.

However, there is evidence that over-expression is due to duplication of subunit 7 {10196}. Regarding to subunit 8^*, evidence was presented to indicate that in Glenlea, one of the standard cultivars for the allele, this subunit is the same as subunit 8 {10808}.

Glu-B1am {1229}. 18 {1229}. **v:** Royo.

Glu-B1an {1229}. 6 {1229}. **v:** BG-2013.

Glu-B1ao {1229}. 7+16 {1229}. **v:** BG-3545.

Glu-B1ap {1229}. 30+31 {1229}. **v:** Marinar.

Glu-B1aq {1229}. 32+33 {1229}. **v:** BG-1943.

Glu-B1ar {1229}. 34+35 {1229}. **v:** Jeja Almendros.

Glu-B1as {1229}. 13 {1229}. **v:** PI 348435.

Glu-B1at {1229}. 13+18 {1229}. **v:** PI 348449.

Glu-B1au {1032}. 37 {1032}. **v:** Shedraya Polesja.

Glu-B1av {03116}. [*Glu-B1r* {3116}]. 7-18 {03116}. **v:** Triticor hexaploid *triticale* {03116}.

Glu-B1aw {03116}. [*Glu-B1s* {03116}]. 6.8-20y {03116}. **v:** Carnac hexaploid *triticale* {03116}.

Glu-B1ax {03137}. [*Glu-B1-XV* {03137}]. *XV* {03137}. **tv:** PI-190922, BG-012302 emmer {03137}.

Glu-B1ay {03137}. [*Glu-B1-XVI* {03137}]. *XVI* {03137}. **tv:** PI 277681 emmer {03137}.

Glu-B1az {03137}. [*Glu-B1-XVII* {03137}]. *XVII* {03137}. **tv:** PI 348620 emmer {03137}.

Glu-B1ba {03122}. [*Glu-B1-XVIII* {03122}]. 13^*+16 {03122}. **v:** PI 348767 spelt {03122}.

Glu-B1bb {03122}. [*Glu-B1-XLX* {03122}]. 6+18' {03122}. **v:** PI 348631 spelt {03122}.

Glu-B1bc {03138}. 6+17 {03138}. **v:** ICDW 20975 {03138}.

Glu-B1bd {03140}. 20+8 {03140}. **v:** Abadja {03140}.

Glu-B1be {10186}. **tv:** *T. dicoccoides* Israel-A {10186}.

Glu-B1bf {10186}. **tv:** *T. dicoccoides* PI 481521 {10186}.

Glu-B1bg {10186}. **tv:** *T. dicoccoides* PI 478742 {10186}.

Glu-B1bh {10327}. 13+22 {10327}. **v:** Grado {10327}; KU-1026 {10327}; KU-1086 {10327}; KU-1094 {10327}; KU-1139 {10327}.

Glu-B1bi {10327}. 13+22.1 {10327}. **v:** KU-1135 {10327}.

Glu-B1bj {10327}. 14*+15* {10327}. **v:** TRI11553/92 {10327}.

Glu-B1bk {10327}. [*Glu-B1be* {10327}]. 6.1+22.1 {10327}. **v:** Hercule {10327}; Rouguin {10327}; Schwabenkorn {10327}; SP3 {10327}; Steiners Roter Tiroler {10327}.

Glu-B1bl {10327}. [*Glu-B1bf* {10327}]. 6.1 {10327}. **v:** KU-3418 {10327}; KU-3446 {10327}; TRI4613/75 {10327}.

Glu-B1bm {10327}. [*Glu-B1bg* {10327}]. 13*+19* {10327}. **v:** KU-3410 {10327}; Renval {10327}; Rechenbergs Fruher Dinkel {10327}; Schlegel {10327}; SP1 {10327}; TRI9885/74 {10327}; Zeiners WeiSer {10327}.

Glu-B1bn {10425}. 7+19 {10425}. **v:** Triticales: Lasko, Dagno, Tewo, Vision, Dato {10425}.

Glu-B1bo {10425}. 7+26 {10425}. **v:** Triticales: Presto, Modus {10425}.

The number 26 was also used to designate a subunit encoded by *Glu-A1k* and *Glu-A1-1k*.

Glu-B1bp {10643}. 7^{**}+8 {10643}. **v:** XM1368-2 {10643}; XM1404-2 {10643}.

Glu-B1bq {10643}. 7+8^{**} {10643}.

Glu-B1br {10807}. 7.1+7.2+8^* {10807}. **v:** H45 {10807}.

Glu-B1bs {10807}. 7.3+7^{OE}+8^* {10807}. **v:** VQ0437 {10807}.

Glu-B1bt {10809}. 17'+18' {10809}. **tv:** TGR-214 {10809}.

Glu-B1bu {10809}. 17'+18^* {10809}. **tv:** TGR-2246 {10809}.

Glu-B1bv {10809}. 13^{**}+8^* {10809}. **tv:** TGR-003 {10809}.

Glu-B1bw {10809}. 8' {10809}. **tv:** TGR-244 {10809}.

Glu-B1bx {10810}. 7+17 {10810}. **v:** CWI-59797, *T. aestivum* var. *ferrugineum* {10810}.

Glu-B1by {10808}. $7b^*$+8 {10808}. **v:** Eshimashinriki {10808}.

Glu-B1bz {10808}. 7^{OE} {10808}. **v:** Attila {10808}; Darius {10808}; Cappelle-Desprez {10808}; Festin {10808}; Petrel {10808}.

Glu-B1ca {10808}. 6+$8b^*$ {10808}. **v:** Appolo {10808}; Brimstone {10808}; Clement {10808}; Nidera Baguette 10 {10808}; Ruso {10808}; Pepital {10808}; Thesee {10808}.

Glu-B1cb {10808}. 7^{OE}+8 {10808}. **v:** ACA 303 {10808}; Courtot {10808}; Demai 3 {10808}; Shinchunaga {10808}.

Glu-B1cc {10808}. 7^{OE}+$8a^*$ {10808}. **v:** Klein Jabal 1 {10808}; Pioneer {10808}; ProINTA {10808}; Redemon {10808}.

Glu-B1cd {10808}. 7^{OE}+$8b^*$ {10808}. **v:** ACA 601 {10808}.

Glu-B1ce {10808}. 7+$8a^*$ {10808}. **v:** Jing 411 {10808}; Tasman {10808}.

In a study including emmer wheats (*T. dicoccon*) {00115}, new subunits named 7^+ (in accessions MG5400/5 and MG30835/1), 8^- (in accessions MG5400/5, MG30835/1, MG5333/1 and MG5507) and 13^- (in accession MG5282/2) were found and provisionally assigned to *Glu-B1*. Until confirmed, they are not included in the *Glu-B1* list.

Glu-B1cf {11490}. 20*+33* {11490}. **tv:** *T. turgidum* ssp. *durum* Mexican landrace accession 22 (CWI52215) {11490}.

Glu-B1cg {11490}. 13+16* {11490}. **tv:** *T. turgidum* ssp. *durum* Mexican landrace accession 19 (CWI52200) {11490}.
Glu-B1ch {11490}. 7+22 {11490}. **v:** *T. aestivum* ssp. *aestivum* cv. Wilbur (CW13735) {11490}.
Glu-B1ci {11490}. 7+22* {11490}. **tv:** *T. turgidum* ssp. *durum* Iranian landrace accession 51 (CWI57280) {11490
Glu-B1cj {11490}. 13*+15* {11490}. **tv:** *T. turgidum* ssp. *durum* Iranian landrace accession 46 (CWI56913) {11490}.
Glu-B1ck {11491}. 15 {11491}. **v:** *T. aestivum* ssp. *compactum* PI 157920 {11491}.
Glu-B1cl {11491}. 14+8 {11491}. **v:** *T. aestivum* ssp. *macha* PI 272554, PI 278660, PI 290507 {11491}.
Glu-B1cm {11491}. 6+8* {11491}. **v:** *T. aestivum* ssp. *macha* PI 428177 {11491}.
Glu-B1cn {11491}. 17 {11491}. **v:** *T. aestivum* ssp. *sphaerococcum* CItr 4531, PI 272581, PI 282452 {11491}.
Glu-B1co {11493}. 20+22* {11493}. **tv:** *T. turgidum* ssp. *durum* Moroccan landraces MGB-2963, MGB-3152 {11493}.
Glu-B1cp {11493}. 20* {11493}. **tv:** *T. turgidum* ssp. *durum* North American cv. MGB-66023 {11493}.
Glu-B1cq [{11492}]. 7+8* {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE048494 {11492}.
Glu-B1cr [{11492}]. 8*.1+20y {11492}. **tv:** *T. turgidum* ssp. *durum* BGE045649 {11492}, BGE047535 {11492}.
Glu-B1cs [{11492}]. 20x {11492}. **tv:** *T. turgidum* ssp. *durum* BGE045673 {11492}.
Glu-B1ct [{11540}]. 6+(8) {11540}. **tv:** *T. turgidum* ssp. *durum* Langdon {11540}.

GLU-D1 {1125,1100}. [*Glt-D2* {420}, *Glu 1D* {1415}, *Glt-D1* {420}]. 1DL {150},{1125},{107},{780},{1100}. **v:** CS.
Five combinations involving 6 HMW subunits [1D (p-t)] are listed in {420}. Eleven additional *GLU-D1* alleles in *T. tauschii* were described {755}. Seven transfers of *Glu-D1a* and 10 of *Glu-D1d* (5+10) from chromosome 1D to chromosome 1A in triticale were described {846}. The subunit 2.2* encoded by *Glu-D1al* and *Glu-D1-1m* in the appropriate list below has an unusually high Mr. Comparison of its N-terminal sequence and amino acid composition with those of subunit 2 (encoded by *Glu-D1-1a*) indicated that its greater Mr could be due to the presence of a larger central repetitive domain, although further evidence suggested that this does not affect the conformational properties of the subunit {02107}. The alleles originally designated *Glu-D1w* (encoding 'subunits' 2 (or 2^t denoting its origin in the *Ae. tauschii* genome) +T1+T2), *Glu-D1af* (encoding 3 (or 3^t)+T1+T2) and *Glu-D1ag* (encoding 1.5 (or1.5^t)+T1+T2) share the component T1 that was originally classified as a HMW glutenin. However, it has since been shown {02108} that this protein is soluble in aqueous ethanol, casting doubt upon this classification. More recently, it was shown {02109}, from one- and two-dimensional gel electrophoresis based upon SDS-PAGE and A-PAGE, and from N-terminal sequencing, that this protein is an omega-gliadin of unusually low electrophoretic mobility in SDS-PAGE, encoded by a locus located on the short arm of chromosome 1D, though distant (13.18 cM) from the principle gliadin-encoding locus on 1D, *Gli-D1*, and 40.20 cM from the high molecular weight encoding locus, *Glu-D1*. The authors named the locus *Gli-DT1* (see Gliadins). Reference to T1 was consequently removed from the *GLU-D1* list. As a consequence of this finding, allele *Glu-D1w* was reused for a distinct allele, and *Glu-D1af* was omitted and will be reused for a future allele, since the combinations of subunits that these alleles originally represented are no longer unique. In {03124}, null alleles were observed for both *GLU-D1-1* and *GLU-D1-2*, which, naturally, are not necessarily the same as those previously reported for this locus, meaning that composite alleles involving them in this study and corresponding to combinations apparently already listed in the Catalogue, may, in fact, represent novel alleles. It was also found that certain subunits of apparently identical relative mobility in SDS-PAGE showed different surface hydrophobocities in RP-HPLC; and

the reverse situation was also observed (the same hydrophobicity, but different electrophoretic mobilities). It was shown {03126} that the relatively small size of a y-type HMW glutenin subunit, named 12.4^t (encoded by *Glu-D1-1t* {03124} - see below) and carried by accession CPI 110750 of *Ae. tauschii*, is due to the deletion of blocks of repetitive motifs, amounting to approximately 200 amino acids, probably caused by unequal crossing-over

Glu-D1a {1116}. 2+12 {1116}. **v:** CS.

Primers were designated that enabled Dx2 to be distinguished from Dx5 and Dy10 from Dy12 {10641}.

Glu-D1b {1116}. 3+12 {1116}. **v:** Hobbit.

Glu-D1c {1116}. 4+12 {1116}. **v:** Champlein.

Glu-D1d {1116}. 5+10 {1116}. **v:** Hope.

Glu-D1e {1116}. 2+10 {1116}. **v:** Flinor (rare).

Glu-D1f {1116}. 2.2+12 {1116}. **v:** Danchi (rare).

Glu-D1f is present at high frequencies in wheats of southern Japan. Its presence may be associated with white salted noodle (Udon) quality {10573}.

Glu-D1g {478}. 5+9 {478}. **v:** BT-2288.

Subunit 9 of *Glu-D1g* (5+9) was so numbered in {478} because its mobility is the same as one of the subunits encoded by *Glu-B1c* (7+9).

Glu-D1h {1145}. 5+12 {1145}. **v:** Fiorello, Italy.

Cultivar Fiorello is given as a standard for *Glu-D1h* encoding subunits 5+12 and for *Glu-D1w* encoding subunits 5^*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1i {107}. Null {107}. **v:** Nap Hal, Nepal.

Glu-D1j {1146}. 2+12^*{1146}. **v:** Tudest.

Glu-D1k {421}. 2 {421}. **s:** CS/Timstein 1D.

Glu-D1k {421} appears to have arisen as the result of a deficiency of subunit 12 from *Glu-D1a* (2+12); subunits 2 and 12 are referred to as D1 and D5 in {421}.

Glu-D1l {759}. 12 {759}. **v:** AUS 10037, Afghanistan.

Glu-D1m {759}. 10 {759}. **v:** AUS 13673, Afghanistan.

Glu-D1n {759}. 2.1+10 {759}. **v:** AUS 14653, Afghanistan.

Glu-D1o {755}. 2.1+13 {755}. **v:** AUS 14519, *T. macha*.

One of the *Glu-D1o* subunits was numbered 13 in {755}; 13 was previously used to number a subunit encoded by *Glu-B1f* (13+16) and *Glu-B1g* (13+19) {1116}.

Glu-D1p {1233}. 36 {1233}. **i:** Iranian landrace accession $3048/5^*$ Sicco.

Glu-D1q {124}. 2+11 {124}. **v:** Flinor.

Glu-D1r {1229}. 2.3+12 {1229}. **v:** PI 348465.

Glu-D1s {1032}. 38 {1032}. **v:** Leningradka.

Glu-D1t {668}. 43+44 {668}. **dv:** *Ae. tauschii* accession $TA2450/2^*$.

Glu-D1u {836}. 2+10' {836}. **v:** Coker 68-15.

Glu-D1v {755}. 2.1+10.1 {755}. **dv:** *Ae. tauschii.*

Glu-D1w {03124}. 5^*+10 {03124}. **v:** Fiorello {03124}.

Note that the cultivar Fiorello is given as a standard for *Glu-D1h* encoding subunits 5+12 and for *Glu-D1w* encoding subunits 5^*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1x {755}. 2+T2 {755}.2^t+12.2^t {03124}. **dv:** *Ae. tauschii.*

Glu-D1y {755}. 3^t+12.2^t {03124}. 3+T2 {755}. **dv:** *Ae. tauschii.*

Glu-D1z {755}. 3+10 {755}. **dv:** *Ae. tauschii.*

Glu-D1aa {755}. 3+10.3 {755}. **dv:** *Ae. tauschii.*

Glu-D1ab {755}. 4.1+10 {755}. **dv:** *Ae. tauschii.*

Glu-D1ac {755}. 4+10 {755}. **dv:** *Ae. tauschii.*

Glu-D1ad {755}. 5.1+10.2 {755}. **dv:** *Ae. tauschii.*
Glu-D1ae {1578}. 2.1^{t}+12.2^{t} {03124}. 2.1+T2 {1578}. **dv:** *Ae. tauschii.*
Glu-D1af. Currently undesignated for reasons given in the preamble to this section.
Glu-D1ag {1578}. 1.5+T2 {1578}. 1.5^{t}+12.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1ah {1578}. 1.5+10 {1578}. **dv:** *Ae. tauschii.*
Glu-D1ai {1578}. 2.1+10.5 {1578}. **dv:** *Ae. tauschii.*
Glu-D1aj {1578}. 1.5+12 {1578}. **dv:** *Ae. tauschii.*
Glu-D1ak {1578}. 3+10.5 {1578}. **dv:** *Ae. tauschii.*
Glu-D1al {02107}. 2.2* {02107}. **v:** MG315.
Glu-D1am {03122}. [*Glu-D1-I* {03122}]. 2+12' {03122}. **v:** PI 348495 spelt {03122}.
Glu-D1an {03122}. [*Glu-D1-II* {03122}]. 2+12* {03122}. **v:** PI 348672 spelt {03122}.
Glu-D1ao {03122}. [*Glu-D1-III* {03122}]. 2.4+12 {03122}. **v:** PI 348473 spelt {03122}.
Glu-D1ap {03122}. [*Glu-D1-IV* {03122}]. 2.5+12 {03122}. **v:** PI 348572 spelt {03122}.
Glu-D1aq {03124}. 1.5^{t}+10.1^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1ar {03124}. 2^{t}+10.1^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1as {03124}. 1.5^{t}+10.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1at {03124}. 3^{t}+10.1^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1au {03124}. 2.1^{t}+10.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1av {03124}. 2^{t}+12.3^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1aw {03124}. 1^{t}+10^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1ax {03124}. 1^{t}+12^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1ay {03124}. 1^{t}+10.1^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1az {03124}. 4^{t}+12.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1ba {03124}. 1^{t}+12.3^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bb {03124}. 1.5^{t}+11^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bc {03124}. 1.5^{t}+10.3^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bd {03124}. 1^{t}+11^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1be {03124}. 2.1^{t}+12.4^{t} {3124}. **dv:** *Ae. tauschii.*
Glu-D1bf {03124}. 2^{t}+12.1^{t} {03124}. **dv:** *Ae. tauschii* {03124}.
Glu-D1bg {03124}. 3^{t}+10.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bh {03124}. 4^{t}+10.1^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bi {03124}. 4^{t}+10.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bj {03124}. 5^{t}+11^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bk {03124}. 5^{t}+10.1^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bl {03124}. 5^{t}+12.2^{t} {03124}. **dv:** *Ae. tauschii.*
Glu-D1bm {03124}. 5^{*t}+null {03124}. **dv:** *Ae. tauschii.*
Glu-D1bn {03124}. 5^{*t}+12 {3124}. **dv:** *Ae. tauschii.*
Glu-D1bo {10091}. 5'+12 {10091}. **v:** W958 {10091}.
This putative new allele encodes two subunits that have very similar electrophoretic mobilities compared to subunits 5+12 encoded by *Glu-D1h*, but analysis using the specific PCR primers for Dx5 described in {10092} and {10093} shows that the x-type subunit of *Glu-D1bo*, provisionally denominated 5' {10091}, does not appear to be the same protein as subunit 5 {10091}. Definitive evidence awaits sequencing information (See note to allele *Glu-D1-1s*).
Glu-D1bp {10327}. 2.1'+12 {10327}. **v:** KU-1034 {10327}.
Glu-D1bq {10304}. [*Glu-D1bp(t)* {10304}]. 2.6+12 {10304}. **v:** Baidongmai {10304}; Hongdongmai {10304}; Hongkedongmai {10304}; Jinbaojin {10304}.
The complete sequence of this subunit was determined {10319}.
Glu-D1br {10426}. 5*t+10.1^{t} {10426}. **tv:** *Ae. tauschii* TD81 {10426}.
Subunit 10.1^{t} possesses a mobility slightly lower than subunit 10 in SDS-PAGE and its deduced amino

acid sequence is similar to subunit 12 (8 amino acid differences) {10426}; the authors used the complete coding sequence to make phylogenetic comparisons with 19 other subunits including both x-type and y-type subunits and concluded that a *Glu-1* gene duplication event occurred about 16.83 million years ago.
Glu-D1bs {10642}. 1.6^{t}+12.3^{t} {10642}. **dv:** *Ae. tauschii* TD16 {10642}.
Glu-D1bt {10568}. 2.1^{t}+12^{t} {10568}. **v:** Syn 396{10568}.
Glu-D1bu {10810}. 2'+12 {10810}. **v:** CWI-64806, *T. aestivum* var. *aestivum* {10810}.
Glu-D1bv {10810}. 2"+10 {10810}. **v:** CWI-65297, *T. aestivum* var. *erythroleucon* {10810}.
Glu-D1bw {10810}. 2"+12 {10810}. **v:** CWI-60509, *T. aestivum* var. *graecum* {10810}.

GLU-Ag^{i}***1*** {374}. 1Ag^{i} {374}. **ad:** Vilmorin 27/*Th. intermedium*.

GLU-E1 {781}. 1ES {781}. **ad:** CS/*E. elongata*.
HMW glutenin y-type subunit Ee1.5 encoded by this locus was sequenced {10439} and compared with other y-type subunits, particularly subunit 1Dy10. It has major deletions in its middle region and is one of the smallest known HMW glutenin subunits. It has an additional Cys residue in the middle of the repetitive domain but lacks one Cys residue commonly found towards the end of this domain. These changes may influence inter- or intra-molecular disulphide bond formation.
Four {10660, 10661} and 11 {10662} alleles were observed in *Agropyron elongatum* (E^{e} genome, 2n = 10X = 70) and named *Aex1* to *Aex5* (producing x-type subunits) and *Aey1* to *Aey10* (producing y-type subunits). *Aex4, Aey7* and *Aey9* were very similar to three alleles in the diploid progenitor *Lophopyrum elongatum* {10439, 10663}. The C-terminal regions of three of the y-type subunits (products of *Aey8, Aey9* and *Aey10*) were more similar to x-type subunits than to other y-type subunits {10662}. The subunit from *Aex4* contained an additional cysteine residue, which may be associated with good processing quality in wheat introgression lines {10662}. Allele *Aey-4* was a chimeric gene formed by recombination of two other genes {10662}.
Chinese *T. aestivum* cultivar Xiaoyanmai carries a subunit with electrophoretic mobility in 10% SDS-PAGE well beyond that of subunits so far observed in *T. aestivum*. It may derive from *Agropyron elongatum*, which was used in the breeding program that led to the variety {1538}. It has not been given a subunit number or allelic designation, because its genetic control has not been elucidated.
Glu-E1a {781}. **ad:** CS/*L. elongatum* W0622 {781}.
Glu-E1b {10644}. **ad:** Langdon/*L. elongatum* DGE-1 {10644}. **al:** *L. elongatum* PI 531719 {10644}.

GLU-H1 {781}. [*Hor 3* {1337}]. 1HL {1337}.1H {781}. **ad:** CS/Betzes {781}. **al:** Various barley cultivars {1337}.

GLU-H^{ch}***1***. 1H^{ch} {1123}. **ad:** CS/*H. chilense*.
38 accessions (natural populations) of *Hordeum chilense* carrying the following 10 subunits were used as the maternal parents of 121 lines of primary tritordeum, and evaluations for associations with bread-making quality initiated {03114}. Subunits 1^{Hch}, 2^{Hch} and 3^{Hch} were previously referred to as H^{ch}a, H^{ch}b and H^{ch}c {03112}.
Glu-H^{ch}***1a*** {03114}. 1^{Hch} {03114}. **al:** *H. chilense* accession H1 {03114}.
Glu-H^{ch}***1b*** {03114}. 2^{Hch} {03114}. **al:** *H. chilense* accession H11 {03114}.
Glu-H^{ch}***1c*** {03114}. 3^{Hch} {03114}. **al:** *H. chilense* accession H7 {03114}.
Glu-H^{ch}***1d*** {03114}. 4^{Hch} {03114}. **al:** *H. chilense* accesion H16{03114}.
Glu-H^{ch}***1e*** {03114}. 5^{Hch} {03114}. **al:** *H. chilense* accession H47 {03114}.
Glu-H^{ch}***1f*** {03114}. 6^{Hch} {03114}. **al:** *H. chilense* accession H220 {03114}.
Glu-H^{ch}***1g*** {03114}. 7^{Hch} {03114}. **al:** *H. chilense* accession H293 {03114}.
Glu-H^{ch}***1h*** {03114}. 8^{Hch} {03114}. **al:** *H. chilense* accession H297 {03114}.
Glu-H^{ch}***1i*** {03114}. 9^{Hch} {03114}. **al:** *H. chilense* accession H252 {03114}.

Glu-H^{ch}1j {03114}. 10^{Hch} {0 3114}. **al:** *H. chilense* accession H210 {03114}.

GLU-H^{t}1 {1037}. 1H^{t}L {1037}. **ad:** CS/*E. trachycaulum*.

GLU-R1 {781, 1356}. [*Sec 3* {1336}]. 1RL {1340,1356}.1R {781, 1336}. **ad:** CS/Imperial; Holdfast/ King II {1340}. **tr:** CS Imperial 1DS.1RL {1356}.
Glu-R1a {03116}. 1^{r}-4^{r} {03116}. **v:** Indiana hexaploid triticale {03116}.
Glu-R1b {03116}. 2^{r}-6.5^{r} {03116}. **v:** Graal hexaploid triticale {03116}.
Glu-R1c {03116}. 6^{r}-13^{r} {03116}. **v:** Almao hexaploid triticale {03116}.
Glu-R1d {03116}. 2^{r}-9^{r} {03116}. **v:** Olympus hexaploid triticale {03116}.
Glu-R1e {03116}. 6.5^{r} {03116}. **v:** Clercal hexaploid triticale {03116}.
Glu-R1f {03115}. 0.8^{r}-6^{r} {03115}. **v:** Carmara hexaploid triticale {03115}.
Glu-R1g {03115}. 5.8^{r} {03115}. **v:** Arrayan hexaploid triticale {03115}.
From study of chromosome substitutions in bread wheat {03117}, it was found that a chromosome 1R carrying HMW secalin subunit 6.5^{r} (*Glu-R1e*), originally derived from the 'Petkus' rye population, was associated with bread making quality (i) intermediate between chromosome 1A carrying the null allele *Glu-A1c* and chromosome 1A carrying HMW glutenin subunit 2* encoded by *Glu-A1b*; (ii) equivalent to a chromosome carrying HMW glutenin subunit 7 encoded by *Glu-B1a*; and (iii) inferior to chromosomes 1D with distinct alleles.
There is a difficulty in the assignment of subunit 6^{r} in the *GLU-R1-1* and *GLU-R1-2* lists, since it appears as an x-type subunit in allele *Glu-R1c* and as a y-type subunit in allele *Glu-R1f*. It is currently provisionally assigned to the *GLU-R1-1* list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.
Five new x-type subunits (plus the null allele) and four y-type subunits were reported in {10094}. They vary principally through duplications and deletions of the tri-, hexa- and nona-peptide motifs found in the central repetitive region of the subunits. Orthologous genes were found to be more closely related than paralogous genes, supporting the hypothesis that gene duplication occurred before Triticeae speciation {10095, 10094}.
GLU-R^{m}**1** {1339}. 1R^{m}L {1340, 1339}. **ad:** CS/*S. montanum* {1340, 1339}.
GLU-S^{l}1 {1228}. 1S^{l}L {1228}. **ma:** In *Ae. longissima 2 /Ae. longissima 10, GLU-S^{l}*1, G*LU-S^{l}3*, one glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one and other {1228} as follows: *GLU-S^{l}*1 – 15.9 cM – *GPI-S^{l}*1 – 38 cM – *GLI-S^{l}*4 – 7.1 cM – *GLU-S^{l}*3 – 0.9 cM – *GLI-S^{l}*1 – 5.6 cM – *GLI-S^{l}*5. *GLU-S^{l}*1 is located in 1S^{l}L and the other loci are in 1S^{l}S.
GLU-Ta1 {10449}. **al:** *Taenitherum crinitum* PI 204577 {10449}.

GLU-A1-1.
Glu-A1-1a. Null. **v:** CS.
Glu-A1-1b. 1. **v:** Hope.
Glu-A1-1c. 2*. **v:** Bezostaya 1.
A PCR marker specific for the *Glu-A1-1c* (Ax2*) allele was developed in {0147}.
Glu-A1-1d. **v:** V74, Spain.
Glu-A1-1e. **v:** 132c, Poland.
Glu-A1-1f. **v:** 112-29, Sudan.
Glu-A1-1g. **v:** Landrace 1600.
Glu-A1-1h. **tv:** PI 94683, USSR, *T. dicoccum*.
Glu-A1-1i. **tv:** CI 12213, India, *T. dicoccum*.
Glu-A1-1j. 1'. **tv:** PI 352359, Germany, *T. dicoccum*; Lambro.
Glu-A1-1k. 26. **v:** BT-2288

Glu-A1-1l. **tv:** Chinook, Canada.
Glu-A1-1m. **tv:** Nugget Biotype 1, Canada.
Glu-A1-1n. 1". **tv:** Corado, Portugal.
Glu-A1-1o. 2^{**}. **tv:** PI 61189, USSR, Aric 581/1.
Glu-A1-1p. 3^{*}. **v:** David 1.
Glu-A1-1q. 2^{***}. **tv:** Melianopus 1528.
Glu-A1-1r. 39. **i:** *T. thaoudar* IPSR 1020006/6* Sicco.
Glu-A1-1s. 41. **i:** *T. thaoudar* G3152/6*Sicco.
Glu-A1-1t {602}. 21^{*} {602}. **v:** W29323, W 3879, W 31169.
Glu-A1-1t is a provisional designation; definitive evidence that subunit 21^{*}, which has a mobility similar to that of subunit 21, is a 'x-type' and not a 'y-type' protein has not been obtained.
Glu-A1-1u {02106}. 2^{*B} {02106}. **v:** Bankuti 1201.
Glu-A1-1v {10327}. 2.1* {10327}. **v:** Grado {10327}; KU-1026 {10327}; KU-1086 {10327}; KU-1094 {10327}; KU-1139 {10327}.
Glu-A1-1w {10327}. 2' {10327}. **v:** TRI14165/91 {10327}.
Glu-A1-1x {10535}. 2" {10535}. **v:** 211.12014 {10535}.
Glu-A1-1y [{11540}]. **tv:** *T. turgidum* ssp. *turgidum* BGE019307 {11540}.
Glu-A1-1z {11106}. [*Glu-A1g* {11106}]. 1.1 {11106}. **v:** Barbela 28 {11106}.
The sequence encoding subunit 1Ax1.1 shows high nucleotide identity with other *GLU-A1* alleles, with the main difference being an insertion of 36 amino acids in the central repetitive region. It is the largest and most acidic subunit currently known at this locus and has been implicated in high dough extensibility in some cv. Barbela wheat lines, although this contrasts with other data showing a similar effect to that of subunit 1Ax1 {11107}.

GLU-A1-2.
Glu-A1-2a. Null. **v:** CS.
Glu-A1-2b. 40. **i:** *T. thaoudar* IPSR1020006/6* Sicco.
Glu-A1-2c. 42. **i:** *T. thaoudar* G3152/6*Sicco.

GLU-B1-1.
Glu-B1-1a. 7. **v:** CS.
A PCR marker (2373 bp) for the *Glu-B1-1a* (Bx7) allele was developed in {0145}.
Glu-B1-1b. 7,7^{*}. **v:** Flinor, Bezostaya 1, Owens, Norstar.
Glu-B1-1c. 7'. **v:** Adonis.
Glu-B1-1d. 6. **v:** Hope.
Glu-B1-1e. 20. **v:** Federation.
Glu-B1-1f. 13. **v:** Lancota.
Glu-B1-1g. 14. **v:** Sappo.
Glu-B1-1h. 17. **v:** Gabo.
Glu-B1-1i. 21.21x {03116}. **v:** Dunav; Foison {03116}.
Glu-B1-1j. 23. **v:** Spica D.
Glu-B1-1k. **tv:** PI 94640, Iran, *T. dicoccum*.
Glu-B1-1l. **tv:** PI 355505, Germany, *T. diccocum*.
Glu-B1-1m. **tv:** PI 352354, Ethiopia, *T. dicoccum*.
Glu-B1-1n. **tv:** PI 94633, Morocco, *T. dicoccum*.
Glu-B1-1o. **v:** Supreza, Canada.
Glu-B1-1p. **v:** Mondor.
Glu-B1-1q. **tv:** Canoco de Grao Escuro, Portugal.
Glu-B1-1r. **tv:** Tremez Mollez, Portugal.

Glu-B1-1s. **tv:** Quaduro, Italy.
Glu-B1-1t. **tv:** Athena, Italy.
Glu-B1-1u. 26. **v:** Cologna 1.
Glu-B1-1v. 28. **v:** Forlani.
Glu-B1-1w. Null. **v:** Olympic mutant.
Glu-B1-1x. 30. **v:** Marinar.
Glu-B1-1y. 32. **v:** BG-1943.
Glu-B1-1z. 34. **v:** Jeja Almendros.
Glu-B1-1aa. 37. **v:** Shedraya Polesja.
Glu-B1-1ab. 6^{*}. **v:** Dawbill.
Glu-B1-1ac {03116}. 6.8 {03116}. **v:** Carnac hexaploid triticale {03116}.
Glu-B1-1ad {03122}. 13^{*} {03122}. **v:** PI 348767 spelt {03122}.
Glu-B1-1ae {10327}. 14* {10327}. **v:** TRI11553/92 {10327}.
Glu-B1-1af {10327}. 6.1 {10327}. **v:** Hercule {10327}; KU-3418 {10327}; KU-3446 {10327}; Rouguin {10327}; Schwabenkorn {10327}; SP3 {10327}; Steiners Roter Tiroler {10327}; TRI4613/75 {10327}.
Glu-B1-1ag {10643}. 7^{**} {10643}. **v:** XM1368-2 {10643}.
Glu-B1-1ah {899}. 7^{OE} {899}. **v:** Benkuti 1201 {10196, 10197}; Glenlea {899}; Klein Universal II {10196}; Tezanos Pintos Precoz {10196}; Tobari {10196}.
Glu-B1-1ai {10807}. 7.1 {10807}. **v:** H45 {10807}.
Glu-B1-1aj 10807}. 7.2 {10807}. **v:** H45{10807}.
Glu-B1-1ak {10807}. 7.3 {10807}. **v:** VQ0437 {10807}.
Glu-B1-1al {10809}. 17' {10809}. **tv:** TGR-214 {10809}; TGR-2246 {10809}.
Glu-B1-1am {10809}. 13^{**} {10809}. **tv:** TGR-003 {10809}.
Glu-B1-1an {10808}. $7b^{*}$ {10808}. **v:** Eshimashinriki {10808}.
Glu-B1-1ao {11490}. 20* {11490}. **tv:** *T. turgidum* ssp. *durum* Mexican landrace accession 22 (CWI52215) {11490}.

GLU-B1-2.
Glu-B1-2a. 8. **v:** CS.
Glu-B1-2b. 9. **v:** Bezostaya 1.
Glu-B1-2c. 16. **v:** Lancota.
Glu-B1-2d. 19. **v:** NS 335.
Glu-B1-2e. 15. **v:** Sappo.
Glu-B1-2f. 18. **v:** Gabo.
Glu-B1-2g. 22. **v:** Serbian.
Glu-B1-2h. 24. **v:** Spica D
Glu-B1-2i. **tv:** PI 355505, Germany, *T. dicoccum*.
Glu-B1-2j. **tv:** PI 352354, Ethiopia, *T. dicoccum*.
Glu-B1-2k. **tv:** PI 94633, Morocco, *T. dicoccum*.
Glu-B1-2l. 11. **v:** BT-2288.
Glu-B1-2m. **v:** Supreza, Canada.
Glu-B1-2n. **v:** Mondor.
Glu-B1-2o. 8^{*}. **v:** Dawbull.
Glu-B1-2p. **tv:** Canoco de Grao Escuro, Portugal.
Glu-B1-2q. **tv:** Tremez Mollez, Portugal, *T. durum*.
Glu1-2r. **tv:** Quaduro, Italy, *T. durum*.
Glu-B1-2s. 18^{*}. **v:** David.
Glu-B1-2t. 27. **v:** Cologna 1.

Glu-B1-2u. 29. **v:** Forlani.
Glu-B1-2v. Null. **v:** Olympic mutant.
Glu-B1-2w. 31. **v:** Marinar.
Glu-B1-2x. 33. **v:** BG-1943.
Glu-B1-2y. 35. **v:** Jeja Almendros.
Glu-B1-2z {03116}. 20y {03116}. **v:** Carnac hexaploid triticale {03116}.
Glu-B1-2aa {03122}. 18' {03122}. **v:** PI 348631 spelt {03122}.
Glu-B1-2ab {03116}. 21y {03116}. **v:** Foison {03116}.
Glu-B1-2ac {10327}. 22* {10327}. **v:** Grado {10327}; KU-1026 {10327}; KU-1086 {10327}; KU-1094 {10327}; KU-1139 {10327}.
Glu-B1-2ad {10327}. 22.1 {10327}. **v:** Hercule {10327}; KU-1135 {10327}; Rouguin {10327}; Schwabenkorn {10327}; SP3 {10327}; Steiners Roter Tiroler {10327}.
Glu-B1-2ae {10327}. 15* {10327}. **v:** TRI11553/92 {10327}.
Glu-B1-2af {10327}. 19* {10327}. **v:** KU-3410 {10327}; Rechenbergs Fruher Dinkel {10327}; Renval {10327}; SP1{10327}; TRI9885/74{10327}; Zeiners Weiser Schlegel {10327}.
Glu-B1-2ag {10643}. [8** {10643}]. **v:** XM1404-2 {10643}.
***Glu-B1-2ah*.** Currently undesignated.
Glu-B1-2ai {10809}. 8' {10809}. **tv:** TGR-244 {10809}.
Glu-B1-2aj {10808}. 8a* {10808}. **v:** Jing 411{10808}; Pioneer {10808}; Tasman {10808}.
Glu-B1-2ak {10808}. 8b* {10808}. **v:** ACA 601 {10808}; Nidera Baguette 10 {10808
Glu-B1-2al {11490}. 33* {11490}. **tv:** *T. turgidum* ssp. *durum* Iranian landrace accession 51 (CWI57280) {11490}.
Glu-B1-2am {11490}. 22* {11490}. **tv:** *T. turgidum* ssp. *durum* Iranian landrace accession 51 (CWI57280) {11490}.
Glu-B1-2an [{11492}]. 8*.1 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE045649 {11492}, BGE047535 {11492}.
Glu-B1-2ao [{11540}]. (8) {11540}. **tv:** *T. turgidum* ssp. *durum* Langdon {11540}.

Eight alleles at *GLU-B1-1* and 10 alleles at *GLU-B1-2* in *T. turgidum* var. *dicoccoides* populations were described in {798}. In a further study using different germplasm of this species {205}, 19 alleles at *GLU-B1* were observed, including 15 not previously observed; the 19 alleles included 11 alleles at *GLU-B1-1* and 14 alleles (including the null allele) at *GLU-B1-2*, although, as the authors pointed out, it was not conclusively clear how many of these alleles were distinct from each other, or from others previously observed.

GLU-D1-1
Glu-D1-1a. 2. **v:** CS.
Glu-D1-1b. 3. **v:** Hobbit.
Glu-D1-1c. 4. **v:** Champlein.
Glu-D1-1d. 5. **v:** Hope.
PCR markers specific for the *Glu-D1-1d* (Dx5) allele were developed in {0145} and {0147}.
Glu-D1-1e. 2.2. **v:** Danchi.
Glu-D1-1f. Null. **v:** Nap Hal, Nepal.
Glu-D1-1g. 2.1. **v:** AUS 14653, Afghanistan.
Glu-D1-1h. 2.3. **v:** PI 348465.
Glu-D1-1i. 38. **v:** Leningradka.
Glu-D1-1j {668}. 43 {668}. **i:** *Ae. tauschii* accession TA2450/2*.
Glu-D1-1k {755}. 4.1 {755}. **dv:** *Ae. tauschii.*

Glu-D1-1l {1578}. 1.5 {1578}. D^{t}x1.5 {10306}. **dv:** *Ae. tauschii* accession SQ-214 {10306}.

A restriction enzyme-based method named the 'restricted deletion method' was used to characterize the ORF of this subunit {10306} (as in the case of subunit D^{t}y10 encoded by *Glu-D1-2u* {10306}. Allele-specific PCR markers were developed based upon SNPs located at the non-repetitive N-terminal {10320}.

Glu-D1-1m {02107}. 2.2* {02107}. **v:** MG315.

Glu-D1-1n {03122}. 2.4 {03122}. **v:** PI 348473 spelt {03122}.

Glu-D1-1o {03122}. 2.5 {03122}. **v:** PI 3484572 spelt {03122}.

Glu-D1-1p {03124}. 1^t {03124}. **dv:** *Ae. tauschii* {03124}.

Glu-D1-1q {03124}. 5^{*t} {03124}. **dv:** *Ae. tauschii* {03124}.

Glu-D1-1r {755}. 5.1 {755}. **dv:** *Ae. tauschii.*

This allele was designated *Glu-D1-1j* in the 1998 Catalogue edition.

Glu-D1-1s {10091}. 5' {10091}. **v:** W958 {10091}.

This putative allele encodes a subunit, provisionally denominated 5' {10091}, that has a very similar electrophoretic mobility compared to subunit 5 encoded by *Glu-D1-1d*, but analysis using the specific PCR primers for Dx5 described in {10092} and {10093} shows that it does not appear to be the same protein as subunit 5 {10091}. Definitive evidence awaits sequencing information (See note to allele *Glu-D1bo*).

Glu-D1-1t {10304}. 2.6 {10304}. **v:** Baidongmai {10305}; Jinbaojin {10305}; Hongdongmai {10305}; Hongkedongmai {10305}.

Glu-D1-1u {10327}. 2.1' {10327}. **v:** KU-1034{10327}. ***Glu-D1-1v*** {10642}. [1.6^t {10642}]. **dv:** *Ae. tauschii* TD16 {10642}.

GLU-D1-2

Glu-D1-2a. 12. **v:** CS.

A PCR marker (612 bp) for the *Glu-D1-2a* (Dy12) allele was developed in {0145}.

Glu-D1-2b. 10. **v:** Hope.

PCR markers (576 bp and 2176 bp) for the *Glu-D1-2b* (Dy10) allele were developed in {0145} and {0147}, respectively.

Glu-D1-2c. 9. **v:** BT-2288.

Glu-D1-2d. Null. **v:** Nap Hal, Nepal.

Glu-D1-2e. 12*. **v:** Tudest.

Glu-D1-2f. 13. **v:** AUS 14519, *T. macha*.

Glu-D1-2g. 36. **i:** Iranian landrace 3048/5* Sicco.

Glu-D1-2h. 11. **v:** Flinor.

Glu-D1-2i {668}. 44 {668}. **i:** *Ae. tauschii* TA2450/2*.

Glu-D1-2j {836}. 10' {836}. **v:** Coker 68-15.

Glu-D1-2k {755}. T1 {755}. **dv:** *Ae. tauschii.*

Glu-D1-2l {755}. T2 {755}. **dv:** *Ae. tauschii.*

Glu-D1-2m {755}. 10.1 {755}. **dv:** *Ae. tauschii.*

Glu-D1-2n {755}. 10.2 {755}. **dv:** *Ae. tauschii.*

Glu-D1-2o {755}. 10.3 {755}. **dv:** *Ae. tauschii.*

Glu-D1-2p {1578}. 10.5 {1578}. **dv:** *Ae. tauschii*. ***Glu-D1-2q*** {03122}. 12' {03122}. **v:** PI-348495 spelt wheat accession {03122}.

Glu-D1-2r {03124}. 12.1^t {03124}. **dv:** *Ae. tauschii.*

Glu-D1-2s {03124}. 12.3^t {03124}. **dv:** *Ae. tauschii.*

Glu-D1-2t {03124}. 12.4^t {03124}. **dv:** *Ae. tauschii.*

Glu-D1-2u {10306}. D^{t}y10 {10306}. **v:** *Ae. tauschii* accession SQ-214 {10306}.

A restriction enzyme-based method named the 'restricted deletion method' was used to characterize the

ORF of this subunit {10306} (as in the case of subunit 1.5 (or D^tx1.5 {10306}) encoded by *Glu-D1-1l* {10306}. This subunit was first recognized as being different from subunit 1- encoded by *Glu-D1-2b* in hexaploid wheat in {10307}.Six combinations involving 5 HMW subunits [1A (u-z)] are listed in {420}, from a study of 109 genotypes including representatives of botanical varieties. Alleles in *T. turgidum* var. *dicoccoides* populations, 12 at *GLU-A1-1* and 3 at *GLU-A1-2*, were described in {798}. In a further study using different germplasm of this species {205}, 14 alleles at *GLU-A1* were observed, including 12 not previously found; the 15 alleles included up to 15 alleles at *GLU-A1-1* (with up to 10 not previously observed), and 5 alleles at *GLU-A1-2* (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously.
In a study including emmers (*T. dicoccum*) {00115}, new subunits named 1^+ and 2^- were found in accessions MG4378/1 and MG5380/1, respectively, and provisionally assigned to *GLU-A1*. Until confirmed, they are not included in the *GLU-A1* list.

Glu-R1-1.
Glu-R1-1a {03116}. 1^r {03116}. **v:** Indiana hexaploid triticale {03116}.
Glu-R1-1b {03116}. 2^r {03116}. **v:** Graal hexaploid triticale {03116}.
Glu-R1-1c {03116}. 6^r {03116}. **v:** Alamo hexaploid triticale {03116}.
Glu-R1-1d {03115}. 0.8^r {03115}. **v:** Carmara hexaploid triticale {03115}.
Glu-R1-1e {03115}. 5.8^r {03115}. **v:** Arrayan hexaploid triticale {03115}.

Glu-R1-2. 1R, 1RL.
Glu-R1-2a {03116}. 4^r {03116}. **v:** Indiana hexaploid triticale {03116}.
Glu-R1-2b {03116}. 6.5^r {03116}. **v:** Graal hexaploid triticale {03116}.
Glu-R1-2c {03116}. 13^r {03116}. **v:** Alamo hexaploid triticale {03116}.
Glu-R1-2d {03116}. 9^r {03116}. **v:** Olympus hexaploid triticale {03116}.
There was difficulty in assigning subunit 6^r in the *GLU-R1-1* and *GLU-R1-2* lists, since it appeared as an x-type subunit in allele *Glu-R1c* and as a y-type subunit in allele *Glu-R1f*. It is currently provisionally assigned to the *GLU-R1-1* list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.

GLU-V1-1.
Alleles and subunits at *GLU-V1-1* and *GLU-V1-2*: The following is analogous to the *GLU-1-1* and *GLU-1-2* lists given earlier to identify x-type and y-type subunits in wheat. It was assumed that where an allele at *GLU-V1* produces only a single subunit, it is an x-type subunit and so encoded by *GLU-V1-1* rather than by *GLU-V1-2*; the electrophoretic mobilities of the subunits are all greater, though some only marginally so, than subunit 7 encoded by *Glu-B1-1a* (an x-type subunit), and extend beyond the mobility of subunit 12 encoded by *Glu-D1-2a* (a y-type subunit) {1651}; therefore, it is quite possible that any one of the subunits designated as encoded by *GLU-V1-1* is, in fact, encoded by *GLU-V1-2*. The designation given here is intended to be the most practically useful until the identities of the genes encoding the alleles are directly established.
Glu-V1-1a {1651}. 71 {1651}. **al:** *D. villosum*.
Glu-V1-1b {1651}. 72 {1651}. **al:** *D. villosum*.
Glu-V1-1c {1651}. 73 {1651}. **al:** *D. villosum*.
Glu-V1-1d {1651}. 74 {1651}. **al:** *D. villosum*.
Glu-V1-1e {1651}. 75 {1651}. **al:** *D. villosum*.
Glu-V1-1f {1651}. 76 {1651}. **al:** *D. villosum*.
Glu-V1-1g {1651}. 77 {1651}. **al:** *D. villosum*.

Glu-V1-1h {1651}. 78 {1651}. **al:** *D. villosum.*
Glu-V1-1i {1651}. 79 {1651}. **al:** *D. villosum.*
Glu-V1-1j {1651}. 80 {1651}. **al:** *D. villosum.*
Glu-V1-1k {1651}. Null {1651}. **al:** *D. villosum.*
Glu-V1-1l {1651}. 81 {1651}. **al:** *D. villosum.*
Glu-V1-1m {1651}. 83 {1651}. **al:** *D. villosum.*
Glu-V1-1n {1651}. 85 {1651}. **al:** *D. villosum.*

GLU-V1-2

Glu-V1-2a {1651}. Null {1651}. **al:** *D. villosum.*
Glu-V1-2b {1651}. 82 {1651}. **al:** *D. villosum.*
Glu-V1-2c {1651}. 84 {1651}. **al:** *D. villosum.*
Glu-V1-2d {1651}. 86 {1651}. **al:** *D. villosum.*

GLU-2

Glu-B2 {277}, {819}. [*XGlu-B2* {277}]. 1BS. **s:** CS*/Cheyenne 1B {277}. **stv:** Langdon*/*T. turgidum* var. *dicoccoides* 1B {277}.
Glu-B2a {00114}. 12 {00114}. **tv:** Mexicali.
Glu-B2b {00114}. Null {00114}. **tv:** Langdon.
GLI-B3 was designated *GLU-B2* {589} until the name of the locus was changed in {1119}.
Glu-B2c {10215}. 12* {10215}. **tv:** Alcala la Real {10215}.
Glu-B2d {11493}. 12.1 {11493}. **tv:** *T. turgidum* ssp. *durum* Moroccan landrace MGB-3125 {11493}.

GLU-3

The *GLU-3* loci are defined as the cluster of LMW glutenin genes previously considered a component of the compound *GLI-1* loci.

More than 30 LMW glutenin complete genes, partial genes or pseudogenes have been sequenced from *Triticum* species (reviewed in {0245}).

In *T. aestivum*, only *GLU-B3* was shown to recombine with the gliadin genes (1.7 +/- 0.8) {1355, 1358}. However, in *T. durum*, recombination was observed for both *GLU-A3* and *GLU-B3* with their respective *GLI-1* loci: the map distance between *GLU-A3* and *GLI-A1* has been estimated as 1.3 +/- 0.4 cM {1242}, and that between *GLU-B3* and *GLI-B1* as 2.0 +/- 0.8 in {1144} and as 2.0 +/- 0.4 in {1242}. It appears that *GLU-B3* is proximal to *GLI-B1*, and there is some evidence that *GLU-A3* is proximal to *GLI-A1* {1242}.

Whereas hitherto it was widely thought that all LMW glutenin subunits were encoded by genes located on the chromosomes of homoeologous group 1, it has been demonstrated that, although the majority of the subunits are indeed controlled by genes on this group, some of the C subunits must be controlled by loci elsewhere in the genome {482}.

A novel type of polymeric protein (M_r approx. 71,000) was reported in the Australian advanced breeding line DD118 {03125}. It participates in the polymeric structure of glutenin (possibly as a chain terminator), and has an M_r of approximately 71,000, could be considered as a D-subunit of LMW glutenin. However, N-terminal sequencing suggests it to be a *Gli-B1* type omega-gliadin that has acquired a cysteine residue through mutation.

In an electrophoretic survey of 51 primary tritordeums {03113}, 20 distinct whole banding patterns (a-t), each consisting of between one and three bands, were observed for D-zone prolamins exhibiting glutenin-like solubility characteristics.

In 85 Japanese common wheat cultivars and 61 elite F_6 breeding lines, 3 alleles were observed at each of *GLU-A3* and *GLU-B3*, and 2 alleles at *GLU-D3* were named according to their parental origins in three doubled haploid mapping populations {03135}.

C-type LMW glutenin subunits in CS were assigned to chromosome groups 1 and 6, and shown to have sequences very similar to those of alpha- and gamma-gliadins {03134}. The authors suggest that they may be encoded by novel genes at loci tightly linked or present within the *GLI-1* and *GLI-2* loci, unlike other LMW glutenin subunits encoded by the *GLU-3* loci.

The HMW and LMW glutenin subunits carried by chromosome $1A^m$ of *T. monococcum* accession G1777 were characterised electrophoretically and evaluated for quality characteristics using recombinant chromosome substitution lines with chromosome 1A of CS {03142}. The HMW subunits from G1777 are promising for bread-making quality, whereas its LMW subunits are promising for biscuit-making quality.

The bread wheat cv. Salmone was shown to carry two DNA fragments designated as SF720 and SF750 located on the chromosome 1B satellite and associated with the presence of two LMW glutenin subunits {03143}. However, the authors suggest that they occur at a locus other than *GLU-B3* due to their relatively high frequency of recombination with *GLI-B3*.

A naming system in which Roman numerals are assigned to whole banding patterns for the LMW glutenin subunit is given in {03131} as an alternative to the LMW-1/-2 system described in {03136}. A further system naming whole banding patterns from LMW-1 to LMW-23 in emmer wheat is described in {03137}. In {00111}, in a study of common and durum wheats from Portugal, the authors used the nomenclature system described in {00113} for the LMW subunits in common wheat, and that described in {00114} for the LMW subunits in durum wheat. The latter system was updated according to {02110} but has been changed herein to new alleles with the earlier durum designation {00114} given as synonyms. In {03116}, it was suggested that *Glu-B3d* (common wheat standard genetic stock) is equivalent to *Glu-B3r* (durum wheat standard genetic stock), and that (referring to article {03127}) LMWsubunits observed in some Portugese triticales could be of the durum type.

A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated *Ch1* to *Ch8*, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the *GLI-1* and *GLU-3* loci. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated {10307}. Characterization of near isogenic lines for the different GLU-3 alleles provides a useful quantification of their contribution to bread making quality {11129}.

Glu-A3 {1358}. 1AS {1358}. **v:** CS.

The first 7 alleles were distinguished using 5 allele-specific primer sets {10185}. Further mainly Australian genotypes with alleles *a* to *f* are listed in {10185}.

In 112 common wheat cultivars from Argentina, 11 microsatellite alleles plus a null allele were found at the *GLU-A3* locus {03123}.

Glu-A3a {481}. **v:** CS.

Glu-A3b {481}. **v:** Gabo.

Glu-A3c {481}. **v:** Cheyenne.

Glu-A3d {481}. **v:** Cappelle Desprez, Orca; Suneca{10185}.

Glu-A3e {481}. **v:** Halberd {10185}; Hope, Insignia.

Glu-A3f {481}. **v:** Rescue.

Glu-A3g {00113}. **v:** Glenlea {10185}.

Glu-A3h {00114, 03116}. [*Glu-A3d'* {03116}]. Null {00114}. **v:** Magistral hexaploid triticale {03116}.

Glu-A3i {02110}. 8^*+11 {02110}. **tv:** Mourisco Fino.

Glu-A3j {00114}. [*Glu-A3a* {00114}]. 6 {00114}. **tv:** Mexicali.

Glu-A3k {00114}. [*Glu-A3b* {00114}]. 5 {00114}. **tv:** Langdon.

Glu-A3l {00114}. [{00114}]. 6+10 {00114}. **tv:** Cocorit.

Glu-A3m {00114}. [*Glu-A3d* {00114}]. 6+11 {00114}. **tv:** Alaga.

Glu-A3n {00114}. [*Glu-A3e* {00114}]. 11 {00114}. **tv:** Blatfort.

Glu-A3o {00114}. [*Glu-A3f* {00114}]. 6+11+20{114}. **tv:** Clarofino.

Glu-A3p {00114}. [*Glu-A3h* {00114}]. Null {00114}. **tv:** Jiloca.

Glu-A3q {10215}. [*Glu-A3i* {10215}]. 5+20 {10215}. **tv:** Fanfarron {10215}.

Glu-A3r {03116}. [*Glu-A3d'* {03116}]. **v:** Magistral hexaploid triticale {03116}.

Glu-A3s {00114}. [*Glu-A3g* {00114}]. 6+10+20 {00114}. **tv:** Claro de Balazote {00114}.

Glu-A3t {10805}. [*Glu-A3*^{m}*a* {10805}]. **dv:** PI 190947, *T. monococcum* ssp. *monococcum* {10805}.

Glu-A3u {10805}. [*Glu-A3*^{m}*b* {10805}]. **dv:** PI 190946, *T. monococcum* ssp. *monococcum* {10805}.

Glu-A3v {10805}. [*Glu-A3*^{m}*c* {10805}]. **dv:** BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.

Glu-A3w {10805}. [*Glu-A3*^{m}*d* {10805}]. **dv:** PI 191097, *T. monococcum* ssp. *monococcum* {10805}.

Glu-A3x {10805}. [*Glu-A3*^{m}*e* {10805}]. **dv:** BGE-013624, *T. monococcum* ssp. *Monococcum* {10805}.

Glu-A3y {10805}. [*Glu-A3*^{m}*f* {10805}]. **dv:** PI 191094, *T. monococcum* ssp. *monococcum* {10805}.

Glu-A3z {10806}. [*Glu-A*^{u}*3-I* {10806}]. **dv:** PI 428139, *T. urartu* {10806}.

Glu-A3aa {10806}. [*Glu-A*^{u}*3-II* {10806}]. **dv:** PI 428327, *T. urartu* {10806}.

Glu-A3ab {10806}. [*Glu-A*^{u}*3-III* {10806}]. **dv:** PI 428340, *T. urartu* {10806}.

Glu-A3ac {10806}. [*Glu-A*^{u}*3-IV* {10806}]. **dv:** PI 428322, *T. urartu* {10806}.

Glu-A3ad {10806}. [*Glu-A*^{u}*3-V* {10806}]. **dv:** PI 428188, *T. urartu* {10806}.

Glu-A3ae {10806}. [*Glu-A*^{u}*3*-VI {10806}]. **dv:** PI 428203, *T. urartu* {10806}.

Glu-A3af {10806}. [*Glu-A*^{u}*3-VII* {10806}]. **dv:** PI 428255, *T. urartu* {10806}.

Glu-A3ag {10806}. [*Glu-A*^{u}*3-VIII* {10806}]. **dv:** PI 428328, *T. urartu* {10806}.

Glu-A3ah {10806}. [*Glu-A*^{u}*3-IX* {10806}]. **dv:** PI 428256, *T. urartu* {10806}.

Glu-A3ai {10806}. [*Glu-A*^{u}*3-X* {10806}]. **dv:** PI 428217, *T. urartu* {10806}.

Glu-A3aj {10806}. [*Glu-A*^{u}*3-XI* {10806}]. **dv:** PI 428335, *T. urartu* {10806}.

Glu-A3ak {10806}. [*Glu-A*^{u}*3-XII* {10806}]. **dv:** PI 428186, *T. urartu* {10806}.

Glu-A3al {10806}. [*Glu-A*^{u}*3-XIII* {10806}]. **dv:** PI 428183, *T. urartu*{10806}.

Glu-A3am {10806}. [*Glu-A*^{u}*3-XIV* {10806}]. **dv:** TRI 11563, *T. urartu* {10806}.

Glu-A3an {10806}. [*Glu-A*^{u}*3-XV* {10806}]. **dv:** PI 427328, *T. urartu* {10806}.

Glu-A3ao {10806}. [*Glu-A*^{u}*3-XVI* {10806}]. **dv:** PI 428253, *T. urartu* {10806}.

Glu-A3ap {10806}. [*Glu-A*^{u}*3-XVII* {10806}]. **dv:** PI 538735, *T. urartu* {10806}.

Glu-A3aq {10806}. [*Glu-A*^{u}*3-XVIII* {10806}]. **dv:** PI 428225, *T. urartu* {10806}.

Glu-A3ar {10806}. [*Glu-A*^{u}*3-XIX* {10806}]. **dv:** PI 538733, *T. urartu* {10806}.

Glu-A3as {10806}. [*Glu-A*^{u}*3-XX* {10806}]. **dv:** PI 428196, *T. urartu* {10806}.

Glu-A3at {10806}. [*Glu-A*^{u}*3-XXI* {10806}]. **dv:** PI 538724, *T. urartu* {10806}.

Glu-A3au {10806}. [*Glu-A*^{u}*3-XXII* {10806}]. **dv:** PI 428191, *T. urartu* {10806}.

Glu-A3av {10806}. [*Glu-A*^{u}*3-XXIII* {10806}]. **dv:** TRI 6734, *T. urartu* {10806}.

Glu-A3aw {10806}. [*Glu-A*^{u}*3-XXIV* {10806}]. **dv:** TRI 11496, *T. urartu* {10806}.

Glu-A3ax {10116}. 6.1 {10116}. **tv:** Buck Cristal {10116}.

The designation of this protein (subunit 6.1) as encoded by *GLU-A3*, previously deduced from its electrophoretic mobility {10116}, was confirmed through mapping studies {11492}. According to {11492}, this subunit is equivalent to that designated 7* in {11539}.

Glu-A3ay {11490}. 6+20 {11492}. **tv:** *T. turgidum* ssp. *durum* landraces BGE047515 and BGE047516 {11492}; Mexican durum landrace accession 10 (CWI52016) {11490}.

Glu-A3az {11490}. 6+10+11* {11490}. **tv:** *T. turgidum* ssp. *durum* Mexican landrace accession 3 (CWI51941) {11490}.

Glu-A3ba {11490}. 5+11 {11492}. **tv:** *T. turgidum* ssp. *turgidum* landrace BGE047535 {11492}; Iranian landrace accession 77 (CWI73342) {11490}.

Glu-A3bb {11493}. 20 {11492}. **tv:** *T. turgidum* ssp. *dicoccon* landrace BGE047498 {11492}; *T. turgidum* ssp. *turgidum* landrace BGE047531 {11492}; *T. turgidum* ssp. *durum* Moroccan landrace MGB-16563 {11493}.
Glu-A3bc {11493}. 5** {11493}. **tv:** *T. turgidum* ssp. *durum* Moroccan cv. MGB-20 {11493}.
Glu-A3bd [{11492}]. 5+22 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047532 {11492}.
Glu-A3be [{11492}]. 5* {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE048495 {11492}.
Glu-A3bf [{11492}]. 5*+20 {11492}. **tv**: *T. turgidum* ssp. *turgidum* BGE048498 {11492}.
Glu-A3bg [{11539}]. 5*+11+20 {11539}. **tv:** *T. turgidum* ssp. *turgidum* BGE018646 {11539}.
Glu-A3bh [{11539}]. 10 {11539}. **tv:** *T. turgidum* ssp. *durum* BGE013622 {11539}.
Glu-A3bi [{11539}]. 5*+11+22 {11539}. **tv:** *T. turgidum* ssp. *turgidum* BGE013089 {11539}.
Glu-A3bj [{11540}]. 5* {11540}. **tv:** *T. turgidum* ssp. *durum* Fanfarron {11540}.
Glu-A3bk [{11540}]. 8* {11540}. **tv:** *T. turgidum* ssp. *durum* BGE019300 {11540}.
Glu-A3bl [{11540}]. 5+8* {11540}. **tv:** *T. turgidum* ssp. *durum* BGE013718 {11540}.

GLU-B3 {1358}. 1BS {1358}. **v:** CS.
Three different approaches were employed to identify putative SNPs used to design gene-specific primers for LMW-GS genes, and six functional STS markers, three for *GLU-B3* and three for *GLU-D3* {10664}. These markers distiguished cultivars with different haplotypes at the *GLU-B3* and *GLU-D3* loci, but there was no clear correlation between the alleles of cultivars defined by protein electrophoretic mobility and the separation patterns of the DNA markers, since all three *GLU-3* loci were multiple copies and each protein electrophoretic mobility allele was controlled by 3-6 coding genes {10665}.
Glu-B3a. **v:** CS.
Glu-B3b {481}. **v:** Gabo, Timstein, Hope.
Glu-B3c {481}. **v:** Insignia, Halberd.
Glu-B3d {481}. **v:** Orca.
Glu-B3e {481}. **v:** Cheyenne.
Glu-B3f {481}. **v:** Radja.
Glu-B3g {481}. **v:** Kharkov, Bungulla.
Glu-B3h {481}. **v:** Thatcher, Rescue.
Glu-B3i {481}. **v:** Norin-61.
Glu-B3j {???}. . **v:** Kavkaz.
Null allele carried by the 1BL.1RS translocation. This allelic designation was originally incorrectly used in the catalogue to name an allele from *T. turgidum* ssp. *durum* that was subsequently redesignated as *Glu-B3ce*, since the Kavkaz allele had precedence.
Glu-B3k {476, 02110}. 8+9+13+16+19 {02110}. **tv:** ALP-153, Dural, Durati, Edmore; Faisca.
Glu-B3l {476}. **tv:** Gionp-1954.
Glu-B3m {03120}. [*Glu-B3b'* {03120}]. **v:** Soissons {03120}.
Glu-B3n {03120}. [*Glu-B3c'* {03120}]. **v:** Courtot {03120}.
Glu-B3o {03116}. [*Glu-B3i'* {03116}]. **v:** Olympus hexaploid triticale {03116}.
Glu-B3p {03116}. [*Glu-B3k* {03116}]. **v:** Alamo hexaploid triticale {03116}.
Glu-B3q {03115}. [*Glu-B3h'* {03115}]. **v:** Torote hexaploid triticale {03115}
Glu-B3r {00114}. [*Glu-B3a* {00114}]. 2+4+15+19 {00114}. **tv:** Mexicali.
Glu-B3s {00114}. [*Glu-B3b* {00114}]. 8+9+13+16 {00114}. **tv:** Langdon.
Glu-B3t {00114}. [*Glu-B3c* {00114}]. 2+4+14+15+19 {00114}. **tv:** Jiloca.
Glu-B3u {00114}. [*Glu-B3d* {00114}]. 2+4+15+17+19 {00114}. **tv:** Mundial.
Glu-B3v {00114}. [*Glu-B3e* {00114}]. 2+4+15+16+18 {00114}. **tv:** Granja Badajoz. ***Glu-B3w***
{00114}. [*Glu-B3f* {00114}]. 2+4+15+17 {00114}. **tv:** Ardente.
Glu-B3x {00114}. [*Glu-B3g* {00114}]. 2+4+15+16 {00114}. **tv:** Claro de Balazote. ***Glu-B3y*** {00114}.
[*Glu-B3h* {00114}]. 1+3+14+18 {00114}. **tv:** Alaga.

Glu-B3z {10116}. 6.1 {10116}. **tv:** Buck Cristal {10116}.
Glu-B3aa {10215}. [*Glu-B3l* {10215}]. 1+3+13*+16 {10215}. **tv:** Blancal de Nules {10215}.
Glu-B3ab {10804}. **v:** Hope {10804}; Nanbukomugi {10804}.
Glu-B3ac {10804}. **v:** ACA 801 {10804}; Klein Proteo {10804}; Thesee {10804}.
Glu-B3ad {10804}. **v:** AC Vista {10804}; Heilo {10804}; Opata 85 {10804}; Ruso {10804}.
Glu-B3ae {11490}. 1+3+16 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 56 (CWI57386) {11490}.
Glu-B3af {11490}. 1+3+17 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 74 (CWI71827) {11490}.
Glu-B3ag {11490}. 2+4+16 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 46 (CWI56913) {11490}.
Glu-B3ah {11490}. 8+9+16 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 65 (CWI57719) {11490}.
Glu-B3ai {11490}. 2+4+14+18 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 62 (CWI57615) {11490}.
Glu-B3aj {11490}. 19 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 77 (CWI73342) {11490}.
Glu-B3ak {11490}. 2+4+6*+15+19 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 69 (CWI71627) {11490}.
Glu-B3al {11490}. 2+4+7*+15+16 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 61 (CWI57614) {11490}.
Glu-B3am {11490}. 1+3+6*+13’+17 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 72 (CWI71759) {11490}.
Glu-B3an {11490}. 8+9+13’+17 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 58 (CWI57522) {11490}.
Glu-B3ao {11490}. 1+3+8’+17 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 50 (CWI57256) {11490}.
Glu-B3ap {11490}. 2+4+6*+9’+14+19 {11490}. **tv:** *T. turgidum* ssp. *durum* accession 78 (CWI73350) {11490}.
Glu-B3aq {11493}. 2+4+8+15+19 {11492}. **tv:** *T. turgidum* ssp. *durum* landraces BGE045634 {11492}; MGB-2963 {11493}.
Glu-B3ar {11493}. 1+3+7+15+18 {11493}. **tv:** *T. turgidum* ssp. *durum* landrace MGB-16563 {11493}.
Glu-B3as {11493}. 1+3+8+13+16+19 {11493}. **tv:** *T. turgidum* ssp. *durum* landrace MGB-3152 {11493}.
Glu-B3at {11493}. 2+4+17 {11493}. **tv:** *T. turgidum* ssp. *durum* landrace MGB-3125 {11493}.
Glu-B3au {11493}. 2+4+7+15+19 {11493}. **tv:** *T. turgidum* ssp. *durum* landrace MGB-5963 {11493}.
Glu-B3av {11493}. 9+13+16 {11493}. **tv:** *T. turgidum* ssp. *durum* landrace MGB-3101 {11493}.
Glu-B3aw [{11492}]. 1+3+8+13+15+18 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047502 {11492}.
Glu-B3ax [{11492}]. 1+3+13*+19 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047504, BGE047506 {11492}.
Glu-B3ay [{11492}]. 1+3+14+15 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047521 {11492}.
Glu-B3az [{11492}]. 1+16 {11492}. **tv:** *T. turgidum* ssp. *dicoccon* BGE045645, BGE047503 {11492}.
Glu-B3ba [{11492}]. 2+4+7+13*+15+19 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE045651 {11492}.
Glu-B3bb [{11492}]. 2+4+15 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE047516 {11492}.
Glu-B3bc [{11492}]. 2+4+15+17+21 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE048494 {11492}.
Glu-B3bd [{11492}]. 4+(7**)+13+15+19 {11492}. **tv:** *T. turgidum* ssp. *dicoccon* BGE045628 {11492}.
The designation of subunit 7** as encoded by *Glu-A3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies {11492}; the subunit was therefore referenced by {11492}.
Glu-B3be [{11492}]. 4+(7**)+13+15+21 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047511 {11492}.
The designation of subunit 7** as encoded by *GLU-A3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies {11492}; the subunit was therefore referenced by {11492}.

Glu-B3bf [{11492}]. 4+(7**)+15+19 {11492}. **tv:** *T. turgidum* ssp. *dicoccon* BGE045629, BGE045676, BGE047499, BGE048499 {11492}.
The designation of subunit 7** as encoded by *GLU-A3* was deduced from its electrophoretic mobility and awaits confirmation by mapping studies {11492}; the subunit was therefore referenced by {11492}.
Glu-B3bg [{11492}]. 4+7***+13+16 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047531 {11492}.
Glu-B3bh [{11492}]. 4+7***+15+19 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE045657 {11492}.
Glu-B3bi [{11492}]. 7+9+14+16 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE047533 {11492}.
Glu-B3bj [{11492}]. 7+13*+15+18 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047512 {11492}.
Glu-B3bk [{11492}]. 7***+8a*+14+17 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE047507 {11492}
Glu-B3bl [{11492}]. 7***+8a*+14*+15+19 {11492}. **tv:** *T. turgidum* ssp. *turgidum* durum wheat landrace BGE048495 {11492}.
Glu-B3bm [{11492}]. 7***+8a*+14*+16+21 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047535 {11492}.
Glu-B3bn [{11492}]. 8+9+14+18 {11492}. **tv:** *T. turgidum* ssp. *durum* BGE045667 {11492}.
Glu-B3bo [{11492}]. 8+13+18 {11492}. **tv:** *T. turgidum* ssp. *dicoccon* BGE048901 {11492}.
Glu-B3bp [{11492}]. 8+13*+16 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047510 {11492}.
Glu-B3bq [{11492}]. 8a*+13*+15+19 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047519 {11492}.
Glu-B3br [{11492}]. 8a*+13*+16 {11492}. **tv:** *T. turgidum* ssp. *dicoccon* BGE047498 {11492}.
Glu-B3bs [{1149}]. (13**)+14+18 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE045632, BGE047532, BGE048498 {11492}.
The designation of subunit 13** as encoded by *GLU-B3* was deduced from its electrophoretic mobility and awaits confirmation by mapping studies {11492}; the subunit was therefore referenced by {11492}.
Glu-B3bt [{11492}]. (13**)+14+19 {11492}. **tv:** *T. turgidum* ssp. *turgidum* BGE047513, BGE048496 {11492}.
The designation of subunit 13** as encoded by *GLU-B3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies {11492}; the subunit was therefore referenced by {11492}.
Glu-B3bu [11539]. 7***+8a*+14*+16+19 {11539}. **tv:** *T. turgidum* ssp. *turgidum* BGE013100 {11539}.
Glu-B3bv [{11539}]. 13+15+19 {11539}. **tv:** *T. turgidum* ssp. *turgidum* BGE020942 {11539}.
Glu-B3bw [{11539}]. 13+17+19 {11539}. **tv:** *T. turgidum* ssp. *durum* BGE013622 {11539}.
Glu-B3bx [{11539}]. 1+3+7*+15+19 {11539}. **tv:** *T. turgidum* ssp. *durum* BGE013590 {11539}.
According to {11492}, this subunit (subunit 7*) is equivalent to 6.1 in {10116}.
Glu-B3by [{11539}]. 1**+2+4+15+17+19 {11539}. **tv:** *T. turgidum* ssp. *durum* BGE08366 {11539}.
Glu-B3bz [{11539}]. 1*+2+4+15+16 {11539}. **tv:** *T. turgidum* ssp. *turgidum* BGE12537 {11539}.
Glu-B3ca [{11540}]. 1+3+13+19 {11540}. **tv:** *T. turgidum* ssp. *durum* BGE018639 {11540}.
Glu-B3cb [{11540}]. 13*+18 {11540}. **tv:** *T. turgidum* ssp. *durum* BGE018657 {11540}.
Glu-B3cc [{11540}]. 13+14+18 {11540}. **tv:** *T. turgidum* ssp. *durum* BGE013724 {11540}.
Glu-B3cd [{11540}]. 2+4+13+15+17 {11540}. **tv:** *T. turgidum* ssp. *durum* BGE030927 {11540}.
Glu-B3ce {476}, {02110}. 4+6*+15+19 {02110}. **tv:** Duramba-B, Duramba-D, Langdon; Mourisco Fino.

GLU-D3 {707}, {1358}. 1DS {707}, {1358}. **v:** CS.
Glu-D3a {481}. **v:** CS.
Glu-D3b {481}. **v:** Gabo.
Glu-D3c {481}. **v:** Insignia, Cappelle Desprez.
Glu-D3d {481}. **v:** Jufy-1 {10813}; Norin-61A.
Glu-D3e {481}. **v:** Orca, Thatcher.
Glu-D3f {10548}. **v:** Cheyenne {10548}.

Glu-D3g {10558}. **v:** Hira-1 {10558}.
Glu-D3h {10558}. **v:** India 115 {10558}.
Glu-D3i {10558}. **v:** Bolac {10558}.
Glu-D3j {10558}. **v:** Hira-2 {10558}.
Glu-D3k {10558}. **v:** Lincoln {10558}.
Glu-D3l {10804}. **v:** Heilo {10804}; Jing411 {10804}; Pepital {10804}; Thesee {10804}.
Glu-D3m {10804}. **v:** Darius {10804}.
Glu-D3n {10804}. **v:** Fengmai 27 {10804}.

GLU-E3 {480}. 1ES {480}. **su:** CS/*E. elongata*.

GLU-S^{l}3 {1228}, {480}. 1S^l {480}. 1S^{1}S {1228}. **su:** CS/*Ae. longissima* {1228}, {480}. **ma:** In *Ae. longissima 2 /Ae. longissima 10* glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one another in {1228} as follows: *GLU-S*^{l}1 – 15.9 cM – *GPI-S*^{l}1 – 38 cM – *GLI-S*^{l}4 – 7.1 cM – *GLU-S*^{l}3 – 0.9 cM – *GLI-S*^{l}1 – 5.6 cM – *GLI-S*^{l}5. *GLU-S*^{l}1 is located in 1S^{l}L and the other loci are in 1S^{1}S.
Glu-U3 {480}. 1U {480}. **su:** CS/*Ae. umbellulata*.
A series of papers {00106, 00107, 00108 and 00109} describe considerable variation in primitive wheats not present in bread wheat (A genome species *T. boeoticum, T. urartu, T. thaoudar, T. aegilopoides, T. monococcum*, and D-genome species *T. tauschii*) for the low molecular weight subunits, sufficient to use them as a source for potentially changing flour properties in bread wheat.
In {00110}, variants for LMW glutenin subunits were reported from study of 24 accessions of einkorn wheat (*T. monococcum* ssp. *monococcum*). Nine of these showed two electrophoretic bands for LMW subunits, arbitrarily designated 'a' and 'b', that appeared to be associated with good bread-making quality.
The isolation of a new low-molecular-weight glutenin subunit gene, located on chromosome 1D, was reported in {0350}.

GLU-4
The following loci, *GLU-D4* and *GLU-D5*, encoding low molecular weight subunits of glutenin (30-32 kDa) were described in {02111}; the proteins encoded by them were first observed earlier {02114, 02115}, and the former was later tentatively assigned the symbol *GLU-4* {02116}, before its chromosomal location was established and the locus definitively named as *GLU-D4* in {02111}. While this locus is located on chromosome 1D (in accordance with the position on the group 1 chromosomes of the remaining glutenin encoding loci found to date), the locus *GLU-D5* is located on chromosome 7D. In SDS-PAGE, the proteins from both loci are detected only in the presence of 4-vinylpyridine added to the sample extract. Their amino acid compositions do not match those of the major prolamin groups; nonetheless, they classify as glutenins based upon solubility, immunological behaviour and N-terminal amino acid sequence (the latter suggesting an evolutionary link with the major (B and C) low molecular weight glutenin subunits).

Glu-D4 {02111}. 1D {02111}. **su:** CS/Langdon 1D(1A); CS/Langdon 1D(1B) {02111}. ***Glu-D4a*** {02111}. **v:** J 24.
Glu-D4b {02111}. **v:** PBW 154.
Glu-D4c {02111}. Null allele. **v:** NI 4.

GLU-5

GLU-D5 {02111}. 7D {02111}. **su:** CS/Langdon 7D(7A); CS/Langdon 7D(7B) {02111}.

A collection of 173 *Ae. tauschii* accessions were analysed for low molecular weight glutenin subunits by SDS-PAGE {02112}; 33 different patterns for B-subunits and 43 for C-subunits were identified, some of which were of identical electrophoretic mobility to those observed in common wheat. Also observed were subunits with the same mobilities as the D-subunits and as the subunits encoded by the *GLU-D4* and *GLU-D5* loci. This variation represents a source of novel germplasm of potential value for breeding programmes aimed at improving the D-genome of common wheat in the context of bread-making quality.
Glu-D5a {02111}. **v:** PBW 154.
Glu-D5b {02111}. Null allele. **v:** K 68.

2.3.2. Gliadins

These are heterogeneous mixtures of alcohol-soluble polypeptides without quaternary structure. The *GLI-1* loci are compound and are now considered to comprise the omega-gliadin and gamma gliadin {982}, {1415} multigene families {494}, which in some circumstances may be divided into *GLI-1-1* and *GLI-1-2*, respectively. The LMW glutenin multigene families, which are closely linked to the *GLI-1* loci {588}, are listed separately as the *GLU-3* set {1358}; information on map distance and gene order in relation to *GLU-3* and the centromere is given in the preamble for the *GLU-3* loci. There is evidence that a few of the omega-gliadin genes are separated from the main omega-gliadin gene cluster {993}.
A catalogue of common wheat gliadin genes and alleles is provided in {11437}.
Variation at the *GLI-1* loci was described earlier {634}, {996}, {1126} and applied in mapping experiments {1243}, {1125}, {196}, {422}, {1120}. A rational system of naming the alleles was produced by Dr. E.V. Metakovsky {988}. This nomenclature is reproduced below. A considerable number of alleles were added to the original list given in {988} and referenced here accordingly. A few alleles have been deleted, because, following much detailed comparison, there is now doubt that they can be reliably distinguished from existing alleles {9981}. The allelic letter in these cases has not been reused. To facilitate practical use of the list, the aim was to give at least three standard cultivars from a range of countries for each allele {9981}. This was achieved for majority of entries and is a change from the original list compiled from {988}, where up to two standards were given. While the three or more standards described almost always include the original standards, some were replaced for various reasons, such as international awareness of the cultivar, availability of seed, or the ease with which an allele can be identified in a particular genetic background {9981}. In the original list, where two cultivars were given as prototypes for an allele, the first named was from the USSR and the second from elsewhere; this is no longer the case, although care was taken to include a Russian cultivar where possible, to maintain a wide base of germplasm in which the alleles are available, as well as to acknowledge the research groups in the country where much of the pioneering work was carried out.
For discussion of null alleles at the *GLI-1* and *GLI-2* loci, see {9984}.
Recombination was observed within the gliadin multigene family at *XGli-A1* {277}. These closely linked genes may correspond to *GLI-A1* and *GLI-A5*, but they were temporarily designated *XGLI-A1.1* and *XGLI-A1.2* until orthology with *GLI-A1* and/or *GLI-A5* is established.
Note: The catalogue entries reproduced here only refer to alleles in *T. aestivum*; there is, however, enormous variation in gliadins in the close relatives of wheat; see, for example, {989} for studies in *T. monococcum* (more than 80 gliadin electrophoretic patterns observed in 109 accessions), {990} for studies in *T. boeoticum* (more than 50 electrophoretic patterns in 60 accessions), and {1076} studies in *T. durum* (19 electrophoretic patterns, referring only to variation in the omego-gliadins, in 243 accessions). In {00110}, variants for omega-gliadins were reported from study of 24 accessions of einkorn wheat (*T. monococcum* ssp. *monococcum*). In {00111}, in a study of common wheat and durum from Portugal, the authors used the nomenclature system described in {00112} for the omega-gliadins. In {00116}, a comparison between spelt and common wheat was carried out for the gliadins using a nomenclature system described in {00118}.
The *GLI-1* loci may be recognised by probes pcP387 {372} and pTag1436 {065}, and by specific

microsatellite primers {252}. Furthermore, it was shown that probe pTag1436 differentiates gliadin alleles rather well; using this probe, families of gliadin alleles and some of their relationships were described {9988}.

Twenty eight gamma-gliadin gene sequences from GenBank were grouped into nine subgroups in {10063}. Primers were developed against some of the subgroups and the chromosomal locations of the gamma-gliadin genes were determined {10063}.

Based upon morphological observation and RFLP analysis, it was proposed that the cultivar 'Chinese Spring' is a strain of the landrace 'Chengdu-guangtou' from the Chengdu Plain, Sichuan Province; this proposal is supported by the observation that CS and the landrace share the same alleles at all nine *GLI-1*, *GLI-2* and *GLU-1* loci {see 01102}.

PCR primers GAG5 and GAG6 were applied to 35 cultivars of closely related spelt and hexaploid wheat, and to eight cultivars of durum, to yield products originating from two gamma-gliadin genes mapped to chromosomes 1B (termed GAG56B) and 1D (termed GAG56D) {01103}. Two alleles for GAG56D (differing in a 9 bp deletion/duplication and single nucleotide polymorphism) were found, one a new allele and the other previously published {01104}. Meanwhile two alleles found for GAG56B among the durum wheats correlated with the presence of gluten quality markers, gamma-gliadins 42 or 45.

1B and 1D sulphur-poor omega-gliadins in cultivar Butte 86 were characterised by RP-HPLC, SDS-PAGE, two-dimensional PAGE, amino acid composition determination and sequencing, matrix assisted laser desorption ionisation-time of flight mass spectrometry and circular dichroism spectroscopy to reveal the detailed nature of the peptides belonging to the two groups, and showing that the complexity of mixtures of the peptides of the 1B group was greater than that of the 1D group {01105}. Although circular dichroism spectra were similar for the two groups of peptides, and suggested a mainly flexible random structure, there was evidence for a significant amount of left-handed polyproline II helical conformation in the case of the 1D components. The authors placed some of the results in the context of the possible ancestor of the B-genome and relationships with the barley C-hordeins and rye omega-secalins.

Eleven new gliadin alleles were found in a collection of 52 Spanish landraces of common wheat {03141}.

A new family of low-molecular-weight gliadin genes located on groups 4 and 7 were reported in {10117}. They appear to influence rheological properties and seem to be closely related to the 17kDa epsilon hordein, important in beer foam stability.

A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated *Ch1* to *Ch8*, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci *GLI-1* and *GLU-3*. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated {10307}.

Transcriptome analysis showed the presence of proteins called avenin-like a and b. The former contained a duplicated sequence of about 120 residues and corresponded to the LMW-gliadins. The latter was not previously characterized but may form part of the glutenin fraction and hence influence quality. These avenin-like proteins showed higher expression levels in three *Aegilops* species (*Ae. caudata, Ae. cylindrica* and *Ae. tauschii*) than in common wheat {10321}.

Four new classes of low molecular weight proteins related to gliadins, though not sufficiently similar to be classified as such, were reported in {02113}. One of the classes has no close association to previously described wheat endosperm proteins.

GLI-1

GLI-A1 {1125, 1334}. [*Gld 1A* {1415}]. 1AS {150}, {634}, {1607}, {1334}. **s:** CS*/Cheyenne {634}. **v:** CS {150}, {1607}, {1334}.

Gli-A1a {988}. **v:** Castan {991}; CS {988}; Mara {9986}; Mentana {9986}; Millewa {00119}.

Gli-A1b {988}. **v:** Bezostaya 1, Mercia {988}; Tracy {991}.

Gli-A1c {988}. **v:** Ukrainka {998}; Gazul {9985}; Sava {994}; Hopps {00119}.

Gli-A1d {988}. **v:** Dankowska {988}; Cabezorro {9985}.

Gli-A1e {988}. **v:** Falchetto {988}; Open {991}; Touzelle {991}.

Gli-A1f {988}. **v:** Mironovskaya 808, Maris Freeman {988}; Arminda {991}.

Note:

An allele **_Gli-A1f*_** is mentioned in {03130}.

Gli-A1g {988}. **v:** Gabo {988}; Adalid {9985}.

Gli-A1h {988}. **v:** Sadovo I {988}; Predela {9981}; Krajinka {9981}.

Gli-A1i {988}. **v:** Saratovskaya 36 {988}.

Gli-A1j {988}. **v:** Lutescens 62 {988}.

Gli-A1k {988}. **v:** Courtot {991}; Skala (heterogeneous) {988}; Soissons {991}; Spada {9986}.

Gli-A1l {988}. **v:** Lesostepka 75 {988}; David {9986}; Salmone {9986}; Mura {9981}.

Gli-A1m {988}. **v:** Marquis {988}; Dneprovskaya 521 {988}; Carat {991}; Liocorno {9986}.

Gli-A1n {988}. **v:** Intensivnaya {988}.

Gli-A1o {988}. **v:** Odesskaya 16 (heterogeneous) {988}; Oderzo {9986}; Cappelle-Desprez {991}; Capitole {991}.

Gli-A1p {988}. **v:** Pyrotrix 28 {988}; Zagore {9981}.

Gli-A1q {988}. **v:** Akmolinka 1 {988}.

Gli-A1r {988}. **v:** Ranniaya 73 {988}; Barbilla {9985}.

Gli-A1s.

Although reported {9986}, this allele is omitted because it requires further confirmation {9981}.

Gli-A1t {9985}. **v:** Jeja del Pais {9985}; Milturum 553 {9981}; Strela {9981}.

Gli-A1u {9985}. **v:** Candeal Alcala {9985}.

Gli-A1v {9981}. **v:** Japhet {9981}; Rouge de Bordeaux {9981}.

Gli-A1w {9984, 9987}. Null allele. **v:** Saratovskaya 29 (mutant) {9987}; E. Mottin {9981}.

Gli-A1x {10805}. [*Gli-A1*^{m}*a* {10805}]. **dv:** PI 191146, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1y {10805}. [*Gli-A1*^{m}*b* {10805}]. **dv:** PI 190947 *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1z {10805}. [*Gli-A1*^{m}*c* {10805}]. **dv:** PI 190946, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1aa {10805}. [*Gli-A1*^{m}*d* {10805}]. **dv:** PI 191097, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1ab {10805}. [*Gli-A1*^{m}*e* {10805}]. **dv:** BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1ac {10805}. [*Gli-A1*^{m}*f* {10805}]. **dv:** BGE-013626, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1ad {10805}. [*Gli-A1*^{m}*g* {10805}]. **dv:** BGE-013628, *T. monococcum* ssp. *monococcum* {10805}.

Gli-A1ae {10811}. [*Gli-A*^{u}*1-I* {10811}]. **dv:** PI-428333, *T. urartu* {10811}.

Gli-A1af {10811}. [*Gli-A*^{u}*1-II* {10811}]. **dv:** PI-428319, *T. urartu* {10811}.

Gli-A1ag {10811}. [*Gli-A*^{u}*1-III* {10811}]. **dv:** PI-428335, *T. urartu* {10811}.

Gli-A1ah {10811}. [*Gli-A*^{u}*1-IV* {10811}]. **dv:** PI-428323, *T. urartu* {10811}.

Gli-A1ai {10811}. [*Gli-A*^{u}*1-V* {10811}]. **dv:** PI-428231, *T. urartu* {10811}.

Gli-A1aj {10811}. [*Gli-A*^{u}*1-VI* {10811}]. **dv:** PI-428194, *T. urartu* {10811}.

Gli-A1ak {10811}. [*Gli-A*^{u}*1-VII* {10811}]. **dv:** PI-428256, *T. urartu* {10811}.

Gli-A1al {10811}. [*Gli-A*^{u}*1-VIII* {10811}]. **dv:** PI-428234, *T. urartu* {10811}.

Gli-A1am {10811}. [*Gli-A*^{u}*1-IX* {10811}]. **dv:** PI-428320, *T. urartu* {10811}.

Gli-A1an {10811}. [*Gli-A*^{u}*1-X* {10811}]. **dv:** PI-428255, *T. urartu* {10811}.

Gli-A1ao {10811}. [*Gli-A*^{u}*1-XI* {10811}]. **dv:** PI-428241, *T. urartu* {10811}.

Gli-A1ap {10811}. [*Gli-A*^{u}*1-XII* {10811}]. **dv:** PI-428235, *T. urartu* {10811}.

Gli-A1aq {10811}. [*Gli-A*^{u}*1-XIII* {10811}]. **dv:** PI-428183, *T. urartu* {10811}.

Gli-A1ar {10811}. [*Gli-A*^{u}*1-XIV* {10811}]. **dv:** PI-428317, *T. urartu* {10811}.

Gli-A1as {10811}. [*Gli-A*^{u}*1-XV* {10811}]. **dv:** PI-427328, *T. urartu* {10811}.

Gli-A1at {10811}. [*Gli-A*^{u}*1-XVI* {10811}]. **dv:** PI-428327, *T. urartu* {10811}.

Gli-A1au {10811}. [*Gli-A^{u}1-XVII* {10811}]. **dv:** PI-428253, *T. urartu* {10811}.
Gli-A1av {10811}. [*Gli-A^{u}1-XVIII* {10811}]. **dv:** PI-428224, *T. urartu* {10811}.
Gli-A1aw {10811}. [*Gli-A^{u}1-XIX* {10811}]. **dv:** PI-538727, *T. urartu* {10811}.
Gli-A1ax {10811}. [*Gli-A^{u}1-XX* {10811}]. **dv:** PI-428211, *T. urartu* {10811}.
Gli-A1ay {10811}. [*Gli-A^{u}1-XXI* {10811}]. **dv:** PI-538724, *T. urartu* {10811}.
Gli-A1az {10811}. [*Gli-A^{u}1-XXII* {10811}]. **dv:** PI-428191, *T. urartu* {10811}.
Gli-A1ba {10811}. [*Gli-A^{u}1-XXIII* {10811}]. **dv:** TRI-6735, *T. urartu* {10811}.
Gli-A1bb {10811}. [*Gli-A^{u}1-XXIV* {10811}]. **dv:** TRI-11494, *T. urartu* {10811}.
Gli-A1bc {10811}. [*Gli-A^{u}1-XXV* {10811}]. **dv:** TRI-6734, *T. urartu* {10811}.
Gli-A1bd {10811}. [*Gli-A^{u}1-XXVI* {10811}]. **dv:** TRI-11496, *T. urartu* {10811}.

GLI-B1 {1125, 1607}. [*Gld 1B* {1415, 1243}, *Gld-B4* {420}, *Gld-B2* {420}, *Gld-B6* {420}, *Gld-B5* {420}, *Gld-B3* {420}, *Gld-B1* {420}]. 1BS {150, 634}.1B {1607}. **s:** CS*/Cheyenne {634}. **v:** CS {150}, {1607}.
Gli-B1a {988}. **v:** CS {988}.
Gli-B1b {988}. **v:** Bezostaya 1 {988}; Carat {991}; Marquis {988}; Liocorno {9986}; Soissons {991}.
Gli-B1c {988}. **v:** Siete Cerros 66 {988}; Prinqual {991}; Loreto {9986}.
Gli-B1d {988}. **v:** Dneprovskaya 521 {988}; Chopin {991}; Petrel {991}; Tiberio {9986}; Yecora {9985}; Neepawa {995}; Suneca {00119}.
Gli-B1e {988}. **v:** Apexal {991}; Fournil {991}; Lutescens 62 {988}; Oderzo {9986}.
Gli-B1f {988}. **v:** Capitole {991}; Cappelle-Desprez {991}; Dankowska {988}; Maris Freeman {988}; Mercia {998}.
Gli-B1g {988}. **v:** Champtal {991}; Galahad {988}; Mara {9986}; Sadovo 1 {988}; Tracy {991}.
Gli-B1h {988}. **v:** Cabezorro {9985}; Krasnodonka {988}; Pepital {991}; Rudi {991}; Tincurrin {00119}.
Gli-B1i {988}. **v:** Ghurka {988}; Insignia {988}.
Gli-B1j {988}. **v:** Cluj 650 {988}.
Gli-B1k {988}. **v:** Crverkapa {994}; De Carolis {9986}; Kremena {988}; Mentana {9986}.
Gli-B1l {988}. **v:** Avrova {9981}; Clement {991}; Damier {991}; Fiocco {9986}; Kavkaz {9981}. *Gli-B1l* encodes secalins ssociated with the 1BL.1RS translocation.
Gli-B1m {988}. **v:** Costantino {9986}; Et.d'Choisy {991}; Pyrotrix 28 {988}.
Gli-B1n {988}. **v:** Intensivnaya {988}.
Gli-B1o {988}. **v:** Aragon 03 {9985}; Levent {988}; Pippo {9986}; San Rafael {9985}.
Gli-B1p {988}. **v:** Inia 66 {9985}; New Pusa 834 {988}.
Gli-B1q {9986}. **v:** Gallo {9986}; Goelent {991}; Goya {991}.
Gli-B1r {995}. **v:** Chinook {995}; Gazul {9985}; Sevillano {9985}.
Gli-B1s {9986}. **v:** Salmone {9986}; Resistente {9986}; E. Mottin {9981}.
Gli-B1t {9985}. **v:** Jeja del Pais {9985}.
Gli-B1u {9985}. **v:** Negrillo {9985}.
Gli-B1v {9985}. **v:** Montjuich {9985}.
Gli-B1w {9981}. **v:** Ardica{9981}; Barbilla (MCB-1017) {9981}.
Gli-B1x {9984, 9987, 991}. Null allele. **v:** Touzelle {991}; Florence Aurora {9985}.
Twelve microsatellite alleles plus a null allele were found at the *GLI-B1* locus tightly linked to *GLU-B3* in 112 bread wheat cultivars from Argentina{03123}.

GLI-D1 {121}, {1125}. [*Gld-D1* {420}, *Gld-D3* {420}, *Gld 1D* {1415}, *Gld-D2* {420}]. 1DS {150}, {121}, {634,} {1607}, {1334}. **s:** CS*/Cheyenne {634}. **v:** CS {150}, {121}, {1607}, {1334}.

Gli-D1a {988}. **v:** CS {988}; Marquis {988}; Mentana {9986}; Prinqual {991}; Saratovskaya 36 {988}.
Gli-D1b {988}. **v:** Bezostaya 1 {988}; Cappelle-Desprez {991}; Etoile d'Choisy {991}; Galahad {988}.
Gli-D1c {988}. **v:** Skorospelka Uluchshennaya (biotype) {988, 9982}.
Gli-D1d {988}. **v:** De Carolis {9986}; Solo {988}.
Gli-D1e {988}. **v:** Gerek 79 {988}.
Gli-D1f {988}. **v:** Carlos {991}; Gabo {988}; Maris Freeman {988}; Orso {9986}.
Gli-D1g {988}. **v:** Fournil {991}; Ghurka {988}; Mironovskaya 808 {988}; Open {991}.
Gli-D1h {988}. **v:** Sadovo I {988}; Zlatostrui {9981}.
Gli-D1i {988}. **v:** Insignia {988}; Napayo (biotype) {995}; San Rafael {9985}; Tselinogradka {988}.
Gli-D1j {988}. **v:** Aubain; Chinook {995}; Inia 66 {9985}; Petrel {991}; Promin {988}.
Gli-D1k {988}. **v:** Cargimarec {991}; Kremena {988}; Mara {9986}; Pippo {9986}.
Gli-D1l {988}. **v:** Artaban {991}; Corin {991}; Longbow {988}.
Gli-D1m {991}. **v:** Heurtebise {991}.
Gli-D1n {981}. **v:** Blanquillo de Toledo (MCB-0950) {9981}.
Gli-D1o {9984, 9987, 991}. Null allele. **v:** Darius {991}; Touzelle {991}; Saratovskaya 29 (mutant) {9987}.

GLI-Ag^{i}1. 1Ag^{i} {168}. **ad:** Vilmorin 27/*Th. intermedium*.

GLI-E1 {781}. 1ES {781}. **ad:** CS/*E. elongata*. ***GLI-H^{t}1*** {1037}. 1H^{t}p {1037}. **ad:** CS/*E. trachycaulum*.

GLI-R1 {1334}. [*SecR1* {1356}, *Sec1* {1336}]. 1RS {1340}, {781}, {1336,} {1334}. **ad:** CS/Imperial{1340}, {781}, {1336}, {1334}; Holdfast/King II{1340, 1334}. **tr:** CS 1DS. Imperial 1RL {1356}.
Sec-12 and *Sec13* are given as allelic alternatives in 1BL.1RS translocation lines by {03132}.
GLI-R^{m}1 {1340}. 1R^{m}S {1340}. **ad:** CS/*S. montanum*.

GLI-S^{l}1 {573}. 1S^{l} {573}. **ad:** CS/*Ae. longissima*.

GLI-U1 {1335}. 1U {150}, {1335}. **ad:** CS/*Ae. umbellulata*. ***GLI-V1*** {111}, {1026}. 1V {111}, {1026}. **ad:** CS/*D. Villosum* {1026}; Creso/*D. villosum* {111}.

In barley, the B and C hordeins are controlled by the *HOR2* and *HOR1* loci, respectively, which are linked {1341} on chromosome 1HS {1063, 1153}. The map distances and homology of the proteins indicate that *HOR1*, the locus closest to the centromere, is equivalent to the omega-gliadins (*GLI-1-1*) in *GLI-1* {1338}.

Three alleles at each of the *GLI-1-1* (omega gliadin) loci were noted {1358}. The complexity of the *GLI-1* compound loci is further emphasized by a report of individual genes being separable by recombination, where *G1d-1A* (a block of gamma and omega genes) is separable by 0.3% from *Gld4-1A* (omega gliadins) which is in turn, separable by 1.5% from *Gld3-1A* (omega gliadins) {1103}.

Variation was described elsewhere {634}, {996}, {1126} and applied in mapping experiments {107}, {196}, {422}, {1120}, {1125}, {1243}. Sixteen combinations of *GLI-B1* and 4 combinations of *GLI-D1* subunits are listed in {420}. Multiple alleles described in {996}, number 15 at *GLI-A1*, 18 at *GLI-B1*, and 8 at *GLI-D1*.

The *Gli-1* alleles present in 57 Yugoslav wheat varieties were reported in {994}.

Gli-DT1 {02109}. 1DS {02109}. **v:** L/18913 (synthetic). **dv:** *Ae. tauschii* AUS18913.

A locus designated *GLI-DT1* controlling an omega-gliadin of *Ae. tauschii* was mapped on the short arm of chromosome 1D between loci *GLI-D1* (strictly *GLI-D*^{t}*1*) and *GLU-D1* (strictly *GLU-D*^{t}*1*), 13.18 cM proximal to the former and 40.20 cM from the latter {02109}. The only omega-gliadin to date identified as being encoded by this locus, namely T1, is of unusually low electrophoretic mobility in SDS-PAGE gels and was formally thought to be a high molecular weight glutenin encoded by the *GLU-D*^{t}*1* locus of *Ae. tauschii* (see note following the *GLU-D1* list in section 'Glutenins'). The authors speculate that, due to their similar relative map positions, the loci *GLI-A4, GLI-D4, GLI-R3, GLI-S*^{l}*4* and this locus, *GLI-DT1*, form a series of '*Gli-4*' orthologous loci. However, this should be interpreted in the light of the above discussion on *GLI-A3* and *GLI-A4*.

Gli-DT1a {02109}. T1. **v:** L/18913 (synthetic). **dv:** *Ae. tauschii* AUS18913.

A 1,200 bp Dra I RFLP was identified as a gene-specific probe for the T1 omega-gliadin {10645}.

GLI-2

Prior to publication {988} allelic variation was demonstrated at all the wheat *GLI-2* loci, including 13 alleles at *GLI-A2*, 11 at *GLI-B2*, and 10 at *GLI-D2*, in a study of 39 cultivars {996}.

GLI-A2 {1125, 1334}. [*Gld 6A* {1415}]. 6A {1334}. 6AS {1122}. **v:** CS.

Gli-A2a {988}. **v:** Cabezorro {9985}; CS {988}; Insignia {988}; Rieti DIV {9986}. ***Gli-A2b*** {988}. **v:** Aradi {9985}; Bezostaya 1 {988}; Rivoli {991}; Tiberio {9986}. ***Gli-A2c*** {988}. **v:** Eagle {00119}; Escualo {9985}; Loreto {9986}; Prinqual {991}; Siete Cerros 66 {988}. ***Gli-A2d*** {988}. **v:** Dneprovskaya 521 {988}; Kenyon (biobype) {995}; Mocho Sobarriba {9985}.

Gli-A2e {988}. **v:** Cobra {991}; Mentana {9986}; Resistente {9986}; Sadovo 1 {988}; Sevillano {9985}.

Gli-A2f {988}. **v:** Adalid {9985}; Gala {991}; Maris Freeman {988}; Sistar {9986}. ***Gli-A2g*** {988}. **v:** Cappelle-Desprez {991}; Ducat {988}; Mahissa 1 {9985}; Mara {9986}.

Gli-A2h {988}. **v:** Apollo {991}; Basalt {9981}; Hereward {988}; Montjuich {9985}; N. Strampelli {9986}.

Gli-A2i {988}. **v:** Krasnodonka {988}; Lesostepka 75 {988}.

Gli-A2j {988}. **v:** Avalon {9981}; Camp Remy {991}; E. Mottin {9981}; Recital {991}.

Gli-A2k {988}. **v:** Akmolinka 1 {988}; Estica {991}; Pyrotrix 28 {988}; Renan {991}; Zena {9986}.

Gli-A2l {988}. **v:** Chamorro {9985}; Champlein {991}; Longbow {988}.

Gli-A2m {988}. **v:** Marquis {988}; Rex {991}; Suneca {00119}.

Gli-A2n {988}. **v:** Mironovskaya 808 {988}.

Gli-A2o {988}. **v:** Calatrava {9985}; Castan {991}; Glenwari {9981}; Lontra {9986}; Touzelle {991}.

Gli-A2p {988}. **v:** Cajeme 71 {9985}; Capitole {991}; Clement{991}; Pliska {988}; S. Lorenzo {9986}; Yecora 70 {9985}.

Gli-A2q {988}. **v:** Candeal Alcala {9985}; Montcada {9985}; Saratovskaya 39 {988}.

Gli-A2r {988}. **v:** Genia l {991}; Open{991}; Riband {988}.

Gli-A2s {988}. **v:** Saratovskaya 36 {998}.

Gli-A2t {988}. **v:** Courtot {991}; Prostor{9981}; Rinconada {9985}; Soissons {991}.

Gli-A2u {988}. **v:** Aragon 03 {9985}; Kirgizskaya Yubileinaya {988}; Saunders {995}; Titien {991}.

Gli-A2v {988}. **v:** Kzyl-Bas {988}.

Gli-A2w {988}. **v:** Bezenchukskaya 98 (biotype) {988}.

Gli-A2x {988}. **v:** Solo {988}.

Gli-A2y {9981}. **v:** Gentil Rosso 202 {9981}; PI 191245 {9981}.

Gli-A2z {9986}. **v:** Gallo {9986}; Giuliana {9986}.

Gli-A2aa {9985}. **v:** Navarro 122 {9985}.

Gli-A2ab {9985}. **v:** Navarro 150 {9985}.
Gli-A2ac {9981}. **v:** Blanquillo de Barcarrota (MCB-0893) {9981}.
Gli-A2ad {9981}. **v:** Hembrilla Soria (MCB-1298) {9981}.
Gli-A2ae {9981}. **v:** Candeal de S.Lorenzo Parrilla (MCB-0932) {9981}.
Gli-A2af {9981}. **v:** Barbilla de Leon (MCB-1292) {9981}.
Gli-A2ag {9981}. **v:** Gluclub {9981}; Tincurrin {9981}.
Gli-A2ah {9981}. **v:** Candeal de Nava del Rey (MCB-0892) {9981}.
Gli-A2ai {9981}. **v:** Blanquillo (MCB-0908) {9981}.
Gli-A2aj {9984, 9987}. Null allele. **v:** Saratovskaya 29 (mutant){9987}.
Gli-A2ak {10805}. [*Gli-A2*^{m}*a* {10805}]. **dv:** BGE-013630, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2al {10805}. [*Gli-A2*^{m}*b* {10805}]. **dv:** PI 094740, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2am {10805}. [*Gli-A2*^{m}*c* {10805}]. **dv:** PI 190942, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2an {10805}. [*Gli-A2*^{m}*d* {10805}]. **dv:** PI 190947, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ao {10805}. [*Gli-A2*^{m}*e* {10805}]. **dv:** PI 190946, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ap {10805}. [*Gli-A2*^{m}*f* {10805}]. **dv:** BGE-013626, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2aq {10805}. [*Gli-A2*^{m}*g* {10805}]. **dv:** PI 191095, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ar {10805}. [*Gli-A2*^{m}*h* {10805}]. **dv:** BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2as {10805}. [*Gli-A2*^{m}*i* {10805}]. **dv:** PI 191096, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2at {10805}. [*Gli-A2*^{m}*j* {10805}]. **dv:** BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2au {10805}. [*Gli-A2*^{m}*k* {10805}]. **dv:** BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2av {10805}. [*Gli-A2*^{m}*l* {10805}]. **dv:** BGE-029108, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2aw {10805}. [*Gli-A2*^{m}*m* {10805}]. **dv:** BGE-013627, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ax {10805}. [*Gli-A2*^{m}*n* {10805}]. **dv:** BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.
Gli-A2ay {10811}. [*Gli-A*^{u}*2-I* {10811}]. **dv:** PI-428333, *T. urartu* {10811}.
Gli-A2az {10811}. [*Gli-A*^{u}*2-II* {10811}]. **dv:** PI-428320, *T. urartu* {10811}.
Gli-A2ba {10811}. [*Gli-A*^{u}*2-II* {10811}]. **dv:** PI-428230, *T. urartu* {10811}.
Gli-A2bb {10811}. [*Gli-A*^{u}*2-IV* {10811}]. **dv:** PI-428319, *T. urartu* {10811}.
Gli-A2bc {10811}. [*Gli-A*^{u}*2-V* {10811}]. **dv:** PI-428239, *T. urartu* {10811}.
Gli-A2bd {10811}. [*Gli-A*^{u}*2-VI* {10811}]. **dv:** PI-428336, *T. urartu* {10811}.
Gli-A2be {10811}. [*Gli-A*^{u}*2-VII* {10811}]. **dv:** PI-428235, *T. urartu* {10811}.
Gli-A2bf {10811}. [*Gli-A*^{u}*2-VIII* {10811}]. **dv:** PI-428234, *T. urartu* {10811}.
Gli-A2bg {10811}. [*Gli-A*^{u}*2-IX* {10811}]. **dv:** PI-428183, *T. urartu* {10811}.
Gli-A2bh {10811}. [*Gli-A*^{u}*2-X* {10811}]. **dv:** PI-428256, *T. urartu* {10811}.
Gli-A2bi {10811}. [*Gli-A*^{u}*2-XI* {10811}]. **dv:** PI-428255, *T. urartu* {10811}.
Gli-A2bj {10811}. [*Gli-A*^{u}*2-XII* {10811}]. **dv:** PI-428224, *T. urartu* {10811}.
Gli-A2bk {10811}. [*Gli-A*^{u}*2-XIII* {10811}]. **dv:** PI-428208, *T. urartu* {10811}.
Gli-A2bl {10811}. [*Gli-A*^{u}*2-XIV* {10811}]. **dv:** PI-428202, *T. urartu* {10811}.]
Gli-A2bm {10811}. [*Gli-A*^{u}*2-XV* {10811}]. **dv:** PI-428217, *T. urartu* {10811}.
Gli-A2bn {10811}. [*Gli-A*^{u}*2-XVI* {10811}]. **dv:** PI-427328, *T. urartu* {10811}.
Gli-A2bo {10811}. [*Gli-A*^{u}*2-XVII* {10811}]. **dv:** PI-428317, *T. urartu* {10811}.
Gli-A2bp {10811}. [*Gli-A*^{u}*2-XVIII* {10811}]. **dv:** PI-428253, *T. urartu* {10811}.
Gli-A2bq {10811}. [*Gli-A*^{u}*2-XIX* {10811}]. **dv:** PI-538742, *T. urartu* {10811}.
Gli-A2br {10811}. [*Gli-A*^{u}*2-XX* {10811}]. **dv:** PI-428232, *T. urartu* {10811}.
Gli-A2bs {10811}. [*Gli-A*^{u}*2-XXI* {10811}]. **dv:** PI-428188, *T. urartu* {10811}.
Gli-A2bt {10811}. [*Gli-A*^{u}*2-XXII* {10811}]. **dv:** PI-428244, *T. urartu* {10811}.
Gli-A2bu {10811}. [*Gli-A*^{u}*2-XXIII* {10811}]. **dv:** PI-538733, *T. urartu* {10811}.
Gli-A2bv {10811}. [*Gli-A*^{u}*2-XXIV* {10811}]. **dv:** PI-428212, *T. urartu* {10811}.
Gli-A2bw {10811}. [*Gli-A*^{u}*2-XXV* {10811}]. **dv:** TRI-6734, *T. urartu* {10811}.

Gli-A2bx {10811}. [*Gli-A^{u}2-XXVI* {10811}]. **dv:** PI-428254, *T. urartu* {10811}.

GLI-B2 {1125, 1607}. [*Gld 6B* {1415}]. 6BS {1122}. 6B {1607}. **v:** CS.
Gli-B2a {988}. **v:** CS{988}.
Gli-B2b {988}. **v:** Bezostaya 1 {988}; Cobra {991}; Gladio {9986}; Sideral {991}.
Gli-B2c {988}. **v:** Courtot {991}; Escuala {9985}; Gabo {988}; Loreto {9986}; Manital {9986}; Prinqual {991}; Siete Cerros 66 {988}; Sinton {995}; Yecora 70 {9985}.
Gli-B2d {988}. **v:** Akmolinka 1 {988}; Cesar {9981}; Friedland {991}; Tselinnaya 20 {988}.***Gli-B2e*** {988}. **v:** Arsenal {991}; Veronese {9986}; Zlatna Dolina {994}.
Gli-B2f {988}. **v:** Basalt {9981}; Maris Freeman {988}; Master {991}.
Gli-B2g {988}. **v:** Capitole {991}; Capelle-Desprez {991}; Galahad {988}; Forlani {9986}.
Gli-B2h {988}. **v:** Castan {991}; Mentana {9986}; Pane 247 {9985}; Partizanka {994}; Sadovo 1 {988}; Sistar{9986}.
Gli-B2i {988}. **v:** Insignia{988}; Robin{9981}.
Gli-B2j {988}. **v:** Farnese {9986}; Funo R250 {9986}; Novosadska Rana 1 {994}.
Gli-B2k {988}. **v:** Skala {988}.
Gli-B2l {988}. **v:** Clement {991}; Longbow {988}; Tracy {991}.
Gli-B2m {988}. **v:** Mironovskaya 808{988}; Open {991}; Renan{991}.
Gli-B2n {988}. **v:** Japhet {9981}; Rouge de Bordeau {9981}; Solo {988}.
Gli-B2o {988}. **v:** Hardi {9981}; Mara {9986}; Odesskaya 16 {988}; Pippo {9986}; Rivoli {991}; Slavjanka {9981}.
Gli-B2p {988}. **v:** Pliska {983}; Champtal {991}; Oderzo {9986}; Recital {991}; Gazul {9985}.
Gli-B2q {988}. **v:** Saratovskaya 39 {988}.
Gli-B2r {991}. **v:** Arminda {991}; Estica {991}; Genial {991}.
Gli-B2s {988}. **v:** Aquila {9981}; Saratovskaya 36 {988}.
Gli-B2t {988}. **v:** Tselinogradka {988}.
Gli-B2u {988}. **v:** Kirgizskaya Yubileinaya {988}.
Gli-B2v {988}. **v:** Declic {991}; Garant {991}; Libellula {9986}; Mahissa 1 {9985}; Poljarka {988}.
Gli-B2w {9986, 995}. **v:** Palata {9986}; Pembina {995}; Rieti DIV {9986}.
Gli-B2x {994}. **v:** Super Zlatna (biotype) {994}; Prostor {9981}; 251/83 {9981}.
Gli-B2y {9986}. **v:** Centauro {9986}; E. Morandi {9986}.
Gli-B2z {9985}. **v:** Maestro {9985}.
Gli-B2aa {9986}. **v:** Salmone {9986}; E. Mottin {9981}.
Gli-B2ab {991}. **v:** Bordier {9981}; Orepi {991}.
Gli-B2ac {991}. **v:** Scipion {991}; Artaban {991}; Riol{991}; Lontra{9981}.
Gli-B2ad {991}. **v:** Champion {991}; Chopin {991}.
Gli-B2ae {991}. **v:** Priam {991}; Etoile d'Choisy {991}; Campeador {9985}; Krajinka (biotype) {994}.
Gli-B2af {9985}. **v:** Montjuich {9985}; Mocho Sobarriba {9985}.
Gli-B2ag {9981}. **v:** Jeja del Pais {9985}; Barbilla de Leon (MCB-1292) {9981}.
Gli-B2ah {9981}. **v:** Rojo de Humanes (MCB-1262) {9981}; Grano de Miracolo {9981}.
Gli-B2ai {9981}. **v:** Blanquillo (MCB-0908) {9981}.
Gli-B2aj {9981}. **v:** Negrete de Malaga (MCB-1754) {9981}.
Gli-B2ak {9981}. **v:** HY320 {9981}; Leader {9981}.
Gli-B2al {9981}. **v:** Dankowska {991}.
Gli-B2am {9981}. **v:** TM-275 {9981}; Uralochka {9981}.
Gli-B2an {9981}. **v:** Eagle {9981}; Glenwari {9981}.
Gli-B2ao {9981}. **v:** Olympic {9981}; Mokoan {9981}.
Gli-B2ap {9981}. **v:** Veda {9981}; Magnif 27 {9981}.

Gli-B2aq {9981}. **v:** Winglen {9981}; Isis {9981}.
Gli-B2ar {9981}. **v:** Arbon {9981}; Roazon {9981}.
Gli-B2as {9981}. **v:** Strela {9981}; Sredneuralskaya {9981}.
Gli-B2at {9981}. **v:** Ranee {9981}; Javelin 48 {9981}.
Gli-B2au {9984, 9987}. Null allele. **v:** Saratovskaya 29 {9987}.

GLI-D2 {1125, 1334}. [*Gld 6D* {1415}]. 6DS {1122}. 6D {1334}. **v:** CS.
Gli-D2a {988}. **v:** CS {988}; Maris Freeman {988}; Sistar{9986}; Tracy {991}.
Gli-D2b {988}. **v:** Bezostaya 1 {988}; Cobra {991}; Farnese {9986}; Partizanka {994}.
Gli-D2c {988}. **v:** Escualo {9985}; Eridano {9986}; Rieti DIV {9986}; Siete Cerros 66 {988}.
Gli-D2d {988}. **v:** Dneprovskaya 521 {988}.
Gli-D2e {988}. **v:** Dollar {9985}; Lada {9981}; Mironovskaya 808 {988}; Open {991}.
Gli-D2f {988}. **v:** Creneau {991}; Kirgizskaya Yubileinaya {988}; Rempart{991}.
Gli-D2g {988}. **v:** Capelle-Desprez {991}; Futur {991}; Galahad {988}; Ghurka {988}; Mec {9986}.
Gli-D2h {988}. **v:** Capitole {991}; Chinook {995}; Eagle {00119}; Garant {991}; Sadovo 1 {988}; Thatcher {995}.
Gli-D2i {988}. **v:** Insignia 49 {00119}; Lario {9986}.
Gli-D2j {988}. **v:** Arcane {991}; Gallo {9986}; Gazul {9985}; Inia 66 {9985}; Mentana {9986}.
Gli-D2k {988}. **v:** Crvencapa {944}; Kzyl-Bas {988}; Skala {988}.
Gli-D2l.
Omitted. No reliable differences compared to existing alleles {9981}.
Gli-D2m {988}. **v:** Marquis {988}; Rex {991}; Rinconada {9985}; Suneca {119}; Veronese {9986}; Yecora 70 {9985}.
Gli-D2n {988}. **v:** Castan {991}; Champlein {991}; Mahissa 1 {9985}; Mercia {988}; Pippo {9986}.
Gli-D2o {988}. **v:** Omskaya 12 {988}.
Cultivars Salmone and Resistente, which carry *Gli-D2aa* {9981}, were erroneously given as standards for allele *Gli-D2o* in {9986}.
Gli-D2p {988}. **v:** New Pusa {988}.
Gli-D2q {988}. **v:** Cook {9981}; E. Mottin {9981}; Fournil {991}; Volshebnitsa (biotype) {988}; Winglen {9981}; Soissons {991}.
Gli-D2r {988}. **v:** Kremena {988}; Mara {9986}; Montcada {9985}.
Gli-D2s {988}. **v:** Akmolinka 1 {988}; Bezenchukskaya 98 {988}; Selkirk (biotype) {995}.
Gli-D2t {9986}. **v:** Golia {9986}; Gabo {9981}; Manital {9986}; Bokal {9981}.
Gli-D2u {9986}. **v:** Loreto {9986}; Martial {991}; Cibalka {9981}.
Gli-D2v {991}. **v:** Epiroux {991}; Arbon {991}.
Gli-D2w {9985}. **v:** Navarro 150 {9985}; Javelin {9981}; Hopps {9981}; Canaleja {9985}.
Gli-D2x {9985}. **v:** Montjuich {9985}; Blanquillo{9985}.
Gli-D2y {9985}. **v:** Candeal Alcala {9985}.
Gli-D2z {9985}. **v:** Aragon 03 {9985}.
Gli-D2aa {9981}. **v:** Salmone {9981}; Resistente {9981}.
Gli-D2ab {9981}. **v:** Rojo de Boadilla de Campos (MCB-1031) {9981}.
Gli-D2ac {9981}. **v:** Albatros {9981}.
Gli-D2ad {9981}. **v:** Hembrilla Soria (MCB-1298) {9981}.
Gli-D2ae {9984, 9987}. Null allele. **v:** Saratovskaya 29 (mutant) {9987

GLI-2 alleles were determined in *57* Yugoslav wheat varieties {994}.

GLI-Ag^{i}2 {374}. 6Ag^i {374}. **ad:** Vilmorin 27/ *Th. intermedium*.

GLI-R
Gli-R2a {03116}. *d1* {03116}. **v:** Carnac hexaploid triticale {03116}.
Gli-R2b {03116}. *d2* {03116}. **v:** Mostral hexaploid triticale {03116}.
Gli-R2c {03116}. *t1* {03116}. **v:** Alamo hexaploid triticale {03116}.
Gli-R2d {03116}. Null {03116}. **v:** Triticor hexaploid triticale {03116}.
Gli-R2e {03115}. *t2* {03115}. **v:** Tornado hexaploid triticale {03115}.

GLI-R^{m}2 {1339}. 6R^{m} {1340, 1339}. **ad:** CS/*S. montanum*.
The location of *Gli-R2* in *S. cereale* is thought to have evolved from *S. montanum* {1339} via a translocation between 2R and 6R {1530}.

GLI-S^{l}2 {573}. 6S^{l} {573}. **ad,su:** CS/*Ae. longissima*.

GLI-U2 {1335}. 6U {1335}. **ad:** CS/*Ae. umbellulata*.

GLI-V2 {111}. 6VS {111}. **ad:** Creso/*D. villosum*.

GLI-3

A *GLI-3* set of loci coding for omega-type gliadins are located 22 to 31 cM proximal to *GLI-1* on the short arms of group 1 chromosomes {422, 1403, 589}.
GLI-A3 {1119, 1403}. [*Gld-2-1A* {1416}]. 1AS {1403}. **v:** Bezostaya 1.
Each of the following *GLI-A3* alleles, apart from *Gli-A3d*, which is a null, controls one minor omega-gliadin with molecular mass about 41k that occurs in the middle of the omega-region of APAGE fractionation. Gliadins controlled by these alleles differ in electrophoretic mobility in APAGE in that the fastest of three known *GLI-A3*-gliadins is controlled by *Gli-A3a* and the slowest by *Gli-A3c* {9983}.
Gli-A3a {9983}. **v:** CS, Prinqual, Courtot, Tselinogradka, Bezenchukskaya 98.
Gli-A3b {9983}. **v:** Bezostaya 1.
Gli-A3c {9983}. **v:** Anda.
Gli-A3d {9983}. Null {9983}. **v:** Saratovskaya 210, Kharkovskaya 6, Richelle.

GLI-B3 {1119}, {422}. [*Glu-B2* {589}, *Gld-B6* {422}]. 1BS {589}, {422}. **s:** CS*/Thatcher1B {422}. **v:** Sicco {589}.
Gli-B3a {589}, {1119}, {422}. **v:** CS.
Gli-B3b {589}. **v:** Sicco.
Gli-B3c {1119}, {422}. **s:** CS*/Thatcher1B.

GLI-R3 {164}. 1RS {164}. **al:** Four inbred lines (R2, J14, 8t, E2666).

GLI-S^{l}3 {1228}. 1S^{l}S {1228}. **ad,su:** CS/*Ae. longissima*. **ma:** In *Ae. longissima 2/Ae. longissima 10*, three gliadin loci, one glucose phosphate isomerase, and two glutenin loci were mapped relative to one another {1228} as follows: *GLU-S^{l}*1 – 15.9 cM – *GPI-S^{l}*1 – 38 cM – *GLI-S^{l}*4 – 7.1 cM – *GLU-S^{l}*3 – 0.9 cM – *GLI-S^{l}*1 – 5.6 cM – *GLI-S^{l}*5. *GLU-S^{l}*1 is located in 1S^{l}L and the other loci are in 1S^{l}S.

Gli-V3 {111}. 4VL {111}. **ad:** Creso/*D. villosum*.

GLI-4

It is not clear how *GLI-S^{l}4* and *GLI-S^{l}5* relate to the *GLI-4* and *GLI-5* sets described below. A locus designated *GLI-A4* controlling omega-gliadins in cv. Perzivan biotype 2 was mapped at 10 cM proximal

to *GLI-A1* on the short arm of chromosome 1A {1205}.
However, Metakovsky *et al.* {9983} have since shown that this locus and *GLI-A3* are, in fact, the same locus. Furthermore, Dubcovsky et al. {277} did not find evidence for the simultaneous presence of both *GLI-A3* and *GLI-A4* in five 1A or 1A^m mapping populations and concluded that *GLI-A4* should be considered *GLI-A3* until conclusive evidence for the former is obtained. For these reasons, variation at the locus *GLI-A4* is not considered.

GLI-5

GLI-5 loci controlling omega-gliadins were mapped to the short arms of chromosomes 1A and 1B, distal to *GLI-1* {1147}. The map distance between *GLI-B5* and *GLI-B1* was estimated as 1.4 cM (recombination value of 1.4 +/- 0.4%), although there was significant variation in recombination ranging from 0% to 5.9% over the six crosses analysed. This variation was attributed to genotypic influence on the frequency of recombination.
GLI-A5 {1147}. 1AS {1147}. **v:** Salmone.
Gli-A5a {9983}. Null {9983}. **v:** CS.
Gli-A5b {9983}. **v:** Marquis.
Allele *Gli-A5b* controls two slow-moving, easily-recognizable omega-gliadins. It is present in all common wheat cultivars having alleles *Gli-A1m* and *Gli-A1r* (and, probably, in those having *Gli-A1e*, *Gli-A1l* and *Gli-A1q*), because earlier (for example, in {988}) two minor omega-gliadins encoded by *Gli-A5b* were considered controlled by these *GLI-A1* alleles {9983}
GLI-B5 {1147}. 1BS {1147}. **v:** Salmone.
Gli-B5a {1147}. **v:** CS.
Gli-B5b {1147}. **v:** Salmone.
In {988}, omega-gliadins controlled by *GLI-B5* (allele *Gli-B5b*) were attributed to alleles at the *GLI-B1* locus (alleles *Gli-B1c, i, k, m, n* and *o*).

GLI-6

GLI-A6 {9983}, {993}. 1AS {9983}.
GLI-A6 was first explicitly described in {9983} but was first observed without designation in {993}. There is strong evidence that it is distinct from *GLI-A3* and *GLI-A5*, mapping distally to *GLI-A1*, with which it recombines at a frequency of 2-5%. Currently three alleles are known, of which *Gli-A6c* is particularly well-described in {9983}: the molecular mass of the omega-gliadin controlled by this allele is slightly lower than those of the omega-gliadins controlled by *GLI-A3* alleles. In {988}, the omega-gliadin controlled by *Gli-A6c* was attributed to *Gli-A1f*. *Gli-A6c* is rather frequent in common wheat and may relate to dough quality (preliminary data {9983}).
Gli-A6a {9983}. Null {9983}. **v:** CS; Bezostaya 1.
Gli-A6b {9983}. **v:** Bezenchukskaya 98.
Gli-A6c {9983}. **v:** Courtot, Anda, Mironovskaya 808.

GLI-7

GLI-A7 {10547}. 1DS {10547}. **dv:** AUS18913 {10547}.
The gamma-gliadin encoded by this locus co-segregated with the T1 omega-gliadin encoded by the *GLI-D^{t}T1* locus (currently included in the Catalogue as locus (*GLI-DT1*). *GLI-A7* was located 0.69 cM from *GLI-D^{t}1* {10547}.

2.3.3. Other endosperm storage proteins

Triticin proteins The triticin proteins {1360} or [Triplet proteins {1357}] are storage globulins with homology to pea legumins and related proteins in oats, rice and several dicotyledonous species {1360}. Triticin gene segments including the hypervariable region were PCR-amplified, with preferential amplification of *TRI-D1* for the only pair of primers giving consistent results {10322}.
TRI-A1. 1AS {1357}. **v:** CS.
Tri-A1a. [*cs* {1358}]. **v:** CS.
Tri-A1b. [*h* {1358}]. **v:** Hope.

TRI-D1 {707}, {1358}, {1357}. 1DS {1357}. **v:** CS.
Tri-D1a. [*cs* {1358}]. **v:** CS.
Tri-D1b. [*i* {1358}]. **v:** India 115.

2.3.4. Enzyme Inhibitors

Inhibitors of alpha-amylase and subtilisin

ISA1
ISA-A1 {908}. 2AL {908}. **v:** CS.
Isa-A1a {908}. **v:** CS.
Isa-A1b {908}. Null allele. **v:** Cajeme 71.

ISA-B1 {908}. 2BL {908}. **v:** CS.
Isa-B1a {908}. **v:** CS.
Isa-B1b {908}. **v:** Bihar.

ISA-D1 {908}. 2DL {908}. **v:** CS.

Orthologous genes were identified in *Ae. speltoides* and *T. timopheevii* {908}. All durum wheats investigated had the genotype *Isa-A1b, Isa-B1b*.

Inhibitors (dimeric) of heterologous alpha-amylase

Chromosome 3BS has duplicated loci controlling two dimeric inhibitors of exogenous a-amylases, one known as 0.53 or Inh I {1260}, and the other as WDA I-3 {1260}. Chromosome 3DS has a homoeologous locus controlling a dimeric inhibitor of exogenous a-amylases, known as 0.19 or Inh III {1260, 0124}, that is closely related to 0.53/Inh I. Intervarietal polymorphism for the WDA-3 protein was identified by isoelectric focussing of water-soluble endosperm proteins {0124}. This was interchromosomely mapped on 3BS using both a DH population of Cranbrook/Halberd, and a set of RILs of Opata 85/W-7984 (ITMI population) {0125}.
Three genome allele specific primer sets were designed for the 3BS and 3DS alpha-amylase inhibitors in cv. Chinese Spring, based upon SNPs. Their validity was confirmed in 15 accessions of *Triticum urartu, Triticum monococcum, Aegilops tauschii* and *Triticum dicoccoides*. The results offered support that the 24 kDa dimeric alpha-amylase inhibitors in cultivated wheat are encoded by a multigene family {10323}, previously proposed in {10324}, as the result of phylogenetic analysis of sequences characterized by cSNPs.
IHA-B1
IHA-B1.1 {1260}. 3BS {1260}. **v:** CS {1260}.

IHA-B1.2.
Iha-B1.2 {0124}. **v:** CS {0124}.
Iha-B1.2a {0124}. 3BS {0124}. **v:** CS {0124, 0125}.

Iha-B1.2b {0125}. Null allele. **v:** Cadoux {0125}; Cranbrook {0125}; Tasman {0125}.

IHA-D1 {1260}. 3DS {1260}. **v:** CS {1260}.

Subtilisin inhibition

SI-1

SI-R1 {529}. 2RS {701}.2R {529}. **ad:** CS/Imperial, Holdfast/King II.

SI-H1 {528}. [*Isa 1* {528}]. 2H {528}. **ad:** CS/Betzes.

SI-2

SI-B2 {701}. 1BS {701}. **su:** Bersee (Koga II).

SI-D2 {701}. 1DS {701}. **v:** Koga II.

SI-H2. [*Ica 2* {528}, *Ica 1* {528}]. 1H {528}. **ad:** CS/Betzes.

SI-R2. 1RS {701}. 1R {529}. **ad:** CS/Imperial {529}. **tr:** Gabo 1BL.1RS {701}.

SI-S^{l}2 {701}. 1S^{l} {701}. **ad:** CS/*Ae. longissima*.

SI-U2 {701}. 1U {701}. **ad:** CS/*Ae. umbellulata*.

Considerable genetic variation for *Si-2* was noted in {701}. A chromosome location for *Si-H2* on 1HL was inferred in {528} but questioned in {701}.

Three subunits of the wheat tetrameric inhibitor of insect a-amylase, CM1, CM3 and CM16, with homology to the dimeric and monomeric a-amylase inhibitors and the trypsin inhibitors, were located by Southern analysis of cDNAs pCT1, pCT2, and pCT3 to 4A, 4B, 4D; 7A, 7B, 7D; and 4A, 4B, 4D, respectively {427}.

Genes encoding proteins which inhibit the action of mammalian and insect, but not cereal, a-amylases, were located in chromosomes 3BS, 3DS and 6DS of Chinese Spring {1260}. Also, genes encoding inhibitors of insect a-amylases were in *H. chilense* chromosomes 4H^{ch} and 7H^{ch} {1262}.

Trypsin inhibition

TI-1

TI-H1. [*Itc 1* {528}]. 3H {528}. **ad:** CS/Betzes.

TI-R1. 3R {529}. **ad:** CS/Imperial.

TI-2

TI-A2 {699}. 5AL {699}. **v:** CS.

TI-B2 {699}. 5BL {699}. **v:** CS.

TI-D2 {699}. 5DL {699}. **v:** CS.
Ti-D2a {699}. **v:** CS.
Ti-D2b {699}. **v:** Champlein.
Ti-D2c {699}. **v:** Synthetic.

TI-Ag^{i}2 {699}. 5Ag^{i} {699}. **ad:** Vilmorin 27/ *Th. intermedium*.

TI-M^{t}2 {699}. 5M^{t} {699}. **ad:** CS/*Ae. mutica*.

TI-R2 {699}. 5RL {699}. **ad:** CS/Imperial. **su:** CS/King II.

TI-S^{l}2 {699}. 5S^{l}L {699}. **ad:** CS/*Ae. sharonensis*.

TI-U2 {699}. 1U {699}. **ad:** CS/*Ae. umbellulata*.

2.3.5. Grain softness protein

GSP-1 {1185}.
GSP-A1 {614}. [GSP {614}]. 5A {614}, {383}. **v:** CS {614}, {0383}; Rosella (GenBank AF177218) {383}.

GSP-B1 {614}. [*GSP* {614}]. 5B {614}. **v:** CS {614}; Glenlea {0385}.
In {1185} sequence of clone TSF33 from cv. Soft Falcon (GenBank X80379) was identical to this allele, as are ESTs for cv. CS (dbEST BJ235798) and cv. CNN (dbEST BE423845).

GSP-D1 {614}. [*GSP* {614}]. 5DS {614}.
Gsp-D1a. **v:** CS {614}; Glenlea {0385}. **dv:** *Ae. tauschii* CPI1110799 (GenBank AF177219) {0383}. **ma:** Co-segregation of *Gsp-D1* and *Ha* {614}.
Gsp-D1b {03105}. **dv:** *Ae. tauschii* TA1583 (GenBank AY252079) *Pina-D1a, Pinb-D1a* {3105}; TA2475 (GenBank AY252087) *Pina-D1a, Pina-D1i* {03105}.
Gsp-D1c {03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY252081) *Pina-D1c, Pinb-D1h* {03105}; CPI110799 (GenBank AF177219) {0383}.
Gsp-D1d. **dv:** *Ae. tauschii* TA2536 (GenBank 252093) *Pina-D1c, Pinb-D2i* {03105}; TA2374 (GenBank AY252046) *Pina-D1d, Pinb-D1i* {03105}; TA2458 (GenBank AY252084) *Pina-D1e, Pinb-D1i* {03105}; TA2436 (GenBank AY252048) *Pina-D1f, Pinb-D1i* {03105}.
Gsp-D1e. **dv:** *Ae. tauschii* TA2527 (GenBank AY252066) *Pina-D1c, Pinb-D1h* {03105}; TA2512 (GenBank AY252092) *Pina-D1d, Pinb-D1i* {03105}; TA2495 (GenBank AY252091) *Pina-D1e, Pinb-D1i* {03105}.
Gsp-D1f. **dv:** *Ae. tauschii* TA1649 (GenBank AY252063) *Pina-D1d, Pinb-D1h* {03105}; TA2455 (GenBank AY252073) *Pina-D1d, Pinb-D1i* {03105}.
Gsp-D1g. **dv:** *Ae. tauschii* TA1599 (GenBank AY252062) *Pina-D1a, Pinb-D1j* {03105}.
Gsp-D1h. **dv:** *Ae. tauschii* TA1691 (GenBank AY252064) *Pina-D1a, Pinb-D1j* {03105}.
Gsp-D1i {03105}. **v:** Yecora Rojo (GenBank AY255771) *Pina-D1b, Pinb-D1a* {03105}. ***Gsp-D1j*** {10077}. **s:** CS*/Red Egyptian 5D, *Pina-D1, Pinb-D1* and *Gsp-D1* {10077}.
In {1185} the sequence of clone TSF69 from cv. Soft Falcon (GenBank S72696) is identical, as are ESTs for cv CS (dbEST BJ237450) and cv CNN (dbEST BE422565). This locus has a large deletion encompassing genes *PINA-D1, PINA-D1* and *GSP-D1* {10077}.
In {1185} partial-sequence clone TSF61 from cv. Soft Falcon (GenBank X80380) was identical to this allele.

2.3.6. Histone H1 proteins

HSTH1-1
HSTH1-A1 {0215}. 5AL {0215}. **v:** CS {0215}.

HSTH1-B1 {0215}. 5BL {0215}. **v:** CS {0215}.

HSTH1-D1 {0215}. 5DL {0215}. **v:** CS {0215}.

HSTH1-2
HSTH1-A2 {0215}. 5AL {0215}. **v:** CS {0215}.
HstH1-A2a {0215}. **v:** CS {0215}.
HstH1-A2b {0215}. Null allele {0215}. **v:** Mara {0215}; 10 others{0215}.

HSTH1-B2 {0215}. 5BL {0215}. **v:** CS {0215}.
HstH1-B2a {0215}. **v:** CS {0215}; 19 others {0215}.
HstH1-B2b {0215}. **v:** Excelsior {0215}.

HSTH1-D2 {0215}. 5DL {0215}. **v:** CS {0215}.
HstH1-D1a {0215}. **v:** CS {0215}; 18 others {0215}.
HstH1-D1b {0215}. **v:** Grekum 114 {0215}; Kirgizsky Karlik {0215}.

The relationship of this gene series with a *Hst-A1, Hst-B1, Hst-D1* series in group 5 chromosomes {0216} based on DNA hybridization studies was not established.

2.3.7 Iodine binding factor

A monomeric water-soluble protein from mature grain which preferentially binds iodine {818}.
IBF-1
IBF-A1 {818}. 5AL {818}. **v:** CS.
Ibf-A1a {818}. **v:** CS.
Ibf-A1b {818}. **v:** Cappelle-Desprez.
Ibf-A1c {818}. **v:** Hope.
Ibf-A1d {818}. **v:** Chris.
Ibf-A1e {818}. **v:** Sears' Synthetic.

IBF-B1 {818}. 5BL {818}. **v:** CS.
Ibf-B1a {818}. **v:** CS.
Ibf-B1b {818}. **v:** Cappelle-Desprez.
Ibf-B1c {818}. **v:** Ciano 67.
Ibf-B1d {818}. **v:** Sears' Synthetic.

IBF-D1 {818}. 5DL {818}. **v:** CS.
Ibf-D1a {818}. **v:** CS.
Ibf-D1b {818}. **v:** Cappelle-Desprez.
Ibf-D1c {818}. **v:** Purple Pericarp.
Ibf-D1d {818}. **v:** Sears' Synthetic.

IBF-Ag^{i}***1*** {818}. 5Ag^{i} {818}. **ad:** Vilmorin/*Th. intermedium*.
IBF-E1 {818}. 5EL {818}. **ad:** CS/*E. elongata*.
IBF-H1 {818}. 4H {818}. **ad:** CS/Betzes.
IBF-R1 {818}. 5RL {818}. **ad:** CS/Imperial, CS/KingII.
IBF-S^{l}***1*** {818}. 5S^{l} {818}. **ad:** CS/*Ae. sharonensis*.
IBF-U1 {818}. 5U {818}. **ad:** CS/*Ae. umbellulata*.

2.3.8 Lipopurothionins

PUR-1

PUR-A1 {351}. 1AL {351}. **v:** CS {351}.
A PCR marker specific for *PUR-A1* was developed in {9976}.

PUR-B1 {351}. 1BL {351}. **v:** CS {351}.
A PCR marker specific for *PUR-B1* was developed in {9976}.

PUR-D1 {351}. 1DL {351}. **v:** CS {351}.
PCR marker specific for *PUR-D1* was developed in {9976}.
A locus in chromosome 5DS affects the level of lipopurothionin {351}.

PUR-R1. 1RL {1261} = 1RS.1BL. **ad:** CS/Imperial. **su:** Several 1R(1B) lines. **tr:** Aurora, Kavkaz.
A PCR marker specific for *PUR-R1* was developed in {9976}.

2.3.9. Lectins

LEC-1

LEC-A1. 1AL {1427}. **v:** CS.

LEC-B1. 1B {1427}. **s:** CS*/Hope 1B.

LEC-D1. 1DL {1427}. **v:** CS.

LEC-U1. 1U {1427}. **ad:** CS/*Ae. umbellulata*.

2.3.10. Puroindolines and grain softness protein

Puroindolines a and b are the major components of friabilin, a protein complex that is associated with grain texture (see 'Grain Hardness'). The name 'puroindoline' and the complete amino acid sequence of puroindoline from cv. Camp Remy was given in {0382}. Hard grain texture in hexaploid wheat results from unique changes in the puroindoline amino acid sequence or, currently, four null forms {0295} of the completely linked genes (max. map distance 4.3 cM) {452}. Tetraploid (AABB, AAGG) wheats lack puroindolines and are consequently very hard {03103}. A searchable database of wheat varieties and their puroindoline genotype is available at http://www.wsu.edu/~wwql/php/puroindoline.php. Grain softness protein-1 is a closely related gene which is closely located to the puroindoline genes {03111, 1185}. 'GenBank' and 'dbEST' refer to sequence databases available at NCBI (also available throught EMBL and DDB).
Reviews {10522, 10523} provide comprehensive descriptions of the molecular genetics and regulation of puroindolines. Morris and Bhave {10524} reconciled the D-genome puroindoline alleles with DNA sequence data. Bonafede et al. {10525, 10526} developed a CS line (PI 651012) carrying a 5A^{m}S.5AS translocation from *T. monococcum*; the translocated chromatin carries A-genome *Pina, Pinb* and *Gsp-1* alleles that confer softer kernel texture.

PINa-1

PINa-A1 {03103, 03104, 03108}. **dv:** *T. urartu* unspecified accession {03103}; TA763 (GenBank AJ302094) {03104, 03108}; TA808 (GenBank AJ302095) {03104, 03108}. ***PINa-A^{m}1*** {0083}. 5A^{m}S {0083}. **dv:** *T. monococcum* DV92 (cultivated), G3116 (spp. *aegilopoides*) (GenBank AJ242715) {0083}; unspecified acession (GenBank AJ249933) {03103}; PI277138 (GenBank AJ302093) {03104}; PI418582 (GenBank AJ302092) {03104}; *T. monococcum* spp. *monococcum* TA2025, TA2026 (GenBank AY622786), TA2037 (GenBank AJ242715) {03108}; *T. monococcum* spp. *aegilopoides*

TA183, TA291, TA546, TA581 (GenBank AY622786) {03108}.
In *T. monococcum PINa-A*^{m}*1* is completely linked to *GSP-A*^{m}*1* {0083}.

PINa-D1 {452}. 5DS {452}. **v:** CS (GenBank DQ363911) {03108}; Capitole (GenBank X69914) {03110}.
This locus has a large deletion encompassing genes *PINa-D1, PINb-D1* and *GSP-D1*. This allelic combination confers a harder kernel texture than *Pina-D1a/Pinb-D1b* {10077}.
Pina-D1a {452}. **v:** Bellevue {0249}; Capitole (GenBank X69914) {03110}; Courtot {0249}; Fortuna {0249}; Galaxie {0249}; Heron {1035}; Renan (GenBank CR626934) {10440}; Soissons {0249}. **v2:** Aurelio *Pinb-D1a* {0249}; Bezostaja *Pinb-D1b* {0249}; Bilancia *Pinb-D1a* {0249}; Bolero *Pinb-D1a* {0249}; Brasilia *Pinb-D1b* {0249}; Centauro *Pinb-D1a* {0249}; Cerere *Pinb-D1b* {0249}; CS *Pinb-D1a* {0249}, {452}; Colfiorito *Pinb-D1b* {0249}; Cologna 21 *Pinb-D1b* {0249}; David *Pinb-D1b* {0249}; Democrat *Pinb-D1b* {0249}; Etruria *Pinb-D1b* {0249}; Francia *Pinb-D1b* {0249}; Gemini *Pinb-D1b* {0249}; Genio *Pinb-D1b* {0249}; Gladio *Pinb-D1b* {0249}; Lampo *Pinb-D1a* {0249}; Leone *Pinb-D1a* {0249}; Leopardo *Pinb-D1a* {0249}; Libero *Pinb-D1a* {0249}; Livio *Pinb-D1a* {0249}; Marberg *Pinb-D1b* {0249}; Mentana *Pinb-D1a* {0249}; Mieti *Pinb-D1b* {0249}; Mose *Pinb-D1a* {0249}; Neviana *Pinb-D1a* {0249}; Newana *Pinb-D1b* {0249}; Oscar *Pinb-D1a* {0249}; Pandas *Pinb-D1b* {0249}; Pascal *Pinb-D1b* {0249}; Penawawa *Pinb-D1a* {03104}; Sagittario *Pinb-D1b* {0249}; Salgemma *Pinb-D1b* {0249}; Saliente *Pinb-D1b* {0249}; Salmone *Pinb-D1b* {0249}; Serena *Pinb-D1a* {0249}; Serio *Pinb-D1b* {0249}; Veda *Pinb-D1b* {0249}; Zena *Pinb-D1b* {0249}. **dv:** *Ae. tauschii* upspecified accession (GenBank AJ249935) {03103}; TA2475 (GenBank AY252037) *Pinb-D1i, Gsp-D1b* {03105}; TA1599 (GenBank AY252011) *Pinb-D1j, Gsp-D1g* {03105}; TA1691 (GanBank AY252013) *Pinb-D1j, Gsp-D1h* {03105}; *Ae. tauschii* unidentified accession (GenBank AJ249935) {03103}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440}.
Pina-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats that carry a hardness mutation in puroindoline b {452}, {1035}, {0082}, {0204}, {0295}.
Pina-D1b {1035}. Null allele. **i:** Falcon/7*Heron, Heron/7*Falcon {03109}; Gamenya Seln.{0203, 0298}; Heron/7*Falcon sel. {0203, 0298}; PI 644080 (Alpowa/ID377s//7*Alpowa) {10429}; Near-isogenic pairs were developed in McNeal, Outlook, Hank, Scholar and Explorer {10527}. **v:** Butte 86 {1035}; Eridano {0249}; Falcon {1035}; Glenlea (GenBank AB262660). This BAC clone also contains *Pinb-D1a* {10431}; Kalyansona{0249}; Super X {0249}; Yecora Rojo {0204}. **v2:** Amidon *Pinb-D1a* {0249}; Ciano *Pinb-D1a* {0249}; Dorico *Pinb-D1a* {0249}; Golia *Pinb-D1a* {0249}; Guadalupe *Pinb-D1a* {0249}; Barra *Pinb-D1a* {0249}; Inia 66 *Pinb-D1a* {0249}; Indice *Pinb-D1a* {0249}; Jecora *Pinb-D1a* {0249}; Manital *Pinb-D1a* {0249}; Mendos *Pinb-D1a* {0249}; Padus *Pinb-D1a* {0249}; Prinqual *Pinb-D1a* {0249}; Sibilia *Pinb-D1a* {0249}.
Present only in some hard hexaploid wheats. *Pina-D1b* is associated with harder texture than *Pinb-D1b* {0177, 0206}.
This allele is now defined as a 15,380 bp deletion versus other possible puroindoline a nulls {10428, 10391}.
Pina-D1c {03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY252031) *Pinb-D1h, Gsp-D1c*; TA2527 (GenBank AY252015) *Pinb-D1h, Gsp-D1e* {03108}; *Ae. tauschii* TA10 (GenBank AY649746) {03108}.
Pina-D1d {03105}. **dv:** *Ae. tauschii* PI452131 (GenBank AJ302098) *Pinb-D1i* {03104}; PI554318 (GenBank AJ302099) *Pinb-D1k* {03104}; TA1649 (GenBank AY252012) *Pinb-D1h, Gsp-D1f* {03105}; TA2374 (GenBank AY251996) *Pinb-D1i, Gsp-D1d* {03105}; TA2512 (GenBank AY252042) *Pinb-D1i, Gsp-D1e* {03105}; TA2455 (GenBank AY252022) *Pinb-D1i, Gsp-D1f* {03105}; TA2536 (GenBank AY252043) {03105}; *Ae. tauschii* TA 1704 (GenBank AY649744) {03108}.
Pina-D1e {03105}. **dv:** *Ae. tauschii* TA2458 (GenBank AY252034) *Pinb-D1i, Gsp-D1d* {03105}; TA2495 (GenBank AY252041) *Pinb-D1i, Gsp-D1e* {03105}.
Pina-D1f {03105}. **dv:** *Ae. tauschii* TA2436 (GenBank AY251998) *Pinb-D1i, Gsp-D1d* {03105}.

Pina-D1g {03105}. **dv:** *Ae. tauschii* TA1583 (GenBank AY252029) *Pinb-D1a, Gsp-D1b* {03105}.

Pina-D1h {10118}. **v:** *X. aegilotriticum* CIGM86.946-1B-0B-0PR-0B (GenBank AY573898) *Pinb-D1o* {10118}.

Pina-D1i {10118}. **v:** *X. aegilotriticum* CIGM87.2784-1B-0PR-0B (GenBank AY573899) *Pinb-D1k* {10118}.

Pina-D1j {10118}. **v:** *X. aegilotriticum* CIGM88.1363-0B (GenBank AY573900) *Pinb-D1o* {10118}.

Pina-D1k {10077}. [homonym: *Pina-D1b/Pinb-D1h(t)*]. **s:** CS*/Red Egyptian 5D substitution line, *Pinb-D1q, Gsp-D1i* {10077}. **v:** Bindokku {10305}; Cheyenne-A {10305}; Chosen 68 {10305}; Gaiyuerui {10316}; KT020-584 {10432}; Saiiku 18 {10305}; Saiiku 44 {10305}; Safangmai {10316}; Tachun2 {10316}; ZM2851 {10316}; ZM2855 {10316}.

This allele is currently used to denote a large deletion of undetermined size that involves *PINa-D1, PINb-D1* and *GSP-D1* {10077}. The deletion of both puroindolines is associated with harder kernel texture than other known puroindoline hardness alleles {10077, 10305, 10432}.

Pina-D1l {10168}. [*Pina-D1c* {10168}]. **v:** Baikezaomai Chinese landraces {10208}; Chengduguangtou {10208}; Guangtouxiaomai {10208}; Sanyuehuang {10208}; Xiaoyuhua {10208}. **v2:** Fortuna (USA) *Pinb-D1a* {10168}; Glenman *Pinb-D1a* {10168}.

Pina-D1l has a C deletion leading to an open reading frame shift and premature stop codon; PINA null, hard kernel texture {10208}.

Pina-D1m {10208}. **v:** Hongheshang (GenBank EF620907) {10208}.

C-to-T substitution: Proline-35 to serine; hard kernel texture {10208}.

Pina-D1n {10208}. **v:** Baimangchun {10208}; Hongheshang (GenBank EF620907) {10208}; Xianmai (GenBank EF620908) {10208}; Yazuixiaomai Chinese landraces {10208}; Yazuizi {10208}; Zhuantoubaike {10208}.

G-to-A substitution: Tryptophan-43 to stop codon; PINA null hard kernel texture {10208}.

Pina-D1o {10311}. **dv:** *Ae. tauschii* RM0182 (GenBank AY608595) {10311}.

Pina-D1p {10316}. **v:** *T. aestivum* Jing 771 (GenBank AY599893) {10316}.

Pina-D1q {10316}. **v:** U29 (GenBank AB181238) {10316}; Muu-27 (homonym 'a2', *Pina-D1p*) {10316}.

PINb-A1 {03104, 03108}. **dv:** *T. urartu* TA763 (GenBank AJ302103) {3104}; TA808 (GenBank AJ302104) {03104, 03108}.

Pinb-D1a {452}. **v:** Hill 81 {452}. **v2:** Adder *Pina-D1a* {0317}; Amidon *Pina-D1b* {0249}; Aurelio *Pina-D1a* {0249}; Barra *Pina-D1b* {0249}; Bilancia *Pina-D1a* {0249}; Bolero *Pina-D1a* {0249}; Centauro *Pina-D1a* {0249}; CS *Pina-D1a* {0249,452}; Ciano *Pina-D1b* {0249}; Dorico *Pina-D1b* {0249}; Fortuna (USA) *Pina-D1b* {0249}; Glenman *Pina-D1b* {0249}; Golia *Pina-D1b* {0249}; Guadalupe *Pina-D1b* {0249}; Inia 66 *Pina-D1b* {0249}; Jecora *Pina-D1b* {0249}; Idice *Pina-D1b* {0249}; Karl *Pina-D1a* {0317}; Lampo *Pina-D1a* {0249}; Leone *Pina-D1a* {0249}; Leopardo *Pina-D1a* {0249}; Libero *Pina-D1a* {0249}; Livio *Pina-D1a* {0249}; Manital *Pina-D1b* {0249}; Mendos *Pina-D1b* {0249}; Mentana *Pina-D1a* {0249}; Mose *Pina-D1a* {0249}; Neviano *Pina-D1a* {0249}; Oscar *Pina-D1a* {0249}; Padus *Pina-D1b* {0249}; Penawawa *Pina-D1a* {03104}; Prinqual *Pina-D1b* {0249}; Serena *Pina-D1a* {0249}; Sibilia *Pina-D1b* {0249}; Sigyn II *Pina-D1a* {0317}. **dv:** *Ae. tauschii* unspecified accession (GenBank AJ249936) {03103}; TA1583 (GenBank AY251981) *Pina-D1a, Gsp-D1b* {03105}.

Pinb-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pinb-D1b, -D1c, -D1d, -D1e,* or *-D1f* mutations {452}, {1035}, {0082}, {0204}, {0295}.

Pinb-D1b {452}. 5DS {452}. **i:** Paha*2/Early Blackhull/5*Paha {0203,0298}; Early Blackhull der./5*Nugaines seln. {0203, 0298}; hard sib sel. from Weston {03107}; PI 644081 (Alpowa/ND2603//7*Alpowa) {10429}. **s:** CS*7/Cheyenne 5D {452}. **v:** Thatcher {0204}; Wanser {452}; hard component of Turkey {0204}; Cheyenne (GenBank DQ363914) {10315}; Renan

(GenBank CR626934) {10440}. **v2:** Bastion *Pina-D1a* {0317}; Bezostaya *Pina-D1a* {0249}; Brasilia *Pina-D1a* {0249}; Cerere *Pina-D1a* {0249}; Colfiorito *Pina-D1a* {0249}; Cologna 21 *Pina-D1a* {0249}; David *Pina-D1a* {0249}; Democrat *Pina-D1a* {0249}; Etruria *Pina-D1a* {0249}; Francia *Pina-D1a* {0249}; Gemini *Pina-D1a* {0249}; Genio *Pina-D1a* {0249}; Gladio *Pina-D1a* {0249}; Marberg *Pina-D1a* {0249}; Mieti *Pina-D1a* {0249}; Newana *Pina-D1a* {0249}; Pandas *Pina-D1a* {0249}; Pascal *Pina-D1a* {0249}; Sagittario *Pina-D1a* {0249}; Salgemma *Pina-D1a* {0249}; Saliente *Pina-D1a* {0249}; Salmone *Pina-D1a* {0249}; Serio *Pina-D1a* {0249}; Veda *Pina-D1a* {0249}; Zena *Pina-D1a* {0249}.

Pinb-D1b is a "loss-of-function" mutation resulting from the replacement of a glycine by a serine at position 46 {452}.

Pinb-D1c {0082}. **i:** PI 644082 (Alpowa/Red Bobs//7*Alpowa) {10429}. **v:** Avle {0082}; Bjorke {0082}; Portal {0082}; Reno {0082}; Tjalve {0082}.

Pinb-D1c is a "loss-of-function" mutation resulting from the replacement of a leucine by a proline at position 60 {0082}.

Pinb-D1d {0082}. **i:** PI 644083 (Alpowa/Mjolner//7*Alpowa) {10429}. **v:** Bercy {0082}; Mjolner {0082}; Soissons (homonym 'b1') {10433}.

Pinb-D1d is a "loss-of-function" mutation resulting from the replacement of a tryptophan by an arginine at position 44 {0082}.

Pinb-D1e {0204}. **i:** PI 644084 (Alpowa/Canadian Red//7*Alpowa) {10429}. **v:** Gehun {0204}; Canadian Red {0204}; Chiefkan {0204}; Yunxianxiaomai {10427}.

Pinb-D1e is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 39 {0204}.

Pinb-D1f {0204}. **i:** PI 644085 (Alpowa/Sevier//7*Alpowa) {10429}. **v:** Abyssinia AV12.4 {10430}; The hard component of Utac{0204}.

Pinb-D1f is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 44 {0204}.

Pinb-D1g {0204}. **i:** PI 644086 (Alpowa/Andrews//7*Alpowa) {10429}. **v:** Andrews {0204}.

Pinb-D1g is a "loss-of-function" mutation resulting from the replacement of a cysteine by a stop codon at position 56 {0204}.

Pinb-D1h {03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY251983) *Pina-D1c, Gsp-D1c* {03105}; TA2527 (GenBank AY251965) *Pina-D1c, Gsp-D1e* {03105}; TA1649 (GenBank AY251963) *Pina-D1d, Gsp-D1f* {03105}; TA10 (GenBank AY649748) {03108}; CPI110799 (GenBank AY159804) {10037}.

Pinb-D1i {03105}. **dv:** *Ae. tauschii* TA2475 (GenBank AY251989) *Pina-D1a, Gsp-D1b* {03105}; TA2536 (GenBank AY251993) *Pina-D1c, Gsp-D1d* {03105}; TA2374 (GenBank AY251948) *Pina-D1d, Gsp-D1d* {03105}; TA2512 (GenBank AY251992) *Pina-D1d, Gsp-D1e* {03105}; TA2455 (GenBank AY251972) *Pina-D1d, Gsp-D1f* {03105}; TA2458 (GenBank AY251986) *Pina-D1e, Gsp-D1d* {03105}; TA2495 (GenBank AY251991) *Pina-D1e, Gsp-D1e*; TA2436 (GenBank AY251947) *Pina-D1f, Gsp-D1d* {03105}; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747) {03108, 10315}; *Ae. tauschii* isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440}.

Q03-002, TA1704, and TA2381 were incorrectly assigned *Pinb-D1w* in the 2006 supplement.

Pinb-D1j {03105}. **dv:** *Ae. tauschii* TA1599 (GenBank AY251962) *Pina-D1a, Gsp-D1g* {03105}; TA1691 (GenBank AY251964) *Pina-D1a, Gsp-D1h* {03105}; *Ae. tauschii* TA1691 (GenBank AY251946) {03108}.

Pinb-D1k. **dv:** *Ae. tauschii* PI554318 (GenBank AJ302108) *Pina-D1d* {03104}.

Pinb-D1l {10119}. **v:** GaoCheng8901 {10119}.

{10208} reported *Pinb-D1b* in Gaocheng 8901.

Pinb-D1m {10118}. **v:** *X. aegilotriticum* CIGM87.2783-1B-0PR-0B (GenBank AY573901) *Pina-D1c* {10118}.
Pinb-D1n {10118}. **v:** *X. aegilotriticum* CIGM92.1708 (GenBank AY573902) *Pina-D1d* {10118}.
Pinb-D1o {10118}. **v:** *X. aegilotriticum* CIGM93.247 (GenBank AY573903) *Pina-D1e* {10118}.
Pinb-D1p {10121}. [*Pinb-D1z* {10316}]. **v:** Dahuangpi (GenBank AY581889) {10316}; Nongda 3213 {10121}; Nongda 3395 {10121}; Qindao landrace {10305}; Qitoubai {10305}; Shijiazhuang 34 {10305}; Zigan {10305}.
The single nucleotide A deletion occurs in the AAAA at position 210-213 and is assigned to the last position at 213. Homonym: *Pinb-D1i(t)* {10305}. This homonym sequence (allele) was incorrectly assigned *Pinb-D1z, 'b3', Pinb-D1u.*
Pinb-D1q {10077}. **s:** CS*/Red Egyptian 5D substitution line, *Pina-D1k, Gsp-D1i* {10077}. **v:** Jingdong 11 (GenBank EF620909) {10313}.
This allele was used originally (2004 supplement) in combination with *Pina-D1k* and *Gsp-D1i* to denote the large deletion that encompasses *PINa-D1, PINb-D1,* and *GSP-D1* {10077} (cf. *Pins-D1k*). The haplotype nomenclature of this deletion is under review. *Pinb-D1q* is currently used to denote the C-to-G SNP at position 218 {10313}.
Pinb-D1r {10209}. [*Pinb-D1h* {10209}]. **v:** Hyb65 (NCBI AJ619022) {10209}.
G insertion: open reading frame shift and premature stop codon; hard kernel texture {10209}.
Pinb-D1s {10209}. **v:** NI5439 (NCBI AJ619021) {10209}.
G insertion as in *Pinb-D1r* and an A-to-G substitution; hard kernel texture {10209}.
Pinb-D1t {10208}. **v:** Guangtouxianmai (GenBank EF620910) {10208}; Hongma{10208}.
G-to-C substitution: Glycine-47 to arginine; hard kernel texture {10208}
Pinb-D1u {10427}. **v:** Tiekemai (GenBank EF620911) {10427}; 31 hard Yunnan endemic wheats (*T. aestivum* ssp. *yunnanense* King) {10427}.
Possesses a G deletion at position 127 leading to a shift in ORF {10427}.
Pinb-D1v {10305, 10316}. [*Pinb-D1i(t)* {10305}, *Pinb-D1r* {10316}]. **v:** Qingdao Landrace 1 {10305}; Qitoubai {10305}; Shijiazhuang 34 {10305}; Tachun 3 (GenBank AY598029) {10316}; Zigan {10305}; homonym 'b5' {10316}.
The original assignment of this allele in the 2006 supplement was incorrect; the sequence/varieties in {10305] are *Pinb-D1p* as listed above for that allele. The following variety/sequence was assigned *Pinb-D1y* in the 2006 supplement; but the original assignment of {10316} is now unchanged.
Pinb-D1w {10314}. [*Pinb-D1q* {10316}]. **v:** Jing 771 (GenBank AY640304, AB180737) {10316}; homonym 'b4' {10316}. **dv:** *Ae. tauschii* 002 (GenBank DQ257553) {10314}; *Ae. tauschii* ssp. *tauschii* TA1704 (GenBank AY649747) {10315}; *Ae. tauschii* ssp. *anathera* TA2381 (GenBank AY649747 {10315}.
This variety/sequence was incorrectly assigned *Pinb-D1x* in the 2006 supplement; the original assignment of {10316} is now unchanged.
Ae. tauschii isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747) {10315}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440} were incorrectly assigned this allele in the 2006 supplement; they are *Pinb-D1i* as listed above.
Pinb-D1x {10528}. **v:** Kashibaipi (GenBank AM909618) {10528}.
Pinb-D1y.
The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Tachun 3 in {10305} is *Pinb-D1v* as listed above. The original assignment of {10316} is now unchanged. Currently there is no assignment for this allele.
Pinb-D1z.
This allele/sequence is identical to, and listed under, *Pinb-D1p*. Currently there is no assignment for this allele.

Pinb-D1aa {10391}. **v:** Changmangtoulongbai (GenBank EF620912) {10391}; Hongtutou 1 {10391}; Hongtutou 2 {10391}.
Pinb-D1ab {10432}. **v:** KU3062 {10432}; KU3069 {10432}; Tuokexunyihao {10528}.
Pinb-D1ac {10570}. **v:** Kashibaipi {10570}; Red Star {10570}.
G to A substitution at position 257 and C to T substitution at position 382 {10570}.

PINa-S1 {03108}. **dv:** *Ae. speltoides* PI 393494 (GenBank AJ302096) {03104}; PI 369616 (GenBank AJ302097) {03104}; *Ae. speltoides* spp. *speltoides* TA2368 (GenBank AY622787), TA1789 (GenBank AY622788) {03108}; *Ae. speltoides* spp. *ligustica* TA1777 (GenBank AY622789) {03108}.
PINa-S^{b}1 {03108}. **dv:** *Ae. bicornis* spp. *typica* TA1954, TA1942 {03108}.
Pina-S^{l}1 {03108}. **dv:** *Ae. longissima* spp. *longissima* TA1912 (GenBank AY622790) {3108}; *Ae. longissima* spp. *nova* TA1921 (GenBank AY622791) {03108}.
Pina-S^{s}1 {03108}. **dv:** *Ae. searsii* TA1837, TA1355 (GenBank AY622792) {03108}.
Pina-S^{sh}1 {03108}. **dv:** *Ae. sharonensis* TA1999 (GenBank AY622796) {03108}.

Pinb-D1b, Pinb-D1c, Pinb-D1d, Pinb-D1e, Pinb-D1f, or *Pinb-D1g* are present in hard hexaploid wheats not carrying the *Pina-D1b* (null) mutation {452, 1035, 0082, 0204}.

Wheats with *Pinb-D1b* were slightly softer and a little superior to those with *Pina-D1b* in milling and bread-making characteristics although there was considerable overlap {0206}.
Transgenic rice with the *Pina-D1a* and *Pinb-D1a* alleles possessed softer grain {0207}.
Genotypes for a selection of North American wheats are given in {0204}.
In *T. monococcum* the gene order was reported to be: tel - *GSP-1 - PINa - PINb* {0083, 10122} whereas in *Ae. squarrosa* it was: tel - *GSP-1 - PINb- PINa* {10037}.
The soft kernel trait was transferred to durum {10899}. The soft kernel trait was transferred to durum; firstly, to Langdon durum Selection 1-674 and then by backcrossing to cv. Svevo {10899}, which was in turn used to develop backcross derivatives in cv. Alzada, Havasu, Kyle, and Strongfield {11444}. Genetic evidence indicated that ~24.4 Mbp from CS chromosome 5DS replaced ~20 Mbp of 5BS {11444}. Further cytogenetic analysis identified the translocation breakpoint in a 39 bp region within a putative glcosyltransferase gene {11489}.
Ikeda et al. {10305} reported a double-null with apparently no *PINa-D1* or *PINb-D1* genes present in **v:** Bindokku, Cheyenne 'A', Chosen 68, Saiiku 18, Saiiku 44, and tentatively assigned it *Pina-D1b/Pinb-D1h(t)*. How this deletion compares with the double null mutation reported by Tranquili et al. {10077} which was assigned *Pina-D1k/Pinb-D1q* is unknown.
Lines possessing the alien-derived genes *Lr57* and *Yr40* lack puroindoline genes and therefore should be hard phenotypes {10770}.

2.3.11. Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator alias Storage protein activator

SPA-1
SPA-A1 {10908}. 1AL {10909}. **v:** Recital {10909}.

SPA-B1 {10908}. 1BL {10909}. **v:** Recital{10908}. **ma:** *Glu-B1* - 1.3 cM - *Spa-B1* {10909}.
Spa-B1a {10908}. **v:** Chinese Spring {10909}; Recital {10908}; Australian genotypes listed in {10908}.
Spa-B1b {10908}. **v:** Renan {10909}; Australian genotypes listed in {10908}.

SPA-D1 {10908}. 1DL {10909}. **v:** Recital {10909}.

After testing an ealier hypothesis that SPA genes affected wheat quality, analyses conducted by both {10908} and {10909} obtained no evidence supporting a significant effect and attributed any variation to the closely linked *GLU-B1* locus.

2.3.12. Salt soluble globulins

GLO-1 are endosperm proteins (23-26 kDa) soluble in salt but not in water {455}.
GLO-1
GLO-A1 {455}. 1AS {455}. **v:** CS. **ma:** Distally located: *GLO-A1*(distal) – 5.2 cM – *GLI-A1* {1077}.

GLO-B1 {455}. 1BS {455}. **v:** CS.

GLO-D1 {455}. 1DS {455}. **v:** CS. **ma:** Distally located: *GLO-D1*(distal) – 2.9 cM – *GLI-D1* {1077}.
GLO-E1 {455}. 1ES {455}. **ad:** CS/*E. elongata*.
GLO-R1 {455}. 1RS {455}. **ad:** CS/Imperial. **su:** 1B/(1R), eg., Salzmunde 14/44.

2.3.13. Serine protease inhibitors *alias* serpins

Serine proteinase inhibitors or serpins are salt soluble proteins (~43 kDa) representing about 4% of the total protein in wheat and barley endosperms. They may have a role in plant defense.
SRP-1
SRP-A1 {10754}. 5AL {10754}.
Srp-B1a {10754}. [*Srp5Ba* {10754}]. **v:** Etawah {10755}; Federation {10755}; Frame {10755}; Pugsley {10754}; Stylet {10755}.
Srp-B1b {10754}. Null allele. **v:** Correll {10755}; EGA Eagle Rock {10755}; Gladius {10755}; Yitpi {10755}.
This allele reduced milling yield by 0.4% {10755}.

SRP-B1 {10754}. [*Srp5B* {10754}]. 5BL {10754}.

SRP-D1 {10754}. 5DL {10754}.

2.3.14. Starch granule proteins

The proteins, designated SGP-1, are starch synthases, encoded by *SsII-A1, SsII-B1* and *SsII-D1* {0042}.
SGP-1* See also starch synthase *SSII-1
SGP-A1 {1615}. 7AS {1615}. **v:** CS.
Sgp-A1a {1615}. **v:** CS.
Sgp-A1b {1615}. Null allele. **v:** Chosen 30, Chosen 57.
Sgp-A1c {1615}. **v:** Hua Non 9.

SGP-B1 {1615}. 7BS {1615}. **v:** CS.
Sgp-B1a {1615}. **v:** CS.
Sgp-B1b {1615}. Null allele. **v:** K79.
Sgp-B1c {1615}. **v:** Gnatruche.
Sgp-B1d {1615}. **v:** Waratah.

P-D1 {1615}. 7DS {1615}. **v:** CS. See also
Sgp-D1a {1615}. **v:** CS.
Sgp-D1b {1615}. Null allele. **v:** T116.

SGP-2
SGP-A2 {1615}. **v:** CS.

Sgp-B2 {1615}. **v:** CS.

Sgp-D2 {1615}. **v:** CS. .

SGP-3* See also starch synthase, *SSI-1
Sgp-A3 {1615}. 7AS {1615}. **v:** CS.
Sgp-A3a {1615}. **v:** CS.
Sgp-A3b {1615}. Null allele. **v:** Norin 61.

Sgp-B3 {1615}. 7BS {1615}. **v:** CS.
Sgp-B3a {1615}. **v:** CS.
Sgp-B3b {1615}. Null allele. **v:** Crest.
Sgp-B3c {1615}. **v:** Spica.

SGP-D3 {1615}. 7DS {1615}. **v:** CS.

A triple null stock (SGP-1 null wheat) is reported in {0137}. Deletion mapping indicated that the gene order on the 7S arms is: centromere - *SGP-1* – *SGP-3* – *Wx* {1615}.

2.3.15. Starch synthase

SSI-1. Starch synthase I proteins are identical to starch granule proteins SGP-3 {0041}.

SSI-A1 {0041}. 7A {0041}.

SSI-B1 {0041}. 7B {0041}.

SSI-D1 {0041}. 7D {0041}.

SSII-1. Starch synthase II proteins are identical to the starch granule proteins SGP-1 {0042}
SsII-A1 {0042}. 7A {0042}.

SsII-B1 {0042}. 7B {0042}. ***SsII-D1*** {0042}. 7D {0042}.

2.3.16. Water soluble proteins

WSP-1. WSP-1 are monomeric grain endosperm proteins identified by their high pI's {817}.
WSP-A1 {817}. 7AL {817}. **v:** CS.
Wsp-A1a {817}. **v:** CS.
Wsp-A1b {817}. **v:** Huntsman.
Wsp-A1c {817}. **v:** Hope.
Wsp-A1d {817}. **v:** Sicco.
Wsp-A1e {817}. **v:** Condor.

WSP-B1 {817}. 7BL {817}. **v:** CS.
Wsp-B1a {817}. **v:** CS.
Wsp-B1b {817}. **v:** Hope.
Wsp-B1c {817}. **v:** Condor.

WSP-D1 {817}. 7DL {817}. **v:** CS
Wsp-D1a {817}. **v:** CS.
Wsp-D1b {817}. **v:** Sears' Synthetic IPSR 1190903.
Wsp-D1c {893}. **v:** T4 = Agatha {890,893}; Indis {890,892}.

WSP-E1 {817}. 7E {817}. **ad:** CS/ *E. elongata*.
WSP-H1 {817}. 7H {817}. **ad:** CS/Betzes.
WSP-H^{ch}1 {817}. 7H^{ch} {817}. **ad:** CS/*H. chilense*.
WSP-S^{l}1 {817}. 7S^{l} {817}. **ad:** CS/*Ae. sharonensis*.
WSP-V1 {817}. 7V {817}. **ad:** CS/*D. villosum*.

2.3.17. Waxy proteins

Waxy protein (granule-bound starch synthase = ADP glucose starch glycosyl transferase, EC 2.4 1.21 = GBSSI) is tightly bound within endosperm starch granules and is involved in the synthesis of amylose {1616}. Waxy variants, characterised by starch granules containing increased amylopectin and reduced amylose, are preferred for Japaness white salted or "udon" noodles {1650}. Similar waxy phenotypes are controlled by orthologous genes in barley, maize and rice but are not known to occur in rye {725}. All combinations of the null alleles were produced in Chinese Spring {0018}. Partial genomic clones of various diploid, tetraploid, and hexaploid wheats were sequenced {0278, 0279}.
A multiplex PCR assay for identifying waxy genotypes is described in {10032}.
WX-1
WX-A1 {1053}, {180}. [*Wx-B1* {1054, 1053}, *Xwx-7A* {179}, {180}]. 7AS {1053}, {180}. **v:** CS. **ma:** Variation in the microsatellite gene *Xsun1-7A* provides a co-dominant marker for this locus {116}.
Wx-A1a {1054}. [*Wx-B1a* {1054}]. **v:** Bao Hua {10989}; CS; Hoshuu. **tv:** Langdon {10989}.
Wx-A1b {1054}. [*Wx-B1b* {1054}]. Null allele. **v:** California {10032}; Kanto 79; Kanto 107; Shino {10032}; Shirodaruma {1617}; Sturdy {10032, 1617}. **v2:** Mochi-Otome *Wx-B1b Wx-D1b* {10032}; Nebarigoshi *Wx-b1b* {10032}. **tv:** Asrodur {0111}; MG826 {03101}; A variant allele was present in one Iranian and one Italian accession {03101}. The complete genomic sequences for the *Wx-A1a* allele from CS {0073} and the cDNA sequence for the *Wx-A1b* allele from Kanto 107 {0075} were determined.
Wx-A1c {1617}. **v:** Pakistan Zairaishi selection {10629}; QT105 {1617}; WB6 {1617}.
Wx-A1d {1616}. **tv:** *T. dicoccoides* KU 8937B {1616}.
Wx-A1e {1616}. **tv:** KU 3659 {10629}; *T. durum* KU 3655 and KU 3659 {1616}.
Wx-A1f {10187}. Null allele. **v:** Turkey-124 {10187}; Turkey-140 {10187}; Turkey-171 {10187}; Turkey-280 {10187}; Turkey-299 {10187}.
Lines with this allele produce a PCR product with a 173 bp insertion in an exon {10187}.
Wx-A1g. *Wx-A1'* {10587}. **v:** PI 348476 {10587}; Spelt accessions PI 348576 {10587}; 2778 Epeautre Noir Velu {10587}.
Wx-A1h {10763}. Null allele. **tv:** Buck Topacio {10763}.
This is probably a unique allele possessing a 1 bp deletion in exon 6 leading to frameshift and a stop codon: partial sequence GQ120523 {10763}.
Wx-A1i {10989}. **v:** KU9259{10989}.
Wx-A1j {10989}. **v:** M1 {10989}.
Functional markers for *Wx-A1c, Wx-A1d, Wx-A1e* and *Wx-Ali* were developed from DNA sequences {10990}.

WX-B1 {1053,180}. [*Wx-A1* {1054, 1053}, *XWx-4B* {179, 180}, *XWx-4A* {961}]. 4AL {1054, 180}. **v:** CS. **tv:** A variant allele was present in three accessions {03101}.
A dominant PCR marker for identifying heterozygotes at the *Wx-B1* locus is reported in {10732}.

Wx-B1a {1054}. [*Wx-A1a* {1054}]. **v:** CS; Joshuu.
The complete genomic sequence for *Wx-B1a* from CS was determined {0073}.
Wx-B1b {1054}. [*Wx-A1b* {1054}]. Null allele. **v:** Kanto 79 {1617}; Kanto 82 {1617}; Kanto 107 {1617}; Norin 98 {1617}; Gabo {1617}; Reward {10032}; Satanta {1617}; Yukon {10032}. **v2:** Mochi-Otome *Wx-A1b Wx-D1b* {10032}; Nebarigoshi *Wx-A1b* {10032}. **v:** For list of Australian wheats, see {1650}. **tv:** Blaquetta (BG-13701) {0111}.
An ELISA-based method was developed for distinguishing wheat lines carrying this null allele {10325}.
Wx-B1c {1617}. **v:** AF24 {10629}; Chousen 40 {0094}; Cikotaba {1617, 10629}; Junguk 12 {1617, 10629}.
Wx-B1d {1616}. **tv:** *T. durum* KU 4213D {1616}; KU 4213D {10629}; KU 4224C {1616}.
Wx-B1e {0027}. **v:** Blue Boy II {0027}; Canthatch {0027}; Eureka {0027}; Gotz {0027}; Norin 44 {0027}; Turkey Red {0027}.
Wx-B1f {0111}. **tv:** BG-12413 {0111}; BG-12415 {0111}.

Wx- $\boldsymbol{B^{S}}$ ***1g*** {10587}. **al:** *Ae. speltoides* 33 {10587}.
Wx- $\boldsymbol{B^{SL}}$ ***1h*** {10587}. **al:** *Ae. longissima* 12 {10587}.

WX-D1 {1053}, {180}. [*XWx-7D* {179, 180}]. 7DS {1053}, {180}. **v:** CS.
Isolation of a wheat cDNA encoding *WX-A1* and *WX-D1* was reported in {0123} and {0167}, respectively.
Wx-D1a {1054}. **v:** CS.
Wx-D1b {1617}. Null allele. **v:** Bai Huo (Baihuomai) {1617}; DHWx12 {0117}. **v2:** Mochi-Otome *Wx-A1b Wx-B1b* {10032}. **ma:** STS marker *Xsun1-7D* produces a distinct band of about 260 bp (compared with the standard 840 bp), indicative of a smaller PCR product, but the gene is non-functional {0116, 0117}; *Xsun4(Wx)-7D* is a perfect marker {0118}.
The complete genomic sequence for *Wx-D1a* from CS {0073} and the cDNA sequence for the *Wx-D1b* allele from Bai Huo {0075} were determined.
Wx-D1c {1617}. **v:** Scoutland {1617}.
Wx-D1d {0118}. **v:** K107Wx1 {0118}; K107Wx2 {0118}; One Iranian and one Italian accession {03101}.
Wx-D1e {0117}. Null allele {0117}. **v:** NP150 {0117}.
STS marker *Xsun1-7D* failed to produce a PCR product {0117
Wx-D1f. [*Wx-d1e* {0234}]. **v:** Tanikei A6599-4 {0234}.Relative to Kanto 107, Tanikei A6599-4 carries an alanine to threonine substitution at position 258 in the mature protein {0234}.

Wx- $\boldsymbol{D^{DN}}$ ***1g*** {10587}. **al:** *Ae. ventricosa* 12 {10587}.

Various hard and soft wheats with alleles *Wx-A1b, Wx-B1b* and *Wx-D1b* are listed in {0304}. 15% of Chinese wheats possessed *Wx-B1* null alleles {10357}.
Isolation of genomic sequences for the genes encoding granule-bound starch synthase (*GBSSI* or *WX*) in *T. monococcum, Ae. speltoides* and *Ae. tauschii* was reported in {0168}. Cloning of a second set of *GBSSI* or *waxy* genes, *GBSSII*, which were shown to be located on chromosomes 2AL, 2B and 2D, was reported in {0167}.

Wheat Gene Catalogue – 3. Pathogenic Disease/Pest Reaction

For disease/pest reaction gene guidelines see Introduction, no. 8.

Note: In listings of multiple alleles, the chromosomes locations and **ma:** citations with generally be given with the particular allele that was located or mapped.

3.1. Abiotic Stress Responses: Dehydrin-response Element Binding Factors

DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers as probes for an orthologous *Dreb1* gene series was placed on chromosomes 3A, 3B and 3D {10729}. SNPs in *DREB-B1* permitted mapping in chromosome 3BL in the ITMI (Opata 85 / W7984) mapping population. See also section 2.2.42.

DREB A1. 3A {10729}.

Dreb-A1 {10729}.

DREB-B1 {10729}. 3BL {10729}. **ma:** *Xmwg818-3B* – 27.3 cM – *Dreb-B1* – 11.2 cM – *Xfbb117-3B* {10729}.

Dreb-B1.

Dreb-B1a {10729}. **v:** Opata 85 {10729}.

Dreb-B1b {10729}. **v:** W7984 {10729}.

DREB-D1.

Dreb-D1 {10729}. 3D {10729}.

3.2. Reaction to Barley Yellow Dwarf Virus

Disease: Barley yellow dwarf; Cereal yellow dwarf

BDV1

Bdv1 {1363, 1379}. 7D {1379}. 7DS {1363}. **i:** Jupeteco 73R (compared to Jupeteco 73S) {1363}. **v:** Anza {1379}; Condor BW3991 {1379}; Tyrant BW3872 {1379}; Hahn BW4097 {1379}; Parrot BW10817{1379}; Siren BW18643 {1379}; Many CIMMYT genotypes. *Bdv1* is completely linked with *Ltn*, *Sr57*, *Lr34* and *Yr18*. See *Ltn*, *Lr34*, *Yr18*.
Note: BW = CIMMYT wheat accession number.

BDV2

Bdv2 {58}. Derived from *Th. intermedium* 7D = T7DS-7Ai#1S.7Ai#1L group.7DL = T7DS.7DL-7Ai#1L {0182}, {552}. **tr:** TC14 {0201}, {59}; H960642 {0182}. **v:** Glover (with TC6) {10491}; Mackellar = LH64C (from tissue culture) {10177}; TC14*2/Hartog {0225}; TC14*2/Spear {0201}; TC14*2/Tatiara {0225}; Yw243, Yw443, Yw642 and Yw1029 (derived by *ph1* induced recombination) see {10177}. **ma:** Distal 10% of 7DL, translocation point between RFLP markers *Xpsr680* and *Xpsr965* {0182}; Complete association with *Xpsr129-7D*, *Xpsr548-7D*, *XksuD2-7D*, *XcslH81-7D*, and *Xgwm37-7D* selected as a diagnostic marker {0225}; Two RGAP and 1 RAPD markers developed for the Yw series also effective for at least TC14 {10177}.
7D = T7DS-7Ai#1S.7Ai#1L {552} **tr:** TC5, TC6, TC8, TC9, TC10 {59}.
1B = T1BS-7A#1S.7Ai#1L {552} TC7 {447}.
7Ai#1S {552} **su:** TAF2 {59}; Lines 5395 & 5395-243AA{552}.
Small recombinant segments are described in a *pontin* series of lines: recombinants were obtained with *Lr19* but not with *Sr25* {11097}.

BDV3

BDV3 in wheat shows distored inheritance that varies with genetic background

Bdv3 {10159}. Derived from *Th. intermedium* cv. Ohahe {10158} 7DS.7DL-7EL {10157}. **v:** P961341 PI 634825 {10157}; P98134 {10159}. **ad:** P107 {10159}. **su:** P29 (7D(7E) {10156}. **ma:** A SSR-BDV marker is described in {10159}.
Further translocation lines with *Bdv3* are described in {10882}.

3.3. Reaction to *Bipolaris sorokiniana*

Diseases: Spot blotch and common root rot.
Spot blotch

The pathogen harbours Tox A in common with *Parastagonospora nodurum*, *Parastagonospora avenaria tritici* and *Pyrenophora tritici-repentis* {11255, 11768}.

SB1

Sb1 {10855}. Partial resistance 7DS {10855, 10856}. **i:** HUW234Ltn+ {10855}. **v:** Saar {10856}; Lines with *Lr34/Yr18/Pm38/Sr57* - see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*, Reaction to *Blumeria graminis*, Reaction to *Puccinia graminis*, Leaf tip necrosis. **ma:** Pleiotropic or closely linked with *Lr34/Yr18/Pm38/Sr57* located between *Xgwm1220-7DS* and *Xswm10-7DS* (1.0 cM interval) {10856}; see also Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia graminis* and Reaction to *Blumeria graminis*. **c:** Putative ABC transporter {10648}.

SB2

Sb2 {11255}. *QSb.bhu-5B* {11255}. 5BL {11255}. **bin:** 5BL1-0.55-0.75. **v:** Ning 8201 {11255}; Yangmai 6 {11255}; YS116 {11255}. **ma:** *Xgwm639-5B* – 1.4 cM – *Sb2* – 0.06 cM – *Xgwm1043-5B* {11255}.

sb2. [*Tsn1* {11255}. **v:** Duster {11376}; Sonalika {11255}. Presumably all genotypes with *Tsn1*.

SB3

Sb3 {11256}. 3BS {11256}. **bin:** 3BS8-0.78 -1.00. **v:** Line 621-7-1 {11256}. **ma:** *Sb3/XWGGC3959* were mapped to a 2.2 cM interval between *Xbarc133/Xbarc147/Xcfp30-3B/XWGGC5911* and *XWGGC4320* {11255}; *XWGGC12798* – 0.08 cM – *SB3XW GGC9893/XWGGC10235* – 0.07 cM – *XWGGC6119* {11255}.

SB4

Sb4 {11592}. 4BL {11592}. **v:** Line 7H9094 {11592}. **ma:** *YK12831* – 1.18 cM – *SB4/YK12828* – 0.01 cM – *YK13104* {11592}.
Line 7H909 was selected from a segregating F_4 line from a cross of resistant cultivars GY17 and Zhongyu 1211 {11592}.

QTL
Yangmai 6 (R)/Sonalika (S): RIL population: AUDPC was controlled by four QTLs derived from Yangmai 6, viz. *QSb.bhu-2AL* (*Xbarc353-2A – Xgwm445-2A*, R^2=0.148), *QSb.bhu-2BS* (*Xgwm148-2B – Xgwm375-2B*, R^2=0.205), *QSb.bhu-5BL* (*Xgwm67-5BL – Xgwm371-5BL*, R^2=0.386) and *QSb.bhu-6DL* (*Xbarc173-6D – Xgwm732-6DL*, R^2=0.225) {10719}.

3.4. Reaction to *Blumeria graminis* DC.

Disease: Powdery Mildew.
Resistance genes and their molecular associations are reviewed in {10141}.

3.4.1. Designated genes for resistance

Note: Chancellor, used as a susceptible genetic background, for some near-isogenic lines probably carries *Pm10* and *Pm15* {1479}. 33 NILs, including 22 resistance genes and 3 genetic backgrounds are listed in {10389}.

PM1

Pm1a {562}. [*Mla* {348}, *Pm1* {130}, *Mlt* {1175}]. 7AL {1305}.7A {1293}. **i:** Axminster/8*Chancellor {132}; CI 14114 = As II/8*Chancellor {132}; CI 13836/8*Chancellor {132}; Kenya C6041/5*Federation {1168}; Norka/8*Chancellor {132}. **s:** CS*5/Axminster 7A {1293}. **v:** Anfield {98}; As II {130}; Axminster {1175,130}; Birdproof {165}; Bonus {1554}; CI 13836 {130}; Converse {1175}; Fedka

{939}; Festival {1554}; Fram I {130}; Huron CI 3315 {1175,1554}; Kenora {1554}; Kenya W744 = C6041 {1175,130}; Norka {1175,130}; Pika {130}; Sweden W1230 {1554}; Thew {1175}; TU 4 {130}; Zhengzhou 871124 {570}. **v2:** Anfield *Pm9* {1287}; BGRC 44514 *Pm3a* {1628}; Mephisto *Pm2 Pm9* {540}; Normandie *Pm2 Pm9* {165}; Pompe *Pm9* {1287}; Ring *Pm9* {1287}; Sappo *Pm2 Pm4b* (Carries *Lr20*) {310}; Solo *Pm2 Pm4b* {52}. **ma:** Co-seg. with *Xcdo347-7A* using NILs{ 864}; Co-segregation or close linkage with three RAPDs; one RAPD converted to a STS {570}; Note: In Solo, *Pm1* is translocated to chromosome 7D {52}; Complete cosegregation of several markers including *Xcdo347-7A, Xpsr121-7A, Xpsr680-7A, Xpsr687-7A, Xbzh232(Tha)-7A, Xrgc607-7A* and *Xsts638-7A* with *Pm1* and *Lr20* was reported in {323}. **c:** Encodes a nucleotide-binding, leucine rich repeat protein with close similarity to *Pm21* {11509}.

Reference {11402} provides further evidence for a non-recombinogenic region in distal chromosome arm 7AL. The region appeared to have re-arrangements involving all three homoeologous group 7 chromosomes. This casts doubt regarding an allelic series at the *PM1* locus {11509}.

Pm1b {562}. **v:** MocZlatka {562}.

Pm1c {562}. [*Pm18* {853}, {562}]. **v:** Blaukorn {0011}; M1N {562},{1628}; M1N was described as an undesignated subline of Weihenstephan M1{540}. **ma:** AFLP marker 18M2 was diagnostic for *Pm1c* {0011}.

Pm1d {562}. **v:** *T. spelta* var *duhamelianum* TRI2258 {562}. **ma:** AFLP marker 18M1 – various *Pm1* alleles 0.9 cM {0011}.

Pm1e {0322}. [*Pm22* {1134}]. **v:** Elia{1134}; Est Mottin {1134}; Ovest {1134}; Tudest {1134}; Virest {1134}.

PM2 *TraesCS5D01G044600* {11503}.

Pm2a{11049}. [*Mlu* {1175}, *Mlx* {1088}, *Pm2* {130}]. [*Mlx* {10885D {1007}; *Pm48* {10935}. 5DS{945}. **i:** CI 14118 = Ulka/8*Chancellor {132}; CI 14119 = CI 12632/8*Chancellor {132}; Federation*4 /Ulka {1168}. **v:** Avalon {96}; Bounty {96}; Claire {11678}; Fenman {96}; Galahad {1531}; H8810/47 {130}; Longbow {1531}; Maris Beacon {1592}; Maris Nimrod {1592}; Maris Sportsman {96}; Maris Templar {1592}; Mattis {11678}; Norman {96}; Orestis {1079}; PI 92378 {1168}; PI 181374{1168}; Sea Island {130}; Sentry {96}; S2303 {945}; Synthetic(Iumillo/*Ae. tauschii*) {1168}; Tobasco {11678}.TP 114/2*Starke deriv {626}; Ulka {1175, 130}; XX186 = *T. durum* Santa Maria/*Ae. squarrosa* BGRC 1458 *Pm19* {853}. **v2:** Apollo *Pm4b Pm8* {541}; Brigand *Pm6* {96}; Brimstone *Pm6* {1531}; CI 12632 *Pm6* {130}; CI 12633 *Pm6* {133}; Compal *Pm4b* {854}; Crossbow *Pm5 Pm6*{98}; Gawain *Pm6* {1531}; Halle Stamm 13471 *Mld* {97}; Heiduck *Pm6* {541}; Hustler *Pm6*{96}; Hornet *Pm8* {1531}; Kinsman *Pm6* {96}; Mardler *Pm6* {96}; Maris Dove *Mld* {1592}; Maris Fundin *Pm6* {96}; Maris Huntsman *Pm6* {1592}; Mephisto *Pm1 Pm9* {540}; Normandie *Pm1 Pm9* {165}; Parade *Pm5 Pm6*{1531}; Rendezvous *Pm4b Pm6* {1531}; Solo *Pm1 Pm4b* {52}; Timmo *Pm4b* {96}; TP 114 *Pm6* {626}; Virtue *Pm6* {96}; Walter *Pm4b Pm6* {1428}. **dv:** *Ae. squarrosa* BGRC 1458 {853}; Forty accessions of *Ae. tauschii* {852}. **ma:** *Pm2* – 3.5 cM –

Xbcd1871-5D using F2s{864}; *Xcfd81-5D* – 2.0 cM – *Pm2* {10366}. **c:** NBS-LRR structure {11270}. GenBank LN999386, protein CZT14023.1. The *TraesCS5D01G044600* allele in susceptible CS and Taichung 29 differed from the *Pm2a* allele by a 7 bp deletion in the first intron {11503}. Several alleged alleles at the *Pm2* locus were are likely *Pm2a* {11503}. Allelism of *Pm2a* and *Pm2b* was based on more than 7,600 F_2 plants. Tobasco was independently reported to have *Pm3a* {10843}.

Pm2b {11049}. Putatively derived from *Agropryron cristatum* [*PmPB3558*{11049}, *PmKM2939* {11049}]. **bin:** C-5DS1-0-0.63. **v:** KM2939 {11049}; PB3558{11075}. **ma:** *Xscar112* – 0.5 cM – *Pm2b* – 1.3 cM – *Xscar203/Xmag6176/Xcfd81-5D*{11049}; *Xcfd81-5D* – 5.5 cM – *PmPB3558* – 3.9 cM – *Xbwm25* – 0.9 cM – *Xbwm21* – 0.9 cM – *Xbwm20* {11075}.
Deleted: Identified as *Pm2a* {11503}.

Pm2c {11061}. [*PmNM* {11061}]. 5DS {11061}. **bin:** 5DS-1-0-0.63. **v:** Niaomai {11061}. **ma:** *Xcfd81-5D* – 0.4/0.1 cM – *Pm2c* – 7.5/4.9 cM – *Xcfd78-5D* {11061}.
Deleted: Identified as *Pm2a* {11503}.

Several alleles of *Pm2* with wheat and alien origins have been reported in Chinese genotypes – see temporary designations. The complex nature of temporarily named powdery mildew resistance genes in the *Pm2* region is discussed in {11380}. Several alleged alleles at the *Pm2* locus are likely *Pm2a* {11503}.

PM3.

PM3 has 92.9% identity with PM8 at the protein level {11398}.

Pm3a {130}, {132}. [*Mla* {1168}]. 1A {1007}.1AS {947}, {943}. **i:** Asosan/8*Chancellor {132} = CI 14120; Asosan/3*Federation {1168}. **v:** Asosan {130}, {1168}; BGRC 44514 *Pm1a* {1628}; Coker 797 {786}; Florida 301 {786}; Florida 302 {786}; Hadden {97}; Halle Stamm {97}; Madrid {10843}; Merker {10843}; Norin 3 {1134}; Norin 29 {1134}; PI 46890 {1439}; Robigus {10843}; Saluda {786}; Tabasco {10843}; Tyler {1419}. **ma:** *Xbcd1434-1A* – 1.3 cM – *Pm3* using NILs{864}; *Xwhs179-1A* – 3.3 cM – *Pm3*{522}. *Xgdm33-1A* – 2.3 cM – *Pm3/Xpsp2999-1A*{313}. Sequence AY939880 {10292}.

Tobasco was independently reported to have *Pm2a* {11678}, *Pm48* {10935}.

Pm3b {130}, {132}. [*Mlc* {165}, *Pm3j* {10405}]. 1A {1007}. **i:** Chul*8/Chancellor = CI 14121 {132}; *T. sphaerococcum**8/Chancellor = CI 15887 {539}. **v:** Chul {165}; Enorm {10843}. **ma:** *Xbcd1434-1A* – 1.3 cM – *Pm3b* using NILs {864}. **c:** The isolation of *Pm3b* is reported in {10064}. The *Pm3b* gene (GenBank AY325736) is a coiled-coil NBS-LRR type of disease resistance gene {10064}.

Pm3c {130}, {132}. [*Pmi* {10405}, *Mls* {1175}]. 1A {1007}, {134}. **i:** Sonora/8*Chancellor {132} = CI 14122; Sonora/4* Federation {1168}; Triticale/8*Chancellor {539}. **s:** CS*7/Indian 1° {134}. **v:**

Borenos {854}; Cawnpore {1628}; CI 3008 {130}; CI 4546 {130}; Hindukush {1628}; Indian {1175}; Sonora {130}, {1168}; Sturgeon {1175}. **c:** Sequence DQ251587, DQ517917 {10405}.

Pm3d {1628}. [*Mlk* {434}, *Ml-k* {540}, {10405}. 1° {1628}. **v:** Axona {0313}; Cornette {0313}; Herold {540}; Indian 4 {0313}; Kadett {0313}; Kanzler {0011}; Kleiber {0313}; Kolibri {540, 542, 1628}; Ralle {540}; Socrates {heterogeneous} {540}; Star {heterogeneous}{540}; Syros {540}; Vergas {10843}. **v2:** Kadett *Pm4b* {540}; Turbo *Pm4b* {540}. **c:** Sequence AY9398881 {10292}. DQ251488, DQ517518 {10405}.

Pm3e {1628}. **v:** Sydney University Accession W150 = AUS 6449 {939, 1628}. **v2:** Cortez *Pm5* allele {10843}. **ma:** *Pm3e* – 7.1 cM – *Xwmc818-1A* {10843}.

Pm3f {1628}. **i:** Michigan Amber/8*Chancellor {1628}; This allele was distinguished from *Pm3c* with only one of 13 pathogen cultures. **v:** Viza {10843}. **c:** Sequence DQ071554 {10292}.

Pm3g {0070}. [*Mlar* {854}]. 1AS {0313}. 1A {0070}. **v:** Avo{1629}; Aristide{1629}; Champetre {0313}; Courtot {1629}; Lutin {0313}; Oradian {0313}; Rubens {0313}; Soissons {0313}; Valois {0313}. **ma:** *Pm3g* – 5.2 cM – *Gli-A5* – 1.9 cM – *Gli-A1* {0070}; *Pm3g* was completely linked to microsatellite *Xpsp2999*{313}. **c:** Sequence DQ251489, DQ517919 {10405}.

The *Pm3a, Pm3b, Pm3d* and *Pm3f* alleles form a true allelic series based on sequence analysis {10292}. Following the cloning and sequencing of *Pm3b* {10064}, 6 other alleles were sequenced {10405}. The Chinese Spring (susceptible) allele, *Pm3CS*, considered to be ancestral and present in many hexaploid and tetraploid wheats, was also transcribed {10405, 10406}. Other wheats possessed a truncated sequence (e.g. Kavkaz), or were null {10405,10406}. Unique markers were developed for all 8 transcribed alleles, and for individual alleles {10405}.

Alleles *Pm3b, Pm3d*, and *Pm3f* were detected in Scandinavian varieties using allele-specific markers {10681}.

PM4 {131}. *TraesSYM2A03G00828360* {11774}.

Pm4a {1464}. [*Pm4* {131}]. 2AL {1464}. **i:** CI 14123 = Khapli/8*Chancellor {131}; CI 14124 = Yuma/8*Chancellor {131}. **v:** Aikang 58 {11753}; Steinwedel*2/Khapli {939}; Yangmai 10 {10176}; Yangmai 11 {10176}. **tv:** Khapli {131}; Valgerado {97}; Yuma {131}. **ma:** Co-seg with *Xbcd1231-2A.2* & *Xcdo678-2A* using F2s{864}; *Xbcd1231-2A.1* – 1.5 cM – *Pm4* – 1.56 cM – *Xbcd292-2A*{864}; *Pm4a* – 3.5 cM – AFLP markers *4aM1* and *4aM2* {11}; *Xbcd1231-2A* was converted to a STS marker and to a *Pm4a*-specific dominant PCR marker {10176}; *Xgwm356-2A* – 4.8 cM – *Pm4a*{10176}. **c:** Similar structure to *Pm4b* {11525}.

Pm4b {1464}. [*Mle* {1591}]. 2° {52}. 2AL {1464}. **i:** Federation*7/*T. carthlicum* W804 {1464}; VPM1/7*Bainong 3217 {11287}. **v:** Achill {540}; Ajax {540}; Arkas {540}; Armada {96}; Atlantis {11}; Boheme {11}; Botri (heterogeneous) {854}; ELS {1591}; Facta {854}; Factor (heterogeneous){854}; Fakon {854}; Fazit {854}; Hermes {540}; Horizont {540}; Maris Halberd;

Max {540}; Olymp {540}; Orbis {540}; RE714 {1220}; Renan {16}; Ronos{1079}; S-25 {52}; S-28 {52}; TP 229 {626,1591}; Weihenstephan M1 {1591}; VPM1 {97}. **v2:** Apollo *Pm2 Pm8* {541,802}; Boxer *Pm5*{541}; Compal *Pm2* {854}; Kadett *Pm3d* {540}; Kronjuwel *Pm8* {541}; Mission *Pm5* {1531, 541}; Rang *Pm1* {52}; Rendezvous *Pm2 Pm6* {1531}; Solo *Pm1 Pm2* {540, 52}; Sorbas *Pm6* {541}; Timmo *Pm2 Pm6* {96}; Turbo *Pm3d* {540}; **v:** Xiaomaomai {11774}; Walter *Pm2 Pm6* {1428}. **ma:** *Pm4b* – 4.8 cM – *Xgbx3119b-2A* {272}; *Xgwm382-2A* – +/-10 cM – *Pm4b* – +/-2 cM – *XgbxG303-2* {354}; STS241 – 4.9 cM – *Pm4b* – 7.1 cM – SRAP *Me8/Em7*$_{220}$ – 4.7 cM – *Xgwm382-2A*{10553}; *Xics13* – 1.3 cM – *Pm4b* – 1.7 cM – *Xics43* covering a 6.7 Mb physical region {11287}. **c:** Encodes a putative chimeric protein of a serine/threonine kinase and multiple C2 domains and transmembrane regions; *Pm4b* undergoes alternative splicing to generate two isoforms, both of which are essential for resistance function {11525}. Genbank: Pm4b_V1 CDS: MT783929; Pm4b_V2 CDS, MT783930. Closest homologue of the C2 domain of *Pm4b* in CS is *TraesCS2A01G557900*.

Pm4c {10583}. [*Pm23* {1618}] 2AL {10583} – earlier reported on 5AL {1618}. **v2:** 81-7241 *Pm8* suppressed{1618, 10583}. **ma:** *Xbarc122-2* – 1.4 cM – *Pm4c* – 3.5 cM – *Xgwm356-2* {10583}.
Pm4b and *Pm4c* are identical at the nucleotide level {11774}.

Pm4d {10744}. 2AL {10744}. **bin:** 2AL1-0.85-1.00. **v:** GR18-1 {11701}; SYMattis {11525, 11775};. Tianmin 668 {11702}; Tm27d2 = WW St2022/Tm27//Amor = TRI 29584 {10744}. **dv:** *T. monococcum* Tm27 {10744}. **v: ma:** A 218 bp fragment was amplified with STS marker *ResPm4* as were other *Pm4* alleles {10744}, Located within the intervals 75.889 – 78.702 Mb {11701} and 76.148 – 76.803 {11702}..

Pm4e {11317}. 2AL {11317}. **v:** D29 {11317}. **ma:** *Xgdm93-2A* – 4.9 cM – *Pm4e/Xsts_bcd1231* – 1.8 cM – *Xhbg327-2A* {113017}; *Xwgrc763-2A* – 0.13 cM – *Pm4e/Xwgrc872-2A/Xwgrc869-2A* – 0.58 cM – *Xwgrc982-2A*, a region of about 6.1 Mb {11335}.
Pm4d and *Pm4e* are identical at the nucleotide level {11774}.

A recessive resistance gene (*pmXXM* {11661}) in Xiaomaomai had a similar protein structure to *Pm4d*, *Pm4e* and *Pm4h* {11661}.

Pm4f. **v:** WATDE0571 {11775}.

Pm4g. **v:** WW-740 {11775}.

Pm4h. **v:** WW-474 {11774}.

Pm4i. **v:** WATDE0048 {11775}.

Pm4j. **v:** WATDE0592 {11775}.

Add note at end of *Pm4* section: Some variants of *PM4* confer resistance to wheat blast {11632, 11735, 11775} – see Reaction to *Magnaporthe grisea*.
PM5. *TraesCS7B02G441700* (susceptible allele) (chr7B: 706.811-706.816 Mb) {11533}.

Pm5a {0257}. *Pm5a* was transferred to hexaploid wheat from *T. dicoccum* via Hope and H-44. Recessive. [*Pm5* {787}, *mlH* {771}]. 7B {964}.7BL {771}. **i:** Hope/8* Chancellor = CI 14125{570}. **s:** CS*6/Hope 7B {964}, {771}. **v:** Alidos {854}; Aotea {964}; Caldwell {786}; Ga 1123 {786}; Galaxie {0257}; Glenwari {964}; Hardired {786}; Hope {964}; H-44 {964}; Kontrast {854}; Kormoran {1079}; Kutulukskaya {257}; Lambros {0257}; Lawrence {964}; Navid {0257}; Pagode {0257}; Redcoat {97}; Redman {964}; Regina {0257}; Renown {964}; Selpek {540}; Sicco {96}, {0257}; Spica {964}; Tarasque{0257}; Warigo {964}; Zolotistaya {0257}. **v2:** Arthur *Pm6*{786}; Coker 983 *Pm6* {786}; Double Crop *Pm6* {786}; Granada *Pm8* {541}; Saar *Pm38 Pm39* {10481}; Sensor *Pm8* {541}. **c:** GenBank MK955160.

Pm5b {0257}. [*Mli* {558}, {540}]. **v:** Aquila{96, 541}; Carimulti {541}; Cariplus {541}; Cucurova {0257}; Dolomit {541}; Falke {541}; Flanders {96}; Fruhprobst {0257}; Ilona {0257}; Ibis {96}; Kirkpinar-79 {0257}; Kontrast {0257}; Kormoran {541}; Krata {541}; Markant {541}; Mercia {1531}; Milan {541}; Nadadores {0257}; Reiher {541}; Rektor{541}; Rothwell Perdix {96}; Siete Cerros {0257}; Severin {541}; Sicco {96}; Sperber {541}; Tukan {541}; Una {0257}; Urban {541}; Wattines {541}; Wettiness {0257}. **v2:** Bert *Pm6* {541}; Boxer *Pm4b* {541}; Crossbow *Pm2 Pm6* {98}; Kristall *Pm8* {541}; Mission *Pm4b* {1531, 541}; Parade *Pm2 Pm6* {1531}. **c:** GenBank MK955159.

Pm5c {257}. 7B {0257}. **v:** *T. sphaerococcum* cv. Kolandi {0257}.

Pm5d {0257}. 7B {0257}. **bin:** 7BL 0.86-1.00 {10542}. **i:** IGV 1-455 = CI 10904/7*Prins {0257}; CI 10904/7*Starke {0257}. **v:** Dream {10542}. **ma:** *Xgwm611-7B* – 2.1 cM – *Pm5d* – 2.0 cM – *Xgwm577-7B* – 1.0 cM – *Xwmc581-7B* {10542}. **c** Same sequence as *Pm5e* {11533}.

Pm5e {0258}. Recessive and hemizygous effective {0258}; usually dominant {11708}. [*mlfz* {0259}]; *PmAL11* {11708}. **i:** H962R {11707). **v:** AL11 {11708}. Baiyouyantiao (previously published as *PmBYYT* {11533}); Fuzhuang 30 {0258}; Hongquanmong (previously published as *PmH* {11533}; Mazhamai (previously published as *Mlmz* {11533}); Tangmai 4 (previously published as *PmTm4* {11533, 10961, 11533}); Xiaobaidongmai (previously published as *Pmxbd* {0258, 11533}). **ma:** *Xgwm1267-7B* – 6.6 cM – *Pm5e* – 12.6 cM – *Xubc405*$_{628}$*-2B* {0258}. KASP marker *AL11-K2488* {11708}. **c:** Identified as a CC-NBS-LRR {11533}. GenBank MK955156.
Although Duanganmang (*PmDGM*) had an identical sequence and UTR to *Pm5e*, a second completely linked gene was postulated to account for a different response pattern to the *Pm5e* control {11705}.

pm5. **c:** CS (susceptible allele): *TraesCS7B02G441700* (chr7B: 706.811-706.816 Mb); GenBank MK955157.

Genotype lists: {0313, 10405, 10406}

PM6

Pm6 {627}. [*Mlf* {626}]. 2B {1088}. **i:** CI 13250/7*Prins {0069}; CI 12559/8*Prins {0069}; Eight Prins derivatives {10576}; PI 170914/7*Prins 6 NILs based on Prins {0139, 0069}. **v:** 1969 IVGS Line

C {626}; Abe {97,1256}; Coker747 {786, 1079}; Mengavi {97}; Oasis {786}; Timgalen {98}; TP 114/2*Starke deriv. B {626}. **v2:** Arthur *Pm5a* {786}, {97}; Brigand *Pm2* {96}; Brimstone *Pm2* {1531}; CI 12632 *Pm2* {1088}, {626}; CI 12633 *Pm2* {1088}, {626}; Crossbow *Pm2 Pm5* {98}; Double Crop *Pm5a* {786}; Garwain *Pm2* {1531}; Greif *Pm5a* {0011}; Heiduck *Pm2* {541}; Hustler *Pm2* {96}; Kinsman *Pm2* {96}; Mardler *Pm2* {96}; Maris Fundin *Pm2* {96}; Maris Huntsman *Pm2* {1592}; Parade *Pm2 Pm5* {1531}; Rendezvous *Pm2 Pm4b* {1531}; Sorbas *Pm4b* {541}; Timmo *Pm2 Pm4b* {96}; TP 114 *Pm2* {626}; Virtue *Pm2* {96}; Walter *Pm2 Pm4b* {1428}. **ma:** Close linkage with *Xbcd135-2B* (1.5+-1.4 cM), *Xbcd307-2B* (4.7 +- 2.5 cM) and *Xbcd266-2B* (4.5 +- 2.4 cM) {69}; Mapped to the interval *Xbcd35-2B-Xpsr934-2B* {139}; However, the fact that Timgalen and a 'CI12632/Cc' line lacked the critical *T. timopheevii* markers {0139} is cause for concern; RFLP marker *Xbcd135-2B* was converted to STS markers *NAU/STS*$_{\mathrm{BCD135-1}}$ and *NAU/STS*$_{\mathrm{BCD135-2}}$ which showed linkage of 0.8 cM with *Pm6* {10576}. *Pm6* was localized to a 0.9 Mb physical region in chromosome 2BL {11451}.

PM7

Pm7. Derived from *S. cereale* cv. Rosen. 4BL {270}, {271}, {389} = T4BS.4BL-5RL {543}, but more recently revised to T4BS.4BL-2R#IL {389}, {380}. **i:** Transec/8*Chancellor. **v:** Transfed {269}; Transec {273}.

PM8

Pm8. Derived from Petkus rye - see *Yr9, Lr26, Sr31*. 1BL.1RS. 1R(1B). **i:** MA1 and MA2, four-breakpoint double translocation lines 1RS-1BS-1RS-1BS. 1BL in Pavon {0084}. **v:** Corinthian {1531}; Dauntless {1531}; Ambassador {1531}; Disponent {541}; GR876 {753}; Halle Stamm {97}; Hammer {98}; Others {1208}; ST1-25 {201}; Slejpner {1531}; Stetson {1531}; Stuart {96}. **v2:** Apollo *Pm2 Pm4b* {541}; Granada *Pm5* {541}; Hornet *Pm2* {1531}; Kristall *Pm5* {541}; Kronjuwel *Pm4b* {541}; Sensor *Pm5* {541}. **tv:** Cando*2/Veery = KS91WGRC14 {381}.
1BS/1RS recombinants 2.9 cM proximal to *Gli-B1/GluB3* {0084}. Crosses between three lines with *Pm8* and Helami-105, a 1BL.1RS line with *Pm17*, indicated that *Pm8* and *Pm17* were allelic {524}. Earlier, these genes were reported to be genetically independent {1463}. **ma:** *Pm8* is located between *Gli/Glu3* and rust resistance genes *Sr31, Lr26* and *Yr9* {11354}. An STS marker distinguished *Pm8* from *Pm17* {0186}. *Pm8* is located between *Gli/Glu3* and rust resistance genes *Sr31, Lr26* and *Yr9* {11354}. **c:** GenBank KF572030. *Pm8* is an orthologue of *Pm3* and an allele of *Pm17* in the rye genome {11276, 11398}. *Pm8* has 92.9% identity with *Pm3* at the protein level {11398}.

PM9

Pm9 {347}. 7AL.7A {347}. **v:** N14 {562}. **v2:** Anfield *Pm1a* {1287}; Mephisto *Pm1a Pm2* {540}; Normandie *Pm1a Pm2* {347}; Pompe *Pm1a* {1287}; Ring *Pm1a* {1287}.

PM10

Pm10 {1482}. 1D {1482}. **v:** Norin 4 {1482}; Norin 26 {1482}; Norin 29 {1482}; Penjamo 62 {1482}; Shinchunaga {1482}. **v2:** *T. spelta duhamelianum Pm11* {1481}.
Pm10 was detected using a culture derived from a hybrid of *B. g. tritici* and *B. g. agropyri*.

PM11

Pm11 {1481}. 6BS {1481}. **v:** Chinese Spring {1481}; Salmon {1481}; *T. compactum* No. 44 {1481}. **v2:** *T. spelta duhamelianum Pm10* {1481}.
Pm11 was detected using a culture derived from a hybrid of *B. g. tritici* and *B. g. agropyri*

PM12

Pm12 {1017}. Derived from *Ae. speltoides*.
The earlier location of 6A {1017} was not correct. 6B = 6BS-6SS.6SL {572}, {598}. 6S^{1}S {598}. **v:** Wembley*6/*Ae. speltoides* #31 {598}, {1017}. **al:** *Ae. speltoides* CL214008 = K {1017}. **ma:** *Pm12* was mapped to a translocated segment proximal to *Xpsr551-6B* {598}; Secondary recombination analysis indicated that *Pm12* was located in the long arm of 6S between *Xwmc105* and *Xcau127* {10517}.

PM13

Pm13. Derived from *Ae. longissima* accession TL01.
T3BL.3BS-3S^1#1S. **v:** Recombinant N12-3 containing 2.82 Mb of 3S^l (11756}. **al:** *Ae longissima* TL01, TL20, TA1910 {11756}. **ma:** STS marker *Xutv13* {0036}; several other markers located in introgressed segments {0036}.
3B {173} = T3BL.3BS-3S^1#1S {389} **v:** R1A {174}; R1B {0055}; R4A {0055}; R6A {0055}. **ma:** *Pm13* was mapped to a translocated 3S^{1}S segment distal to *Xcdo-460-3B* {0036}; Two markers, *AelMLKL-1* and *AelMLKL-8*, developed {11756}.
3D {173} = T3DL.3DS-3S^1#1S {389}. **v:** R2A{0055}; R2B {0055}. **tv:** R1D {174}.
3S^1#1S. **al:** *Ae. longissima*.

c: Encodes a mixed lineage kinase domain kinase-like (MLKL) or kinase fusion protein (FLP) {11756}.

PM14

Pm14 {1478}. 6B {1478}. **v2:** Akabozu *Pm10Pm15* {1478}; Kokeshikomugi *Pm15* {1478}; Norin 10 *Pm15* {1478}.
Pm14 and *Pm15* were detected using hybrids between *B. g. tritici* and *B. g. agropyri* cultures.

PM15

Pm15 {1478}. 7DS {1478}. **v2:** Akabozu *Pm14* {1478}; Chinese Spring *Pm11* {1478}; Kokeshikomugi *Pm14* {1478}; Norin 4 *Pm10* {1478}; Norin 10 *Pm14* {1478}; Norin 26 *Pm10* {1478}; Shinchunaga *Pm10* {1478}; *T. macha subletschumicum Pm10*{1478}; *T. compactum* No. 44 *Pm11* {1478}.
Pm14 and *Pm15* were detected using hybrids between *B. g. tritici* and *B. g. agropyri* cultures.

PM16

Pm16 {1201}. 4A {1201}. 5B {10217}. **v:** Line 70281 = Norman/*3 Beijing 837 {10217}; Norman lines with resistance from *T. dicoccoides* CL1060025{1201}. **tv:** *T. dicoccoides* CL1060025 {1201}. **ma:** *Pm16* – 5.3 cM – *Xgwm159-5B* {10217}.
To account for the different chromosome locations a 4A-4B translocation was suggested {10217}. Based on the 5B location and similar disease responses *Pm16* and *Pm30* may be the same {10217}.

PM17

Pm17 {97}, {544}, {838}.
1AS = T1AL.1R#2S {389}, {185}, {1624} **v:** Amigo {561}; Century {216}; Embrapa 16 {11355}; Hugenoot {11355}; McCormack {10758}; Nekota {21}; Neobrara {21}; TAM107 {216}; TAM200 {216}; TAM201 {216}; TAM202 {21}; TAM303 {10758}; Tribute {10758}; TXGH13622 {11355}. **al:** Insave rye Nr 10458 {11398}. **c:** *Pm17* shares 96% nucleotide identity with *Pm8* (83% at the protein level) and low but significant identity with *Pm3CS* {11355}. GenBank MH077963.
1BS = T1BL.1R#2S {561} **v2:** Helami 105 *Pm5* {561}. **ma:** A STS marker distinguished *Pm17* from *Pm8* {0286}; *Pm7* – 7.8 cM – *Xmwg68-1R* – 10.9 cM – *Sec-1* in 1RS {10167}.
Pm8 and *Pm17* were reported to be allelic {524}, see note under *Pm8*.

Pm17 is allelic with *Pm8* in rye and orthologue of *Pm3* {11398}.

PM18. **Deleted,** see *Pm1c*.

PM19

Pm19 {853}. 7D {853}. **v:** *T. durum* 'Moroccos 183'/*Ae. tauschii* AE 457/78 {853}. **v2:** Synthetic XX186 *Pm2* {853}. **dv:** *Ae. tauschii* {853}.

PM20

Pm20 {386}. [*M1P6L* {543}]. 6BL = T6BS.6R#2L {386}, {389}, {543}. **v:** KS93WGRC28 = PI 583795 {386}, {382}; 6RL. **su:** 6R{6D} {543}. **ad:** 6R addition {543}. **al:** Prolific rye {543}.

PM21

Pm21 {1177}. 6AS = T6AL.6VS#2 {1177, 11714}. **bin:** 6VS 0.45-0.58 {10859}. **v:** Yangmai 18 {11352}; 9 independent translocations {1177}; A derivative named HP33 was described as a ‘cryptic’ translocation {11275}. **ma:** RAPD *OPH17*$_{1900}$ (synonym 'OPH17-1900') was associated with *Pm21* and RAPD *OPH17*$_{1000}$ (synonym OPH17-1000') with its absence {1176}; RAPD OPH17$_{1400}$ and SCAR markers SCAR$_{1400}$ and SCAR$_{1265}$ associated with *Pm21* are described in {14}; Marker NAU/Xibao15, developed from a serine/threonine gene upregulated by powdery mildew infection, acts as a co-dominant marker for lines carrying *Pm21* {10519}; Potentially useful markers are provided in {10918}. Genetic mapping in a resistant × susceptible *D. villosum* cross identified two RGA candidate loci (markers

6VS-09.4 and 6VS.09.4b) co-segregating with *Pm21* and overlapped by an EMS-induced susceptible mutation {11352}. **c:** *Pm21* is likely the serine/threonine kinase gene *Stpk-V* {10859}. *NLR-V1*, one of two *NLR-V* genes in HP33, was identified as the candidate for *Pm21* {11275}. GenBank MF716955. Silencing of *NLR-V1* compromised *Pm21* resistance in the T6AL.6VS lines described below and decreased the level of resistance in the T6DL.6VS lines described below {11275}. Marker *6VS-09.4* but not marker *6VS-09.4b* was deleted in a susceptible mutant indicating that the former was *Pm21* – the protein product had a CC-NBS -LRR structure – GenBank MF370199 {11353}. This gene was different from *Stpk-V* {11275} but was quite similar to *NLR-V1* {11353}.
6AL.6AS-6VS#2S {11578}.

Pm21, PmV and *Pm12* were shown to be orthologous and diagnostic markers for each gene were developed in {11704}.
See also *PmV*.
See also *PM31*.

Three lines, Pm97033, Pm97034 and Pm07035, with a 6DL.6VS translocation were developed from a different source of *H. villosa* {10194}. These may carry *Pm21*.

See also *PmV*.

PM22 {1134}. **Deleted.**

***Pm22*. Deleted,** renamed as *Pm1e*.

PM23 **Deleted.**

***Pm23*. Deleted,** Renamed as *Pm4c*.

***PM24*.** TraesCS1D02G058900; AET1Gv20142700. This locus is also named *RMG1* (*RWT4*) – see Reaction to *Magniporthe grisea*.

Pm24 {571, 11414}. [*Pm24a* {571}, *Pm24b* {10994}, *WTK3* {11414}]. 6D {571}. 1DS {0150}. **bin:** 1DS5-0.54-1.00. **v:** Baihulu {10994, 11414}; Chiyacao {571}; Hongmangmai {11414}; Hulutou {11413, 11414}. **ma:** *Xgwm789-1D/Xgwm603-1D* – 2.4 cM – *Pm24/Xgwm1291-1D* – 3.6 cM – *Xbarc229-1D*{10109, 10957}; *Xgwm789/Xgwm603-1D* – 2.4 cM – *Pm24* – 6 cM – *Xbarc229-1D* {10109, 10957, 10994}. Located in a 9.3 cM region flanked by *Xgwm337-1D* and *Xcfd83/Xcfd72-1D* {11413}. **c:** *Pm24* encodes a tandem kinase protein with putative pseudokinase domains. The gene was designated *Wheat Tandem Kinase 3* (*WTK3*) – this gain of function mutation was conferred by a 6 bp deletion of lysine/glycine codons (K400G401) in the KIN1 domain {11414}. GenBank MK950855. The same candidate gene was predicted for *PmDTM* in Datoumai (11556), but according to those results Chiyacao, Hulutou and Datoumai showed differential responses to an array of *Bgt* isolates {11414}.

PM25

Pm25 {1343}. [*PmTmb* {1344, 1343}]. 1A {1343}. **v:** PI 599035 = NC94-3778{1344}. **v2:** NC96BGTA5 = Saluda*3/PI 427662 *Pm3a* {1343}. **dv:** *T. monococcum* PI 427662 {1343}. **ma:**

Linked with 3 RAPDs, the nearest, OPAG04950, at 12.8 +/- 4.0 cM {1343}; Associated with 3 RAPDs {1344}.

PM26

Pm26 {0001}. Recessive {0001}. 2BS {0001}. **s:** Bethlehem*8/*T. turgidum* var. *dicoccoides* 2BS {0001}. **tv:** *T. turgidum* var. *dicoccoides* TTD140 {0001}. **ma:** Co-segregation with *Xwg516-2B* {0001}.

PM27

Pm27 {0002}. 6B (6B-6G) {0002}. **v:** Line 146-155-T {0002}. **tv:** *T. timopheevii* var. *timopheevii* K-38555 {0022}. **ma:** 6BS......*Xpsr8/Xpsr964-6B – Pm27 – Xpsr154/Xpsr546-6B* ......6BL {0002}; Co-segregation with *Xpsr3131-6B* {0002}.

PM28

Pm28 {0022}. 1B {0022}. **v:** Meri {0022}.

PM29

Pm29 {0129}. Derived from *Ae. ovata*. 7DL. **v:** Pova {0129}. **ma:** Location confirmed by co-segregation with molecular markers {0129}.

PM30

Pm30 {0163}. [*MIC20*] 5BS{0163}. **v:** 87-1/C20//2*8866 Seletion {0163}. **ma:** *Pm30* – 5.6 cM – *Xgwm159-5B* {0163}.
Pm30 could be the same as *Pm16* {10217}.

PM31 **Deleted.** This gene designation {0301} is not valid; subsequent studies {10918} showed the gene is *Pm21*.

Pm31 {0301}. [*mlG* {0301}]. 6AL {0301}. **v:** G-305-M/781//3*Jing411 {0301}. **tv:** *T. dicoccoides* G-305-M {0301}. **ma:** cent....*Pm31* – 0.6 cM – *Xpsp3029.1-6A* – 2.5 cM – *Xpsp3071-6A* {0301}.

PM32

Pm32 {10025}. Derived from *Ae. speltoides* {10025}. 1B=1BL.1SS{10025}. **v:** L501 = Rodina*6/*Ae. speltoides* {10025}.

PM33

Pm33 {10205}. [*PmPS5B* {10205}]. 2BL {10205}. **v:** Am9 = *T. carthlicum* PS5/*Ae. umbellulata* Y39 {10205}. **tv2:** *T. carthlicum* PS5 *PmPS5A* {10205}. **ma:** *Xgwm536-2B* – 18.1 cM – *Pm33* – 1.1 cM – *Xwmc317-2B* – 1.1 cM – *Xgwm111-2B* – 1.8 cM – *Xgwm383-2B*{10205}.

PM34

Pm34 {10241}. 5DL {10241}. **v:** PI 604033 = NC97BGTD7 = Saluda*3/*Ae. tauschii* TA2492 {10241}. **dv:** *Ae. tauschii* TA2492 {10241}. **ma:** *Xbarc177-5D* – 5.4 cM – 2.6 cM – *Xbarc144-5D* {10241}.

PM35

Pm35 {10342}. 5DL {10342}. **v:** NC96BGTD3 = PI 603250 = Saluda*3/TA2377 {10342}. **dv:** *Ae. tauschii* ssp. *strangulata* TA2377 {10342}. **ma:** *Xcfd26-5D* – 11.9 cM – *Pm35* {10342}.

PM36

Pm36 {10356}. 5BL {10356}. **bin:** 5BL6-0.55-0.76 {10356}. **tv:** MG-FN14999, a durum backcross line 5BIL-29 {10356}; *T. turgidum* ssp. *dicoccoides* MG29896 {10356}. **ma:** *Xcfd7-5B* – 10.7 cM – *Pm36* – 0.8 cM – *EST BJ261636* – 8.9 cM – *Xwmc75-5D* {10356}; 5BIL-42 identified as the derivative with shortest *T dicoccoides* segment; *IWB7454* (537.36 Mb, Svevo RefSeq) – *PM36* – *IWB22904* (538.44 Mb) {11709}.

PM37

Pm37 {10372}. 7AL {10274, 10372}. **v:** PI 615588 = NC99BgTAG11 = Saluda*3/PI 427315{10372}. **tv:** PI 427315 = *T. timopheevii* ssp. *Ameriacum* {10372}. **ma:** *Pm37* (PmAG11) was about 15 cM proximal to a cluster of markers that earlier co-segregated with *Pm1* {10372}; A cross indicated linkage between *Pm37* and *Pm1*{10372}; *Xgwm332-7A* – 0.5 cM – *Pm37* – 0.5 cM – *Xwmc790-7A* – 15.5 cM – *Pm1* {10372}.
A further gene derived from *T. monococcum* PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3/PI 427772 {10479}. A single resistance gene was identified on chromosome 7AL in hexaploid germplasm NC96BGT4 (a *T. monococcum* derivative). This gene was proximal to *Pm1* and considered to be different from *Pm37*, although possibly allelic {10274}.

PM38 *TraesCS7D03G0183600*

Pm38 {10373}. Adult plant resistance 7DS {10374}. **i:** RL6058 = Tc*6/PI 58548{10374}. **v:** Lines with *Sr57/Lr34/Yr18*. **v2:** Saar *Pm5a Pm39* {10481}. **ma:** *Xgwm1220-7D* – 0.9 cM – *Lr34/Yr18/Pm38* – 2.7 cM {10374}. **c:** ABC transporter; See *Lr34*.
This gene is identical to *Yr18, Sr57, Lr34* and *Ltn* and confers stem rust resistance in some genetic backgrounds; see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*.

PM39

Pm39 {10481}. Adult plant resistance 1BL {10481,10480}. **i:** Avocet-R+Lr46/Yr29 = Avocet-R*3//Lalb mono 1B*4/Pavon 76 {10480}. **v:** Genotypes with *Lr46/Yr29*; see Reaction to *Puccina* *triticina*, Reaction to *P. striiformis*. **v2:** Saar (CID: 160299, SID: 188) *Pm5a Pm38* {10481}. **ma:** *Xwmc719-1BL* – 4.3 cM – *Lr46/Yr29/Pm39* – 2.5 cM – *Xhbe248-1BL* {10481}.

PM40

Pm40 {10539}. Derived from *Th. intermedium* {10539}. *Pm40* was not derived from *Th. intermedium* {11710}. 7BS {10539}. **bin:** C-7BS-1-0.27. **v:** GRY19 {10539}; Partial amphiploid TAI7047 {10539}; Yu {10539}; PI 672538 {11710}; Yu24 {10539}. **ma:** *Xwmc426-7B* – 5.9 cM – *Xwmc334-7B* – 0.2 cM – *Pm40* – 0.7 cM – *Xgwm297-7B* – 1.2 cM – *Xwmc364-7B* {10539}; *Xwmc-7B* – 0.58 cM – *Pm40* – 0.26 cM – *BF291338* {11710}. Flanked by EST markers *BF478514* and *BF291338* {11711}. **c:** *TraesCS7B01G164000*, an NLR with an additional NBS region was identified as a candidate {11711}.

PM41

Pm41 {10551}. Derived from *T. dicoccoides*. 3BL {10551}. **bin:** 0.63-1.00. **v:** XXX = 87-1*4/Langdon/IW2 {10551}. **tv:** Langdon/IW2 Seln. XXX {10551}; *T. dicoccoides* IW2 {10551}. **ma:** *BE489472* – 0.8 cM – *Pm41* – 1.9 cM – *Xwmc687-3B*{10551}. **c:** Encodes a unique CC-NBS-LRR gene {11454}. GenBank MN395289. Orthologs: in tv: Zavitan (*TRIDC3BG077810*) and Svevo (*TRITD3Bv1G261150.1*), and common wheat cv. Claire, but not in Chinese Spring {11454}.
Pm41 and associated marker alleles showed strongly distored inheritance with reduced frequencies relative to Langdon alleles {10551}.

PM42

Pm42 {10559}. Derived from *T. dicoccoides.* Recessive. 2BS {10559}. **bin:** 2BS-0.75-0.84. **v:** P63 = Yanda 1817/G303-1M/3*Jing 411 {10559}. **tv:** *T. dicoccoides* G303-1M {10559}. **ma:** *BF146221* – 0.9 cM – *Pm42* – *Xgwm148-2B* {10559}.

PM43

Pm43 {10560}. Derived from *Th. intermedium*. 2DL {10560}. **v:** Line CH5025 = 76216-96/TAI7045//2*Jing 411 {10560}; Partial amphiploid TAI7045 {10560}. **al:** *Th. intermedium* Z1141 {10560}. **ma:** *Xwmc41-2D* – 2.3 cM – *Pm43* – 4.2 cM – *Xbarc11-2D* {10560}.

PM44

Pm44 {10790}. 3AS {10790}. **v:** Hombar {10790}. **ma:** Flanked by SSR markers distally located in chromosome arm 3AS {10790}. **CURATOR'S NOTE**: This gene nane was based on a pre-publication request; the publication cannot be located.

PM45

Pm45 {10791}. [*Pm57-6D* {10790}]. 6DS{10791}. **v:** Line NWG0099 {10791}. **v2:** D57{10791}. **ma:** Close linkages are reported in the draft manuscript.

PM46

Pm46 {10847}. Partial resistance. 4DL {10847, 10678}. **bin:** Distal to break point 0.56 FL{10678}. **i:** RL6077 = Thatcher*6/PI250413 {10847,10678}. **v:** Chapingo 48 {11070}. **ma:** Pleiotropic or closely linked with *Lr67/Yr46/Sr55/Ltn3* and aassociated with *Xgwm165-4D* and *Xgwm192-4DL* {10847, 10678}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmenbrane helices {11070}.

PM47

Pm47 {10912}. Reccessive. [*PmHYLZ* {10912}]. 7BS{10912}. **bin:** 7BS1-0.27-1.00. **v:** Hongyanglazi {10912}. **ma:** *Xgpw2119-7B* – 7.5 cM – *BE606897* – 1.7 cM – *Pm47* – 3.6 cM ascob– *Xgwm46-7A* {10912}.

PM48

Pm48 {10935}. Identified as *Pm2a* {11678}. [*Pm46* {10935}]. 5DS {10935}. **bin:** 5DS1. **v:** Tabasco {10935}. **ma:** *Xgwm205-5D* – 17.6 cM – *Pm48* – 1.3 cM – *Xmp510(BE498794)* – 1.8 cM – *Xcfd81-5D* {10935}.

PM49

Pm49 {10938, 10937}. [*Ml5323* {10937}]. 2BS {10937}. **bin:** 2BS-0.84-1.00. **tv:** *T. dicoccum* MG5323 {10937}. **ma:** *Xcau516-2B* – 7.2 cM – *Pm49* – 4.1 cM – *XCA695634* {10937}.

PM50

Pm50 {10942}. 2AL {10942}. **bin:** C-2AL1-0.85. **v:** K2 TRI29907 {10942}. **tv:** *T. dicoccum* M129 {10942}. **ma:** *Xgwm294-2A* – 2.9 cM – *Pm50* {10942}.
K2 is a backcross derivative of German winter wheat cv. Alcedeo with *T. dicoccum* accession M129 as donor of mildew resistance {10942}.

PM51

Pm51 {11026}. Putative *Th. ponticum* derivative. [*PmCH86* {11026}]. 2BL {11026}. **bin:** 2BL6-0.89-1.00. **v:** CH7086 {11026}. **ma:** *Xwmc332-2B* – 3.2 cM – *Pm51* – 1.5 cM – *BQ246670* {11026}.

PM52

Pm52 {11029}. [*MlLX90* {11028, 11029}]. 2BL {11028}. **bin:** 2BL-0.35-0.50. **v:** DH51302 {11715}; Jimai 22 {11714}; Liangxing 99 {11028, 11029, 11716}; Shimai 26 {11715}. **ma:** *Xcfd73-2B* – 5.3 cM – *Xwmc441-2B* – 0.2 cM – *XBE604758* – *Pm52* – 2.9 cM – *Xgwm120-2B* {11028}; *XBE604758* – 5.5 cM – *Xics34* – *Pm52* – 0.8 cM – *Xics30* – 6 additional *ics* markers – *Xgwm120* {11029}. Located in a 533.6 – 612.9 Mb interval {11716}.

PM53 **Curator's note:** A publication of this gene could not be located.

Pm53 {11045}. Derived from *Ae. speltoides*. [*PmNC-S16* {11045}]. 5BL {11045}. **v:** NC09BGTS16, PI669386 = Saluda*3/TAU829 {11045}. **al:** *Ae. speltoides* TAU829 {11045}. **ma:** *Xwmc759/Xgwm499-5B/IWA6024* – 0.7 cM – *Pm53* – *IWA2454* – 5.9 cM – *Xgwm408-5B* {11045}.

PM54

Pm54 {11050}. [*PmA2K* {11050}]. 6BL {11050}. **bin:** 6BL-0.450-1.00. **v:** AGS2000 PI612956 {11050}. **ma:** *Xgpw2344-6B* – 1.00 cM – *wPt-9256* – *Pm54* – 1.2 cM – *Xbarc134-6B* {11050}.

PM55 **c:** CC-NBS-LRRR {11742}.

Pm55 {11108}. Derived from *Dasypyrum villosum*. [*Pm5VS* {11108, 11109}]. 5AS (5VS.5AL) {11108}. 5DS (5VS.5DL) {11109}. **v:** NAU421 {11108}; NAU415 {11108, 11109}. **ma:** A 730 bp 5*EST-237* band is associated with chromosome 5VS {11109}; 5VS also carries puroindoline genes; therefore all lines with this gene will be soft (5VS.5DL) or supersoft (5VS.5AL).
The backgrounds of NAU415 and NAU 421 are Chinese Spring. The PM resistance conferred by this gene gradually increases from the third leaf stage and reaches an immunity level by the seventh leaf stage.

Pm55**a** {11742}. *Pm55* {11108}. Growth stage and tissue-specific. [*Pm5VS*#4S{11108, 11109}]. 5AS (5AL 5VS#4S) {11108}. **v:** NAU185 {11742}.
This allele has a closely linked dominant inhibitor {11742}.

The backgrounds of NAU415 and NAU 421 are Chinese Spring. The PM resistance conferred by this gene gradually increases from the third leaf stage and reaches an immunity level by the seventh leaf stage.

Pm55b {11742}. 5DS (5DL.5VS) {11109}. **v:** NAU421 {11108}; NAU415 {11108, 11109}; NAU {11742}; TF5V-1 {11742}. **ma:** A 730 bp 5*EST-237* band is associated with chromosome 5VS {11109}.

5VS also carries puroindoline genes; therefore all lines with this gene will be soft (5VS.5DL) or supersoft (5VS.5AL).

Pm55a and *Pm55b* interact differently with the *Pm55a* inhibitor *SuPm55* {11742}.

PM56

Pm56 {11155}. Derived from *S. cereale*. 6AS (T6AL.6RS) {11155}. **v:** LM47-6 {11155}. **al:** *S. cereale* cv. Qinling {11155}.
Study of misdivision products from a double monosomic 6A, 6R located *Pm56* to the subterminal region of 6RS {11155}.

PM57

Pm57 {11159}. Derived from *Ae. searsii*. 2BL (T2BS·2BL-2S^S#1) {11159}. **v:** Line 89-346, TA5108{11159}; Line 89(5)69, TA5109 {11159}; Line898(6)88 {11728}; TA5109 {11728}. **ad:** BCS+2S^S#1 TA3581 {11159}. **c:** Encodes a tandom kinase with putative kinase-pseudokinse domains followed by a von Willebrand domain and orthologue of *Lr9* (88.3% amino acid similarity) {11728}. Line 89-346 has a 28% distal *Ae. searsii* segment and line 89(5)69 has a 33% distal *Ae. searsii* segment {11159}.

PM58

Pm58 {11171}. Derived from *Ae. tauschii*. [*PmTA1662* {11171}]. 2DS {11171}. **v:** U6714-A-011, PI 682090 {11320}; U6714-B-056, PI 682089 {11320}. **dv:** *Ae. tauschii* TA1662 {11171}. **ma:** Co-segregation with KASP^{TM}markers *K-TP331370, KTP338253, K-Tp15990* and *K-Tp313873* {11171}. Co-segregating marker *Xkasp68500* developed from *AET2Gv20068500* distinguished TA1662 from random common wheat accessions {11749}.

PM59

Pm59 {11214}. [*Pm181356* {11214}]. 7AL {11214}. **bin:** 7AL15-0.00-1.00. **v:** PI 181356 {11214}. **ma:** *Xwmc525-7A* – 1.8 cM – *Xmag1759* – 0.5 cM – *Pm18156* – 5.7 cM – *Xmag1714* – 20.0 cM – *Xcfa2257-7A* {11214}.

PM60

Pm60 ex *T. urartu* {11250}. [*PmR2* {11250}]. 7AL {11250}. **bin:** 7AL16-0.86-1.00. **dv:** PI 428196 {11250}; PI 428210 {11250}; PI 428215{11250}; PI 428306 {11250}; PI 428309 {11250}; PI 428310 {11250}; PI 538737 {11250}; PI 538751 {11250}. **c:** NBS-LRR; the sequence in PI 428309 (GenBank MF996807) is 4,365 bp. The sequence in PI 428215 (designated *Pm60a*; GenBank MF996808) has a 240 bp insertion relative to PI 428309 whereas PI 428210 (designated *Pm60b*, GenBank MF996806) lacks the same sequence, which corresponds to two LRRs {11250}. Transformants with *Pm60a* conferred resistance to a lower number of *Bgt* isolates than transformants with *Pm60* or *Pm60b* {11663}.

PI 428210 carries an adjacent gene (possibly a paralog) that conferred resistance to a *Bgt* isolate virulent to *Pm60* and *Pm60b* {11663}.
Two of three resistant haplotypes of *Pm60* were transferred to common wheat (11651}.

Pm60 ex *T. dicoccoides* {11551}. *TRIDC7AG077150*. **v:** 3D249 (derivative of WE18) {11608}, Ruta {11551}. **itv:** WEW G18-6 / LDN RIL 154 {11551}; G18-16 {10886, 11551}. **t*v:*** *MlWE18* {11608}; *MlIW72* {10545, 11609}, *MlIW172* {11095}, *PmG16* {10886, 11551}. **v** Ruta {11551}. **ma:** *Xuhw386-7A* – 0.3 cM – *Pm60* – 1.4 cM – *Xuhw-7A* {11551}.
Further resistant haplotypes were identified for *MlIWE6* (MW375704) and *MlIW113* and *PmIW226* (MW375704) {11761}. Evidence of allelic variation was also presented {11761}.
The cloned *PM60* sequences from the diploid and tetraploid sources differed by 8 SNP that changed 6 amino acids {11551}.

***pm60*.** **dv:** G1812 {11250}.

Gene *PmU*, flanked by *Xwmc273-7A* and *Xpsp3003-7A*, was transferred to common wheat from *T. urartu* accession UR206 (JIC 10100015) {11402}. *Xwmc273-7A* was 7.8 cM proximal to *PM60* {11250}.

PM61

Pm61 {11290}. 4AL {11290}. **bin:** 4AL4-0.8-1.00. **v:** Xuxusanyuehuang {11290}. **ma:** *Xgwm160-4A* – 0.23 cM – *Pm61* – 0.23 cM – *Xicsx79* {11290}.
Pm61 was considered to be at a different locus to *MlIW30*, a dominant gene in *T. dicoccoides* accession IW30 and its hexaploid derivative Line 2L6 {11289}.

PM62

Pm62 {11321}. [*Pm2VL* {11321}.] Adult-plant resistance. 2BS·2VL#5 {11321}. **v:** NAU1823 {11321}. **ma:** *X2L4g9P4/Hae111* {11159}.

PM63

Pm63 {11331}. *Pm628024* {11331}. 2BL {11331}. **bin:** 2BL6-0.89-1.00. PI 628024 {11331}. **v:** PI 628024 {11331}. **ma:** *Xwmc175-2B* – 1.7 cM – *Xstars419-2B* – 0.6 cM – *Pm63* – 1.1 cM – *Xbcd135.2 – 2B*; 710.3 – 723.4 in the CS RefSeq 1.0 {11331}.

PM64

Pm64 {11346}. [*PmWE35* {11346}]. 2BL {11346}. **bin:** 2BL4-0.5-0.89. **v:** WE35 {11346}. **tv:** *T. dicoccoides* G-573-1 {11346}. **ma:** *Xwmc175-2B* – 1.12 cM – *Pm64/Xgwm47-2B* – 2.18 cM – *Xwmc332-2B* {11346}. Complete repulsion linkage with *Yr5* in 644 F_3 lines {11346}.

PM65

Pm65 {11356}. [*PmXM208* {11356}]. 2AL {11356}. **v:** Xinmai 208 {11356}. **ma:** *Xhbg327-2A* – 4.4 cM – *XresPm4/XTaAetPR5* – 0.6 cM – *PmXM208* – 1.6 cM – *Xbarc122-2A* {11356}. An allelism test of *Pm65* and *Pm4a* showed a recombination value of 10.3 cM based on the frequency of susceptible F_2 plants {11356}.

Putative *Pm65* allele {11752}. *Pm351817* {11752}. **v:** PI 351817 {11752}. **ma:** *Stars-KASP662* (771.21 Mb, CS RefSeq 2.1) – 0.9 cM – *Pm351817* – 0.6 cM – *Stars-KASP656* (771.81 Mb). 2.5 cM proximal to a marker for *Pm4* {11752}.

PM66

Pm66 {11364}. 4BS (4BL·$4S^{l}$#7S) {11364}. **v:** TA3465 {11364}. **al:** *Ae. longissima* (unknown accession). **ma:** $4S^{l}S$ markers developed in {11364}.

PM67

Pm67 {11426 *Pm1V#5* {11426}. 1D (1DL.1VS#5) {11426}. **v:** NAU18105 {11426}. **su:** NAU18103 (1V(1D)) {11426}. **al:** *Dasypyrum villosum* 011140 {11426}.
Lines with *Pm67* showed complete immunity as seedlings but adult plants produced some conidial development on leaves whereas the culms, leaf sheaths and spikes were mildew-free {11426}.

PM68

Pm68 {11466}. 2BS {11466}. **bin:** 2BS-0.84-1.00. **tv:** *T. durum* TRI 1796 {11466}. **ma:** *Xdw04* (TRITD2Bv1G010030, chr2B:21587671-21591163) – 0.22 cM – *PM68* – 0.22 cM – *Xdw12* (TRITD2Bv1G010880, chr2B:23374401-23375310) – 3.0 Mb – *PM26/Xcau516-2B* (TRITD2Bv1G012960, chr2B:26398438-26414596) – 36.8 cM – *PM42* {11466}.

PM69

Pm69 {11541}. *PmG3M* {11302}. 6BL {11302}. **bin:** 6BL-0.7-1.00. **v:** Ruta + Pm69 {11627}. **itv:** Svevo + Pm69 {11627}. **tv:** *T. dicoccoides* G-305-3M {11302, 11627} TD116180 (University of Haifa Wild Cereal Gene Bank), CGN19852 (Netherlands Centre for Genetic Resources) {11541}. **ma:** *Xgpw7262-6B* – 6.9 cM – *PM69* (*PmG3M*) – 4.5 cM – *Xedm149-6B* {11302}. **c:** *Pm69* comprises Rx_N with RanGAP interaction sites, NB-ARC, and LRR domains {11627}. GenBank KY825226.1. Collinearity analyses indicated homoeology with *SR13* {11627}.

PM70

Pm70 [{11724}]. 3BS (by association with *Sr2* and *Lr27* {11723}. **s:** CS (Hope 3B) {11723}. **v:** Hope {11723}. **tv:** Yaroslav emmer {11723}. **ma:** Association of *Pm70* with *Sr2, Sr27* and *Pbc1* {11723}.

MLO

Mlo mutants in barley confer durable resistance to powdery mildew; most *mlo* mutants have deleterious effects on plant growth and morphology, but a few selected for negligible deleterious effects have been widely used in barley breeding. Most species have *MLO* homologs. *MLO* is considered a gene for susceptibility since overexpression leads to increased haustorial index {11743}. ***TaMLO-A1***, ***TaMLO-B1*** and ***TaMlo-D1*** located in chromosome arms 5AL, 4BL and 4DL {11743} are 98% and 99% identical at the nucleotide and protein levels, respectively {11744}.
Plants with combined *Tamlo-A1*, *Tamlo-B1* and *Tamlo-D1* mutations were resistant to powdery mildew {11744} but exhibit abnormal growth {11745}. A mutant with a 304 bp targeted deletion in *TaMLO-4B* had normal phenotype when combined with the mutant orthologs {11745}. This mutation led to ectopic activation ofa closely linked gene *TaTMT3B* (*Tonoplast monosaccharide transportase 3*, *TraesCS4B02G322000*) leading to a normal plant phenotype {11745}.

<u>Genotype lists</u>: Chinese wheats{1608, 572}; Finnish wheats {0028}; French wheats {1629}; Hungarian wheats {02104}; Western Siberian wheats{1101}. Others {0313, 10405, 10406}

Complex genotypesDrabent {heterogeneous} *Pm2 Pm4bPm9/Pm1 Pm2 Pm4b Pm9* {1287};
Nemares *Pm1 Pm2Pm4b Pm6 Pm9* {1287};
Planet, Sappo & Walter *Pm1 Pm2 Pm4b Pm9* {096,097,540,1287,1428} Scandinavian wheats {10681}.

3.4.2. Suppressors of *PM* resistance genes

Some wheats which on the basis of cytological and rust tests carry 1RS from Petkus rye, do not express resistance due to presence of a suppressor {385}. Zeller & Hsam {1625} located a suppressor of *Pm8* and *Pm17* in chromosome 7D of Caribo. Mildew resistance was suppressed in Florida, Heinrich, Ikarus, Olymp and Sabina, which are derivatives of Caribo with 1BL.1RS. According to Ren *et al.* {1209}, *SuPm8* does not suppress *Pm17*. Hanusova *et al.* {492} listed 16 wheats that carry a suppressor of *Pm8*; 111 wheats did not carry the suppressor. In contrast, a high frequency of suppression occurred in CIMMYT wheats {108}, {1208}. Further genotypes are identified in {491}, {11025}. Although Line 81-7241 carries *Pm8* as well as *Pm23*, evidence was presented to indicate that *Pm8* was suppressed in Line 81-7241 {1618} and, by inference, indicated that Chinese Spring possessed *SuPm8*.

SuPm8 {1209}. 1AS {1209}. **v:** Wheats with *Gli-A1a* {1209} including CS; Lists in {1208}, {491, 108}.
Pm8 was suppressed when locus *Pm3* is transcribed (including Chinese Spring and Thatcher which have no currently detectable *Pm3* resistance alleles) {10828}.

3.4.3. Temporarily designated genes for resistance to *Blumeria graminis*

PmHHXM. *PmXNM* {11748}. **v:** Xiaonanmai {11748}. **ma:** *PmXnm* was flanked by markers *caps213923* (744.11 Mb) and *kasp511718* (744.41 Mb) {11748}.

PmHYM [{11732}]. *pmHYM* {11732}. Recessive. 7BL {11732}. **v:** Hongyoumai {11732}. **ma:** Allelic with *Pm5e* and *mlXBD* and differed in specificity from lines carrying *Pm5a, Pm5b, Pm5e* and *MlXBD* {11732}.

Pm2Mb {11662}. 2DL {11662}. **v:** 2DL-$2M^bL$ translocation lines. **ad:** CS + $2M^b$ TA7733 {11662}. **ma:** Mapped to a FL 0.49 – 0.667 region containing 19 2Mb-specific markers {11662}.

PMTR1 & PMTR3I. *SECCE6Rv1G0382290.*

PmTR1 & ***PmTr3*** {11686}. 6RS {11686}. **v:** TR1 and TR3 were described as stable wheat lines derived from different triticale sources; TR1 had post-seedling ('age-dependent') resistance and TR3 had all stage resistance. **c:** These genes were shown to be allelic and the different responses were attributed to differences in expression {11686}. Both proteins had similarity to Pm12 and Pm21, but differed from Pm8, Pm17 and Pm50 {11686}.

PmV {11703}. T6DL.6VS#4S {11703}. **v:** Yangmai 22 {11703}.

Pm6Sl {11597}. Derived from *Ae. longissimum*. 6A and 6B {11597}. **ad:** CS + $6S^l$#3 TA7548 {11597}. **v:** T27 (Ti6AS.6AL-$6S^l$#3-6AL) {11597}; R43 (T6BS.6BL-$6S^l$#3^l#3 {11597}. **al:** *Ae. longissimum* TA1910 (11597). **ma:** Mapped to a distal $6S^l$#3 interval of 42.8 Mb flanked by markers *Ael58410* and *Ael5799* {11597).
Pm6S^l conferred resistance to 28 of 30 Chinese *Bgt* isolates {11597}.

Pm10V-2 {11380}. 5DS {11380}. **bin:** 5DS-0-0.63. **v:** 10V-2 {11380}. **ma:** *Xbwm25-5D/Xswgi066-5D* – 1.2 cM – *Pm10V-2/*several markers – 1.2 cM – *Xcfd-5D* {11380}.

Pm2026 {10604}. [*pm2026* {10604}]. Recessive {10604}. 5A^{m}L {10604}. **bin:** 5AL17-0.78-1.00 {10604}. **dv:** *T. monococcum* TA2026 {10604}. **ma:** *Xcfd39-5A* – 1.8 cM – *Xcfd1493-5A/Xmg2170-5A* – 0.9 cM – *Pm2026* – 2.5 cM – *Xgwm126-5A* {10604}.

PmAF7DS {11291}. 7DS {M10891}. **v:** Arina {11291}. **ma:** *Xpsr160-7D* – 1.3 cM – *Xgwm350a-7D* – 4.7 cM – *PmAF7DS* – 9.9 cM – *Xbarc184/Xgwm111-7D* {11291}.
Three of 61 Israeli *Bgt* isolates were avirulent: all three isolates were from tetraploid wheat accessions. It is possible that the gene may be present in many common wheat accessions.

PmAS846 {10926}. 5BL {10926}. **bin:** 5BL14-0.75-0.76. **v:** N9134 {10926}; N9738{10927}. **tv:** *T. dicoccoides* AS846 {10926}. **ma:** *XMAG2498-5B* – 1.3 cM – *Pm36/XBJ261635* – 1.1 cM – *PmAS846* – 1.3 cM – *XFCP1-5B* {10927}.

PmCn17 {10686}. 1BS=1BL.1RS {10686}. **v:** Chuannong 17 {10686}. **al:** *S. cereale* R14 {10686}.

pmDHT {11447}. Recessive. 7BL {11447}. **v:** Dahongtou S761 {11447}. **ma:** *XBE443877/Xwmc526-7B* – 0.8 cM – *pmDHT* – 0.8 cM – *Xgwm611/Xwmc581-7B* – 0.9 cM – *XBF473539/Xgwm577-7B* – 0.9 cM – *Xgwm577-7B* {11447}.

PmG3M {11302}. 6BL {11302}. **bin:** 6BL-0.7-1.00. **tv:** *T. dicoccoides* G-305-3M {11302}. **ma:** *Xgpw-6B* – 13.6 cM – *PmG3M* – 3.5 cM – *Xuhw213-6B* – 5.7 cM – *Xedm149-6B* {11302}.

PmJM23 {11445}. 5DS {11445}. **v:** Jimai 23 {11445}. **ma:** *Xytu3004* – 0.7 cM – *PmJM23/Xytu201/Xbwm21/Xcfd81-5D* – 1.8 cM – *Xswgi068/Xbwm20* {11445}.

PmG16 {10886}. 7AL {10886}. **bin:** 7AL16 0.86-0.90. **tv:** *T. dicoccoides* G18-16 {10886}. **ma:** *Xgwm1061/Xgwm344-7A* – 1.2 cM – *PmG16/wPt-1424/wPt6019* – 2.4 cM – *wPt-0494/wPt9217/Xwmc809-7A* {10886}.

PmHNK {10706}. 3BL {10706}. **v:** Zhoumai 22 {10706}. **ma:** *Xgwm108-3BL* – 10.3 cM – *PmHNK* – 3.8 cM – *Xwmc291-3BL* {10706}.

PmHNK54 {10897}. 2AL {10897}. **bin:** 2AL1 C-0.85. **v:** Zheng9754{10897}. **ma:** *Xgwm372-2A* – 5.0 cM – *PmHNK54* – 6.0 cM – *Xgwm312-2A* {10897}.

PmHo {11176}. 2AL {11176}. **v:** Mv Hombar {11176}. **ma:** *XwPt-665330* – 0.3 cM – *PmHo* – 0.1 cM – *XwPt-3114* {11176}.

PmHHXM {11565}. 4AL {11565}. **v:** Honghuaxiaomai {11565}. **ma:** Located in a 1.77 Mb (0.18 cM) region flanked by *Xkasp475200* and *Xhnu522* {11565}.

PmKN0816 {11598}. 2BL {11598}. **v:** KN0816 {11598}. **ma:** Mapped to a region of chromosome carrying *Pm6*, *Pm33*, *Pm51*, *Pm64* and *PmQ* but distinguished from each other by specificity {11598}.

PmLS5082 {11629}. 2BL {11629}. v: LS5082 {11629}. ma: Located in the interval 710.3 – 711.0 Mb {11629}.

PmLX66 {11162}. *PmLX66* was allelic with *Pm2* {11162}. 5DS{11162}. **v:** Liangxing 66 {11162}. Identified as *Pm2a* {11503}.

PmLK906 {10476}. Resistance is recessive {10476, 10477}. 2AL{10476, 10477}. **v:** Lankao 90(6)21-12 {10476}; Zhengzhou 9754{10476}. **ma:** *TacsAetPR5-2A/Pm4* – 3.9 cM – *Xgwm265-2A* – 3.72 cM – *Pm39* – 6.15 cM – *Xgdm93-2A* {10476, 10477}; *TacsAetPR5-2A* was converted to an STS marker {10477}

PmNJ3946 {11677}. 3AS {11677}. **dv:** *T. monococcum* Line NJ3946 {11677}; PI 191097 = TA2032 {11677}. **ma:** *Xbarc294-3A* – 1.1 cM – *PmNJ3946* – 0.8 cM – *Xwgrc5153-3A* {11677}.

PmPBDH {11647}. 4AL {11647}. **v:** PBDH {11647}. **ma:** Mapped to a 3.2 cM interval, 719.1-726.2 Mb (CS RefSeq 1.0) {11647}.
Cytology failed to detect a putative *Agropyrum cristatum* segment in PBDH {11647}.

PmPs5A {10205}. 2AL{10205}. **v:** AM4{10205}. **tv2:** *T. turgidum* subsp. *carthlicum* pS5 *Pm33*{10205}. **ma:** *Xgwm356-2A* - 10.2 cM - *PmPS5A*; *PmPS5A* is located at or near the *Pm4* locus{10205}.

PmQ {11461}. Recessive. **v:** Hongxinmai {11461}. **ma:** *Xstars419-2B* – 0.6 cM – *Xicsq405 2B* – 0.8 cM – *PmQ* – 0.2 cM – *XWGGBH913-2B* {11461}.
PmQ is very close to *Pm51, Pm63* and *Pm64*.

PmXQ-0508 {11734}. 2AS {11734}. **v:** Line XQ00508 {11734}. **ma:** Located to 226.7 kb interrval {11734}. All F_2 plants in crosses with lines having *Pm26* (1,226 plants), *Pm42* (1,198 plants) and *Pm26* (1,583 plants) were resistant to the test isolate but the response arraye of the lines appeared to be diferente {11734}.

PmSGD {11453}. Recessive. 7BL {11453}. **v:** Shangeda {11453}. **ma:** *SNP2-58* – 0.4 cM – *PmSGD* – 0.8 cM – *SNP2-46* {11453}.

PmTb7A.1{11130}. 7AL {11130}. **bin:** 7AL 18-0.90-1.00. **dv:** *T. boeoticum* PAU5088 *PmTb7A.2* {11130}. **ma:** Mapped to a 4.3 region flanked by *wPt4553* and *Xcfa2019-7A* {11130}; Estimated to be 46 cM proximal to *Pm1* {11130}.

PmTb7A.2 {11130}. 7AL {11130}. **dv:** *T. boeoticum* PAU5088 *PmTb7A.1* {11130}. **ma:** Mapped to a 0.8 cM region flanked by *MAG1759* and *MAG2185b* in the region of *Pm1* {11130}.

PmTm4 {10961}. 7BL {10961}. **bin:** 7BL10-0.78-1.00. **v:** Tanmai4 {10961}. **ma:** *Xgwm611-7B* – 7.0 cM – *PmTm4* – 14.6 cM – *Xest92* – 2.9 cM – *Xbarc1073/Xbarc82-7B* {10961}; *XWGGC6892* – 0.6 cM – *PmTm4/XWGGC5746* – 0.03 cM – *XWGGC891* {11452}.

PmTx45 {11374}. Recessive. 4BL {11374}. **bin:** 4BL5-0.85-1.00. **v:** Tian Xuan 45 {11374}. **ma:** *Ax-110673642* – 3.0 cM – *PmTx45* – 2.6 cM – *ILP4B01G266900* {11374}.

PmU {11251}. 7AL {11251}. **dv:** UR206 {11251}. **ma:** *Xwmc273-7A* – 2.2 cM – *PmU* – 3.8 cM – *Xpsp3003-7A* {11251}.
PmU was transferred to, and was effective in, common wheat.

PmW14 {11162}. *PmW14* is allelic with *Pm2* {11162}. 5DS {11162}. **v:** Wennong 14 {11162}. Identified as *Pm2a* {11503}.

PmWE99 {11166}. Derived from *Thinopyrum intermedium*. 2BS{11166}. **bin:** 2BS-0.84-1.00. **v:** WE99. **ma:** *Pmwe99* – 10.4 cM – *Xgwm148-2B* – 3.1 cM –*Xbarc55-2B* {11162}.
GISH failed to detect alien chromatin.

Pmx {11009}. Reccessive. 2AL {11009}. **bin:** 2AL1-0.58-1.00. **v:** Xiaohongpi {11009}. **ma:** *Xhbg327-2A* – 0.6 cM – *Pmx/Xsts-bcd1231* – 8.9 cM – *XresPm4/Xgpw4456-2A* {11009}.
This gene and close markers showed distorted segregation ratios and some discrepancy of markers relative to *Pm4* alleles {11009}.

PmY39 {10367}. 2U(2B) {10367}. **su:** Laizhou 953*4/Am9 (Am9 = *Ae. umbellulata* Y39/*T. turgidum* ssp. *carthlicum* PS5) {10367}. **dv:** *Ae. umbellulata* Y39 {10367}. **ma:** Associated with 2U markers *Xgwm257, Xgwm296* and *Xgwm319* {10367}.

PmYm66 {10619}. 2AL {10619}. **v:** Yumai 66 {10619}. **ma:** *XKsum193-2A* – 2.4 cM & 3.6 cM – *PmYm66* {10619}.

Ml3D32 {10892}. 5BL {10892}. **bin:** 5BL 0.59-0.76. **tv:** *T. dicoccoides* I222 {10892}. **v:** 3D232 {10892}. **ma:** *Xwmc415-5B* – 1.3 cM – *Ml3D232* – 3.3 cM – *CJ832481*{10892}; Co-segregation with 8 EST markers including an NBS-LRR analogue {10892}.

MlAB10 {10873}. 2BL {10873}. **bin:** 2BL6 0.89-1.00. **v:** NC97BGTAB10, PI 604036 {10873}. **tv:** *T. dicoccoides* PI 471746 {10873}. **ma:** *Xwmc445-2B* – 7 cM – *MlAB10*{10873}.

Ml-Ad {854}. **v:** Adlungs Alemannen {854}.

Ml-Br {854}. **v:** Bretonischer Bartweizen {854}.

Mld {96}. 4B{97}. **v2:** Halle 13471 *Pm2* {96}; H8810/47 *Pm2* {96}; Maris Dove *Pm2* {96}. **tv:** *T. durum* line {96}.

Ml-Ga {854}. **v:** Garnet {854}; Many old German cultivars {854}.

MlHLT {18057}. *Pm24* {11414}. 1DS {11257}. **v:** Hulutou {11257}. **ma:** *Xgwm-1D* – 1.7 cM – *Xwggc3026* – 1.5 cM – *MlHLT* – 2.1 cM – *Xwggc3148* – 4.0 cM – *Xcfd83-1D* {11257}.

MlIW72 {10545}. See *Pm60.* 7AL {10545}. **bin:** FL 0.86 {10545}. **tv:** *T. dicoccoides* IW72 {10545}. **ma:** *Xmag1759-7A* – 8.2 cM – *MlIW72* – 3.3 cM – *Xmag2185-7A* – 1.6 cM – *Xgwm344-7A* {10545}.

MlIW30 {11289}. [*MLIW30* {11289}]. 4AL {11289}. **bin:** Line 2L6 {11289}. **v:** Line 2L6 {11289}. **tv:** *T. dicoccoides* IW30 {11289}. **ma:** *Xbarc78-4A* – 1.00 cM – *XB1g2020.2* – 0.1 cM – *MlIw30* – 0.1 cM – *XB1g2000.2* – 2.6 cM – *Xgwm350-4A* {11289}.

MlIw170 {10921}. 2BS. **bin:** 2BS3-0.84-1.00 {10921}. **tv:** *T. dicoccoides* IW170 {10921}. **ma:** *XcauG2* – 0.6 cM – *MlIw170/Xcfd238-2B* – 2.15 cM – *XcauG8/BF201235/Xwmc243-2B* {10921}; *Iw1* – 18.77 cM – *MlIw170* {10921}.
This gene is located in the same region as *Pm26* {10921}.

MlIW172 {11095}. 7AL {11095}. **bin:** 7AL-16-0.86-0.90. **tv:** *T. dicoccoides* IW172 {11095}. **ma:** *WGGC4664/WGGC4665/WGGC4668* – 0.44 cM – *MlIW172* – 0.7 cM – *WGGC4659* {11095}.

Mljy {0339}. Recessive, hemizygous-effective {0339} 7B {339}. **v2:** Jieyan 94-1-1 *Pm8* {0339}.

Mlm2033 {10393}. 7AL {10393}. **dv:** *T. monococcum* TA2033 {10393}. **ma:** *Xmag1757/Xmag2185* – 2.7 cM – *Mlm2033/Xmag2185* – 1.3 cM – *Xgwm344-7A* {10393}; *Xmag1757* – 5.9 cM – *Mlm2033/Xmag2185/Xgwm344/Xgwm146-7A* – 4.7 cM – *Xmag1986* {10393}; *Xmag1757/Xmag1714/Xmag1759* – *Mlm2033* – 0.9 cM – *Xmag2185/Xgwm344-7A*{10393}; *Xwgrc353/Xwggc4659* – 0.84 cM – *Mlm2033/Xmag8626/Xmag9060/Xmag2185/Xmag5240* – 0.06 cM – *Xmag8415/Xmag8220* {11190}.

Mlm80 {10393}. 7AL {10393}. **dv:** *T. monococcum* ssp. *aegilopoides* M80 {10393}. **ma:** *Xmag1757/Xmag1759* – 3.6 cM – *Mlm80* – 0.7 cM – *Xmag2166/Xgwm344-7A* {10393}; *Xwggc4655* – 0.29 cM – *Mlm80* – 0.57 cM – *Xwgrc253/Xwgrc271* {11190}.
Mlm2033 and *Mlm80* appeared to be allelic and their relative locations suggest they are allelic with *Pm1* {10393}.

MlNFS10 {11666}. 4AL {11666}. **tv:** *T. turgidum* ssp. *dicoccoides* NFS10 {11666}. **ma:** Located to a 0.3 cM interval of 2.1 Mb (729275816-731365462) in CS refseq 1.0 {11666}.
Considered to be located at a different locus to *Pm61* and *MlIW30* {11666}.

MlNCD1 {11004}. 7DS {11004}. **bin:** 7DS4-0.61-1.00 {11004}. **v:** NC96BGD1 PI597348 {11004}; Saluda*3/TA2570 {11004}. **ma:** *Xgwm635-7D* – 5.5 & 8.3 cM – *MlNCD1* – 16.2 cM & 13.6 cM – *Xgpw328-7D*{11004}.

mlRd30 {10175}. Reccesive 7AL {10175}. **v:** RD30 {10175}; TA2682c {10175}. **ma:** *Xgwm344-7A* – 1.8 cM – *mlRD30* – 2.3 cM – *Xksuh9-7A* {10175}.
TA2682c carries a second dominant gene located in chromosome 1A {10175}.

Mlre {1220}. 6AL {0142}. **v2:** RE714 *Pm4b* {0142, 1220}. **tv:** *T. dicoccum* 119 {1220}. *Mlre* showed a residual effect on the quantitative expression of APR in the presence of *B. graminis* pathotypes considered virulent for *Mlre* in standard seedling tests {0016}. In addition to *Mlre*, a QTL for resistance effective at the seedling stage was associated with microsatellite marker *Xgwm174-5D* {0142}.

Mlsy {339}. Recessive, hemizygous-effective {0339} 7B {0339}. **v:** Siyan 94-2-1 {0339}.

MlUM15 {11216}. Derived from *Aegilops neglecta.* 7AL {11216}. **bin:** 7AL15-0.99-1.00. **v:** NC09BGTUM15 {11216}. **al:** *Ae. neglecta* TTCC 223 {11216}. **ma:** *Xwmc525-7A*/*IWA8057* – 0.7 cM – *Xcfa2257-7A* – 0.4 cM – *MlUM15* – 0.8 cM – *Xcfa2240-7A* – 2.8 cM – *Xmag2185* – 3.4 cM – *IWA29295* – 4.0 cM – *IWA4434* {11216}.

MlWE74 {11589}. 2BS {11589}. **v:** WE74 {11589}. **tv:** *T. dicoccoides* G-748-M {11589}. **ma:** Mapped to a 799.9 kb region corresponding to physical region 25.48-26.28 in CHr2_Zavitan v2.0 (26.59-27.01 in IWGSC RefSeq v1.0) {11589}. The relationship to *Pm26* and *MlIW170* was not established {11589}.

Mlxbd {0259}. Recessive and hemizygous-effective {0258} 7B {0259}. **v:** Xiaobaidong {0258}.

MlTd1055 {10029}. **tv:** *T. dicoccoides* 1055 {10029}.

MlWE74 {11665}. 2BS {11665}. **v:** WE74 = YD1817/G-748-M//7*ND01 {11665}. **tv:** *T. dicoccoides* G-748-M {11665}. **ma:** Co-segregated with *WGGBD425* {11665}.Located in the same region as *Pm26, MlIW170*, and *MlWE74* {11665}.

Mlzec1 {10127}. [*MLZec* {10127}]. 2BL {10127}. **v:** Zecoi 1 = Ralle*3/*T. dicoccoides* Mo49 {10127}. **tv:** *T. dicoccoides* Mo49 {10127}. **ma:** Distally located in chromosome 2BL {10127}; *Xwmc356-2B* – 2.0 cM – *PmZec1* {10127}.

Ml92145E8-9 {11436}. 2AL {11436}. **bin:** 2AL1-0-0.85. **v:** Line 92145E8-9 {11436}. **ma:** *Xwmc181-2A* – 9.3 cM – *Xsdauk682-2A* – 2.8 cM – *Ml92145E8-9* – 0.8 cM – *Xsdauk-2A* – 18.7 cM – *Xgwm356-2* {11436}.

Unnnamed resistance gene {11612}. *WTK4* {11612}. 7D {11612}. **dv:** *Ae. tauschii* Ent-079 {11612}; Ent-080 {11612}; Ent-085 {11612}; Ent-102 {11612}. **v:** Synthetic derivatives of the above diploid accessions {11612}. **ma:** Located within a 60 kb insertion relative to the AL8/78 reference genome in region 4.76 – 5.06 Mb {11612}. **c:** Wheat tandom kinase; MW295405 {11612}.

A normally inherited resistance to powdery mildew in wheat-*Th. intermedium* translocation line 08-723 (?B-?S^t.6AL) was reported in {11035}.

3.4.4. QTLs for resistance to *Blumeria graminis*

QTL: Several QTLs were detected in two RE714/Hardi populations when tested at two growth stages and with different cultures over three years. The most persistent and effective QTL was located in the vicinity

of *Xgwm174-5D* {0272}. Three QTLs, *QPm.vt-1B*, *QPm.vt-2A* and *QPm.vt-2B*, with additive gene action, accounted for 50% of the variation in a population developed from Becker/Massey {0284}. These QTLs were confirmed by the addition of extra markers to the Becker/Massey map and in a separate analysis of USG 3209 (A Massey derivative)/Jaypee (susceptible) {10505}. USG 3209 possessed *Pm8* (1BL.1RS) and an unknown specific resistance factor and their combination had a positive effect on APR even though neither was effective against the races used to identify the QTL {10505}. QTLs on chromosomes 1A, 2A, 2B, 3A, 5D, 6A and 7B were detected in a RE714/Festin population in multiple locations and over multiple years. The QTL on chromosome 5D was detected in all environments and all years and was associated with markers *Xgwm639-5D* and *Xgwm174-5D*. Resistance was contributed by RE714. A QTL coinciding with *MlRE* on 6A was also detected in all environments. The QTL on chromosome 5D and 6A accounted for 45% to 61% of the phenotypic variation {0354}.
Ae. tauschii CIAe8 **(R) /** ***Ae. tauschii*** **PI 574467 (S):** Resistance conferred by recessive genes *pmAeCI8_2DS* (14.48 – 16.32 Mb) and *pmAeCI8_7DS* {4.72 – 4.98 MB); the former overlapped the location of dominant *Pm58* and the latter was likely *WTK4* located in a ~60 kb insertion and encoding a wheat tandom kinase {11695}.

Avocet R(S)/Saar (R): F6 RILs: QTL located on chromosomes 1BL (close to *Xwmc44-1B*) (*Pm39*), 7DS (*Xgwm1220-7D*) (*Pm38*) and 4BL (*XwPt-6209*) (resistance allele from Avocet R {10481}.

AGS 2000 (*Pm3a* + *Pm8* / Pioneer 26R61 (*Pm8*). *QSuSuPm.uga-1AS(SuPm8)* with an inhibitory effect on powdery mildew response was located at or near *Pm3a*. *QPm.uga-7AL* from Pioneer 26R61 flanked by *Xcfa2257-7A* and *Xwmc525-7A* was in the region of the *Pm1* locus, even though the test culture was virulent for known *Pm1* alleles {11025}.

CI 13227(S) / Suwon 92(R): SSD population: APR (field resistance) was closely associated with *Hg*. *Xpsp2999-1A* and *Xpm3B.1* and *Xpm3B.2* were designed from the *Pm3b* sequence {REF}.

Fukuho-Komugi / Oligoculm: DH population: QTL for adult plant resistance located on 1AS (R^2=22%, *Pm3* region, *Xgdm33 - Xpsp2999*), 2BL (R^2=8%, *Xwmc877.1-Xwmc435.1)* and 7DS (R^2=10%) derived from Fukuho-komugi, and 4BL (R^2=6% at one of two sites, *Xgwm373-Xgwm251*) from Oligoculm {10335}. The QTL on 7DS, flanked by *Xgwm295.1-7D* and *Ltn*, is likely to be *Lr34/Yr18*.

Jingdong 8 / Aikang 58 (R): RIL population: *Pm4a* and several QTL from both parents {11753}.

Liangxing 99 / Zhongzuo 9504: RIL population: A QTL *Qaprpm.caas.2B* in the same region as *Pm52* and APR QTL *Qaprpm.caas.7A* in a 1.3 cM region flanked by *Xicscl726*-7AL and *XicsK128-7A* {11716}.

Lumai 21(R) / Jingshuang 16(S):, F_3 lines: Three QTLs from Lumai 21: *QPm.caas-2BS, Xbarc98-2BS – Xbarc1147-2BS* interval, R^2=0.106-0.206; *QPm.caas-2BL, Xbarc1139-2BL – Xgwm47-2BL* interval, R^2=0.052-0.101; and *QPm.caas-2DL, Xwmc18-2DL – Xcfd233-2DL* interval, R^2=0.057-0.116 {10707}.

RE9001(R) / Courtot(S) RIL population: *QPm.inra-2B* (R^2 = 10.3-36.6%), in the vicinity of *Pm6*, was consistent over environments {10360}. Eleven QTL, detected in at least one environment were identified by CIM {10360}.

SHA3/CBRD(S)/Naxos(R): RIL population: A major QTL on chromosome 1AS accounted for 35% of the phenotypic variation; other QTL from Naxos were on 2DL, 2BL and 7AL. Although SHA3/CBRD possessed a *Pm3* allele suppressed *Pm8* which appeared to be effective in Norway {10934}.

Tianmin 668 / Jingshuang 16: RIL population: Three QTL in chromosome arms 2AS (3,573 – 4.347 Mb), 2BL (56.844 – 70.698 Mb), and 5AL (4.412 – 4.719 Mb) were detected in Tianmin 666; *Pm4d* (2AL) identified in the same line was not effective in the field {11702}.

QPm.sfr-1A {0051}. 1A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr1201-1A* and *Xpsr941-1A* {0051}.

QPm.sfr-1B {0051}. 1B {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xsfr3(LRR)-1B* and *Xpsr593-1B* {0051}.

QPm.sfr-1D {0051}. 1D {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr168-1D* and *Xglk558-1D* {0051}.

QPm.sfr-2A {0051}. 2A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr380-2A* and *Xglk293-2A* {0051}.

QPm.sfr-2D {0051}. 2D {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr932-2D* and *Xpsr331-2D* {0051}.

QPm.sfr-3A {0051}. 3A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xpsr598-3A* and *Xpsr570-3A*{0051}.

QPm.sfr-3D{0051}. 3D {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr1196-3D* and *Xsfr2(Lrk10)-3D* {0051}.

QPm.sfr-4A.1 {0051}. 4A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xgwm111-4A* and *Xpsr934-4A*{0051}.

QPm.sfr-4A.2 {0051}. 4A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xmwg710-4A* and *Xglk128-4A* {0051}.

QPm.sfr-4B {0051}. 4B {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xpsr593-4B* and *Xpsr1112-4B* {0051}.

QPm.sfr-4D {0051}. 4D{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xglk302-4D* and *Xpsr1101-4D* {0051}.

QPm.sfr-5A.1 {0051}. 5A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr644-5A* and *Xpsr945-5A* {0051}.

QPm.sfr-5A.2 {0051}. 5A {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr1194-5A* and *Xpsr918-5A* {0051}.

QPm.sfr-5B {0051}. 5B {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0051}. **ma:** Associated with *Xpsr580-5B* and *Xpsr143-5B* {0051}.

QPm.sfr-6B {0051}. 6B {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xpsr167-6B* and *Xpsr964-6B* {0051}.

QPm.sfr-7B.1 {0051}. 7B {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno {0051}. **ma:** Associated with *Xpsr593-7B* and *Xpsr129-7B* {0051}.

QPm.sfr-7B.2 {0051}. This QTL corresponds to *Pm5* {0051}. 7B {0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xglk750-7B* and *Xmwg710-7B* {0051}.

QPm.ipk-2B {0255}. 2BS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {2055}; Resistance was contributed by Opata {0255}. **ma:** Associated with *Xcdo405-2B* and *Xmwg950-2B* {0255}.

QPm.ipk-4B {0255}. 4B {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}; Resistance was contributed by W-7984 {0255}. **ma:** Associated with *Xcdo795-4B* and *Xbcd1262-4B* {0255}.

QPm.ipk-7D {0255}. 7DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}; Resistance was contributed by Opata {0255}. **ma:** Associated with *Xwg834-7D* and *Xbcd1872-7D* {0255}.

QPm-tut-4A {11154}. 4AL {11154}. **v:** DT4AL-TM Line 8.1 {11154}. **tv:** *T. militinae* (AAGG) {11154}.
The 7G segment carrying this resistance likely replaces most of the 7BS segment known to be part of chromosome 4A {11154}.

PmSE5785 {11084}. Recessive 2DL {11084}. **v:** SE5785, Snipe/Yav79//Dack/Teal/3/*Ae. squarrosa 877* {11084}; NO7728-1 {11084}; NO7728-2{11084}. **ma:** *Xbarc59-2D* – 3.6 cM – *PmSe5785* – 4.6 cM – *Xwmc817-2* {11084}. Bainong 64(R) / Jingshuan 16(S). DH lines: Four QTL from Bainong 64: *Qpm.caas.1A*.
Xbarc148-1A – *Xgwmc550-1A* interval. R^2=0.074-0.099; *QPm.caas-4DL* proximal to *Xwmc331-4D*. R^2=0.15-0.23; *QPm.caas-6BS*, proximal to *Xbarc79-6BS*, R^2=0.09-0.13; and *QPm.caas-7AL*, proximal to *Xbarc174-7AL*, R^2=0.067-0.071 {10680}.

Additional temporarily named genes and QTL are listed in {11655}.

3.5. Reaction to *Cephalosporium gramineum*

Disease: Cephalosporium stripe QTL: Coda (more resistant)/Brundage (less resistant): RIL population: 7 QTLs identified based on whiteheads; three from Coda - *QCs.org-2D.1* (nearest marker C, R^2=0.11), *QCs.orp-2B* (nearest marker *Xwmc453-2B*, R^2=0.08), and *QCs.orp-5B* (nearest marker *Xgwm639-5A*, R^2=0.12) and four from Brundage (*QCs.orp-2D.2* (nearest marker *Xbarc206-2D*, R^2=0.04), *QCs.orp-48* (nearest marker *wpt-3908*, R^2=0.05), *QCs.orp-5A.1* (nearest marker *wpt-3563*, R^2=0.08), *QCs.orp-5A.2* (nearest marker *B1*, R^2=0.05) {10836}.

3.6. Reaction to *Cephus* spp. See also Stem solidness.

Pest: Wheat stem sawfly. North American species *C. cinctus*; European species *C. pygmeus*. Resistance to wheat stem sawfly is associated with solid stem (see also: Stem solidness).
Tetraploid wheat

Qsf.spa-3B {10351}.

3.7. Reaction to *Cochliobolus sativus* Ito & Kurib.

Disease: Cochliobolus root rot.***CRR***

Crr {764}. Recessive. 5BL {764,765}. **v:** Apex {764}; Cadet {765}.

3.8. Reaction to *Colletotrichum cereale*

RCC1

Rcc1 {10939}. 5AL {10939}. **v:** Chinese Spring {10939}; Norin 4 {10939}; Shinchunaga {10939}. **ma:** *Xbarc165-5A* – 1.2 cM – *Rcc1* – 12.8 cM; *Xgwm671-5A* – 0.7 cM – *Xwmc415-5A* {10939}.

rcc1. **v:** Hope {10939}.

Susceptibility to this non-pathogen of common wheat is rare, with only one susceptible genotype being documented. A few susceptible tetraploid genotypes were identified {10939}.

3.9. Reaction to *Diuraphis noxia* (Mordvilko)

Insect pest: Russian aphid, Russian wheat aphid.

DN1

Dn1 {286}. 7DS {0211}.7D {1288}. **bin:** 7DS-0.36-0.73 {11225}. **i:** Betta-Dn1:PI 634768 {0211, 0004, 10277}; Caledon {0004}; Gariep {0004}; Karee-Dn1 {0211}; Limpopo-Dn1 {0004}; Tugela-Dn1:PI591932 {0211, 0004, 10277}. **v:** PI 137739 {286}. **ma:** *Xgwm111-7D*$_{210}$ – 3.20 +/- 0.20 cM – *Dn1* {0211}.
VIGS silencing of *5AL-B4* on chromosome 5A compromised resistance conferred by *Dn1* suggesting a decoy role {11333}.

Tests of allelism indicated that *Dn1, Dn2, Dn5, Dn6,* and *Dnx* and four uncharacterized lines were identical or closely linked {11225}.

DN2

Dn2 {286}. 7DL {863}.7DS {286}. **i:** Betta-Dn2:PI 634769 {286}, {10277}; Karee-Dn2:PI 663774 {286}, {10277}; Tugela-Dn2: PI 634772 {286} ,{10277}. **v:** PI 262660 {286,863}. **ma:** *XksuA1-7D* – 9.8 cM – *Dn2* {863}; Myburg et al. {9968} identified two SCAR markers that mapped 3.3 cM proximal to *Dn2* {9968}; *Xgwm111-7D*$_{200}$ – 3.05 +/- 0.18 cM – *Dn2*{286}; *XksuA1-7D* – 9.9 cM – *Dn2* – 2.8 cM – *Xgwm437-7D* {0353}.
According to Saidi & Quick {1250}, *Dn1* and *Dn2* are probably allelic. Reference stocks with each gene showed allelism with a gene in PI 262605.

DN3

Dn3 {1086}. Recessive. **v:** *Ae. tauschii* SQ24/*T. turgidum* TD65{1086}. **dv:** *Ae. tauschii* SQ24 {1086}.

DN4

Dn4 {1250}. 1DL {863}, 1DS {11225}. **i:** Yumar {10397}. **v:** Ankor {10397}; CORWAI {260}; CI 2401 {260}; Halt {0209}; PI 151918 {260}; PI 372129 {1250}; Prairie Red {10397}. **ma:** *Xabc156-1D* – 11.6 cM – *Dn4* {863}; *Xgwm106-1D* – 7.4 cM – *Dn4* – 12.9 cM – *Xgwm337-1D*{0352}; *Xgwm106-1D* – 5.9 cM – *Dn4* – 9.2 cM – *Xgwm337-1D* {10128}.
Dn4 and an uncharacterized gene in PI 151918 were allelic or tightly linked {11225}.

DN5

Dn5 {1249}. 7D {259}. 7DS {286}. 7DL {287}, {10396}, {10310}. **i:** Betta-DN5 {286}; Palmiet derivative 92RL28 {287}; Palmiet DN5 {0004}. **v:** STARS - 9302W-sib {259}; PI 294994 {259}. **ma:** A SCAR marker developed from the RAPD fragment OPF14$_{1083}$ mapped 5.5 cM proximal to *Dn5* {0172}; *Xgwm111-7D*$_{220}$ – less than 3.20 cM – *Dn5* {286}.
Issues relating to the confused arm location and mapping of *Dn5* is discussed in {10310}. Genetic mapping indicated that *Dn5* is located in chromosome 7DS, but cytological analysis showed it was located in 7DL {10396}. It was also suggested {10396} that the Palmiet Dn5 line {0004} may not have *Dn5* {10396}.

DN6

Dn6 {1250}. 7D. **bin:** 2AL1-0.85-1.00. **v:** CI 6501 {260}; PI 243781 {1249,1250}. **ma:** *Dn6* – 3.0 cM – *Xgwm111* {352}. *Xgwm44-7D* – 11.6 cM – *Xgwm111-7D* – 3.0 cM – *Dn6* {11225}.

DN7

Dn7 {9918}. Derived from *S. secale* cv. Turkey 77 {9918} [*Dn2414* {10478}]. 1R {9918}. 1B = 1BL.1RS {9918}. **v:** 93M45-14 {9918}; 94M370 {10188}; STARS 02RWA2414-11 {10474}. **ma:** *Xbcd1434-1R* – 1.4 cM – *Dn7* – 7.4 cM – *Xksud14-1R* {10188}; *Xhor2-1R* – 1.7 cM – *Dn7* – 1.0 cM – *Xscb241-1R* {10474}; Marker *Xrems1303*$_{320}$ was amplified only in genotypes resistant to biotype 3 and presumably possessing *Dn7* {10474}.

DN8

Dn8 **{**286}. 7DS {286}. **i:** Karee-Dn8:PI 634775 {10277}. **v2:** PI 294994 *Dn5Dn9* {286}. **ma:** *Xgwm635-7D*$_{100}$ – less than 3.20 cM – *Dn8* {286}.

DN9

Dn9 {286}. 1DL{286}. **i:** Betta-DN9:PI 634770 {10277}. **v2:** PI 294994 *Dn5Dn8* {286}. **ma:** *Xgwm642-7D*$_{180}$ – less than 3.20 cM – *Dn9* {286}.

Dn10 {11211}. **bin:** 7DL-0.1-077. **v:** PI 682675 {11211}. **ma:** *Xcfd14*-7D – 2.3 cM – *Xgwm437-7D* – 9 cM – *Dn10* – 29.1 cM – *Xwmc488-7D* {11211}; *Xcfd14*-7D – 3.6 cM – *Xgwm437-7D* – 11.3 cM – *Dn10* – 35 cM – *Xwmc488-7D* {11211}; *Dn626580* – 2.0 cM – *Dn2401* – 8.4 cM – *Dn624151* {11211}.

Temporary designations

Dnx {286}. 7DS {286}. **v:** PI 220127 {286}. **ma:** *Xgwm111-7D*$_{210}$ – 1.52 +/- 0.15 cM – *Dnx* {286}. *Dnx* was considered to be located at a locus different from *Dn1, Dn2* or *Dn5* {286}, which were likely to be identical or allelic.

Dn1881 {10145}. 7BS {10145}. **tv:** Line 1881 {10145}. **ma:** *Xgwm46-7BS* – 10.1 cM – *Dn1881* – 12.8 cM – *Xgwm333-7BL* {10145}.

Dn2401 {11078}. 7DS {11078}. **v:** CI2401, PI97812 {11078}. **bin:** 7DS-0.37-0.61 {11211}. **ma:** *Xbarc214-7D* – 1.1 cM – *Dn2401* – 1.8 cM – *Xgwm473 -7D* {11078}.

Dn100695 {11226}. 7DS M19026}. **v:** IG 100695 {11226}. **ma:** *Xgwm44-7D* – 13 cM – *Xcfd14-7D* – 15.7 cM – *Dn100695*.

Dn626580 {10981}. 7DS {10981}. **v:** PI 626580 {10981}. **ma:** *Dn626580* – 1.8 cM – *Xbarc214-7D* – 3.2 cM – *Xgwm473-7D* – 3.2 cM – *Xgwm473-7D* {10981}.

QTL: QTLs for antixenosis were associated with *Xpsr687-7D* (7DS) and *Xgwm437-7D* (7DL) in CS/CS (Synthetic 7D) {10136}. Separate antibiotic effects were demonstrated for the same chromosome {10136}.
A QTL, *QDn.unlp.6A*, for antixenosis was associated with *Xgwm1393-6AL* and *Xgwm1150-6AL* in a CS/CS(Synthetic 6A) DH population {10216}.

3.10. Reaction to *Eurygaster Integriceps*

Sunn pest

EI1

Ei1 {11201}. 4BS {11201}. **bin:** 4BS4-C-0.27. **ma:** *IWB73001 – Ei1/BS00022785 – IWB9610* {11201}.

3.11. Reaction to *Fusarium* spp.

3.11.1. Disease: Fusarium head scab, scab

Type II resistance. Whereas much of the recent genetic work involved FHB caused by *F. graminearum*, according to {10514}, *F. culmorum* is more damaging than *F. graminearum* in terms of FHB severity, kernel damage, yield reduction and DON/NIV contamination. Mesterhazy et al. {0006} reported a strong genetic correlation in resistance to different species of *Fusarium*.

FHB1

Fhb1 {10403,10214}. [*QFhs.ndsu-3BS* {9925}, {175}]. 3BS {9925}. **i:** HC374/3*98B69-147 {10214}; Sumai 3*5/Thatcher {10214}. **v:** HC-147-126 {10444}; Rollag {11071}. **v2:** Alsen *Fhb5*{11071, 11237}; BW278 *Fhb2* {10225}; Carberry *Fhb5* {11237 }; ND744 *Fhb5* {11237}; ND3085 *Fhb5* {11237}; Sumai 5 *Fhb2 Fhb5* {10314, 11237}. **ma:** *XSTS3B-80* – 0.2 cM – *Fhb1* – 1.1 cM – *XSTS3B-142*{10214}; Placed in a 1.2 cM interval flanked by *XSTS3B-189* and *XSTS3B-206* {10403}; *Xgwm389*-3B – 3.0 cM – *Sr2/csr2* – 0.4 cM – *Xgwm389*-3B – 2.0 cM – *Fhb1/UMN10/*UMN$_{v2}$ (coupling) {11210}. *Xgwm493-3B* and *Xgwm533-3B* were confirmed as useful markers {11237}. **c:** A pore-forming toxin-like gene product encodes a chimeric lectin with two agglutinin domains and an ETX/MTXZ toxin domain {11205}.
The relationship of *Fhb1* to *Fhs1* or *Fhsb2* {1096} is unknown. Lines combining *Fhb1*and *Sr2* are reported in {11170}; *Fhb1* is located about 2 cM proximal to *Sr2*. SYN1 / Ocoroni DH population: three

QTL from SYN1 were identified, *QFhs.cim-2D* (PVE 25%), *QFhs.cim-7A* (PVE 4.7%) and *Qfhs.cim-7A* (PVE 4.2%) {11165}.
A marker study found that 14 of 66 wheats with putative FHB resistance shared markers indicative of the 3BS QTL in Ning 7840, Sumai 3, Wangshuibai and possibly Wuhan 3, plus Japanese landraces Shinchunaga and Shirasu No 1 {10115}. The original source may be the landrace 'Taiwan Wheat' rather than Funo {10115}.

FHB2

Fhb2 {10225}. 6BS {10225}. **v:** pbE85{10444}. **v2:** BW278 *Fhb1* {10225}; Sumai 3 *Fhb1* {10225}. **ma:** *Xgwm133-6B* – 4 cM – *Fhb2* – 2 cM – *Xgwm644-6B* {10225}.
The relationship of *Fhb2* to *Fhs1* or *Fhs2* {1096} is unknown.

FHB3

Fhb3 {10529}. 7DS = T7AL.7Lr#1S{10529}. **v:** TA 5608{10529}. **al:** *Leymus racemosus* {10529}. **ma:** Three PCR markers, *Be586744-STS, BE404728-STS* and *BE586111-STS*, were developed {10529}. The level of type 2 resistance conferred by *Fhb3* was similar to that of Sumai 3 {10529}.

FHB4

Fhb4 {10884}. [*Qfhi.nau-4B*{10282}]. 4BL {10883,10282}. **bin:** 4BL5-0.86-1.00. **i:** Mianyang 99-323*4/Nanda 2419/Wangshibai {10885}. **v2:** Wangshuibai *Fhb5* {10884}. **ma:** Located in a 1.7 cM segment flanked by *Xhbg226-4B* and *Xgwm149/Xmag4580-4B* {10883}.
Although plants with *Fhb-4* were taller than the recurrent parent, the height difference was not associated with the *Rht-B1* locus {10885}.

Type I resistance (% infected plants) in this cross was attributed to 10 chromosome regions among which *Qfhi.nau-4B* (*Xwmc349-4B – Xgwm149-4B* - $r^2 = 0.75$), *XFhi.nau-5A (Xwmc96-5A – Xgwm304-5A* - $R^2 = 0.27$) and *Qfhi.nau-5B (Xgwm408-5B – Xbarc140-5B*) from Wangshuibai were detected in at least 3 of 4 years {10282}. A significant additive effect of QTL on 6D and 2A was also observed {10282}.

FHB5

Fhb5 {10896}. [*Qfhi.nau-5A* {10282 }; *Qfhs.ifa-5A* {10076}]. 5AS {10896}. **bin:** C-5AS3-0.75. **i:** Mianyan 99-323 and PH691 backcross derivatives selected for *Qfhi.nau-5A*{10896}. **v2:** Alsen *Fhb1*{11237}; Carberry *Fhb1* {11237}; ND744 *Fhb1* {11237}; ND3085 *Fhb1* {11237}; Sumai 5 *Fhb1 Fhb2* {10314, 11237}; Wangshuibai *Fh4b* {10896}. **ma:** Mapped to a 0.3 cM interval between *Xbarc117/Xbarc358/Xgwm293/Xgwm304-5A* and *Xgwm415-5A* {10896}.
Closely linked in coupling with *Qflw.nau-5A* for narrow leaf width, but recombination is reported in {11041}.
According to {11487} *Fhb5* might be the same as *Qfhs.ifa-5Ac* but the issue remained ambivalent.

FHB6

Fhb6 {11048}. Derived from *Elymus tsukushiensis* syn. *Roegneria kamoji* 1AS {11048}.
T1AL.1AS-1E^{ts}#1S {11048} **v:** TA5660, KS14WRRC61 {11048}.
T1AL.1AS-1E^{ts}#1S {11048} TA5093 {11048}. **ma:** Three CAPS and one KASPar SNP (*wg1S-snp1*) markers were developed {11048}.
TW.1E^{ts}#1S{11048} **v:** TA5655 {11048}.
TA5660 is in Chinese Spring background; TA5093 is in Everest background.

FHB7

Fhb7 {11060}. Derived from *Thinopyrum ponticum* [*FhbLoP* {11118}].
T7DS.7D1-7el$_2$L {11060} **v:** SDAU1881 {11060}.
T7DS.7D1-7el$_2$L {11060} SDAU1886 {11060}. **ma:** Flanked by 7el$_2$ markers *Xcfa2240* and *XsdauK66* in a 1.7 cM interval {11060}. Located to a 245 kb region flanked by *Xsdau86* and *Xsdau88* {11483}.
T7DS.7el$_2$ {657} **v:** KS24-2 {657}.
c: Gene Tel7E01T1020600.1 encodes a glutathione S-transferase that detoxifies trichothecene toxin {11483}. Sequence data can be found at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA540081.

FHB8

Fhb8 {11676}. 7D {11676}. **i:** Wangshuibai/4*PH691 7D-NIL1 {11676}; Wangshuibai/4*PH691 7D-NIL2 {11676}. **v2:** Wangshuibai *Fhb1 Fhb2 Fhb4 Fhb5*{11676}. **ma:** *Xwgrb1500* (93.9 Mb, RefSeq 1.0) – *Fbhb8/Xwgrb1587* – *Xwgrb1559* (96.5 Mb) {11676}.

FHB9

Fhb9 {11727}. *QFhb-2DL* {11719}. 2DL {11727}. **v:** Shi4185 / Shijiazhuang8 RIL92 (11727}; Ji5625 / Wheaton NILs {11719}. **v2:** Shi4185 + additional QTL in chr. 4A, 3D and 5D {11727}; Ji5625 {11719}. **ma:** Located in an 8.0 Mb (2.21 cM) region (KASP-525 – KAS-12056, 525.9 – 533.8, Mb, CS RefSeq 2.1) {11727}; 524.9 – 531.0 Mb {11719}.

Other names

Fhs1 {1096}. **v:** Line A {1096}. **v2:** Ning 7840 *Fhs2* {1096}.

Fhs2 {1096}. **v:** Line B {1096}. **v2:** Ning 7840 *Fhs1* {1096}.
A major QTL was associated with several linked AFLP markers tentatively located in chromosome 7BL of Ning 7840 {0005}.

QTL
QTLs for resistance to *Fusarium graminearum* detected in the cross Renan/Recital {10069}. All resistance alleles, except *QFhs.inra-3A*, were contributed by Renan. LOD scores and percent of variation explained by the QT (R^2) are average of three years of field tests.

QFhs.inra-2A {10069}. **ma:** Associated with *Xgwm382c-2A* (LOD=6.3, R^2=14.4%).

QFhs.inra-2B {10069}. **ma:** Associated with *Xgwm374-2B* (LOD=7.6, R^2=12%).

QFhs.inra-3A {10069}. **ma:** Associated with *Xbcd372-3A* (LOD=3.7, R^2=6.2%).

QFhs.inra-3B {10069} . **ma:** Associated with *Xgwm383b-3B* (LOD=5.4, R^2=10.5%).

QFhs.inra-5A.1 {10069}. **ma:** Associated with *Xpsr170a-5A* (LOD=3.8, R^2=5%).

QFhs.inra-5A.2 {10069}. **ma:** Associated with *Xgwm639b-5A* 8LOD=6.6, R^2=14%).

QFhs.inra-5A.3 {10069}. **ma:** Associated with *B1* (LOD=6.3, R^2=8.5%).

QFhs.inra-5D {10069}. **ma:** Associated with *Xcfd29-5D* (LOD=4.4, R^2=7%).

QFhs.inra-6D {10069}. **ma:** Associated with *Xcfd42-6D* (LOD=2.7, R^2=6.6%).

QFhs.ndsu-2A {9925,175}. 2AL {9925}. **v:** Sumai 3/Stoa RI mapping population; the QTL was contributed by Stoa {9925}. **ma:** Association with RFLP *XksuH16-2A* (LOD >3) {9925,175}.

QFhs.ndsu-3AS {10482}. 3AS {372}. **tv:** *T. turgidum* var. *dicoccoides.* Recombinant substitution lines LDN and LDN(Dic-3A). The resistant allele was contributed by *T. dicoccoides*{372}. **ma:** Associated with *Xgwm2-3A* (explained 37% of the phenotypic variation){372}; *QFhs.ndsu-3AS* was placed within a 11.5 cM region flanked by TRAP marker loci *Xfcp401-3A* and *Xfcp397.2-3A* {10482}; This gene was transferred to durum cultivars using the closely linked marker *Xgwm2-3A* {11367}. This gene is unlikely to be a homoeologue of *Qfhs.ndsu-3BS = Fhb1* {10482}.

QFhs.ndsu-3B {9925,0175}. 3BS {9925}. **v:** Sumai 3/Stoa RI mapping population; the QTL was contributed by Sumai 3 {9925,0175}. **ma:** Association with *Xbcd907-3B.2* (LOD >3) {9925} and microsatellite markers *Xgwm1533-3B* and *Xgwm493-3B* {0175}; *QFhs.ndsu-3B* from Sumai 3 was associated with microsatellite loci *Xgwm533-3B* and *Xgwm274-3B* in certain Sumai 3 derivatives {10062}. In Ning 894037 the QTL has the same location and similar SSR bands to Sumai 3 {10085}. STS marker SRST.3B1 was mapped between *Xgwm533-3B* and *Xgwm389-3B* and associated with *QFhs.ndsu-3B* {10072}. *QFhs.ndsu.3B* was associated with markers *Xgwm533-3B, Xbard133-3B, Xbarc147-3B* and *Xgwm493-3B* {10073}.
This QTL explained 42% of the variation in Sumai 3/Stoa {0175}.
Two additional QTL for resistance to *Fusarium graminearum* were identified in the croSumai3/Stoa {0175}. The QTL on 4BS was associated with *Xwg909-4B* and the QTL on 6BS was associated with *Xbarc101-6B* and *Xbcd1383-6B* {0175}. The QTL associated with markers *Xgwm493-3B/Xgwm533-3B* (explaining 24.8 % of the variation), and *Xbarc101-6B/Xbcd1383-6B* were also identified in a RIL population from the cross ND2603/Butte 86 {0175}. In addition, one QTL on chromosome 3AL associated with *Xbcd941-3A* and one on chromosome 6AS associated with *XksuH4-6A* were identified in RILs from the cross ND2603/Butte 86 {0175}.

Remus / CM-82036 (a Sumai 3 derivative): DH population: Resistance QTL on chromosome 3BS associated with *Xgwm493-3B* and *Xgwm533-3B* {0240}. Additional QTL in this cross were detected on

chromosome 5A, associated with *Xgwm293-5A* and *Xgwm304-5A*, and possibly on 1B, associated with *Glu-B1* {0240}.
Two major genes with additive effects were reported in crosses between Sumai 3 (resistant) and two susceptible cultivars {0174}. One of the genes was assigned to 5AL based on linkage to the dominant awn suppressor *B1* (RF 15.1-21.4%).

Alve (S) / Line 685 R: DH population: QTL on chromosomes 4D (*Rht-D1*), 3BS, 5A and 2BL {10972}. Two resistance QTL were needed to counteract the negative effect of the *Rht-D1b* semi-dwarfing allele {10972}.

Arina (R) / Forno (S): Three QTLs, *QFhs.fal-6DL* (R^2=22%), *QFhs.fal-5BL.1* (in Forno, R^2=14%) and *QFhs.fal.4AL* (R^2=10%) and 5 minor QTLs in 2AL, 3AL, 3BL, 3DS and 5DL were detected {10172}.

Arina / Riband DH lines: QTL affecting ADUPC were identified in 1BL(2), 2B, 4DS, 6BL and 7AL (Arina), and 7AL and 7BL (Riband). The most effective was the 4DS QTL that appeared to be an effect of *Rht-D1a* rather than height *per se* {10464}.

Baishanyuehuang (R) / Jagger (S): RIL population: Four genes/QTLs derived from the resistant parent included *Fhd1* (R^2=0.16), *Qfhb.hwwg-3BS c*(R^2=0.09), *Qfhb.hwwg-3A* (R^2=0.05-0.08) and *Qfhd.hwwg-5A* (R^2=0.05 in one trial) {10950}.

Cansas (moderately resistant) / Ritmo (susceptible): Map based analysis across environments revealed seven QTL, *QFhs.whs-1BS* (1RS), *QFhs.whs-3B* (not *Fhb1*), *QFhs.whs-3DL, QFhs.whs-5BL* '(renamed *Qfhs.lfl-1BL* in {10768})'*,* *QFhs.whs-7AL* and *QFhs.whs-7BL* (cumultatively, R^2 = 0.56). The chromosome 1D gene was primarily involved in resistance to fungal penetration and the others in resistance to spread {10503}. There were significant correlations of FHB response with height and heading date {10503}. *Qfhs.lfl-1BL* was verified in $F_{4:7}$ lines and detected in Biscay, History and Pirat {10768}. The renamed *Qfhs.lfl-1BL* reduced FHB severity by 42% relative to lines lacking it {10698}. This gene was also present in Biscay, History and Pirat {10698}.

CS / CS(Sumai 3 7A): *QFhb7AC*, nearest marker *Xwmc17-7A*, explained 22% of phenotypic variance for Type II and 24% of phenotypic variance for Type III resistance {10798}.

Chris / Frontana: In a reciprocal backcross analysis of Chris monosomics/Frontana, Frontana chromosomes 3A, 6A and 4D reduced visibly diseased kernels, kernel weight and DON content, whereas Frontana chromosomes 2A, 2B, 4B and 7A increased the same traits {10398}. Further study of the 3A, 6A and 4D reciprocal substitution lines indicated that chromosome 3A of Frontana had the largest effect on incidence, severity, spread and kernel damage, 4D less so and 6A possibly not at all {10900}.

DH181(R)(Sumai 3 / HY 386 Seln.): QTL identified in 2DS, 3AS, 3BS, 3B Cent. region, 4DL, 5AS, 6BS {10213}.

Dream(R) / Lynx(S): RIL population: Following inoculation with *F. culmorum* 4 QTL for AUDPC were identified on chromosomes 6AL (R^2=19%), 1B (12%), 2BL (11%) and 7BS (21%). The resistance allele

in 1B came from Lynx and was associated with T1BL.1RS {10260}.
Dream*4 / Lynx lines were developed by selection of QTL on chromosomes 6AL, 7BS and 2BL. Lines carrying *QFhs.lfl-6AL* and *QFhs.lfl-7BS* were more resistant than lines lacking them; the 2BL QTL effect was not verified {10470}.

Chokwang (R) / Clark (S): *Qfhb.ksu-5DL.1* associated with *Xbarc239-5D* (R^2=0.24) {10276}, *Qfhb.ksu-4BL.1* associated with *Xbarc1096-4B* (R^2=0.13) {10276}, and *Qfhs.ksu-3BS.1* marginally associated with the region of *Fhb1* (R^2=0.1) {10276}.Ernie (Res) / MO94-317 (Sus): 243 F8 RIL population. Four QTLs from Ernie detected as follows: *Qfhs.umc-2B*, linked to *Xgwm278-2BS*, R^2 = 0.04 {10456}; *Qfhs.umc-3B*, linked to *Xgwm285-3BS*, R^2 = 0.13 {10456}; *Qfhs.umc-4B*, linked to *Xgwm495-4BL*, R^2 = 0.09 {10456}. *Qfhs.umc-5A*, linked to *Xgwm165-5A*, R^2 = 0.17 {10456}. Evidence was provided to suggest the QTL acted additively {10456}.

Frontana (R) / Remus (S): Major QTLs in chromosomes 3AL (*Xgwm270-3AL – Xdupw227-3A* region) and 5A (*Xgwm129-5A – Xbarc-5A* region) accounted for 16% and 9% of the phenotypic variation (mainly type 1 resistance) over 3 years {10174}.

Frontana (MR) / Seri82 (S): F3 and F3:5 populations: QTLs were located in chromosomes 1BL (R^2=7.9%), flanked by AFLP markers, 3AL (R^2=7.7%), flanked by *Xgwm720-3A* and *Xgwm121-3A*, and 7AS (R^2=7.6%), flanked by anAFLP and *Xgwm233-7A* {10349}.

G16-92 (R) / Hussar (S): Two QTL for resistance to *F. culmorum* were identified on chromosome 1A (resistance from Hussar) (R^2 = 0.01) and 2B (resistance from G16-92) (R^2 = 0.14) {10588}.

Glenn (R) / MN00261-4 (S): RIL population: three of 15 QTL for FHB response and heading date were stable and explained >10% of the phenotypic variation; these were located on chromosome arms 5BL, 6BS (possibly *Fhb2*) and 7AS {11568}.

Grandin (S) / PI277012 (I): DH population: Two QTLs, *Qfhb.rwg-5A.1* on 5AS ($R^2$0.06-0.2) and *Qfhb.rwg-5A.2* on 5AL (R^2=0.12-0.2) conferred type I and II resistance and reduced DON content {0147}. The new QTL on 5AL was closely but not completely linked with gene *q* which is present in PI277012 {10860}.

Hobbit Sib / *T. macha* 4A: DH population: Type I resistance and DON accumulation:: Both traits were assigned to a small region distal to *Xgwm601-4A* and cosegregating with *Xgwm165-4A* {10254}.

Huapei 57-2 /Patterson: Four QTL on chromosomes 3BS (associated with *Xbarc133-3B*), 3BL (*Xgwm247-3B*) and 3AS (*Xgwm5-3A*) from Huapei 57-2, and 5BL (*Xbarc59-5B*) from Patterson {10026}. Huapei 57-2, Ning 7840 and Sumai 3 carried common alleles in the *Xgwm533-3B, Xgwm493-3B, Xbarc147-3B* and *Xbarc133-3B* region {10026}.

Luke (S) / AQ24788-83 (R): RIL population: *QFhb.cau-7DL* near marker *Xgwm428-7DL* was equally effective as *Fhb1* {11358}.

Nanda2419 (S) / Wangshuibai (R): 8 QTLs were identified; those with large effects were associated with *Xgwm533-3B.3 – Xgwm533-3B.1* (W), *Xwmc539-6B* (W) and *Xs1021m-2B – Xgwm47-2B* {10190}.

Nanda 2419 / Wangshuibai: Backcross-derived NILs with *Qfh.nau-2B, Qfhs.nau-3B, Qfhi.nau-4B* (syn. *Fhb4*), and *Qfhi.nau-5A* were developed with Mianyang 99-323 as the recurrent parent {10884}. Type IV resistance (proportion of Fusarium-damaged kernels) was attributed to five QTLs, four from Wangshuibai. Those with the largest effects included *QFdk.nau-2B* (from Nanda 2419), *QFdk.nau-3B* and *QFdk.nau-4B* {10577} with each accounting for more than 20% of the phenotypic variation.

Ning 7840 / Clark: QTLs were located in chr. 3BS, 2BL and 2AS. The most effective QTL was probably in the interval flanked by deletions 3BS-3 and -8 and was close to *Xgwm533-3B* and *Xbarc147-3B* {0328}. RIL population: Three resistance gene analogue (RGA) sequences putatively assigned to chromosome 1AL explained 3.37-12.73% of the phenotypic variation in FHB response among F7 and F10 populations {10364}. STS marker FHBSTS1A-160 was developed from one of the RGA.

Patterson (mod sus) / Fundulea 201R RILS: QTLs accounting for 19% and 13% of phenotypic variation were found on chromosomes 1BL (*Xbarc8-1BS – Xgwm131-1BL* region) and 3AS (*Xgwm674-3A/Xbarc67-3A* region) {10114}. Two weak QTLs were possibly associated with chromosomes 3D (Patterson allele) and 5AS {10114}.

Patterson (open florets) / Goldfield (closed florets): RILs: narrow flower opening was correlated with FHB resistance. The major QTL effect associated with narrow flower opening and low FHB incidence occurred in map interval *Xbarc200 – Xgwm210* (29% of variation in FHB incidence); these genes were probably located in chromosome 2BS {10243}.

Pelikan (S) / G93010 (= Bussard / Ning 8026) (R): *Qfhs.Ifl-7BS/5BL* and *Qfhs.Ifl-6BS* (probably *Fhb2*) from Ning 8026 reduced disease severity by 30% and 24%, respectively, and by 46% when combined {10594}. Other resistance genes were located on chromosomes 1AS (*Qfhs.Ifl-1AS* from Pelikan), and 2AL and 7AL (from Ning 8026) {10594}.

PI 672538 (R) / L661 (S): F_2:F_3 population. QTL identified in chromosomes 2B and 3B. The latter was considered different from *Fhb1* {11648}.

Renan / Recital: Of the QTLs for resistance detected in the cross all alleles, except *QFhs.inra-3A*, were contributed by Renan. LOD scores and percentages of variation explained by the QTL (R^2) were averages of three years of field tests {10069}.

Spark (MR) / Rialto (S): DH population: Of nine QTLs identified across all environments, seven alleles for resistance came from Spark and two from Rialto. The largest effect on Type 1 resistance (*Xfhs.jic-4D.2*) was associated with the *Rht-D1b* allele in Rialto which made lines more susceptible. Other QTLs occurred on chromosomes 1B (1B.1R), 4D (*Qfhs.jic-4D.2*), 2A,3A (each, 2 QTLs), 5A and 7A. *Xfhs.jic-4D.2* had little effect on Type 2 resistance {10603}.

Soissons (relative resistant) / Orvantis (susceptible): Increased susceptibility associated with the *Rht-D1b* allele was further confirmed in crosses of semi-dwarf cultivars Apache, History and Romanus {10793}.

Sumai3 (R) / Y1193-6 (S): RIL population: Three resistance QTL on chromosomes 3BS, 6BL and 2DS with R^2 values of 0.26, 0.11 and 0.19, respectively; the last was derived from Y1193-6 {11001}.

SYN1 / Ocoroni DH population: three QTL from SYN1 were identified, *QFhs.cim-2D* (PVE 25%), *QFhs.cim-7A* (PVE 4.7%) and *Qfhs.cim-7A* (PVE 4.2%) {11165}.

Treho (S) / Heyne (MR): RIL population: Three QTLs from Heyne, viz *Qfhb.hwwg-3AS* (R^2, up to 0.18), *Qfhb.hwwg-4DL* (R^2=0.14-0.23) and *Qfhb.hwwg-4AL* (R^2, up to 0.18) {11005}.

W14(R) / Pioneer 2684(S) population: QTL in 3BS and 5AS accounted for 33%, 35% and 31% of the phenotypic variation for disease spread, kernel infection and DON accumulation in greenhouse experiments, and 34% and 26% of variation for FHB incidence and severity in the field {10239}. Flanking markers were *Xbarc133-3B* & *Xgwm493-3B* and *Xbarc117-5A* & *Xbarc56-5A* {10239}.

Wuhan-1 / Nyubai{10623}: Two QTLs were located on chromosomes 2DL and 3BS (distal) {10020}. A QTL for seedling resistance in the Wuhan/Nyubai population was associated with the *Qwmc75-5B* locus, R^2 = 0.138. The relationship of this resistance to crown rot resistance was unknown {10624} (see Reaction to *F. pseudograminearum*).

Wuhan-1 / Maringa: Field resistance: QTLs were located on chromosomes 2DS, 3BS (proximal) and 4B {10020}. Resistance to DON accumulation: QTLs were located on chromosomes 2DL and 5DS {10020}.

VA00W-38 (mod. R) / Pioneer26R46 (S): RIL population: Consistent QTL from VA00W-38 detected on chromosomes 1BL, 2A, 2DL, 5B, 6A and 7A explained 6.5-21.3% of the phenotypic variation; one QTL from 24R46 was identified on chromosome 7A {11022}. Major QTL on 2DL, 6A and 5B decreased FHB index, Fusarium damaged kernels, and DON, respectively {11022}. Veery (S) / CJ9306 (R): Four QTLs, *XQFhs.ndsu-3BS* (*Xgwm533b – Xgwm493*), *QFhs.nau-2DL* (*Xgwm157 – Xwmc-041*), *QFhs.nau-1AS* (*– Xbarc148*) and *QFhs.nau-7BS* (*Xgwm400 – Xgwm573*) accounted for 31, 16, 10 and 7%, respectively, of the average phenotypic variation over three years {10490}

Wangshuibai / Alondra 'S': A stable QTL was associated with *Xgwm533-3B* in each of 3 years, QTLs in 5B (*Xgwm335-5B*), 2D and 7A were detected in 2 years {10268}.

Wangshuibai / Annong 8455: RIL population: CIM analysis over 2 years detected QTL for FHB response on chromosome 3B (R^2=0.17) and 2A (R^2=0.12) and for DON levels in 5A (R^2=0.13), 2A (R^2=0.85) and 3B (R^2=0.06) {10447}. The regions involved were *Xgwm533-3B – Xbarc133-3B, Xgwm425-2A*, and *Xgwm186-5A – Xgwm156-5A* {10447}.

Wangshuibai / Seri 82: F3:F5 populations: QTL on chromosome 3BS (*Xgwm533-3B – Xs18/m12-3B*) and 2DL (*Xgwm539-2D – Xs15/m24-2D*) accounted for 17% and 11%, respectively, of the phenotypic variance {10264}.

Wangshuibai (R) / Wheaton (S): QTLs located in chromosome 3BS (*Xbarc147-3B*, R^2=37% & *Xbarc344-3B*, R^2=7%), 7AL (*Xwms1083-7A*, R^2=10%) and 1BL (*Xwms759-1B*, R^2=12%) {10200}.

Wheaton (I) / Haiyanzhong: RIL population: Four QTLs, *Qfhb.uhgl-7D* [syn. *Qhb.hyz-7D*], nearest marker *Xwmc121-7D*, R^2=0.16-0.2), *Qfhb.uhgl-6B.1* [*Qhb.hyz-6B.1*], R^2=0.4), *Qfhb.uhgl.6B.2* [*Qhb.hyz-6B.2*], R^2=0.07), *Qfhb.uhgl-5A* [*Qhb.hyz-5A*], R^2=0.04-0.07) were from Haiyanzhong, and *Qfhb.uhgl-1A* [*Qhb.hyz-1A*], R^2=0.05) was from Wheaton {10837}.

Of 54 lines with reported FHB resistance, 6, including CM-82036, Ning 7840 and Wuhan 3, had the same 5-marker haplotype as Sumai 3, and 4 lines possessed 4 of the markers. Twenty-nine lines, including Frontana, had no marker allele in common with Sumai 3, whereas 13 lines had 1 to 3 alleles in common with it {10113}. *Qfhs.ndsu-3B* and the 5 marker loci were placed in 3BS deletion bin 0.78-0.87 {10144}.

Haplotype diversity among a large number of FHB resistant and susceptible (mainly Canadian) germplasms indicated similarities in Asian, Brazilian and other materials {10173}. Brazilian cv. Maringa was more similar to Asian types than to other Brazilian lines {10173}.

For review see {0283}. A review of 52 mapping studies is provided in {10593

Bobwhite plants transformed with AtNPR1, an *Arabidopsis thaliana* gene that regulates SAR activities, displayed a heritable type II response equal to that of Sumai 3 {10237}.

Associations between response to FHB caused by *F. culmorum* and the semi-dwarfing locus *Rht-D1* in crosses Apache / Biscay, Romanus / Pirat and History /Rubens (Biscay, Pirat and Rubens carry *Rht-D1b*) were reported in {10574}. Genotypes with the semi-dwarf alleles tended to be more susceptible. }.

Tetraploid wheat

Ben*2 / Tunisian 108: BIL population: nine QTL for FHB resistance of which new QTL *Qfhb.ndsu-2B* and *Qfhb.ndsu-3BL* and *Qfhb.ndsu-5A* and *Qfhb.ndsu-7BL* were the most important {11382}.

Langdon / Langdon (DIC-2A): RICL population: Increased susceptibility of the *T. dicoccoides* Israel A substitution line relative to Langdon was mapped to a 22 cM interval spanned by *Xgwm558-2A* and *Xgwm445-2A* {10613}.

Strongfield /*T. carthlicum* (Blackbird): Field resistance identified in chromosome 2BL (*Xgwm55-2B*), and 6BL (*Xwmc397-6B*) (coincident with *Fhb2* {10225}.

***T. dicoccum* line Td161 crossed to three durum parents:** small effect QTL were detected on chromosomes 3B, 4B, 6A, 6B and 7B; all except the 6A QTL were located at previously known positions {10993}.

***T. dicoccoides* Mt. Gerizim#36 /*2 *T. durum* Helidur**: F_6 lines: two QTL for type2 resistance located on chromosome 3A (*Xbarc45-3A* - *Xbarc67-3A* and 6B (*Xs13m22-2* - *Xgwm626-6B* {11088}.

Qfhs.crc-2BL {10445}. **tv:** Strongfield {10445}. **ma:** Spanning 16 cM, this QTL peaking on *Xgwm55-2B* explained 23% of the phenotypic variation {10445}.

Qfhs.crc-6BS {10445}. **tv:** *T. turgidum* var. *carthlicum* cv. Blackbird{10445}. **ma:** Spanning 23 cM and peaking on *Xwmc397* this QTL accounted for 23% of the phenotypic variation {10445}.

Qfhs.ifa-5A{10076}. Associated mainly with resistance to fungal penetration {10073}. 5A {240, 10076}. **v:** Remus/CM-82036 {10076}. **ma:** Associated with markers *Xgwm293-5A, Xgwm304-5A, Xgwm1057-5A, Xbarc117-5A, Xbarc186-5A, Xbarc100-5A* and *Xbarc40-5A* {10073}. Fine mapping divided this QTL into two components, *Qfhs.ifa-5Ac* located in the centromere region at 245.9 Mbp and a less effective *Qfhs.ifa 5AS* located at 290 Mbp. Both QTL were significantly associated with higher anther extrusion and plant height {11487}.

Qfhs.fcu-7AL {10401}. **sutv:** LDN-DIC 7A {10401}. **tv:** *T. turgidum* var. *dicoccoides* PI 78742 {10401}. **ma:** Located in an interval 39.6 cM thie QTL accounted for 19% of the phenotypic variation in a RIL population of Langdon/LDN-DIC 7A; nearest marker *Xbarc121-7AL* {10401}.

Qfhs.ndsu-3AS {10402}. **sutv:** LDN-DIC3A {10402}. **tv:** *T. dicoccoides*{10402}. **ma:** Located in an interval spanning 29.3 cM this QTL accounted for 37% of the phenotypic variation; peak marker, *Xgwm2-3A*{10402}.

QFhs.pur-2D {10085}. **v:** Alondra{10085}. **ma:** Located on 2DS between SSR markers *Xgwm296-2D* and *Xgwm261-2D* {10085}.

QFhs.pur-7El {10489}. 7DS.7DL-7el$_2$ {10489}. 7el$_2${10489}. **su:** K2630{10489}. **v:** K11695 = 7DS.7DL-7el$_2$ {10489}; KS10-2 = 7el$_2$S.7el$_2$L-7DL {10489}; KS24-1 and KS24-2 = 7DS.7el$_2$ {10489}. **ma:** *Qfhs.pur-7el$_2$* was flanked by *BE445653* and *Xcfa2270-7D*{10489}; These markers were also present in KS10-2{10489}. See *FHB7*.

3.11.2. Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* speciesQTL

2-49 / W21MMT70: DH lines: Three QTLs fo seedling resistance, viz. *QCr.usq-1D.1,* and a weaker QTL on chromosome 7A from 2-49 and *QCr.usq-3B.1* (R^2=0.41) from W22MMT70 {10883}.

2-49 (partially resistant) / Janz (susceptible): DH population: Analysis of partial seedling resistance indicated major QTL in chromosomes 1D (R^2=0.21) and 1A (R^2=0.09) and minor QTL in 2A, 2B (from Janz), 4B and 7B {10132}.

W21NMT70 / Mendos: DH population: three consistent QTLs for seedling resistance were identified with CIM; these were located in chromosome 5D and 2D (resistance alleles from W21NMT70) and 2B (resistance allele from Mendos) {10358}.

Kukri (R) / Janz (S): DH population: Simple interval mapping in the region Pst1 ACG.Mse1 CAC - *Xgwm251-4B* accounted for 48% of the variation in crown rot response {10034}.

Lang (S) / *T. spelta* CSCR6 (R): RIL population: tested under controlled conditions with *F. pseudograminearum* and *F. graminearum*: *Qcrs.cpi-3BL* from CSCR6, R^2=0.49 and *Qcrs.cpi-4B* from Lang R^2=0.23 {10703}. Six of 9 NIL pairs made by MAS for *Xgwm01081-3B* earlier located near the 3BL QTL {10703} in CSCR6 showed significant differences (P <0.01) in crown rot response {10891}.*Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495;* R^2 up to 0.49, validated in other crosses {10723}. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23 {10723}. Shishoumai (R) / Sanyuehuang (S): $F_{2:3}$ population. *Qfcr.sicau.1B-4* – 641.36 – 645.13 Mb – reduced the crown rot response by up to 39.7% of the phenotypic variation {11674}.
Sunco / 2-49: DH population: Three QTLs for seedling resistance, viz. *QCr.usq-1D.1* and *QCr.usq-4B.1* (R^2=0.19) from 2-49 and *QCr.usq-2B.1* from Sunco {10883}.

Sunco / Macon: RIL population: QTLs were located in chromosomes 2B, 3B, 4B and 4D. *Qcrs.wsu-3BL* from Macon and flanked by *Xgwm299-3B* was the most effective {10932}.

Sunco / Otis: RIL population: QTLs were located in chromosomes 2B, 3B, 4B and 7A. *Qcrs.wsu-3BL* from Otis was the most effective {10932}.

UC1110 / PI 610750: RIL population: Three QTL had an additive effect: *QFCR.heau-6A* (R^2 = 0.078 – 0.102) from UC1110; and *QFCR.heau-2A* (R^2 = 0.052 – 0.070) and *QFCR.heau-2D* (R^2 = 0.072 – 0.093) from PI 610750 {11548}.

Wuhan / Nyubai: A QTL for seedling resistance to *F. graminearum* was associated with the *Qwmc75-5B* locus, R^2 = 0.138. The relationship of this resistance to crown rot resistance is unknown {10624}Three crosses involving EGA Wylie: *Qcrs.cpi-5Ds* (R^2 = 0.31) and *Qcrs.cpi-2DL* (R^2 = 0.221). Two additional QTL on chromosome 4BS were associated with plant height {11243}.Nine NIL sets derived from three crosses of Australian wheat cultivars and *T. spelta* CSCR6: *Qcrs.cpi* was flanked by *Xcfp1822-3B* and *Xgwm181-3B* {11244}.

3.12. Reaction to *Heterodera avenae* Woll.., *H. filipjeva* (Madzhidov) Stelter

Cereal root eelworm; cereal cyst nematode.

CRE1

Cre1. [*Cre* {1388}]. 2BL {1579,1580}. 2B {1388}. **i:** AP = Prins*8/AUS10894 {1579}. **v:** AUS 10894 {1056}; Beulah {10013}; Chara {10163}; Goldmark {10013}; Goroke {10013}; Kellalac {10013}; Loros CI 3779 {10013}; Mira {10163}; Mitre {10163}; Ouyen {10013}; RE8670 {10013}; Silverstar {10013}; VI252 {10013}; VI727 {10013}. **ma:** *Xglk605-2B* - 7.3 cM - *Cre1* - 8.4 cM - *Xcdo588-2B/Xabc451-2B*{1579}; A PCR-based assay was developed from *Xglk605-2B* {1580}; Co-segregation with *Xcsl107-2B*. Four of 6 land varieties possessed *Xcsl107-2B*. A variant haplotype of *Xcsl107-2B* was present in AUS4930 {10013}; *Xcdo36-2B* – 7.5 cM – *Xbcd1231-2B/XAtPPr5/Xcsl107-2B/Cre1*{10013}.

CRE2

Cre2 {238}. Derived from *Ae. ventricosa* 10 {238}, {9991}. 6M^v {9991}. **v2:** H-93-8 *Cre6* {238}. Although H-93-8 is a double M^v(5A), 7M^v(7D) substitution line, *Cre2* was presumed to be located in a separate undetected translocated 6M^v segment {9991}.

CRE3

Cre3. [*CcnD1* {329},*Ccn-D1* {328}]. 2DL {328}. **v:** Synthetic hexaploids {329}. **dv:** *Ae. tauschii* accessions AUS 18912 {328}; AUS 18913 {328}; CPI 110809 {329}; CPI 110810 {328}. **ma:** Co-linearity with 2BL for *Xcdo-36-2D* and *XAtPPr5/Xbcd1231-2D/G4/G12/Cre3* (see *Cre1*) {10013}.

CRE

Cre4. [*Ccn-D2* {328},*CcnD2* {329}]. 2D {328}. **dv:** *Ae. tauschii* accessions AUS 18914 {329}; CPI 110813 {328}.

CRE5

Cre5 {0107}. Derived from *Ae. ventricosa* {0107, 0009}. [*CreX* {9, 0183}, *QCre-ma2A* {11394}.]. 2AS {0107} = 2A-2N^v-6N^v. **v:** VPM1 {0107}; Many VPM1 derivatives {0107}. **v2:** Madsen *Cre9* {11102}.
Notable exceptions of lines with *Lr37, Sr38* and *Yr17*, but lacking *Cre5* include Trident and Line L22 {0107}; however a contribution of the *Cre5* region was detected in Trident/Molineux {10343}. **su:** Moisson 6N^v(6D){0183}. **dv:** *Ae. ventricosa* 10 {0183}. **ma:** Associated with the *Xgwm359-2A* (R^2=8%) – *Xwmc177-2A* (R^2=7%) region in Trident/Molineux{10343}.
Two resistance gene analogues similar to the candidate gene *Cre3* were isolated from the *Ae. ventricosa* segment carrying *Cre5*.
Cre5 conferred resistance to *H. avenae* but not to *H. filipjevi* {11394}.

CRE6

Cre6 {0138}. Derived from *Ae. ventricosa* {0138}. 5N^v {0138}. **ad:** Moisson + 5N^v {0138}. **v:** H-93-35 {0138}. **v2:** H-93-8 *Cre2* {0138}.

CRE7

Cre7 {104}. Derived from *Ae. triuncialis* {0105}. [*CreAet* {0105}]. **v:** TR353 derivatives {0105}.

CRE8

Cre8 {220}. [*CreF* {138}, {12}]. 6BL {0220}, on basis of linkage with *Xbcd1-6B* and *Xcdo347-6B* {220}. **v:** Barunga {220}; Festiguay {220}, {12}; Frame {220}, {138}; Molineaux {220}. **ma:** Linked to RFLP loci *Xbcd1-6B* and *Xcdo347-6B*. The 6B location of the *Xcdo347* probe used in this study was confirmed by nulli-tetrasomic analysis{220}; Associated with the *Xgwm147-6B* ($R^2 = 24\%$) – *Xcdo247-6B* ($R^2 = 12\%$) region in Trident/Molineux {10343}; The map in {10343} was reversed: *Cre9* was located closer to the end of chromosome 6BL {11081}; Six markers that can be screened by KASP^{TM} and *wri15* developed from a SNP were reported {11081}.

CRE9

Cre9 {11394}. [*QCre-ma7D* {11394}]. **v:** VPM-1/Moisson 951{11394}. **v2** Madsen *Cre5* {11394}; VPM-1 *Cre5* {11394}. **ma:** Flanked by *Xics7D-27-7D* and *BS00129645* {11394}. KASP markers *BS00021745*, *BS00150072*, and *BS00154302* were developed {11394}.
Cre9 conferred resistance to Chinese isolates of *H. filipjevi* but not to *H. avenae*.

Temporay designations

CreR {318}, {133}. 6RL {133}. **ad:** Wheat + 6R {318}; Wheat + 6RL {318}; Various deletion stocks {318}. **su:** CS + 6R(6D) {133}. **al:** Rye accession T701-4-6 {133}; Triticale T-701{318}. **ma:** Cent......*XksuF37* 3.7 cM – *CreR* {133}; Deletion mapping indicated *CreR* was located near *Got-R2* {318}.

CreX {10486}. Derived from *Ae. variabilis* 2AS or 2DS {10486}. **ad:** Line M {10487}. **v:** Line D {10486}. **ma:** RAPD markers $OP02_{1000}$, $OpR4_{1600}$, $OpV3_{450}$ {10486}.

CreY {10486}. Derived from *Ae. variabilis* 3BL {590}. **v:** Line X {10487}. **ma:** Co-segregation with RAPD $OpY16_{1065}$ {0103} which was converted to SCAR16 {10486}.
May be the same gene as *Rkn-mn1* (see reaction to *Meloidogyne naasi*).

QTL

QCre.pau-1A {10749}. 1AS {10749}. **dv:** *T. monococcum* Tm 14087 *QCre.pau-2A* {10749}. **ma:** *QCre.pau-1A* was mapped in a 3.6 cM interval in a *T. boeoticum* Tb 5088 / Tm 14087 RIL population and was flanked by *Xcfa2153-1A* and *BE444890* {10749}; R^2=0.26{10749}.
QCre.pau-1A was transferred to tetraploid and hexaploid lines {10749}.

QCre.pau-2A {10749}. 2AS {10749}. **dv:** *T. monococcum* Tm 14087 *QCre.pau-1A* {10749}. **ma:** *QCre.pau-2A* was mapped in a 4.00 cM interval flanked by *BE498358* and *Xwmc358-2A* {10749}; R^2=0.13{10749}.

Qcre.src-1B was located to the *Xwmc719-1B* (R^2=12%) – *Xgwm140-1B* (R^2=12%) region in Trident/Molineux {10343}.

For review {11309}.

3.13. Reaction to *Magnaporthe* spp.

3.13.1. Reaction to *Magnaporthe grisea* (Herbert) Barr: Syn. *Pyricularia oryzae*

M. grisea is a pathogen of blast on many graminaceous species, the best known of which is rice. In Brazil a related form has become a pathogen of wheat. The wheat pathotype(s) (MoT) is different from those attacking other species such as rice, oat, millets and weeping lovegrass.

RMG1 *TraesJAG1D03G00423690*; *TraesCS1D02G058900*; this locus is also named *PM24* {11414, 11632}

Rmg1 {10461; 10462}. [*Rwt4* {0302}]. 1D {10462}. **s:** CS (Cheyenne 1D) {10462}. **v1:** Cheyenne {10462}; Norin 26 {10462}; Shin-chunaga {10462}. **v2:** Norin 4 *Rmg6* {0302, 11470}. **c** Candidate gene encodes a 916 amino acid protein with a wheat tandom kinase (WTK) domain {11632}.
Rmg1 was present in 87% of surveyed genotypes {11470}.

RMG2

Rmg2 {10461}. 7A {10461}. **i:** CS (Thatcher 7A) {10461}. **v2:** Thatcher *Rmg3* {10461}.

RMG3

Rmg3 {10461}. 6B {10461}. **i:** CS (Thatcher 6B) {10461}. **v2:** Thatcher *Rmg2* {10461}.

RMG4

Rmg4 {10639}. 4A {10639}. **v:** Norin 4 {10639}; Norin 26 {10639}; Norin 29 {10639}; P168 {10639}; Shin-chunaga {10639}; *T. compactum* No. 24 {10639}.
Confers resistance to *Digitaria* isolate Dig41 at 26C {10639}.

RMG5.

Rmg5 {10639}. 6D {10639}. **s:** CS (Red Egyptian 6D) {10639}. **v:** Red Egyptian {10639}.
Confers resistance to *Digitaria* isolate Dig41 at 26C {10639}.

RMG6. *TraesCS1D02G029900.*

Rmg6 {10948 11504}. [*Rwt3* {11470, 11504}]. 1DS {10948}. **v1:** Chinese Spring {10948}; Shin-Chunaga {10948}, Transfed {11470}. **v2:** Chinese Spring *Rmg9* {11504}, Norin 4 *Rmg1* {10948, 11470}. **ma:** *Xwmc432-1D* – 9.6 cM – *RMG6* – 6.6 cM – *Xwmc222-1D* {10948}; 11.60 – 11.80 Mb {11632}. **c:** Candidate gene encodes an NRL with 1,069 amino acids (11632}.
Rmg6 was present in 77% of surveyed genotypes 11470}. *Xwmc432-1D* – *RMG9* – 5.0 cM – *RMG6* – *Xwmc222-1D* {11504}.
A second gene in chromosome 1D designated *Rwt4* {0302} (*TraesCS1D02G058900* {11632}) (was present in CS and Norin 4. **c:** *Rwt4* was identified as wheat tandom kinase {11632}.

Genes *Rwt3* and *Rwt4* were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.
Rmg6 and a second gene with a weaker effect conferred resistance to a selected *Triticum x Lolium* isolate {10948}.

RMG7

Rmg7 {11046}. 2AL {11083}. **tv:** *T. dicoccum* KU112 {11046}; KU120 {11046}; KU1222 {11046}. **ma:** *Xcfd50-2A* – 5.6 cM – *Rmg7* – 15.1 cM – *Xhbg327-2A* {11083}. **c:** The sequence of *Rmg7* was identical to *Pm4a* {11735}. *Rmg7* has the same specificity as *Rmg8* {11735}.
Rmg7 and Rmg8 recognise the same *Avr-Rmg8* effector {11775}.

RMG8

Rmg8 {11083}. 2BL {11083}. **bin:** 2BL6-0.89-1.00. **v:** S615 {11083}. **ma:** *Xwmc317-2B* – 12.1 cM – *Rmg8* – 22.4 cM – *Xbarc159-2B* {11083}. **c:** The nucleotide sequence of *Rmg8* was identical to *Pm4f* {11735}. *Rmg8* has the same specificity as *Rmg7* {11735}.
According to {11083} markers linked to *RMG8* were independent of those linked to RMG7. The *Pm4a* allele in some accessions is located in chromosome 2B {11735}.
Among *PM4* alleles *Pm4a, Pm4b and Pm4d* conferred resistance to both MoT and *Bgt*; *Pm5f* conferred resistance to MoT but not *Bgt*, and *Pm4f* was ineffective against both pathogens {11735}.

RMG9

Rmg9 {11504}. [*Rwt6* {11504}. 1D {11504}. **v2** Chinese Spring *Rmg6* {11504}. **ma:** *Xwmc432-1D* – *RMG9* – 5.0 cM – *RMG6* – *Xwmc222-1D* {11504}.

RMG10

Rmg10 {11736}. 2DS {11736}. **v:** Line 6051 (amphiploid Langdon / KU-2097) Permanent genbank accession number needed {11736}. **dv:** *Ae. taushii* KU-2097 {11736}. **ma:** *Xbarc-2D* – 7.8 cM – *Ms-4* – 7.8 cM – *RMG10* – 8.3 cM – *MS12* – 4.7 cM – *Xwmc503-2D* {11736}.

RMG11

Rmg11 {11755}. 7AS {11755}. **tv:** *T. dicoccum* St19, KU-114 {11755}. **ma** *IMT_5* – 1.0 cM – *RMG11* – *IMT_6/IMT_7* – 1.1 cM – *Xgwm635*-7A{11755}.
The *Rmg11* resistance remained effective at 30ºC {11755}.

Temporary desigations

RmgGR119 {11652}. **v:** GR119 *Rmg8* {11652}.

RmgTd(t) {10949}. 7BL {10949}. **tv:** *T. dicoccoides* KU109 {10949}. **ma:** *Xhbg338-7B* – 10.5 cM – *Rmg7* {10949}.

RmgTd(t) was detected with a white culture of an *Avena* pathogen isolate backcrossed to a wheat isolate. A virulence to *RmgTd(t)* was completely associated with white color of the pathgen isolate {10949}. The white color appeared as a mutant variant during backcrossing.

The wheat blast pathogen became established on wheat cultivar Anahuac (*rmg1 rmg6*) in Brazil in the mid-1980s. It was initially avirulent on cultivars such as IAC-5 with *Rmg6* but later acquired virulence allowing it to attack most wheat genotypes {11470}.

3.13.2. Reaction to *Magnaporthe oryzae*

RMG8

Rmg8. *Rmg8* also confers resistance to the wheat form of the pathogen. Its response is not sufficiently effective when present alone, but is enhanced in the presence of *RmgGR119* {11263}.
AVR-Rmg8 was isolated and shown to be a small protein with a putative signal peptide. This protein was recognized by both *Rmg8* and *Rmg7* {11272}.

RmgGR119 {11263}. **v:** GR119 {11263}.
RmgGR119 confers resistance to the wheat form of the pathogen and its response is enhanced in combination with *Rmg8* {11263}.

Near-isogenic lines with the T2A-2NS translocation from *Ae. ventricosa* displayed reduced levels of spike blast, but there was little effect on seedling leaf blast response {11265}: **v:** Milan; VPM1.
Wheat cultivars carrying the 2NS translocation from *Aegilops ventricosa* had 50.4 to 72.3% less head blast than those without 2NS when inoculated with an older isolate (MoT) of *Magnaporthe oryzae* (*Triticum* pathotype) under growth chamber conditions. When inoculated with recently collected isolates from wheat, cultivars with 2NS had 64.0 to 80.5% less head blast {11127}.
A review of wheat blast {11776}.

3.14. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

Insect pest: Hessian fly.

H1

H1 {1087}. **i:** Dawson/3*Poso, 6179 {1087}. **v2:** Big Club 43 *H2* {1441}; Dawson *H2* {166}, {1087}; Poso 42 *H2* {1441}.

H2

H2 {1087}. **i:** Dawson/3*Poso, 6232 {1087}. **v2:** Big Club 43 *H1* {1441}; Dawson *H1* {166}, {1087}; Poso 42 *H1* {1441}.

H3

H3 {156}. Recessive. 5A {1105}, {425}. Based on the location of *H9* on chromosome 1AS, *H3* may also be located on chromosome 1AS {10252, 10231}. **i:** Carol = Newton-207*5/Larned {1107}. **v:** Ace {426}; Arthur {426}; Becker {749}; Cardinal {750}; Dual {1273}; Frankenmuth {341}; Georgia 1123 {426}; GR855 {751}; GR876 {753}; Ike {10252}; Ionia {426}; Larned {824}; Logan {426}; Monon {157}; Norkan {904}; Ottawa {547}; Purdue B 36162 A13-12 {156}; PI 468960 {1439}; Redcoat {1273}; Reed {1273}; Riley {1273}; Roland {148}; Russell {426}; Shawnee {547}; Titan {747}; Todd {426}; W38 {156}. **v2:** Clara Fay *H6* {375}. **ma:** Cosegregation of *H3* and a RAPD {296}.
Allan et al. {019} considered that *H3* and *H4* might be allelic. Also suggested by Shands and Cartwright {1317}. Linkage of 10.5 +/- 2% involving *H3* and *Pm3a* in PI 468960 was attributed to a chromosome 1A/5A translocation {1437}.

H4H4. [*h4* {1441}]. Recessive. 1AS {11634}. *H4* confered resistance to race A, but not to race B. **v:** Dixon {1441}; Java {1441}. **ma:** Mapped to interval 6.64 – 728 Mb {11634}. KASP markers developed {11634}.

H5

H5 {1317}. Temperature sensitive {1413}. 1AS {1222}. **v:** Abe {162}; Arthur 71 {162}; Beau {875}; Downy {1223}; Magnum {10252}; Oasis {1109}; Ribeiro {1317}; Sullivan {1110}. **tv:** Giorgio 331-4 {1090}; PI 94567-6 {1317}; PI 94571-14 {1317}. **ma:** Cosegregation of *H5* and two RAPDs {296}.

H6

H6 {19}. Based on the location of *H9* on chromosome 1AS, *H6* may also be located on chromosome 1AS {10252,10231}. 5A{425}. **i:** Erin = Newton-207*7/Arthur 71 {1107}; Flynn = Newton-207*7/Knox 62 {1107}. **v:** Adder {1319}; Benhur {426}; Caldwell {1421}; Compton {1318}; CI 12855 {19}; Excel {752}; Fillmore {1106}; Knox 62 {426}; Lathrop {426}. **v2:** Clara Fay *H3* {375}. **tv:** Purdue 4835 A4-6 {1105}. **tv2:** PI 94587 *H11 H16* {19}. **ma:** Cosegregation with three RAPDs {296}.

H7 and *H8*

H7 & H8 {425}. Duplicate factors. *H7* is located in chromosome 5D {026}. **v:** Adena {748}; Seneca {425,26}.

H7. 6AS {11511}; 5D {026}. **ma:** Mapped as a major QTL (PVE 0.61 – 0.78) in a 6 Mb interval flanked by GBS6A205 and GBS6A215 {11511}.
With relocation of *H7* to chromosome arm 6AS there are issues of overlap with *H31*.

H8. 2B {11511}. **ma:** Mapped as a minor QTL (PVE, 0.03 – 0.05) {11511}.

The *H7* and *H8* genes were variously described as duplicate {026}, complementary and additive {11511}.

H9

H9 {1420}. 1AS {10252,10231}. 5A {162}. **i:** Iris = Newton-207*7/Ella {1107}. **v:** Ella {875}; Line 822-34 {162}. **v2:** Elva CI 17714 *H10* {162}; Line 812-24 *H10* {1421}; Line 817-2 *H10* {1421}; Stella *H10* {875}. **ma:** Cosegregation with two RAPDs {296}; *STS-Pm* – 1.7 cM – *SOP005*$_{909}$ – 0.6 cM – *Xksu11/Xcnl76/Xgdm3* – 0.5 cM – *Xgwm176/Xpsp2999/Xcfa2153-1A* – 0.5 cM – *Xbarc263-1A* – 1.2 cM – *H9 - Xwmc24-1A* {10231}; *Xcfa2153-1A* – 0.5 cM – *H9* – 0.3 cM – *Xbarc263-1A* {10252}.

H10

H10 {1104}. May be identical to H9 {10252}. 1AS {10252}. 5A {162}. **i:** Joy = Newton-207*3/IN76529A5-3-3 {1107}. **v:** IN76529 {875}. **v2:** Elva CI 17714 *H9* {162}; Line 817-2*H9* {162}; Stella *H9* {875}. **ma:** Cosegregation with one RAPD and close linkage to another RAPD {296}; *Xcfa2153-1A* – 0.5 cM – *H10* – 1.3 cM – *Xbarc263-1A* {10252}; *Xrapd9-2-1000/Xpsp2999-1A/Xgps7072-1A* – 2.2 cM – *H10* {10252}.

H11

H11 {1422}. 1A {1222}. 1AS {10252}. **i:** Karen = Newton-207*4/IN916-1-3-1-47-1 {1107}. **v:** Kay {875,375}; Line 916 {1422}; Line 920 {1422}; Line 941 {1422}. **tv2:** *T. turgidum* PI 94587 *H6 H16* {1422}. **ma:** Close linkage with two RAPDs{296}; *Xcfa2153-1A* – 0.3 cM – *H11* 1.7 cM – *Xbarc363-1A* {10252}.

H12

H12 {1092}. 5A {1098}. **i:** Lola = Newton-207*4/Luso {1107}. **v:** Luso {1092}. **ma:** Cosegregation with one RAPD and close linkage of *H12* to another RAPD {296}.

H13

H13 {1104}. 6DS {10251, 10388}. 6DL {441}. **i:** Molly = Newton-207*7/3/KU221-19/Eagle/ KS806 {1107}. **v:** AGS 2010 {11008}; AGS 2026 PI 658065 {11008}; KS81H1640HF {441}; Oglethrope PI 657986 {11008}; PI 562619 {10388}; SW34=Langdon/*Ae. tauschii* RL 5544 {10388}; *T. turgidum* var. *durum* cv. Gulab KU 134/*Ae. tauschii* KU 2076, KU 221-14 {525}; *T. turgidum* var. *persicum straminium* KU 138/*Ae. tauschii* KU 2076, KU221-19 {525}. **dv:** *Ae. tauschii* KU 2076 {525}. **ma:** Cosegregation with a RAPD{296}; *Xgdm36-6D* – 2.7 cM – *H13/Xcfd132-6D* – 1.1 cM – *Xcfd213-6D* {10251}; *Xcfd132-6D* – 3.7 cM – *H13* {10388}.

H14

H14 {875}. 5A {875}. **tv:** IN 81601A2-3-3 {875}. **tv2:** ELS 6404-160 *H15* {875}. **ma:** Cosegregation with a RAPD {296}.

H15

H15 {875}. 5A {875}.Based on the location of *H9* on chromosome 1AS, *H15* may also be located on chromosome 1AS {10231}. **tv:** IN81602C5-3-3 {875}. **tv2:** ELS 6404-160 *H14* {875}.

H16

H16 {1106}. 5A {1098}. 1AS {11058}. **bin:** 1AS-3-0.86-1.00. **v:** P921682 {11058}. **tv:** IN 80164H5-2-9 {1106}; N80164 {1097}. **tv2:** PI 94587 *H6 H11* {1106}. **ma:** Cosegregation of *H16* and a RAPD{296}; *Xpsp2999-1A* – 3.7 cM – *H16* – 5.5 cM – *Xbarc263/Xwem6B-1A* {11058}.

H17

H17 {1090}. 5A {1090}. 1AS {11058}. **bin:** 1AS-3-0.86-1.00. **v:** P921680 {11058}. **tv:** PI 428435 {1090}. **ma:** Cosegregation of *H17* and a RAPD {296}; *Xpsp2999-1A* – 6.27 cM – *H17* – 5.1 cM – *Xbard263/Xwem6B-1A* {11058}.

H18

H18 {1090}. **v:** Marquillo {426,874}; Redlant {10715}; Shield {198}.

H19

H19 {1089}. **tv:** PI 422297 {1089}; This germplasm possesses a second gene which is allelic or closely linked with *H16* {1089}; IN84702 {1097}. **tv2:** PI422297 *H29* {1097}.

H20

H20 {25}. 2B {25}. **tv:** Jori {25}.

H21 H21. 2B {383} = 2BS.2R#2L {389}. **v:** Hamlet = KS89WGRC8 {1312}; KSWR 69-2-4-3 {383}; KS85HF 011-5 {383}. **ad:** KSWR 297h-1-1-9 {383}. **al:** Chaupon rye {383}. **ma:** A RAPD amplified by primer OPE-13 was shown to co-segregate with *H21* {9938}; STS primer set SJ07 was developed to identify 2RL, and hence *H21* {233}.

H22

H22 {1199}. 1D {1199}. 1DS {10381}. **v:** KS86WGRC1 {1199}; KS85WGRC01=*Ae. tauschii* TA1644/Newton//Wichita {1199}; PI 572542 {10388}. **ma:** *Xgdm33-1D* – 1.0 cM – *H22* – 0.3 cM – *Xhor2KV-1D* – 0.5 cM – *Xgpw7082-1D* {10381}.

H23

H23 {1199}. 6DS {10251}. 6DL {1199}. 6D{442}. **v:** KS89WGRC03 = TA1642 / 2*Wichita {10251,442}; PI 535766 {10388}. **al:** *Ae. tauschii* TA1642 {10251}. **ma:** *H23* – 6.9 cM – *XksuH4-6D*{861}; Maps to same region as *H13* {10262}.

H24

H24 {1199}. 6DL {861}. 3D {1199,442}. **v:** KS89WGRC6 {442}; PI 535769 {10388}. **ma:** *H24* – 5.9 cM – *Xbcd451-6D/Xcdo482-6D* {861}.

H25

H25.
6B{384} = T6BS.6BL-6R#1L {389} **v:** 88HF16 = WGRC17 {384}.
4B {384} = T4BS.4BL-6R#1L {389} 88HF79, 88HF80 = WGRC18, 88HF81, 88HF117 = WGRC19 {384}.
4A {384} = Ti4AS.4AL-6R#1L-4AL {389} 89HF17, 89HF18, 89HF25, 88HF32, 88HF51, 88HF89 = WGRC20 {384}.
6R. **al:** Balbo rye {384}.

H26

H26. 4D {217}. 3DL {10388}. **bin:** 3DL3-0.81-1.00. **v:** KS92WGRC26 {217}; SW8 = Langdon/*Ae. tauschii* CIae 25 {10388}. **dv:** *Ae. tauschii* TA2473 {217}. **ma:** *Xcfd211-3D* – 7.5 cM – *H26* – 2.9 cM – *Xwgc7330-3D* – 4.0 cM – *Xgwm3-3D* {10388}. *Xrwgs-3D* – 3.2 cM – *H26/Xrwgs11-3D* – 1.0 cM – *Xrwgs12-3D* {10846}.
H26 is very close to *H32* {10846}.

H27

H27 {235}. $4M^v$ {235}. **su:** H-93-33 {235}. **al:** *Ae. ventricosa* No. 10 {235}; *Ae. ventricosa* No. 11 {235}.

H28

H28 {171}. 5^A {171}. **tv:** PI 59190 {171}.

H29

H29 {1095}. [*H27* {171}]. 5A {1097}. **tv:** PI422297 *H19* {1097}.

H30

H30 {256}. Derived from *Ae. triuncialis* {0256}. **v:** TR-3531 {256}. **al:** *Ae. Triuncialis* {256}.

H31

H31 {332}. 5BS {332}. **v:** P961696{332}. **tv:** CI 3984{332}. **ma:** STS marker *Xupw4148-5B* – 3 cM – *H31* {332}.

H32 {10137}. 3DL {10137}. **bin:** 3DL3-0.81-1.00. **v:** Synthetic W7984 {10137}. **ma:** *Xgwm3-3D* – 1.7 cM – *H32* – 1.7 cM – *Xcfd-3D* {10137}; *Xrwgs10-3D* – 0.5 cM – *H32/Xrwgs11-3D* – 0.5 cM – *Xrwgs12-3D*{10846}. KASP markers developed {11633}.
H32 is very close to *H26* {10846}.

H33

H33 {10954}. 3AS {10954}. **v:** Line 97211 {10954}. **tv:** PI 134942 {10954}. **ma:** *Xgwm218-3A* – 10 & 7 cM – *H33* – 28 & 25 cM – *Xhbg-3A* {10954}.

H34

H34 {11018}. [*Qhf.hwwg-6B* {11018}]. 6BS {11018}. **v:** Clark {11018}. **ma:** Flanked by *Xsnp921-6B* and *Xsnp2745-6B* within a 4.5 cM region, R^2 = 0.38-0.42 {11018}.

Halotype analysis was used to postulate *Ae. tauschii*-derived genes *H13, H22, H23, H26* and *H32* in a set of synthetic wheat lines {10983}.

H35 in chromosome arm 3BS and ***H36*** in chromosome arm 7AS were named for one major and one minor QTL in common wheat line SD06165 {11512}.

Temporary designations:

Hdic {10262}. 1AS {10262}. **v:** KS99WGRC42 {10262}. **tv** *T. dicoccum* PI 94641 {10262}. **ma:** *Xcfa2153-1A* – 1.4 cM – *Hdic* – 0.6 cM – *Xgwm33-1A* {10262}.

HNC09MDD14. [*Hf-NC09MDD14* {10844}]. 6DS {10843}. **v:** NC09MDD14 PI 656395 {10843}. **dv:** *Ae. tauschii* TA2492 and/or TA2377 {10843}. **ma:** *Xgdm36-6D* – 1.5 cM – *HNC09MDD14/Xcfd123-6D* {10843}; *HNC09MDD12* could be allelic to, but is different from, *H13* {10843}.

HR61 {11008}. 6AL {11008}. **bin:** 6AL8-0.90-1.00 {11008}. **v:** 26R61 PI 612153 {11008}. **ma:** Mapped as a QTL (R^2=0.63) flanked by *Xgwm427-6A* and *wPt-731936* {11008}.

H_{WGRC4} {10251}. 6DS{10251}. **v:** KS89WGRC04 = TA 1695 / 3*Wichita {10251}. **ma:** Allelic with *H13* {10251}.

A recombination value of 12.0% between leaf-rust reaction {possibly *Lr10*} and Hessian-fly reaction in Selection 5240 was reported {018}.

QTL:

Qhf-hwwg-1A {11018}. 1AS {11018}. **v:** Clark *H34* {11018}. **ma:** Closely linked to *Xwgm33-1A* {11018}; Located within a 6 cM region flanked by *Xwgm33-1A* and *Xsnp5150-6B*, R^2=0.1 {11018}.

QHf.hwwg-6BS {11635}. 6BS {11635}. **v:** Chokwang {11635}. **ma:** Located to interval 6BS 6.029 – 10.779 Mb (CS RefSeq v2.0) {11635}. KASP markers developed {11635}.

QHf.hwwg-6BS {11635}. 6BS {11635}. **v:** Chokwang {11635}. **ma:** Located to interval 6BS 6.029 – 10.779 Mb (CS RefSeq v2.0) {11635}. KASP markers developed {11635}.

QH.icd-2A {11510}. Putatively derived from *T. dicoccum* {11510}. 2AL. **ma:** Linked with *Ax-94980581I* {11510}.

QH.icd-5B {11510}. 5BS. **tv:** DWHF01 {11510}.
Possible overlap with *H31* {11510}.

Qhara.icd-6B {11510}. 6BS. **tv:** *T. timopheevii* subsp. *ameniacum* derivatives: DWHF02 {11510}; Chaoui {11510}; Icamoram7d {11510; Marouane {11510}; Nassira {11510}. **ma:** Linked with *Ax-95181449* {11510}.

Duster (R) / Billings: DH population: *QHf.osu.1A.2* (Syn. *QHf.osu-1A*^{d}), $R^2 = 0.88$, delimited to a 2.7 cM region flanked by *GBS07851* and *GBS10205* {11324}. This was a distinct locus 11.2 cM proximal to *QHf.osu.1A*.

Jagger (S) / 2174 9 (R): RIL population: *QHf.osu-1A* (Syn. *Qhf.osu*^{74} ($R^2 = 0.70$) and *QHf.osu-2A* ($R^2 = 0.18$) {11325}. The QTL in chromosome 1A appeared to be co-linear with several previously named *H* genes in tetraploid wheat; the gene in 2A was in repulsion with the 2N segment present in Jagger {11325}.

***Mayetiola destructor*-tolerance QTL**

QHft.nc-7D in chromosome arm 7DS conferring tolerance to Hessian fly in line LA03136E71 is reported in {11513}.

***Mayetiola-destructor* susceptibility gene-1**

Mds-1A {112327}. [*Mds-1*] {11327}. 3AS {11327}. **v:** No allelic variation demonstrated. **c:** EST CD453475, GenBank JN162442; *Mds-1A* encodes a 151 amino-acid protein with 96% identity with HSP16.9 {11327}. Homoeologues are present in chromosomes 3B and 3D. Silencing of *Mds-1* expression caused immunity in otherwise FHB-susceptible genotypes {11327}.

3.15 Reaction to *Meloidogyne* spp.

Root rot nematode, root knot eelworm

RKN1

Rkn1{632}. [*Rkn* {632}]. 6D {10799}. **dv:** *Ae. tauschii* G3489. **v:** Prosquare, a synthetic hexaploid of Produra/*Ae. tauschii* G3489 {632}.

RKN2

Rkn2 {1621}. Derived from *Ae. peregriina (variabilis)* {1621}. [*Rkn-mn1* {1621}]. 3B {590}. **v:** X8 = CS/*Ae. peregrina* No. 1//Rescler/3/Lutin {1620}; X35 {1620, 1621}. **ma:** Co-segregation with RAPD *OpY16*$_{1065}$ and close linkage with several markers including *Est-B5* {103}; converted to SCAR Y16

{10486}; May be the same as *CreY* (see reaction to *Heterodera avenae*) on chromosome $3S^V$ from *Ae. variabilis* translocated to 3BL {10800}.

RKN3

Rkn3{10801, 11264}. Derived from *Ae. ventricosa* 2NS translocation into 2AS {10801}. **v:** VPM1, Lassik (PI 653535) {10801}. **ma:** Resistances to *M. javanica* and *M. incognita* mapped to the 2NS translocation in BC_6F_3 near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation {10801}.

3.16. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter, *Zymoseptoria tritici*

Disease: Septoria tritici blotch

STB1

Stb1. [*Slb1* {1586}]. 5BL {10123}. **bin:** FL 5BL-11 - 5BL-14 {10123}; **v:** Bulgaria 88 {1586}; Oasis {1586}; P881072-75-1 {10123}; SO852 {10123}; Sullivan {1586}. **ma:** Close linkage with 2 RAPD markers at >0.68 and 1.4 cM in P881072-75-1 {10123}; Cent.....*Xbarc74-5B* – 2.8 cM – *Stb1* {10123}.

STB2

Stb2. [*Slb2* {1586}]. 1BS {10976}. 3BS {10105}. **v:** Nova Prata {1586}; Veranopolis {1586}. **ma:** *Xgwm389-3B/Xgwm533-3B* – 1.0 cM – *Stb2* – 3.7 cM – *Xgwm493-3B* {10105}; *Stb2* is neither on 3BS nor linked with *Xgwm389-3B* {10976}; *Xwmc406-1B* – 6.0 cM – *Stb2* – 5.0 cM – *Xbarc008-1B* {10976}.

STB3

Stb3. [*Slb3* {1586}]. 7AS {10556, 11191}. 6D, {10105} (according to {10556} this location is not correct. **v:** Israel 493{1586}. **ma:** *Xcfa2028-7A* – 12.4 cM – *Stb3/Xwmc83-7A* – 2.1 cM – *Xbarc222-7A* {11191}.

STB4

Stb4 {1410}. 7DS {10140}. 7D {326}. **v:** Cleo {1410}; Gene {10010}; Tadinia {10140,1410}; Tadorna {1410}. **ma:** *XAGG/CAT10* – 4.0 cM – *Stb4* – 0.7 cM – *Xgwm111-7D* – 1.4 cM – *XATCG/CAAA5* ....Cent {10140}; *Stb4* – 0.7 cM – *Xgwm111-7D* {10140}.
Stb4 segregated independently of *Stb1* but its relationship with *Stb2* and *Stb3* is unknown. Genetic analysis of Tadinia indicated single gene segregation (assumed to be *Stb4*) with a Californian culture but a different single gene segregated with South American isolates {10140}.

STB5

Stb5 {0186}. Identified using *M. graminicola* IPO94269 {0186}. Derived from *Ae. tauschii* accession 37-1 {0186}. 7DS {0186}. **v:** Baldus {11446}; Bezostaya {0187}; Chaucer {11446}; Hereward

{0187}; Israel 493 {11446}; Longbow {11446}; Olaf {11446}; Sears' Synthetic {0186}; Senat {11446}; Shafir {0}; Veranopolis {11446}; Vivant {0187}. **su:** CS*8/(Syn7D) {0186}. **dv:** *Ae. tauschii* 37-1 {0186}. **ma:** *Rc3* – 6.6 cM – *Stb5* – 7.2 cM – *Xgwm44-7D* – Centromere{186}; *Stb6* – 2 cM – *Xgwm369-3A* {0187}.

STB6

Stb6 {0187}. Confers resistance to *M. graminicola* isolate IPO323 but not to isolate IPO94269 {0187}. [*TaWAKL*4 {11434}]. 3AS {0187}. **v:** Amigo {10448}; Arina {10448}; Amada {10448}; Atlas 66 {10448}; Ble Seigle {10448}; Bon Fermier {10448}; Cadenza {11434}; Chinese Spring {10448}; Bezostaya 1 {10495}; Flame {187, 11434}; Gene {10448}; Heines Kolben {10448}; Hereward {10448}; Poros {10448}; Senat {10448}; Shafir {10448}; Tadinia {10448}. **v2:** Bulgaria 88 *Stb1* {10448}; Israel 493 *Stb3* {10448}; Kavkaz-K4500 *Stb7 Stb10 Stb12* {10011}; TE9111 *Stb7 Stb11* {10012}; Veranopolis *Stb2* {10448}. **tv** *Stb6* is common in *T. dicoccum* {11434}. **ma:** A resistance gene from Senat located at or near the *Stb6* locus was mapped 5 cM from microsatellite *Xgwm369-3A* on chromosome arm 3AS {10067}; *Xgwm369-3A* – 4.3 cM – *Stb6* – 3.8 cM – *Xgwm132-3A* {11434}. **c:** Encodes a wall-associated receptor kinase (WAK)-like protein {11434}.

STB7

Stb7 {0311}. 4AL {0311}. **v:** ST6 = Estanzuela Federal. **v2:** Kavkaz-K4500 *Stb6 Stb10 Stb12* {10011}; TE9111 *Stb6 Stb11* {10012}. **ma:** *Xwmc219-4A* – 0.8 cM – *Xwmc-4A* – 0.3 cM – *Stb7* {0311}; *Stb7* was closer to *Xwmc313-4A* than to *Xwmc219-4A* {10011}.

STB8

Stb8 {0326}. 7BL {0326}. **v:** Synthetic hexaploid W7984 (parent of ITMI population) {0326}. **ma:** *Xgwm146-7B* – 3.5 cM – *Stb8* – 5.3 cM – *Xgwm577-7B* {0326}.

STB9

Stb9 {10027}. Culture IPO89011 2BL{10027}. **v:** Courtot {10027}; Tonic {10027}. **ma:** *Xfbb226-2B* – 3 cM – *Stb9* – 9 cM – *XksuF1b-2B* {10027}.

STB10

Stb10 {10011}. Confers resistance to cultures IPO94269 and ISR8036, but not to IPO87019 {10011}. 1D {10011}. **v2:** Gene *Stb5* {11446}; Frontana *Stb5* {11446}; Kavkaz-K4500 L.6.A.4 *Stb6 Stb7 Stb12* = JIC.W9995 {10011}; Mentana *Stb5* {11446}. **ma:** Associated with *Xgwm848-1D* {10011}.

STB11

Stb11 {10012}. Confers resistance to isolate IPO90012 {10012}. 1BS{10012}. **v:** JIC W 9996; TE9111. **v2:** TE9111 *Stb6 Stb7* {10012}. **ma:** Distal to *Xbarc008-1B* {10012}.

STB12

Stb12 {10011}. Confers resistance to cultures ISR398, ISR8036 and IPO87019 {10011}. 4AL {10011}. **v2:** Kavkaz-K4500 *Stb6 Stb7 Stb10* {10011}. **ma:** *Stb12* was closer to *Xwmc219-4A* than to *Xwmc313-4A* {10011}.

STB13

Stb13 {10347}. Confers resistance to Canadian cultures MG96-13 and MG2 {10347} 7BL {10347}. **v:** DH line 90S05B*01 {10347}; DH line 98S08C*03 {10347}. **v2:** Salamouni *Stb14* {10347}. **ma:** *Xwmc396-7B* – 9 cM – *Stb13*{10347}; *Xwmc396-7B* – 7 cM – *Stb13* {10347}.

STB14

Stb14 {10348}. Confers resistance to Canadian isolate MG2 but not to MG96-13 {10347} 3BS {10348}. **v:** DH line 98S08A*09 {10348}. **v2:** Salamouni *Stb13* {10347}. **ma:** *Xwmc500-3B* – 2 cM – *Stb14* – 5 cM – *Xwmc623-3B* {10348}.

STB15

Stb15 {10341}. Confers resistance to Ethiopian culture IPO88004 {10341} 6AS {10341}. **v:** Riband {10341}. **v2:** Arina *Stb6* {10341}. **ma:** *Stb15* – 14 cM – *Xpsr904-6A* {10341}.

STB16

Stb16 {10879}. Seedling and adult plant resistance [*Stb16q* {10879}]. 3DL {10879}. **v2:** Synthetic W-7976 *Stb17* {10879}. **ma:** Associated with *Xgwm494-3D* and mapped as a QTL, R^2=0.4-0.7 in seedling tests and 0.28-0.31 in mature plants {10879}.

STB17

Stb17 {10879}. Adult plant resistance 5AL {10879}. **v2:** Synthetic W-7976 *Stb16* {10879}. **ma:** Associated with *Xhbg247-5A* and mapped as a QTL, R^2=0.12-0.32 {10879}.

STB18

Stb18 {10827}. Confers resistance to IPO0323, IPO98022, IPO98046 {10827} 6DS {10827}. **v2:** Balance *Stb6 Stb11* {10827}. **ma:** Mapped as a QTL located in a 8.8 cM region spanned by *Xgpw3087-6D* and *Xgpw5176-6D* {10827}.

STB19

Stb19 {11360}. Derived from synthetic wheat. 1DS {11360}. **v:** Lorikeet {11360}. **ma:** KASP markers snp_4909967 and snp_1218021 {11360}.

See {11332, 11361} for reviews.

Temporary designation

TmStb1 {11446}. Resistance to IPO323. **dv:** *T. monococcum* MDR043 {11446}.

QTL

Four QTLs for resistance to *Mycosphaerella graminicola* were identified in replicated field experiments in a double haploid population from **Savannah (susceptible)/Senat (resistant)**. Senat contributed all the alleles providing resistance {10067}.

QStb.riso-2B was mapped on chromosome arm 2BL linked to SSR marker *Xwmc175-2B* (LOD>5, R^2>17%) {10067}.

QStb.riso-3A.2 was mapped on chromosome arm 3AS linked to SSR markers *Xwmc489-3A, Xwmc388-3A* and *Xwmc505-3A* (LOD >4, R^2>18%). Also detected at the seedling stage {10067}. *Xgwm369-3A* is present on chromosome arm 3AS {0187}. A resistance gene from Senat located at or near the *STB6* was mapped 5 cM from *Xgwm369-3A* on chromosome arm 3AS {10067}.

QStb.riso-6B was mapped on the centromeric region between SSR markers *Xwmc494-6B* and *Xwmc341-6B* (LOD >16, R^2 >68%). Also detected at the seedling stage {10067}.

QStb.riso-7B was mapped on chromosome 7B close to SSR marker *Xwmc517-7B* (LOD>4, R^2>11%) {10067}.

ITMI Population: Three QTL, ***QStb.ipk-1DS, QStb.ipk-2DS*** and ***QStb.ipk-6DS*** conferred seedling-stage resistance to 2 isolates, whereas 2 QTL ***QStb.ipk-3DL*** and ***QStb.ipk-7BL*** conferred separate adult-stage resistances to each isolate {10151}.

A weak QTL, ***QStb.psr-7D.1***, giving partial resistance to Portuguese isolate IPO92006, was detected in the *Xcdo475b-7B - Xswm5-7B* region in chromosome 7DS {10341}.

Apache / Balance: Analyses with a panel of *M. graminicola* cultures identified QTLs on chromosomes 1BS (Apache, considered to be *Stb11*), 3AS (Balance, considered to be *Stb6*), 6DS (Balance, named as *Stb18*), 7DS (Apache, considered to be *Stb4*) and 7DL (Apache) {10827}.

Florett / Biscay (S): RIL population: two QTLs for APR were located on chromosomes 3B and 6D {10901}.

Solitar (R) / Mazurka (S): DH population: Resistance under field conditions was associated with QTL on chromosomes 5A, 6D and 7D which accounted for 20% of the genotypic variation; all three were derived from Solitar, but there was no evidence that *Stb6* and *Stb11*, also present in Solitar, were involved {10984}.

Spelt HRTI1410 (R) / three wheat parents: 135 DH lines: mapped using SNP polymorphisms common to all three S parents: four QTL identified on chromosome 5AL (74.2 – 82.4 cM; r^2 = 0.18); 4B (52.9 –

56.9 cm, $r^2 = 0.09$) contributed by the susceptible parents; and 7B.1 (41.2 – 57.0 cM, $r^2 = 0.09$), and 7B.2 (58.2 – 67.4 cM, $r^2 = 0.15$) contributed by the susceptible parents {11430}.

Steele-ND (R) / ND735 (S): RIL population: A consistent QTL ($R^2=0.1$) for seedling resistance flanked by DArT markers *XwPt-7101* and *X377410* was mapped to chromosome 5BL in the region of *Stb1* {10992}. Two other QTLs on chromosomes 1D and 7A were detected in single experiments {10992}.

Tuareg / Biscay (S): RIL population: two QTLs for APR were located on chromosomes 4B and 6B {10901}.

For a review of qualitative and quantitative resistance {11439}.

3.17. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano); *Parastagonospora nodorum*

Disease: Septoria nodorum blotch, Stagonospora nodorum blotch.

3.17.1. Genes for resistance

SNB1

Snb1 {856}. 3AL {856}. **v:** Red Chief {856}. **v2:** EE8 *Snb2* {856}.

SNB2

Snb2 {856}. 2AL {856}. **v2:** EE8 *Snb1* {856}.

SNB3

Snb3 {1594}. 5DL {1594}. **s:** CS*/Synthetic 5D {1594}. **v:** Synthetic {1594}. **dv:** *Ae. Tauschii* {1594}.

Temporay names

SnbTM {856} ,{857}. 3A {857}. 3AL {856}. **v:** Cooker {10210}; Hadden {10210}; Missouri {10210}; Red Chief {10210}; 811WWMN 2095 {10210}; 86ISMN 2137 {10210}. **tv:** *T. timopheevii*/2*Wakooma {856}; *T. timopheevii* PI 290518. *T. timopheevii* derivatives: S3-6 {857}; S9-10 {857}; S12-1 {857}. **ma:** *UBC521*$_{650}$ – 15 cM – *SnbTM* – 13.1 cM – *RC37*$_{510}${212}.
UBC521$_{650}$ was converted to a SCAR marker {0212}.
Allelism of the hexaploid wheat gene and the *T. timopheevii SnbTM* was suspected but not confirmed.

QTL
A QTL analysis of SNB response in the **ITMI population** found significant effects associated with chromosome 1B (probably *Snn1*) and 4BL, with an interactive effect involving the 1BS region and a

marker on chromosome 2B {10009}. An additional QTL on 7BL was effective at a later stage of disease development {10009}.

Arina / Forno: RIL population {10065}. Two QTLs for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in. *QSng.sfr-3BL* was associated with marker *Xgwm389-3B* and explained 31.2% of the variation with resistance contributed by Arina {10065}. The 4BL QTL, *QSng.sfr-4BL*, was associated with *Xgwm251-4B* and explained 19.1% of the variation. Resistance was contributed by Forno {10065}. A QTL on 5BL, *QSng.sfr-5BL*, overlapped with QTLs for plant height and heading time {10065}. *QSng.sfr-3BS* peaked 0.6 cm proximal to *Xsun2-3B* {10465}. Association mapping involving 44 modern European cultivars indicated that the association was retained in a significant proportion of genotypes {10465}.

Br34 / Grandin: Three QTLs with resistance effects from BR34; *Qsnb.fcu-5BL.1* (*Tsn1*), $R^2 = 0.63$, *Qsnb.fcu5BL.2,* $R^2 = 0.06$, and *Qsnb.fcu-1BS* (vicinity of *Snn1*), $R^2 = 0.10$ {10458}. QTL analysis of the RIL population with Culture Sn6 revealed four QTLs, *Qsnb.fcu-2DS* ($R^2 = 0.3 - 0.49$) associated with *Snn2*, *Qsnb.fcu-5BL* ($R^2 = 0.14 - 0.2$) associated with *Tsn1, Qsnb.fcu-5AL* ($R^2 = 0 - 0.13$) associated with *Xfcp13-5A*, and *Qsnb.fcu-1BS* ($R^2 = 0 - 0.11$) associated with *Xgdm125-1BS* {10507}.

Forno (S) / Oberkulmer spelt (R): Among 204 RILs leaf and glume response were genetically different but correlated (R^2=0.52). Ten QTLs for glume blotch (SNG) resistance were detected, 6 from Forno. A major QTL (R^2=35.8%) was associated with q. Eleven QTLs (4 from Forno) affected leaf blotch; 3 of these (chromosome 3D, 4B and 7B) with R^2>13% were considered potential candidates for MAS {10250}.

HRWSN125 (R) / WAWHT2074 (S): Constant detection of *QSnl.daw-2DL* for flag leaf resistance, and *QSng.daw-4BL* for glume resistance over two years {10584}.

ITMI population: A major QTL, coinciding with *Snn1*, was located in chromosome 1BS ($R^2 = 0.58$, 5 days after inoculation), minor QTL were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL {10009}.
P91193D1 (partially resistant) / P92201D5 (partially resistant) RIL populations were tested in Indiana and Western Australia for glume resistance. Two QTL were identified: *Qng.pur-2DL.1* from P91193D1 (R^2 = 12.3 in Indiana and 38.1% in WA, respectively; *Xgwm526.1-2D - Xcfd50.2-2D*) and *QSng.pur-2DL.2* from P99201D5 (R^2 = 6.9% and 11.2%, respectively; *Xcfd50.3-2D - wPT9848*) {10471}.

Liwilla / Begra: DH population: Four QTLs, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B and 5D. A longer incubation period and lower disease intensity were contributed by Liwilla {10045}. A QTL, *QSnl.ihar-6AL*, identified in DH lines of Alba (R) / Begra (S) accounted for 36% of the phenotypic variance in disease severity and 14% of the variance in incubation period {10143}.

Salamouni/Katepwa: RIL population: Two QTLs. *QSnb.fcu-1A* (*Snn4*) (R^2=0.24) and *QSnb.fcu-7A* (R^2=0.16) were associated with SNB response to isolate Sn99CH 1A7a {10867}.

Tetraploid wheat
Langdon / Langdon (*T. turgidum* ssp. *dicoccoides* Israel-A 5B): *QSnb.ndsu-5B* located 8.3 cM proximal to *tsn1* for tan spot resistance; R^2 = 0.38 {10597}.

A summary of QTL analyses is provided in {10726}.

3.17.2. Sensitivity to SNB toxins (necrotrophic effectors)

A discussion on the origin and role of host-specific toxins is provided in {10726}.

TSN1

Tsn1. Sensitive to SnToxA, which is functionally identical to Ptr ToxA {10459}. **v:** Cheyenne {7}; Forno {10725}; Hope {7}; Jagger {7}; Kulm {10458, 10030, 346}; ND495 {7}; Timstein {7}; Trenton {315}. **dv:** Two *Ae. speltoides* accessions {10756}. **tv:** Langdon {10458}; Some *T. dicoccoides* accessions {10756}. **c:** *Tsn1* has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA {10756}. See reaction to *Pyrenophora tritici repentis* {10458}.

tsn1 {10207}, {346}. Insensitivity (disease resistance) is recessive {346}. 5BL {346}. **v:** AC Barrie {10153}; AC Cadillac {10153}; AC Elsa {10153}; BR34 {7}; CEP17 {7}; Chinese Spring {7}; Erik {10030, 7}; Hadden {10155}; Laura {10153}; Line 6B-365 {10155}; Red Chief {10155}; 1A807 {7}; 1A905 {7}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122. **v2:** Grandin *Snn2 Snn3* {10507}. **tv:** Altar 84 {7}; D87450 {7}; *T. dicoccoides* Israel A {10506}. **ma:** *Xbcd1030-5B* – 5.7 cM – *tsn1* – 16.5 cM – *Xwg583-5B*{346}; – 3.7 cM – *Xbcd1030-5B*{7}; *Xfgcg7-5B* – 0.4 cM – *Tsn1/Xfcg17-5B* – 0.2 cM – *Xfcg9-5B*{10207}; *Xfcg17-5B* – 0.2 cM – *Tsn1* – 0.6 cM – *Xfcg9-5B*{10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM {10337}. *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1/XBE425878/Xfcc1/XBE443610* {10413}; This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B* {10724}.
Australian cultivars with *Tsn1* and *tsn1* are listed in {10540}.
Tetraploid wheat
In a reevaluation study Faris and Friesen {10688} attributed all of the variation in SNB response to the presence or absence of *SnTox1*.

Genotype list in {10724}.

snn1tsn1. Atlas 66 {10458}; BR34 {10458}; Erik {10458}; Opata 85 {10458}; ND688 {10458}.

SNN1

Snn1 {10008}. *TaWAK* {11341}. Sensitivity to SnTox1 is dominant {10008} 1BS {10008}. **bin:** 1BS.sat.18. **s:** CS-DIC 1B {10008}. **v:** CS {10008}; Grandin {10008}; Kulm {10008}; M-6 {10960}; ND495 {10008}. **ma:** *Snn1* – 4.7 cM – *XksuD14-1B* {10008}; *XksuD14.2-1BS* – 0.4 cM – *Snn1/XBE498831/XBF474204* – 0.4 cM *Xpsp3000-1BS/XBE422980/XBE637568/ZBE605202* {10727};

XksuD14.2 – 0.34 cM – *Snn1/XBE498831/XBF474204* – 0.12 cM – *XBF29322* – 0.04 cM – *Xpsp3000-1BS/XBE422980/XBE637568/XBF605202* {10727}; *Xfcp618-1B* – 1.9. cM – *Snn1* – 0.16 cM – *Xfcp624-1B* {11433} KASP marker *Bs00093078_51* was developed at Wang map position 8.361 in the UK MAGIC population {11133}. **c:** *Snn1* encodes a wall-associated kinase (WAK) {11341}. GenBank: KP091701.
Lebsock durum carried an intact *Snn1* but it was not expressed {11433}.
Snn1 was present in some *T. dicoccum* accessions, 73% of durum accessions and 16% of common wheat accessions {11341}.

snn1. **i:** CS*/*T. dicoccoides* 1B {10008}. **su:** CS/Hope 1B {11341}. **v:** Br34 {10008}; Erik {10008}; Opata 85 {10008}.

SNN2

Snn2 {10507}. Sensitivity to SnTox2 is dominant {10507}. 2DS {10507}. **v:** BG223 {10507}. **v2:** Grandin *Tsn1 Snn3* {10507}. **ma:** *Xgwm614-2D* – 7.6 cM – *Snn2* – 5.9 cM – *Xbarc95-2D* {10507}; *XTC253803* – 3.6 cM – *Snn2* – 0.4 cM – *Xcfd-2D* {10724}.

snn2. **v:** Atlas 66 {10724}; Br34 {10507}; Cheyenne {10724}; Chinese Spring {10724}; Jagger {10724}; Opata 85 {10724}; Salamouni {10724}; TAM 105 {10724}.

SNN3

Snn3-B1. *Snn3* {10507, 10728}. Sensitivity to SnTox3 is dominant {10728} 5BS {10507, 10728, 11637}. **bin:** 5BS-6{10507}. **v:** BG220 {10960}; Hope {11637}; Katepwa {11637}; Opata 85 {11637}; Timstein {11637}; Sumai 3 {11637}. 39% of a panel of wheat accessions {11637}. **dv:** 2.4% of a panel of *Ae. speltoides* accessions {11637}. **v2:** Grandin *Tsn1 Snn2* {10507, 10728}. **ma:** *Snn3* – 1.4 cM – *Xcfd20-5BS* {10507}.

Snn3-D1 (11637}. 5DS {116373}. **dv:** *Ae. tauschii* TA2377 {11637}. 12% of a panel of *Ae. tauschii* accessions {11637}. **ma:** *Xbarc130-5D* – 1.3 cm – *SNN3-B3/Xcfd18/Xhbg-5D* – 1.3 cM – *XBE446811* – 1.6 cM – *Xgwm190-5D* {11637}.
These likely homoeologous genes (*Snn3*-B1 and *Snn3-D1*) recognize the same pathogen effector (toxin) {11637}.

snn3. **v:** BR34 {10507}.

SNN4

Snn4 {10725}. Sensitivity to SnTox4 is dominant {10725} 1AS {10725}. **bin:** 1AS3-0.86-1.00 {10725}. **v:** Arina {10725}; Katepwa {10867}; Salamouni {10867}. **ma:** *XBG262267/* – 0.9 cM – *Snn4* – 1.6 cM – *Xcfd58.1-1AS* {10725}.

snn4. **v:** Forno {10725}.

SNN5

Snn5 {10925}. 4BL {10925,11205}. **bin:** 4BL5-0.85-1.00. **tv:** *T. carthlicum* PI 94749 {10925}. **tv2:** Lebsock *Tsn1 Snn3-B1* {11203}. **ma:** *Xbarc163/Xcfd-4B* – 13.3 cM – *Snn5* – 2.8 cM – *Xwmc349-4B* {10925}.

snn5. **tv:** LP749-29 {10925}; PI 94749 {10925}.

SNN6

Snn6 {11206}. 6AL {11206}. **v:** Opata 85 {11206}; RIL ITMI137 {11206}. **ma:** Flanked by *XBE424987* and *XBE403326* {11206}.

***snn6*.** **v:** Synthetic W-7984 {11206}.

SNN7

Snn7 {11292}. Sensitive to SnTox7. 2DL {11292}. **bin:** 2DL-9-0.75-1.00. **v:** Timstein {11292}. **ma:** *Xcdf267-2D* – 2.3 cM – *Xgdm6-2D* – 0.9 cM – *Snn7/Xcfd44-2D* – 1.8 cM – *Xgwm349-2D* – 11.3 cM – *Xgwm311-2D* {11292}.

QTL

QSnn.niab-5A.1 {11133}. **v:** Identified in the UK MAGIC population {11133}.

ITMI population: A major QTL, coinciding with *Snn1*, was located in chromosome 1BS ($R^2 = 0.58$, 5 days after inoculation), minor QTLs were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL {10009}.

P91193D1 / P92201D5: RIL population: tested in USA and Australia: *QSng.pur-2DL.1* from P91103D1, R^2=0.123 (Indiana) and 0.381 (South Perth); and *QSng.pur-2DL.2* from P92201D5, R^2=0.069 (Indiana) and 0.112 (South Perth) {10776}.

Host sensitivity genes in US southern winter wheats are listed in {1241}.

3.18. Reaction to *Pratylenchus* spp.

Root lesion nematode; prats

3.18.1. Reaction to *Pratylenchus neglectus*

RLNN1

Rlnn1 {0121, 0374}. 7AL {0121}. **v:** Excalibur {0121}; Krickauff {0121}. **ma:** Mapped between markers *Xpsr121-7A* and *Xgwm344-7A* and 9 cM proximal to *Lr20* {0374}.

3.18.2. Reaction to *Pratylenchus thornei*

QTLs were located on chromosomes 2BS and 6DS {0122, 11501}. These QTL were fine mapped in a Sokoll (MR) / Krichauff DH population and further crosses: *QRlny.sk-2B* was mapped to a 1.4 cM/2.19 Mbp region; *QRLnt.sk-6D* was mapped to a 3.5 cM/1.77 Mbp region {11501, 11502}.

3.19. Reaction to *Puccinia coronata* var. *hordei.*

CR1

Cr1 {10956}. 5DL {10956}. **v:** Chris CItr 14108 {10956}. **ma:** *Xwmc41.2-5D* – 11.3 cM – *Cr1* – 16.8 cM – *Xgdm63-5DL* {10956}.

3.20. Reaction to *Puccinia graminis* Pers.

Disease: Black rust; black stem rust; stem rust.
Note: Some near-isogenic lines are based on Marquis. The genes present in the Marquis background are not listed for those NILs.

SR1. Deleted - see *Sr9d.*

SR2

Sr2 {677}. Recessive allele. Adult plant response. 3BS {499}. **s:** CS*6/Hope 3B {499}. **v2:** HD2009 *Sr30* {10632}; Warigo *Sr7b Sr17* {499}; Suneca *Sr8a Sr17* {485}; Hopps *Sr9d* {499}; Lancer *Sr9d Sr17* {679}; Scout *Sr9d Sr17* {679}; See also {1040,499}. **ma:** *Xgwm389-3B* – 2.7 cM – *Sr2* – 1.1 cM – *Xglk683-3B*{358}; .....*Xglk683*(STS *Xsun2-3B*) – 0.5 cM – *Xgwm533-3B* {358}; These SSR loci were located within FL 0.87 - 0.75 {0358}; All 27 lines with *Sr2* carried a 120 bp allele at *Xgwm533-3B*; A 120 bp allele in 4 cultivars lacking *Sr2* differed from the *Sr2* associated allele at 4 base positions {0358}; STMs for the *Xgwm533-3B* locus had increased specificity as markers for *Sr2* {10142}; Tightly linked CAPS marker csSr2 based on a SNP proved superior to *Xgwm533-3B* as a marker for *Sr2* {10786}; *Xgwm389*-3B – 3.0 cM – *Sr2/csr2* – 0.4 cM – *Xgwm389*-3B – 2.0 cM – *Fhb1/UMN10/*UMN$_{v2}$ (coupling) {11210}; *Bs0006276* – 0.3 cM – *Yr57* – 1.3 cm – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B* {11480}.
Sr2 is associated with pseudo-black chaff {742, 1102} and seedling chlorosis (see {149}) and occurs very frequently in commercial wheats, especially in germplasm produced and distributed by CIMMYT. *Sr2* has probably remained effective since the 1920s.
Lines combining *Sr2* and *Fhb1* are reported in {11170}; *Sr2* was located about 2 cM distal to *Fhb1*.

SR3 & SR4

Sr3 & Sr4 {47}. **v:** Marquillo - based on early data. No stocks for the individual genes available.

SR5

Sr5 {47}. 6D {1308}, {939}, {1626}. 6DS {939}. **i:** I *Sr5*-Ra {828}; I *Sr5*-Rb {828}; Sr5/7*LMPG {685}; Thatcher/10*Marquis {686}. **s:** CS*6/Thatcher 6D {1308}. **v:** Admonter Fruh {72}; Dacia

{979}; Dong-Fang-Hong 2 {564}; Dong-Fang-Hong 6 {564}; Feng-Kong {563}; Hochzucht {46}; Hybrid 80-3 {72}; Jubilejna {68}; Juna {76}; Kanred {1308}; Ke-Fang 1 {564}; Stabil {72}; Viginta {71}; Vrakunski {72}. **v2:** Amika *Sr31* {76}; An-Hewi II *Sr8a* {564}; Beijing 10 *SrTmp* {564}; Dong-Xie 3 *Sr31* {563}; Dong-Xie 4 *Sr31* {563}; Erythrospermum 974 *Sr8a* {72}; Glenlea *Sr6 Sr9b* {327}; Istra *Sr31* {76}; Jing-Hong *Sr17* {564}; Jing-Hong 2 *Sr17* {564}; N.P.789 *Sr11* {1555}; Qing-Chung 5 *Sr6 Sr11* {564}; Solaris *Sr31* {76}; Victor *Sr6 Sr8a* {979}. **ma:** Flanked by *Xbarc183-6D* and *wPt3879* {11232}.

SR6

Sr6 {687}. [*SrKa1* {1167}]. 2D {1577, 1293, 1308}. 2DS {942}. **bin:** 2DS5 - 0.47 - 1.00 {10714}. **i:** I *Sr6*-Ra {828}; Kenya 58/10*Marquis {675, 468}; Sr6/9*LMPG {685}. **s:** CS*5/Red Egyptian 2D {1308}. **v:** Africa 43 {669}; Eureka {468, 844}; Kenya stocks {1167, 669, 1557, 687, 673, 670, 689}; McMurachy {679}; Shield {198}. **v2:** Bowie *Sr8a* {1553}; Eurga *Sr11* {1553}; Fortuna *Sr7a* {679}; Gamut *Sr9b Sr11* {1555}; Glenlea (heterogeneous) *Sr5 Sr9b* {327}; Kentana 52 *Sr7a* {1577, 678}; Kiric 66 *Sr7b* {979}; Lerma Rojo 64 *Sr7b Sr9a* {979}; No. 466 *Sr9b Sr10* {689}; Red Egyptian *Sr8a Sr9a* {1308}, {687}; Siete Cerros *Sr11* {33}; Victor I *Sr5 Sr8a* {979}. **ma:** *Sr6* – 1.1 cM – *Xwmc453-2D* – 0.4 cM – *Xcfd43-2D* {10714}; *Xgwm102-2D* – 0.9 cM – *Xgpw94049-2D* – 5.6 cM – *Sr6*z – 1.5 cM – *Xwmc453/Xcfd43-2D* {10870}. See also {1553}.

SR7* [*Sr7 {830}]. 4AL {1308}, {939}. 4A {1293}, {830}, {671}.

Sr7a {830}. [*Sr7* {687}]. **i:** Egypt Na101/6*Marquis {468}; Kenya 117A/6*Marquis {468}; Sr7a/9*LMPG {685}. **s:** CS*7/Kenya Farmer 4B {830}; CS*8/Sapporo 4B {830}. **v:** Egypt Na101 {669}; Jagger *Sr38* {11420}; Kenya stocks{669}, {687}, {673}, {670}, {689}; Sapporo Haru Komugi Ichigo {689}. **v2:** Egypt Na95 *Sr9b Sr10* {687}; Fortuna *Sr6* {679}; French Peace *Sr9a Sr13* {680}; Kentana 52 *Sr6* {689}; Khapstein *Sr13 Sr14* {674}; W3746 *Sr12* {1371}. **ma:** *Xwmc313-4A* – *SNP1067* – 0.8 cM – *Sr7a* – 2.7 cM – *Xbarc78-4A* – 2.7 cM – *SNP7126* {11420}.

Sr7b {830}. **i:** I *Sr7b*-Ra {828}. **v2:** Warigo *Sr2 Sr17* {499}; Kiric 66 *Sr6* {979}; Roussalka *Sr8a* {979}; Red Bobs *Sr10* {308}; Nell *Sr17* {1565}; PI 177906 *Sr28 SrTmp* {11419}; Spica *Sr17* {939}; Marquis *Sr18 Sr19 Sr20* {675}, {830}. **ma** Located at 147-164 Mb in the Wang et al. (2014) consensus map {11419}.

SR8 6A {1293, 1308}. 6AS{929}, {1368}.

Sr8a {1368}. [*Sr8* {687}]. **i:** I Sr8a-Ra {828}; Red Egyptian/10*Marquis {686}; Sr8a/9*LMPG {685}. **s:** CS*5/Red Egyptian 6A {1308}. **v:** Harvest {11418}; Marimp 3 {979}; Mentana {844}; Strampelli {979}. **v2:** An-Hewi II *Sr5* {564}; E-Gan-Zao *Sr17* {564}; Erythrospermum 974 *Sr5* {72}; Frontana *b* {689}; Golden Valley *Sr17* {979}; Hartog *Sr2 Sr12* {127}; Magnif G *Sr9b* {689}; Pitic 62 *Sr9b* {33}; PI 177906 *Sr7b SrTmp* {11419}; Red Egyptian *Sr6 Sr9a* {687}; Rio Negro *Sr9b* {689}; Roussalka *Sr7b* {979}; SD4297 *Sr28* {11418}; Suneca *Sr2 Sr17* {485}; Victor 1 *Sr5 Sr6* {979}. **ma:** Terminally located; SNP markers within 2 cM {11416}. *Sr8a* – 2.2 cM – *Xgwm459*-6A {11418}.

Sr8b {1368}. [*SrBB*]. **v:** Barleta Benvenuto {1368}; Klein Titan {1368}. **v2:** Bezostaya *Sr5* {979}; Klein Cometa *Sr30* {1368}. **tv:** According to Luig {841} one of the genes in Leeds is *Sr8b*. **tv2:** Arrivato *Sr9e Sr13* {10607}. **ma:** *Sr8b* – 4.6 cM – *Xgwm334-6A* {10607}.
This could be the gene located on chromosome 6A in ST464-A1 {10473} and one of the genes present in ST464, a parent of Leeds.

Sr8155B was also reported to be located at locus {11758}.

SR9* [*Sr9 {676}]. 2B {1308}, {671}, {677}, {828}. 2BL{946}, {1582}, {1307}, {944}, {951}}. *TraesCS2B03G1225900*. **c:** Encodes an NB-LRR immune receptor containing a long LRR domain {11747}. Ortholog of *Sr21* with about 85% identity {11747}.

Sr9a {676}. [*Sr9* {687}]. **i:** I*Sr9a*-Ra {828}; Red Egyptian/10*Marquis {686}; Sr9a/9*LMPG {685}. **s:** CS*4/Red Egyptian 2B {1308}. **v2:** Red Egyptian *Sr6 Sr8a* {687}; French Peace *Sr7a Sr13* {680}; Excel *Sr8a Sr17* {752}. **ma:** *Xbarc101-2B/Xgwm12-2B* – 2.7 cM – *Xgwm47-2B* – 0.9 cM – *Sr9a/Xwmc175-2B* {10472}.

Sr9b {468}. [*SrKb1* {468}, *Sr9* {687}]. **i:** Kenya 117A/10*Marquis {686}; *Sr9b*/10*LMPG {685}. **s:** CS*7/Kenya Farmer 2B {939}. **v:** Gamenya {844}; Kenya stocks {669}, {1557}, {687}, {673}, {67}, {689}. **v2:** Egypt Na95 *Sr7a Sr10* {636}; Festival *Sr15* {1553}; Frontana *Sr8a* {689}; Gamut *Sr6 Sr11* {1555}; Glenlea *Sr5 Sr6* heterogeneous {327}; Kenora *Sr15* {1553}; Magnif G *Sr8a* {689}; No. 466 *Sr6 Sr10* {689}; Pitic 62 *Sr8a* {33}; Rio Negro *Sr8a* {689}; Robin *Sr11* {879}; Veadeira *Sr10* {687}. See also {1553}. **c:** SR9B differs from SR9H and SR9G by different single amino acids {11747}.

Sr9c. Originally reserved for *Sr36*, but later **deleted**.

Sr9d {678}, {831}. [*Sr1* {676}, {47}, {677}]. **i:** Hope/10*Marquis {677}; H-44/10*Marquis {677}; I Hope 2B-Ra {828}; Sr9d/8*LMPG {685}. **v:** Hopps *Sr2* {1040}. **v2:** Lancer *Sr2 Sr17* {679}; Scout *Sr2 Sr17* {679}. **tv:** Arnautka {939}; Mindum {939}; Spelmar {939}.

Sr9e {951}. *Srv* {1391}, *Srd1v* {642}, *SrKn* {11590}. *TRITD2Bv1G223210*. **v:** Line Td31-5R PI700734 {11514, 11590}; SST 16 {1324}; SST 33 {785}; SST 66 {785}; SST 3R {1324}; Vernstein {845}. **v2:** Combination III *Sr36* {841}; Sunstar *Sr8a Sr12* {939}. **tv:** ST464-A2 {10473}; Svevo {11590}; Vernal emmer {1391}; CI 7778 {845}; *Sr9e* occurs in many tetraploid wheats {1378, 939}. **tv2:** Arrivato *Sr8b Sr13* {10607}; Kronos *Sr13* {11590}; ST464 *Sr13* {10473}. **ma:** *Xgwm191-2B* – 5.5 cM – *Sr9e* – 0.7 cM – *Xgwm47-2B* {10607}. *SrKn* was mapped to a 0.29 cM region flanked by *pku4856F*$_2$*R*$_2$ and *pku4917F*$_3$*R*3 {11590}.

Sr9e_h1. **v:** Vernstein {11747}. **tv:** CI 7778 {11747}.
Sr9e_h2. **tv:** Kronos and other lines with *Sr9e* {11747}.
Haplotypes *_h1* and *_h2* code for proteins with several amino acid differences {11747}.

Sr9f {826}. **v:** Chinese Spring {826}; Not present in the near-isogenic I*Sr9a*-Ra {826}. **Deleted** {11747}. The *Sr9f* homolog protein in CS is non-functional indicating that the gene named *Sr9f* in CS is not an *Sr9* allele {11747}.

Sr9g {965}. **s:** CS*7/Marquis 2B *Sr16* {965}; CS*4/Thatcher 2B *Sr16* {965}. **v2:** Celebration *Sr12 Sr16* {965}; Eagle *Sr26* {842}; Hochzucht *Sr5 Sr12* {965}; Lee *Sr11 Sr16* {965}. **tv:** Acme {965}; Iumillo {965}; Kubanka {965}. See also {504}. **c:** SR9G differs from SR9H by a single amino acid {11747}.

Sr9h {11010}. [*SrWeb* {10858}, *SrWLR* {11485}.]. 2BL {10858, 11010}. **v:** Matlabas {10058, 11486}; RL6203 {11010}. **v2:** Gabo 56 CI 14035 *Sr11* {11010}; Gabo CI 12795 *Sr11* {11010}; Timstein CI 12347 *Sr11* {11010}; Webster RL6201 *Sr30* {10858}. **ma:** *Xgwm47-2B* – 1.4 cM – *SrWeb* – 12.5 cM – *Xwmc332-2B*{10858}; *wPt-3132* - 1.9 cM - *Sr9h* - 1.9 cM - *wPt-8460*{11010}; *Sr9h* - 20.7 cM - *Sr28* {11010}; *Xgwm47-2B* – 1.8 cM – *Sr9h* (*SrWLR*) – 7.0 cM – *Xwmc332-2B* {11485}; *AWA543-HRM* – *Sr9h* – *Xgwm47-2B*.
Although {11149} concluded that *Sr28* was present in VL404 and Janz it is more likely that the gene described is the linked gene *Sr9h*. *Sr9h* was frequently present in landraces with field resistance to early isolates of the *Pgt* race Ug99 group {11147}.

SR10

Sr10 {687}. 2B {686}, {939}. **i:** Egypt Na95/4*Marquis {468}. **v:** Federation {939}; Geneva {1412}; Hazen {49}; Kenya stocks {669}, {687}, {673}, {670}. **v2:** Egypt Na95*Sr7a Sr9b* {687}; No. 466 *Sr6 Sr9b* {689}; Red Bobs *Sr7b* {308}.

SR11

Sr11 {468}. [*Sr11* {687}, *Sr12* {687}]. 6BL {1297}. 6B {1309, 1293, 671, 1143}. **i:** I *Sr11*-Ra {828}; Lee/10*Marquis {686}. **s:** CS*7/Kenya Farmer 6B {830}; CS*9/Timstein 6B {1308}. **v:** Charter {844}; Flevina {72}; Gabo {687}; Kenya stocks {1557, 673, 670, 844}; Sonora 64 {33}; Sylvia {71}; Timstein {1308, 687}; Tobari 66 {33}; Yalta {844}. **v2:** Charter *Sr9h* {11177}; Eurga *Sr6*{1553}; Gamut *Sr6 Sr9b* {1555}; Lee *Sr9g Sr16* {687}; N.P.790 *Sr5* {1555}; Qing-Chung 5 *Sr5 Sr6* {564}; Robin *Sr9b* {879}; Prospect *SrWld* {197}; Trident *Sr38* {11177}; See also {1553}. **ma:** *KASP_6BL_IWB46893* – 0.3 cM – *Sr11/KASP_6BL_IWB10724* – 0.3 cM – *KASP_6BL_IWB72471* {11177}.
A resistance gene allelic with *Sr11* was found in Chinese Spring {938}, but the *P. graminis* culture for its detection was lost.

SR12

Sr12 {1332}. Recessive. 3BS or centromeric region {11103}, {682}, {968}, {1332}. 3BL {11104}. **s:** CS*7/Marquis Selection 3B *Sr16* {1332}; CS*5/Thatcher 3B *Sr16* {1332}. **v:** Marquillo {682}; Tincurrin {939}; Windebri {939}. **v2:** Condor *Sr8a* {11105}; Celebration *Sr9gSr16* {939}; Condor Thatcher *Sr5Sr9gSr16* {939}; RL6058 (a Thatcher derivative) {11104}; W3746 *Sr7a* {1371}. **tv:**

Postulated for several durums {1378}. **ma:** *IWA6086 – Sr12 – IWA4613* {11104}.
Sr12 is more widespread and probably more effective in conferring resistance than is usually acknowledged {939}. Although the association of field resistance and *Sr12* was not definitive allelism or close linkage is clearly involved {11104}.

SR13

Sr13 {674. **ma:** *Xwmc59-6A* – 5.7 cM – *Sr13* {10607}; *CD926040 – Sr13 – BE471213*{10777}; CD926040 – *SR13 – BE471213* {10777}; Markers *Xgwm427-6A* and *AFSr13S* (proximal) and *Xdupw-6A* (distal) showed variable but close (<10 cM) linkage with *SR13* in six durum crosses – these markers were variously applicable across durum backgrounds, but only *Xgwm427-6A* was variable in a range of hexaploid derivatives with *Sr13* likely originating from a single source {11146}. **c:** *Sr13* was identified as a CC-NBS-LRR gene with three resistance haplotypes in two specificities {11217}; later, four resistance haplotypes and four specificities {11584}.

Sr13a {674}, {11217}, {11584}. 6AL {929}. **bin:** 6AL-8**. i:** Khapstein /9*LMPG {685}, {11217}; Khapstein / 10*Marquis *Sr7b* {686}; Sr13/9*LMPG {685}. **v2:** Khapstein *Sr7a Sr14* {674}; Machete *Sr2* {10607}. **itv:** Rusty-KL-B {11584}; Rusty-KL-C {11584}. **tv:** Cando {11584}; Durox {11584}; Grenora {11584}; Kronos PI 576168 {11217}; Lakoto {11584}; Maier {11217}; Mountrail {11584}; Renville {11217}; Strongfield {11584}; Transend {11584}; Wells {11584}. **tv2:** Khapli *Sr7a Sr14* {674}. **c:** KY825225 (Resistance haplotype R1) {11217}.

Sr13b {11217, 11584}. **itv:** Im-C2 {11584}; Im-7B {11584}; Rusty-14803 {11584}. **tv:** Ben {11584}; Botno {11584}; Calvin {11584}; Carpio {11584}; D99656 {11217}; D15143 {11584}; Joppa {11584}; Kofa PI 584336{10777; 11217}; Lebsock {11584}; Leeds *Sr92* Sr8b {11584}; Lloyd {11584}; Medora PI 496260 {10777, 11217}, CItr 7777 {11584}; Munich {11584}; ND Grano {11584}; ND Riveland {11584}; Pierce {11584}; Rugby {11584}; Sceptre {10777, 11584}; Svevo {11584}; *T.* carthlicum PI 387696 {11584}; *T. polonicum* CItr 14803 {11584}; Tioga {11584}; Vic {11584}; Ward {11584}. **c:** GenBank KY225226 (Resistance haplotype R2) {11217}.

Sr13c {11584}. **itv:** 8155-B2 {11584}; 8155-C2 {11584}; Rusty-SR464-C1 {11584}; ST464-C1 {10473, 11584}. **tv:** Alkabo {11584}; Altar 84 {11584}; CItr 7771 {11584}; D101073 {11584}; Langdon {11217, 11584}; PI 352548 {11584}; ST464 *Sr9e* {10473, 11584}. **c:** GenBank KY924305 (Resistance haplotype R3 {11217).

Sr13d {11584}. **itv:** CAT-A1 {11584}. **tv:** Camadi Abdu Tipo #103 {11584}. **c:** MW033594 (Resistance haplotype R4 {11584}.

Alleles of many of the *Sr13* genotypes listed under **tv:** were identified by sequence markers; those entries are likely to carry additional resistance genes.

Haplotypes of other germplasm previously listed are unknown: **v2:** French Peace *Sr7a Sr9a*{680}. **tv2:** Arrivato *Sr8b Sr9e* {10607}.

Unspecified allele. tv: {11280}.

A resistance gene in Khapstein/9*LMPG and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However, the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance locus mapped in {10778} could not be *SR13*.

SR14

Sr14 {674}. 1BL {933}. **i:** Khapstein/10*Marquis {686}. **v:** Line A {933}. **v2:** Khapstein *Sr7a Sr13* {674}. **tv2:** Khapli *Sr13* {674}.

SR15

Sr15 {1554}. 7AL {1305}. 7A {1293, 1554}. **v:** Present in stocks possessing *Pm1 and Lr20* {931}, {1554}; See Reaction to *Blumeria graminis* and Reaction to *P. triticina*. **ma:** Associated with clustered markers {323}.

SR16

Sr16 {830}. [*Srrl2* {1238}]. 2B {1308}, {830}. 2BL {1307}. **i:** I *Sr16*-Ra {828}; I Th3B-Ra {832}. **s:** CS*7/Marquis 2B *Sr9g* {1581}; CS*4/Thatcher 2B *Sr9g* {1308}; CS*5/Thatcher 3B *Sr12* {832}. **v2:** Thatcher *Sr5 Sr9g Sr12* {939}; Lee *Sr9g Sr11* {939}. *Sr16* is allelic with a gene in Kota (*SrKt2* {932}) {939}.

SR17

Sr17. Recessive. [*sr17* {964}]. 7B {771}. 7BL {964}, {10565}. **s:** CS*6/Hope 7B {964}. **v:** Forno {10511, 10565}. **v2:** E-Gan Zeo *Sr8a* {564}; Golden Valley *Sr8a* {979}; Jing-Hong 1 *Sr5* {564}; Jing-Hong 2 *Sr5* {564}; Lancer *Sr2 Sr9d* {679}; Nell *Sr7b* {1565}; Scout *Sr2 Sr9d* {679}; Suneca *Sr2 Sr8a* {485}; Present in many stocks possessing *Pm5*{964}; See Reaction to *Blumeria graminis*. **ma:** *Xwmc273-7B* – 15.3 cM – *Sr17* {10565}.

SR18

Sr18 {54}. [*SrMn1* {1263}, *Srmq1* {99}, *SrPs1* {1263}, *SrG2* {844}, *Srrl1* {1238}]. 1D {1582, 1308, 54}. **i:** I Hope 1D-Ra {828}; Sr18/8*LMPG {685}. **s:** CS*6/Hope 1D {1308}. **v:** Present in the majority of wheat stocks{828}.
Stocks **not** possessing *Sr18*: Brevit {54}; Chinese Spring {828}; Eureka {54}; Federation {54}; Gular {54}; Kenya C6042 {54}; Koala {54}; Little Club {828}; Morocco {54}; Norka {54}; Prelude {828}; Yalta {54}.

SR19

Sr19 {29}. [*Srmq2* {99}]. 2B {29}. 2BS {1582}. **v:** Mq-B {29}. **v2:** Marquis *Sr7b Sr18 Sr20* {29}.

SR20

Sr20 {29}. [*Srmq3* {1238}, *Srrl3* {1238}]. 2B {29}. **v:** Mq-C {29}; Rl-C {29}. **v2:** Reliance *Sr5 Sr16 Sr18* {29}; Marquis *Sr7b Sr18 Sr19* {29}.

SR21

Sr21 {1460}. 2AL {1460, 1464}. **i:** Sr21/8*LMPG {685}. **v:** CSSr21 {M10115}; Hexaploid derivatives of *T. monococcum*{939}. **tv:** Tetraploid derivatives of *T. monococcum*{939}. **dv:** Einkorn CI2433 {1460, 11110}; Dv92 *Sr35* {10876}; G2919 *Sr35* {10876}; Various *monococcum* accessions. See also *Sr45* which has similar specificity to *Sr21.* **ma:** FD52726 – 0.25 cM – *Sr21* – 0.05 cM – EX594406 {11110}. **madv:** *CJ961291* – 0.02 cM – *Sr21* – 0.04 cM – NLR pseudo-gene cluster {11315}; A diagnostic marker was developed from the cloned gene {11315}. **c:** *Sr21* is a CC-NBS-LRR gene of 4,872 bp; 44 diploid accessions with *Sr21* were classified as five haplotypes – viz. Haplotype R1, MG582649, 28 accessions including DV92 (and CSSr21); Hap R2, GenBank MG601519, six accessions; Hap R3, MG601520, one accession; Hap R4, MG601521); and six accessions, Hap R5, MG601522, three accessions {11315}.

SR22

The stem rust resistance *Sr22* from *T. monococcum* was cloned and was shown to encode a CC-NBS-LRR gene {11404}. The gene model for the allele in susceptible CS is Ref Seq v1.1 *TraesCS7A02G499600***.**

Sr22a {11514}. *Sr22* {1460}. 7A {649}. 7AL {1460}. **bin:** 7AL-0.74-0.86; 7AL-13 0.83-0.89 {10869}. **i:** Marquis*4//Stewart*3/*T. monococcum* {649, 1460}; Sr22/9*LMPG {685}; Others {1112}. **v:** CS/3/Steinwedel*2//Spelmar/*T. boeoticum* {1460}; Schomburgk {880}; Steinwedel*2//Spelmar/*T. boeoticum* {1460}; Others {1112}; Recombinant line reported in {10772, 10773}. **tv:** Spelmar/*T. boeoticum* {1460}; Stewart*6/*T. monococcum* RL 5244 {649}. **dv:** Various *T. monococcum* accessions {649, 1460}. **ma:** Hexaploid derivatives with *Sr22a* carried 'alien' segments of varying lengths; the shortest segment was distal to *Xpsr129-7A* {1112}; See also{158}; *Xcfa2123-7A* – 6 cM – *Sr22* – 5.9 cM – *Xcfa2019-7A* {10263}; Multiplex marker *cssu22* based on STS markers derived from cloned fragment csIH81 was developed in {10772}; This marker gave positive results for *Sr22* in all recombinant lines including those reported in {10773}; Recombined lines with shortened introgressions from diploid wheat are reported in {10869}; the shortest was U5616020-154 {10869}. **c:** *Sr22* encodes a CC-NBS-LRR protein with 941 aa {11213}. EBI LN883743, GenBank CUM44200.1.

Sr22b {11514}.*SrTm5* {11208}. 7A^{m}L {11208}. **dv:** *T. monococcum* ssp. *monococcum* PI 277131-2 *Sr21 Sr22b Sr60* {11208, 11385}; PI 306540 *Sr21 Sr22b Sr60 SrTm4* {11208, 11385}. **i:** PI 306540 (2x)/Kronos (4x)//Clear White (6x)///*3 Fielder {11514}; PI 700735 {11514}. **ma:** *SrTm5/IWB25012/IWB44281/IWB405527/Sr22GMF/GMR* – 0.8 cM – *IWB6942* {11208}; *pkw4995* (RefSeq v1.1 *TraesCS7A02G499500*) - 0.04 cM – *SrTm5* – 0.04 cM- *pkw4999* (RefSeq v1.1 *TraesCS7A02G499900*) {11514}. **c:** *Sr22b* has an insertion of a large (13.8-kb) retrotransposon in its second intron {11514}.The predicted Sr22b NLR protein is 95.7 to 96.7% identical to proteins translated

from six *Sr22a* resistant haplotypes {11514}.
Allelism of *Sr22a* and *Sr22b* was based on more than 2,200 gametes {11514}.

SR23

Sr23 {950}. The following chromosome locations are consistant with the finding that the first location was based on Rescue monosomics. Rescue differs from CS by a 2B-4B reciprocal translocation {939}. 2BS {939}. 4B {950}. **v:** Exchange {950}; Warden {950}; *Sr23* is always associated with *Lr16* {950}. **v2:** Etoile de Choisy *Sr29* {950}.

SR24

Sr24 {956}. Derived from *Thin. elongatum.*
3DL = T3DS.3DL-3Ae#1L {389, 956}. **i:** Sr24/9*LMPG {685}; Sears' 3D/*Ag* translocations {1300, 956}. **v:** Agent {956}; Blueboy II {956}; Collin {901}; Cloud {956}; Cody {1284}; Ernest {10845}; Fox {956}; Gamka {785}; Karee {785}; Keene {10845}; Kinko {785}; Palmiet {785}; Sage {825, 1024}; SST 23 {1324}; SST 25 {785}; SST 44 = T4R {785, 1324}; SST 102 {785}; Torres {128}; Wilga {785}. **v2:** Siouxland *Sr31* {1283}; List of Australian genotypes {340}.
1BS {185} = T1BS = 1BS-3Ae#1L{389, 600}. **tr:** Amigo {1463, 389, 600}; Millenium {10845}; Teewon {389, 600}. Note: Amigo and some derivatives also carry a 1AL.1RS translocation with resistance from rye {1463}.
3Ae#1 **su:** Chinese Spring 3Ag {3D} {1304}; TAP48 {389}. **ma:** *Xbarc71-3Ag* was considered a better marker for *Sr24* than STS Sr24#12 {10845}.
SR24 is completely linked in coupling with *LR24* {956} and often with red grain colour. See Reaction to *P. triticina*.

SR25

Sr25 {956}. Derived from *Thin. elongatum.* 7DL = T7DS.7DL-7Ae#1L {388, 657, 291, 956}. **i:** Sears' CS 7D/7Ag translocations {1300}, {956}; Sr25/9*LMPG {685}. **v:** Agatha *Sr5 Sr9g Sr12 Sr16* {956} = T4 {1323}; Mutant 28 {388}; Misr 1 (Oasis/Skauz//4*BCN/3/2*Pastor) {11260}.
7AL = T7A-7Ae#1L {330} Sears' 7A/7Ae#1L No. 12 {1304}, {330}; Sears' 7D/7Ag#11 carries neither *Sr25* nor *Lr19* {939}.
7Ae#1L. **su:** Chinese Spring + 7Ae#1L(7D) {1304}.
See *Lr19*, reaction to *Puccinia triticina*.
Sr25/Lr19 often show complete linkage in wheat {956}.
Knott {681} obtained two mutants (28 and 235) of Agatha with reduced levels of yellow pigment in the flour. One of these mutants lacked *Sr25*. Marais {890} reported that a gene very similar to *Sr25* was present in the putative Inia 66 x *Thin. distichum* derivative, Indis. Marais {890}, {892} also obtained mutants with reduced yellow pigment in Indis derivatives and some of these lacked *Sr25*.

SR26

Sr26 {956}. Derived from *Thin. elongatum*. 6AL {364} = T6AS.6AL-6Ae#1L {389}, {388}. **i:** Sr26/9*LMPG {685}. **v:** Avocet {364}; Flinders {1449}; Harrier {939}; Jabiru {956}; King {1451}; Kite {956}; Knott's 6A-6Ae#1L translocation to Thatcher {672}; Takari {253}. **v2:** Bass *Sr36* {1450}; Eagle *Sr9g* {956}. **ma:** Detected with several RFLP probes {138}; A PCR marker, Sr26#43 was reported in {10257}. Four KASP markers were developed for the original translocation (FL 0.85). WA-1 (AUS91435) a derivative with a shortened 6Ae#1 segment (FL 0.32), amplified only *sunKASP_224* and *sunKASP_225* {11336}. The latter was diagnostic for accession AGG91586WHEA *SrB*, a derivative of line WA-5 (AUS91436) {11338}. PCR markers based on NLR genes in homoeologous group 6 chromosomes were used to confirm that WA-2 Type 1 was the smallest secondary translocation carrying *Sr26* {11357}.
Secondary recombinants with shortened 6AL#1L segments involving chromosomes 6A and 6D are reported in {11141}; five 6A recombinants were accessioned in the Australian Winter Cereals Collection.
c: Encodes an NLR protein; GenBank MN531843 {11528}.

SR27

Sr27. Derived from *S. cereale*. 3A (T3A-3R) = T3AS.3R#1S {389}, {10162}, {896}, {3}. **i:** Sr27/9*LMPG {10162}, {685}. **v:** WRT wheat-rye translocation, available in CS, Thatcher and Pembina backgrounds. Translocated from Imperial rye to Chinese Spring by Acosta {10162}, {3}; Widespread in triticales{1384}, {10162}, {966}.
3A = T3AL.3RS {896}. **v:** W964 = 3RS.3AL.1/4* Inia 66 {896}; W968 = 3RS.3AL.1/5* Condor {896}; W970 = 3RS.3AL.88/5*SST3 {896}.
3B = T3BL.3R#1S {896}. **v:** W966 = 3RS.3BL.26/4*Inia 66 {896}.

c: *Sr27* encodes an NLR with closest similarity to *Sr13* among cloned wheat *Sr* alleles {11561}.

SR28

Sr28 {932}. 2BL {932}. **i:** Line AD {932}. **v:** SD 1691, CI 12499 {11148}. **v2:** Kota *Sr7b Sr18* {932}; SD4297 *Sr8a* {11419}. **ma:** Xwmc332 – 1.4 cM – Sr28 – 6.0 cM – wPt-7007{11148}; Sr28 – 1.6 cM – wPt-7004 {11148}; Sr28 – 0.6 cM – wPt-7004 {11148}.
Although {11149} concluded that *Sr28* was present in VL404 and Janz it is more likely that the gene described is the linked gene *Sr9h*.
The *Sr28* allele in SD4297 was originally reported as *Sr9h* {11418}.

SR29

Sr29 {313}. [*SrEC* {955}]. 6DL {313}. 6DS {1626}. **i:** Prelude/8*Marquis//Etoile de Choisy {313}. **v:** Hana {71}; Hela {76}; Mara {68}; Slavia {76}; Vala {76}. **v2:** Etoile de Choisy *Sr23* {955}.

SR30

Sr30 {688}. [*SrW*]. 5DL {688}. **i:** Sr30/7*LMPG - Lines 1, 2, and 3 {685}. **v:** Festiguay {688}; Mediterranean W1728 {1369}; Webster {688}. **v2:** HD2009 *Sr2* {10632}; Klein Cometa *Sr8b* {1368};

Relatively common in Australian and Mexican wheats. Various unnamed accessions {208}, {1321}. **ma:** *Xcfd12-5D* – 9.0 cM – *Sr30* – 16.6 cM – *Xgwm292-5D* {10858}.
According to {10858} Webster RL6201 carries a second gene *SrW* that confers resistance to the race Ug99 group.

SR31

Sr31. Derived from *S. cereale* cv. Petkus. See also Reaction to *P. striiformis, Yr9*: Reaction to *P. triticina, Lr26*
1B = T1BL.1RS = T1BL.1R#1S {389} or 1R(1B). **i:** MA1 and MA2 four-breakpoint double translocation lines 1RS-1BS-1RS.1BL in Pavon {84}. **v:** Amika {heterogeneous} *Sr5* {76}; Cougar {267}; Feng-Kang 2 {563}; Feng-Kang 8 {563}; Gamtoos {785}; GR876 {753}; Jing-Dan 106 {563}; Jan 7770-4 {563}; Lu-Mai 1 {563}; Rawhide (heterogenous) {267}; Yi 78-4078 {563}. **v2:** Dong Xie 3 *Sr5* {563}; Dong Xie 4 *Sr5* {563}; Istra *Sr5* {76}; Solaris *Sr5* {76}; Siouxland *Sr24* {1283}. **tv:** Cando*2/Veery = KS91WGRC14 {381}. **ma:** 1BS/1RS recombinants 4.4 cM proximal to *Gli-B1/Glu-B3* {84}; Several markers tightly linked with *Sr31* were indentified in {377}; A SCAR marker, SCSS30.2$_{576}$ was developed{10359}; *Xscm09-1R*$_{208}$ {10845}.
Sr31 seems to be different from the rye-derived gene in Amigo and related materials {10270}.

SR32

Sr32. Derived from *Ae. speltoides*.
2A {939}, {1304} = T2AL.2S#1L-2S#1S {389}. **v:** C95.24 {389}.
2B {1304 } = T2BL-2S#1S {389}. **v:** C82.1 = P80-14.1-2{389}.
2D {1304} = T2DL-2S#1L.2S#1S {389}. **v:** C82.2 = P80-139.1-4 {389}, {1304}; C82.3 = P80-132.2-2 {1304}, {939}; C82.4 = P80-153.1-2 {1304}, {939}; Deben {10283}.

C82.2 was shown to have two resistance genes – *Sr32* in the short arm isolated as 70type1 (AUS91442) and *SrAe1t* in the long arm isolated as 70typeII (AUS91441), 122typeII (AUS91444), and line 247 (AUS91446) {11779}.

SR33

Sr33. [*SrSQ* {650}]. 1DS {620}. 1DL {650}. **v:** RL 5405 = Tetra Canthatch/*Aegilops squarrosa* RL 5288 {650}. **dv:** *Ae. tauschii* PI 603225 {11012}; TOWWC0153 = TA2466 {11685}. **ma:** linked with *Gli-D1*; *Xmwg60-1D* – 5.8 cM – *Sr33* – 2.2 cM – *Xwmg2083-1* {360}; *Xwmc432-1D* – 0.3 cM – *Xwmc336-1D* – 1.0 cM – *Sr33* – 4.2 cM – *Xwmc222/Xcfa2158-1D* {11012}; Flanked by *BE405778* and *BE499711* within a 1 cM region {10987}. **c:** *Sr33* encodes a CC-NBS-LRR protein and is orthologous to *Sr31, Sr50* and the barley powdery mildew locus *Mla* {10987}. GenBank KF031291, 4,639 bp; protein CUM44200.1. *Sr33* is a paralogue of *Sr66* {11685} with 83% homology {11405}.

SR34

Sr34 {967}. Derived from *Ae. comosa*.
2A {967} = T2AS-2M#1L.2M#1S {389} **v:** CS 2A-2M 4/2 {967}.
2D {967} = T2DS-2M#1L.2M#1S {389} **i:** Sr34/6*LMPG {685}. **v:** Compair {967}; CS 2D-2M 3/8 {967}; Various addition, substitution and translocation lines with *Yr8* {967}.
2M {967}. **su:** Chinese Spring 2M(2A) {967}.

SR35

Sr35 {957}. [*SrTm1* {1522}]. 3AL {957}. **bin:** 3AL8 0.85-1.00. **i:** Marquis*5/G2919 {10876}. **v,tv:** Tetraploid and hexaploid derivatives of *T. monococcum* {957}. **dv:** DV92 *Sr21* {10876}; G2919 *Sr21* {10876}; *T. monococcum* C69. 69 Selection {957}; G2919 {957}. **ma:** *Sr35* was mapped to a 5.1 cM interval between *XBF483299* and *XCJ656351* in diploid wheat{10712}; Mapped in diploid wheat to a 2.2-3.1 cM region between *Xbf483299* and *XCJ656351* and corresponding to a 174 bp region in *Brachypodium*{10876}. **c:** *Sr35* is a CC-NBS-LRR gene {10988}.
Sr35 was postulated in 21 accessions of *T. monococcum* subsp. *monococcum* {11288}.

SR36

Sr36 {939}. [*SrTt1* {949}]. 2BS {939}. **i:** Sr36/8*LMPG {685}. **v:** Arthur {939}; Arthur 71 {1324}; Flemink {1324}; GK Kincso {235}; Gouritz {1324}; Idaed 59; Maris Fundin {70}; Mengavi {949}; SST 101 {1324}; SST 107{785}; Timvera {949}; *T. timopheevii* derivatives {949}; Zaragoza{785}; Others {572, 10609}. **v2:** Bass *Sr26* {1450}; Combination III *Sr9e* {939}; Timson *Sr5 Sr6* {939}. **tv:** *T. Timopheevii* {949}. **ma:** *Xgwm42* – 0.8 cM – *Sr36/Xstm773-2-2B/Xgwm31-2B/Xwmc477-2B* {10609}; *Xgwm319-2B* – 0.9 cM – *Sr36/Xstm773-2-2B/Xwmc477-2B* {10609}; *Xgwm429-2B* – 0.8 cM – *Sr36/Xstm773-2/Xgwm319/Xwmc477-2B*{10824}; *Xgwm319-2B* – 0.9 cM – *Sr36/Xstm773-2/Xwmc477-2B* {10824}; Of four markers *Xwmc477-2B* was the best, but it is not a perfect marker {10845}.

Sr37

Sr37 {939}. [*SrTt2* {949}]. 4BL {939}. **v,tv:** *T. timopheevii* and derivatives {949}, {484}; Line W {949}.

SR38

Sr38 {62}. Derived from *Ae. ventricosa*. 2AS {62}. 6M^v = 2MS-6MS.6ML or 2MS-6ML.6MS {0009}. **i:** RL 6081 = Thatcher + Lr37. This line will carry additional genes from Thatcher. **v:** CDS Stanley {11579}; Mace {11579}; Moisson derivatives Mx12 and Mx22 {0213}; VPM1 {62}; SY Mattis {11579}. **v2** Jagger *Sr7a* {11420}. **ma:** The 2NS translocated segment carrying *Sr38* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682* to *XksuH9*; PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}.
Sr38 is linked with *Lr37* and *Yr17*. See Reaction to *P. triticina Lr37* and *P. striiformis tritici Yr17*. SCAR markers SC-372 and SC-385 were developed in {10796}.

SR39

Sr39 {646}. Derived from *Ae. speltoides*. = 2SL-2SS#2.2SL#2 {11037}. 2B {651}. **v:** RL 5711 {651}, {646}. **tv:** Amphiploid RL 5347 = *Ae. speltoides/T. monococcum* {651}. **ma:** *Sr39* is closely linked with *Lr35* {651}; A SCAR marker was developed {9923}.
Lines with shortened alien segments are reported in {10741}. Although *Sr39* produces similar responses to *Sr32*, also derived from *Ae. speltoides*, recombination studies based on three crosses showed independent inheritance {646}. *Sr39* segregated independently of *Lr13* {651}. *Sr39* may be present in DAS15 in combination with *Sr47*. A Ti2BL.2BS-2SS-2BS translocation {10872} separated from *Sr47* in DAS15 could contain *Sr39* - see *SrAEs7t*.
Further lines with shortened segments are described in {11037} along with tightly linked co-dominant STS markers.

SR40

Sr40 {302}. Derived from *T. araraticum*. 2BS {302} = T2BL/2G#2S{389}. **i:** RL 6087 = RL 6071*7/PGR 6126; RL 6088 = RL 6071*7/PGR 6195 {302}. **tv:** *T. araraticum* PGR 6126 {302}; PGR 6195 {302}. **ma:** *Xwmc661-2B* – 6.4 cM – *Sr40* – 0.7 cM – *Xwmc344-2B* – 2.0 cM – *Xwmc477-2B* {10825}; *Xwmc661-2B* – 7.8 cM – *Sr40* – 2.5 cM – *Xwmc474-2B* – 1.0 cM – *Xwmc477-2B* {10825}.

SR41

Sr41 {1215}. 4D {1215}. **v:** WDR-B1 {1214}. **v2:** Waldron *Sr5* (heterogeneous) *Sr11* (heterogeneous) {1215}.

SR42

Sr42 {938}. 6DS {938}. **v:** PI595667 {11087}. **v2:** Norin 40 *Sr54* {938}; PI410954 *Sr24* {11087}. **ma:** *Xcfd49-6D* – 5.5 cM – *Xbarc183-6D* – 0.5 cM – *Sr42/FSD_RSA* – 11.8 cM – *Xbarc301-6D*; *Xcfd6D* – 5.9 cM – *Sr42* – 46.9 cM – *Xcfd13-6D* {10952}; *Xcfa49-6D* – *Sr42/IBW31561/IBW30767* – *FSDRSA* {11087}.
The likelihood that *Sr42* is the same as *SrTmp* and *SrSha7* (see below) is discussed in {11035} where Blouk#1, Coni#1, Niini#1, Phunye#1, Ripper and Tinkio1 were shown to carry a gene, or closely linked genes, on chromosome 6DS. If they are the same, this list would be enlarged to include Digalu, Gambo, Koshan 09 and Morvarid {11035}. Nearest markers *Xbarc183-6D* and *Xcfd49-6D* but not in consistent order {11035}. *Sr42* co-locates with *SrCad, SrNini, SrSh7* and *SrTmp*. Three haplotypes were identified in {11087}: C-C-T, AC Cadillac, Peace, PI595667; T*-C-T, Norin 40, Eagle 10, Ember, Guard, Ripper, Shield; T-C-T, Triumph 64, CnSSrTMP64, Blouk, Digalu, Pfunye, Robin, PI410954. A genetic analysis of six lines, Blouk, Coni, Niini, Pfuneye, Ripper and Tinkio, is reported in {11132}. All had single genes with linkage to *Xcfd49-6D* ranging from 3.9 – 12.5 cM and the genes were not clearly distinguished from *Sr42* or *SrTmp* {11132}.

A resistance allele at the *SR42* locus, possibly *SrTmp* or a new allele, was identified in South African cultivars Komati, Koonop, Limpopo and SST387 {11725}. This gene was likely derived from Betta {11725}.

SR43

Sr43. Derived from *Th. elongatum*. 7DS-7el$_2$S.7el$_2$L {11076}. 7D.
7DL = T7DL-7Ae#2L.7Ae#2S {389}, {657}. **tr:** KS10-2 {653}.
7D = T7DS.7Ae#2L {389}, {657}. **v:** KS23-9 {653}; KS24-1 {653}; KS24-2 {653}.
Derivatives RWG33 and RWG34 with shortened alien segments were reported in {11076}. **c:** *Sr43* isolated from RWG34 encoded a protein kinase fused to 2 domains of unknown function {11631}.
Sr43 confers higher resistance at low temperature {11631}.

SR44

Sr44{389}. Derived from *Th. intermedium*.
T7DS-7J#1L.7J#S 7J#1L {389}. **v:** Line 86.187 TA5657 {939}; Several 7A-7Ji#1L translocations {89}.
T7DL.7J#1S {11011} **v:** TA5657 {11011}.
7J#2, 7J#2S **su:** Group 7 alien substitution lines with 7J#1 and 7J#1S{939}. **ad:** TAF2 = L1{169}.

SR45

Sr45 {894}. [*SrD* {934}, *SrX*]. 1D {897}. 1DS {894}. **v:** 87M66-2-1 {894}; 87M66-5- 6 {897}; Thatcher + *Lr21*, RL5406 {894}, {934}; Various backcross derivatives developed at PBI Cobbitty{1461}. **dv:** *Ae. tauschii* RL5289 {894, 934}. **su:** CS1D5406 {11134}. **ma:** *Xgwm106-1D/BE44426* – 1.82 cM – *Sr45* – 0.39 cM –*csssu45/Af45* {11134}. **c:**. *Sr45* encodes a 1,230 aa CC-NBS-LRR protein {11213}. NCBI LN883757.
Tests of natural and induced mutants of *P. graminis* f. sp. *tritici* indicated that *Sr45* had identical specificity to *Sr21* {934}. One race distinguishing *Sr45* and *Sr21* is reported in {11134}. Cloning of both *SR45* and *SR21* showed that the genes were different.

SR46

Sr46 {10538}. 2DS {10538}. **bin:** 2DS5-0.47-1.00. **v:** L-18913 / Meering selections R9.3 {10538}; R11.4 {10538}; R14.2 {10538}. **v2:** L-18913 = Synthetic Langdon / *Ae. tauschii* var. *meyeri* AUS 18913 *Sr9e* {10538}. **dv:** *Ae. tauschii* var. *meyeri* AUS18913 {10538} = CIae 25 {11268}; *Ae. tauschii* TA1703 {11268}. **ma:** Co-segregation with RFLP *Xpsr649-2DS* at both the diploid and hexaploid levels {10538}; A PCR-based marker, *csSC46* was developed from a BAC clone containing *Xpsr649* {10538}. *Xgwm210-2D* – 3.9 cM – *Sr46* – 5.6 cM – *Xcfd36-2D* – 0.3 cM – *Xwmc111-2D* {11268}. **madv:** Flanked by *Xgwm1099-2D* and *Xbarc297-2D* {11405}. **c:** Cloned by AgRenSeq and map-based methods *Sr46* has a CC-NBS-LRR structure {11405}. GenBank MG851023.
Sr46 was more effective at higher temperatures in laboratory tests {11268}.

SR47

Sr47 {10549}. Derived from *Ae. speltoides.* 2BS {10872}. 2B = 2BL-2SL-2BL.2BS {10549}. **tv:** DAS15 {10549}. **tv:** RWG35 {10872}; RWG36 {10872}; RWG37 {10872}.
2B=2BL-2SL-2BL.2BS. **v:** RWG35 {10872}. Further markers were used to identify the introgressions in RWG25, RWG26, and RWG27 {10872}. STS marker *Xrwgs38* was diagnostic for the *Sr47* segment in DAS35 and DAS36 {11319}.

2B=2BL-2SL-2BL.2BS **v:** RWG36 {10872}.
al: *Ae. speltoides* PI 369590 {10549}. **ma:** Located in the interval *Xgwm47-2B* – *Xgpw4165-2B* {10872}. Further markers were used to identify the introgressions in RWG25, RWG26, and RWG27 {10872}. STS marker *Xrwgs38* was diagnostic for the *Sr47* segment in DAS35 and DAS36 {11319}.
Further chromosome engineering on DAS15 showed that the alien segment carried two resistance genes. The gene on 2BL was considered to be *Sr47* based on low infection type. The second gene located in 2BS produced a low infection type similar to *Sr39* and was located in a similar position to that gene {10872}.

SR48

Sr48 {10564}. [*SrAn1* {10565}]. 2DS {11653}. 2AL{10564, 10565}. **bin:** 2AL1-0.85-1.00 {10564}. **v:** Arina {10564, 10511, 10565}. **v2:** Arina *Sr56* AUS 91457 {10851}. **ma:** *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}; *Sr48* is considerably distal to the most distal of published markers, all of which are proximal to *Yr1*; *sun_KASP239* – 0.9 cm – *SR48* – 3.5 cM – *Xxib59-2D* {11653}.
The revised chromosome location was attributed to a chromosome 2A-2D translocation that explained the earlier reported linkage between *SR48* and *YR1*.

SR49

Sr49 {10704}. 5BL {10704}. **v:** Mahmoudi AUS 28011 {10704}. **ma:** *sun479* – 0.9 cM – *Sr49* – 1.5 cM – *sun209* – 0.5 cM – *Xwmc471-5BL* {10704}.

SR50

Sr50 {10745}. [*SrR* {377}]. 1DS {10745}. **ad:** CS + Imperial 1R {377}. **v:** Line T6-1 AUS 91434 {10745}. T1DL.1RS-DR.A1 {11316}. **al:** *S. cereale* cv. Imperial. **ma:** Line T6-1 retains the rye marker AW2-5 {10745}. **c:** GenBank KT725812, 3,508 bp. *Sr50* encodes a CC-NBS-LRR protein homologous to the barley *Mla* gene {11316}. GenBank KT725812.
In rye *Sr50* may be allelic with *Sr31*; however in wheat they can be regarded as separate loci *Sr50* is located in a small interstitial segment not detected by GISH. Line T6-1 lacks the *Sec-1* allele from rye {10745}.

Sr51

Sr51 {10803}. Homoeologous group 3 {10803}; 3S^{S}S {10803}
3A (3AL.3S^{S}S {10803}. **v:** TA5619{10803}.
3B (3BL.3S^{S}S) {10803}. **v:** TA5620{10803}.
3D (3DL.3S^{S}S) {10803}. **v:** TA5621{10803}.

3D (3DS-3S^SS.3S^SL) {10803}. **v:** TA5622{10803}. **al:** *Ae. searsii* TA2355 {10803}. **ma:** 3S^S-specific markers are provided in {10803}.

SR52

Sr52 {10774}. 6A (6AS.6V#3L) {10774}. **v:** TA5617 {10775}. **ma:** 6V3-specific EST-STSmarkers are given in {10775}.
The seedling response conferred by *Sr52* is temperature-sensitive.

SR53

Sr53 {10789}. Derived from *Ae. geniculata* 5D {10789}.
T5DS5DL-5M^gL-5DL {10789}. **v:** TA5630 (U6154-124) {10789}.
T5DL-5M^gL-5M^gS {10789}. **v:** TA5625 (U6200-64) {10789}.
T5DL-5M^gL-5M^gS {10789}. **v:** TA5643 (U6200-117) {10789}. **al:** *Ae. geniculata* TA10437 {10789}.
ma: Closest markers: *BE443102/Mbo1* and *BE442600/Mse1* {10789}.
The three translocation lines are re-engineered derivatives of TA5599 (5DL-5M^gL.5M^gS {10789}).

SR54

Sr54 {10816}. 2DL {10816}. **v2:** Norin 40 *Sr42* {10816}. **ma:** *Xcfd-283-2D* – 8.1 cM – *Sr54*/linkage block of 18 markers – 15.8 cM – *Xwmc167-2D* {10816}.
The possibility of a large alien linkage block was supported by the fact that many of the associated markers were null {10816}.

SR55

Sr55 {10847}. Adult plant resistance 4DL {10847, 10678}. **bin:** Distal to break point 0.56 FL{10678}.
i: RL6077=Thatcher*6/PI 250413 {10847, 10678}. **v:** Chapingo 48 {11070}. **ma:** Pleiotropic of closely linked with *Lr67* and *Yr46* and associated with *Xgwm165-4D* and *Xgwm192-4DL*{10847,10678}.
c: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.
Sr55 is pleiotropic or closely linked with *Lr67*, *Yr46*, *Pm46* and *Ltn3*.

SR56

Sr56 {10851}. Adult plant resistance [*QSr.sun-5BL* {10565}]. 5BL {10851, 10565}. **bin:** 5BL160-0.79-1.00. **v:** AF533 {10851}. **v2:** Arina *Sr48* AUS 91457 {138}. **ma:** *Xsun209* (SSR) – 2.6 cM – *Sr56* – 1.2 cM – *Xsun320* (STS from wPt-7665) {10851}.
In the earlier QTL analysis of an Arina/Forno population *QSr.sun-5BL* accounted for 12% of the PVE {10565}. In the present study of an Arina/Yitpi RIL population stem rust response segregated as a single gene. The response phenotype was 40-50 MS-S.

SR57

Sr57 {10861}. Adult plant resistance. 7DS {10861}. **bin:** 7DS4. **su:** Lalbahadur(Perula7D) GID 5348503 and GID 5348496 {10648, 10861}. **v:** Chinese Spring {10861}; Wheat accessions with *Pm38/Lr34/Yr18*, see Reaction to *Blumeria graminis*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia triticina*, Leaf tip necrosis. **ma:** See Reaction to *Puccinia triticina*. **c:** Putative ABC transporter{10648}.
Further evidence for the effects of this gene on stem rust response can be found in {299}, {10565}, {10733}, {10863}, {10864}, {10865}, {10866}.

SR58

Sr58 {10965}. 1BL {10965}. **v:** *Lr46* Deletion Mutant 109 (GID 5349718) {10965}; *Lr46* Deletion Mutant 111 (GID 5349716) {10965}. **su:** Lalbahadur(Pavon 1B) (GID 519245) {10965}.

SR59

Sr59 {11066}. Derived from *Scale cereale* 2D (T2DS.2RL) {11066}. **v:** TA5094 {11066}. **su:** SLU238 (2R(2D)) {11066}. **al:** VT828041 (6X triticale) {11066}. **ma:** Three rye-based KASP markers identified lines with *Sr59* {11066}.

SR60

Sr60 {11208}. 5A^{m}S {11208}. **dv:** PI 277130 {11385}; PI 277131-2 {11385}; PI 277135 {11385}; PI 306540 {11385}; PI 306545 {11385}; PI 306547 {11385}; PI 428158 {11385}; PI 435001 {11385}. **dv2:** PI 306540 *Sr21 SrTm4 SrTm5* {11208}. **v:** PI 689563, PI 306540/Kronos/2/UC1361/4UC12014-36 {11385}. **ma:** *Pinb-5A^{m}S……GH724575/DK22976/CA5012332* – 0.25 cM – *Sr60/LRRK123.1* – 0.19 cM – *CJ942731/CJ884584* {11208}; *GH724575* – 1.56 cM – *Sr60/ LRRK123.1* – 0.52 cM – *FD475316* {11208}. *Sr60F2R2* {11385}. **c:** *Sr60* from *T. monococcum* PI 306540 encodes a 724 amino acid protein with two putative kinase domains designated *Wheat Tandem Kinase 2* (*WTK2*) {11208,11385}. GenBank MK629715 {11385}. The gene is orthologous to *T. aestivum* gene *TraesCS5A02G005400* {11385}.
Sr60 in UC12014-36+Sr60 (PI 689563) is linked with puroindoline genes for grain softness that were also introgressed from the diploid parent {11385}.

SR61

Sr61 {11397}. *SrB* {11337}. Derived from *Th. ponticum* 11397}. 6A = T6AS.6AL-6Ae#1-6Ae#3 {19018}; 6Ae#3 {11338}. **v:** AGG91586WHEA *Sr26* {11397}. **su:** W3757 = SA8123 {11337}, a (6Ae#3(6D) line {11338}. **ma:** *SrB* was recombined with a 6Ae#1 segment possessing *Sr26*. Marker *sunKASP_225* {11336} was diagnostic for the recombined line AGG91586WHEA {11338}. **v2:** AGG91586WHEA *Sr26* {11397}. **c:** Encodes a 880 amino acid NLR protein; GenBank MN531844 {11528}.
The recombinant AGG91586WHEA was produced after crossing the shortened 6Ae#1 recombinant WA-5 (AUS91436) carrying *Sr26* with SA8123. A separate line carrying *Sr61* alone is currently being selected for *Ph1* homozygosity.

SR62

Sr62 {11524}. *Sr1644-1Sh* {11519}. 1BS = T1S^{Sh}S.1S^{Sh}L-1BL {11524}. **v:** Zahir*4 / *Ae. sharonensis* AS_1644, JIC DPRM0081 {11524}. **ma:** Mapped in *Ae sharonensis* to a 480 kb interval on chr arm 1^{Sh}S {11519}. **c:** Cloned from *Ae. sharonensis* and validated in transformed wheat. *Sr62* is tandom kinase with both domains required for function {11524}. *Sr62* has a kinase-pseudokinse (tandom kinase) structure with both components required for resistance function, 740 amino acids {11524}. GenBank MZ826707.

1DS (T1S^{Sh}S.1S^{Sh}L-1DL). **v:** JIC DPRM0092 {11524}. **al:** *Ae. sharonensis* AS_1644 {11519}.

SR63

Sr63 {11554}. Adult plant resistance. *QSrGH.cs-2AL* {11554}. 2AL {11554}. **tv:** GH/M14 RIL49 XXXXX {11554}; GH/M14 RIL188 AUSXXXX {11554}. **tv2:** Glossy Huguenot *Sr58* (syn *QSrGH.cs-1BL*) AUS2499 {11554}. **ma:** *IWA200-KASP_32429* – 2.7 cM – *Sr63* – 3.0 cM – *IWB4881*-2AL {11554}.

SR64

SR64 {11644}.Derived from *Thinopyrum*.
4D = T4DL·4J^SS {10788}. **v:** KS93WGRC27 {404}; Mace (PI 651043) {11681}.
4D = T4DL·4DS-4J^SS {11644}. **i:** Line E*6/rec213 (*Sr64, Wsm1*) = GSTR 527 {11644, https://npgsweb.ars-grin.gov/gringlobal/accessiondetail?id=2158211}. **v:** KS08WGGRC50 {11644, 10788}. **ma:** KASP markers developed in {11643}.

SR65

Sr65 {11682}. *SrH2* {11682}. 1AS {11682}. **v:** Hango-2 FLW6-Selection AGG95499WHEA {11682}. **ma:** *KASP_7944/ KASP_11804* (2,3 Mb, CS REfSeq 2,1) – 2.6 cM – *SR65* – 2.0 cM – *KASP_12147 / KASP21832 / sunCS_265* {11682}. CHS21_002378110 bp, respectively.

SR66

Sr66 {11685}. *SrTA1662* {11012}. 1DS {11012}. **v:** KS05HW14 {11405}. **dv:** *Ae. tauschii* TA1662 {11012}; TOWWC0017 = TA11134 11685}; TOWWC0033 = TA1582 {11685}; TOWWC0104 = TA1658 {11685}. **ma:** *Xwmc432-1D* – 4.4 cM – *SrTA1662* – 4.4 cM – *Xwmc222-1D* {11012}. **c:** An *SrTA1662* candidate identified by AgRenSeq encoded a CC-NBS-LRR candidate gene (GenBank MG763911) with 83% homology to *Sr33* {11405}. GenBank MW526949 {11612}. *Sr66* is a paralogue of *Sr33* {11685}.

SR67

***Sr67*. v2:** KU168-2 *Sr57* = XXXXXX {11687; 11688}. 6AL {11688}. **ma:** Mapping data indicates that *Sr67* (61.80 – 61.80 Mb) is distal to *Sr13* {61.6437} (CS REFSeq v2) {11688}.

Consensus maps of many reported genes and QTL for stem rust resistance are provided in {11202}.

Temporay designations

SrA {323}. **v:** SW55-1 {323}; SW56-1 {323}. **v2:** SW33-5 *Sr9a Sr13* {323}; SW54-3 *Sr9d Sr13* {323}.

SrAes7t {10872}. 2BS = T2B.2BS-2SS-2BS {10872}. **v:** Line 0797 {10872}. **ma:** Sr39#50s {10741, 10872}.
SrAes7t may be identical to *Sr39* {10872}.

SrCad {10733}. 6DS {10733}. **v:** AC Cadillac {10733}; AC Crystal {10733}; AC Foremost {10733}; AC Karma {10733}; AC Taber {10733}; AC2000 {10733}; Peace {10733}; 5700 {10733}. **ma:** Lines with *Bt10* {10733}; *Xcfd49-6D* – 7.7 cM – *SrCad* – 1.5 cM – FSD_RSA/*Bt10* – 14.1 cM – *Xbarc301-6D* – 0.8 cM – *Xbarc173-6D* {10733}; *Xcfd49-6D* – 7.2 cM – *SrCad* – 1.8 cM – FSD-RSA/*Bt10* – 14 cM – *Xcfd75-6D* {10733}.

SrND643 {11092}. 4AL {11092}. **bin:** 4AL4-0.8-1.00. **v:** Kenya Sunbird {11092}; Kenya Tai {11092}; ND643/2*Weebill1 GID6302736 {11092}. **tv:** ND643 {11092}. **ma:** *Xwmc776-4A* – 2.9 cM – *Xgwm350-4A* – 0.5 cM – *SrND643* – 4.1 cM – *Xwmc219-4A* {11092}.

SrPan3161 {11722}. 4DS {11722}. **v:** Tugela {11722}. **v2:** PAN 3161 *Sr57/Lr34* {11722}. **ma:** *RHT-D1* – 12.8 cM – *Xwmc-720-4D* 1.8 cM – *SRPan3161* – 1.8 cM – *Xgpc8038Xwmc52/Xgpc7414/Xcfd23/Xpsp3103-4D* {11722}.

SrPI94701 {11780}. 5BL {11780}. **tv:** PI 94701 {11780}. **ma:** Mapped to a 0.17 cM region flanked by *pku69124* and *pku69228* and corresponding to 1.04 and 2.15 Mb in the Svevo REfSeq 1.0 and CSRefSeq 2 genomes {11780}.

SrPI410966 {11180. 2BS {11180}. **v:** PI 410966 {11180}.
The marker profile for this gene was very similar to that of a line with *Sr36* {11180, 10825}. Specificity tests were not reported.

SrTA10276-2V {11395}. 2V {11395}. **ad:** TA7753 {11395}. **al:** *D. villosum* TA10276 {11395}.

SrTm4 {11111}. Reccessive. 2A^{m}L {11111}. **dv:** Monogenic line TmS4-260 {11673}. **dv2:** *T. monococcum* PI306540 *Sr21 Sr22b Sr60* {11111, 11673}. **bin/contig:** IWGS_2AL_contig6401556. **ma:** BQ461276 – 1.6 cM – *SrTm4* – 0.5 cM – DR732348/*Xgwm526/Xgdm93-2A* {11111}. Mapped to a 0.06 cM interval – 763.67 – 763.67 Mb in CS RefSeq 2.1 {11673}. A 593 kb inversion within the candidate region was completely associated with resistance {11673}.
SrTm4 was postulated in several *T. monococcum* accessions originating from the Balkans region – all had the inversion {11673}.

SrTm5 (11208}. 7A^{m}L {M11208}. **dv:** *T. monococcum* PI 277131-2 {11208}. **dv2:** *T. monococcum* PI 306540 *Sr21 Sr60 SrTm4* {11208}; A further 10 *T. monococcum* accessions, all with the same inversion {11754}. **ma:** *SrTm5/IWB25012/IWB44281/IWB405527/Sr22GMF/GMR* – 0.8 cM –

IWB6942 {11208}. Located in a 0.37 cM interval flanked by *CD903048* (762.56 Mb) and *DK65885/Xgwm526-2A* (763.83 Mb, CS RefSeq 2.1) {11754}; reduced to a 593 kb 0.06 cM (762.67 – 763.67 Mb) region in PI 206540 relative to CS with an inversion breakpoint located in the promoter of a candidate gene {11754}.
May be allelic with *Sr22* {112308}.

SrTmp {1230}. *SrSha7* {11057}; *SrA2K* {11691}; *QSr.nc.*6D {11691}. 6DS. **v:** AGS2000 {11691}; Bai-Yu-Bao {564}; Beijing 9 {564}; Beijing 11 {564}; Digalu {11132, 11057}; Ember {11152}; Fertodi 293 {977}; Guard-1 {11152}; Kenya Robin {11152, 11057}; KS91WGRC11 {M22059}. Martonvasari 5 {977}; Mironovska = Mironovskaya 808 {68, 977}; Morvarid {11132}; Nung-Ta 139 {564}; Overland {11152}; Parker {977}; Ripper {11132}; Shield {11152}; Trison {1230}; Triumph 64 {1230, 841, 977}; Xuzhou 14 {564}; Yen-An 15 {564}. **v2:** Beijing 10 *Sr5* {564}; PI 177906 *Sr7b Sr28* {11419}; MD01W28-08-11 *Sr31* {11691}. **ma:** *SrTmp* – 3.1 cM – *IWB49086* {11419}.
The possibility of this gene being present in a number of South African cultivars, including Betta = Klein Impacto, is discussed in {10941}.

SrWld {1230}. **v2:** Prospect *Sr11* {197}.

SrZdar {67}. 1B {67}. **v:** Zdar {67}.

Sr1RS$^{\text{Amigo}}$ {10845}. 1AS (T1AL.1RS) {389}, {1624}. **v2:** Amigo *Sr24* {10845, 1464}. **ma:** *Xscm09-1R*$_{224}$ {10845}.
This alien segment also carries *Pm17* - see *Pm17*

Sr8155B1 {11580}. Recessive. 6AS {11580}. **v:** Choteau / Mountrail Der. SXD 43 PI 681713 {11580}; Marruecos*2/CItr 8155 {11580}. **tv:** Alkabo 11580}; Renville {11580}. **tv2:** Grenora *Sr13* {11580}; Munich *Sr13* {11580}. **ma:** Co-segregation with *KASP_6AS_IWB10558* {11580}.
Also predicted in durum accessions Belzer, Dilse, Lloyd, Divide and Montrail {11580}.

Sr10171 {10936}. 7DS {10936}. **v:** Genetic stock to be designated {10936}. **dv:** *Ae. tauschii* TA10171 {10936}. **ma:** *Sr10171* – 0.9 cM – *Xgdm88/Xwmc827-7D* – 1.9 cM – *Xcfd30-7D* {10936}.

Sr10187 {10936}. [*SrTA10187* {11181}]. 6DS {10936}. **v:** Genetic stock to be designated {10936}. **dv:** *Ae. tauschii* TA10187 {10936}. **ma:** *Xcfd49-6D* – 1.9 cM – *Sr10187* – 13.6 cM – *Xbarc173-6D*{10936}; *6DS0027* – 0.2 cM – *Sr10187* – 0.2 cM – *6DS00273* {11181}; *Sr10187* – 0.2 cM – *6DS0039* {11181}.

Sr10526 {11249}. 6DS {11249}. **v:** CItr 105026 {11249}. **ma:** *IWB36391/IWB34477* – 2.9 cM – *Sr15026* – 3.0 cM – *IWA4000* {11249}; *IWB36391* – 0.4 cM – *IWB262* – 2.6 cM – *Sr15026* – 1.3 cM – *IWB49086* {11249}.
Sr10526 was detected with races QFCSC and TTTTF. When the same DH and RIL populations were tested with race TRTTF there was evidence for complementary resistance genes on chromosomes 6DS and 6AS, one of which was *Sr10526*. When the populations were tested in the field in Kenya with Ug99 races *QSr.abr-6AS.1* (R^2 = 0.1 – 0.3) was detected {11249}.

Th. ponticum-derived, stem rust resistant line WTT34 with a T5DS.5DL-Th chromosome pair is reported in {11783}.

Additional temporary designations are listed in {1230}.
Genotype lists: {323}, {970}, {10270}, {10511}, {10697}.

Complex genotypes:
AC Taber: *Sr2, Sr9b, Sr11, Sr12* {9905}.
Centurk: *Sr5* {979}, *Sr6* {979}, *Sr8a, Sr9a* {979}, *Sr17* {979}.
Chris: *Sr5* {679}, {1371}, *Sr7a* {1371}, *Sr9g* {1371}, *Sr12* {1371}.
Egret: *Sr5* {939}, *Sr8a* {939}, *Sr9b* {939}, *Sr12* {939}.
FKN: *Sr2, Sr6, Sr7a, Sr8a* {791}, *Sr9b* {791}.
H-44: *Sr2, Sr7b* {677}, *Sr9d* {677}, *Sr17.*
Hartog: *Sr2* {127}, *Sr8a, Sr9g, Sr12* {939}.
Hope: *Sr2* {677}, *Sr7b* {677}, *Sr9d* {677}, *Sr17.*
Kenya Plume: *Sr2* {1370}, *Sr5* {1370}, *Sr6* {1370}, *Sr7a* {1370}, *Sr9b* {1370}, *Sr12* {1370} *Sr17* {1370}.
Khapstein: *Sr2, Sr7a, Sr13* {674}, *Sr14* {674}.
Lawrence: *Sr2, Sr7b* {939}, *Sr9d, Sr17.*
Lerma Rojo 64: *Sr2, Sr6, Sr7b* {979}, *Sr9a* {979}.
Madden: *Sr2, Sr9b, Sr11, Sr13* {842}.
Manitou: *Sr5* {679}, *Sr6* {679}, *Sr7a, Sr9g* {965}, *Sr12* {939}.
Mendos: *Sr7a* {939}, *Sr11* {879}, *Sr17, Sr36.*
Pasqua: *Sr5, Sr6, Sr7a, Sr9b, Sr12*. Gene *Lr34* acted as an enhancer of APR {9905}.
PI 362698: *Sr5, Sr8a, Sr12, Sr15?, Sr16* {11347}.
PI 362698: *Sr5, Sr8a, Sr12, Sr15?, Sr16* {11347}.
PI 60599: *Sr7a* {689}, *Sr8a, Sr9b, Sr10.*
Redman: *Sr2, Sr7b* {939}, *Sr9d* {939}, *Sr17.*
Reliance: *Sr5* {1308}, *Sr16* {1238}, *Sr18*, *Sr20.*
Renown: *Sr2, Sr7b* {939}, *Sr9d* {939}, *Sr17.*
Roblin: *Sr5, Sr7a? Sr11, Sr12.*
Selkirk: *Sr2* {499}, *Sr6* {468}, *Sr7b* {499}, *Sr17, Sr23* {950}.
Thatcher: *Sr5* {1308}, *Sr9g* {965}, *Sr12* {939}, *Sr16* {1308}.
Timgalen: *Sr5* (heterogeneous) {1555}, *Sr6* {1555}, *Sr8a, Sr36.*
WW15 = Anza = Karamu = T4: *Sr5* {939}, *Sr8a* {939}, *Sr9b* {939}, *Sr12* {939}.

QTL:

Arina / Forno: *Qsr.sun-5BL* {10565}; resistance contributed by Arina, associated with *Xglk356-5B*, R^2 = 11-12% {10565}. *Qsr.sun-7DS* {10565}; resistance contributed by Forno, associated with markers *XcsLV34* and *Xswm10* diagnostic for *Lr34/Yr18* {10565}.

Avocet S / Pavon 76: RIL population of lines lacking *Sr26*:Five QTLs, *QSr.cim-3B(Sr2), QSr.cim-1B(Lr46/Yr29/Pm39* region) and *QSr.cim-3D* (R^2=0.2) from Pavon 76; *QSr.cim-4B* and *QSr.cim-5A* from Avocet S {10975}.

Carberry (Resistant in Canada) / AC Cadillac (Resistant in Canada and Kenya): DH population: QTLs effective in Kenya were located in chromosomes 2B, 5B, 7B and 7D, those effective in Canada were on 3B (*Sr2*), 5A and 5B; those effective in Kenya and Canada were on 4B and 6D (*Sr2*); both parents had *Lr34/Sr51* {11040}

HD2009 / WL711: RILs: Three of several QTLs gave consistent effects across environments, viz. *QSr.sun-3BS*, R^2 = 0.09-0.15, probably *Sr2, QSr.sun-5DL*, R^2 = 0.2-0.44, probably *Sr30*, and *QSr.sun-7A*, R^2 = 0.07-0.13, nearest marker *wPT-4515* {10632}.

PBW343 (S) / Muu (I): RIL population:4 consistent QTLs were identified, *QSr.cim-2BS, QSr.cim-3BS(Sr2)* and *Sr.cim-7AS* from Muu, and *QSr.cim-5BL* from PBW343 {11019}.

RL6071 / RL6058(R): RIL population: RL6058, a Tc backcross line with *Lr34/Sr57* is more resistant than Tc. Enhancement of resistance in both Kenya and North America was attributed to a QTL in the region *wPt5044 – Xgwm-2B* in chromosome 2BL {10902}.

Spark / Rialto: DH population: *Sr5* and *Sr31* were derived from Rialto and *QDr.sun-3BS* (*Xgwm1034-3B – BS00010945* region and *QSR.sun-5A* (*Xgwm445-5A – Xgwm205-5A* region) were derived from Spark {11231}.

Suppressor of Stem Rust Resistance 1

A suppressor of stem rust resistance in cv. Canthatch was known from the 1980s based on the response of an extracted tetraploid and aneuploid derivatives of Canthach as well as mutation analysis ({11410, 11411}) and references therein.

SuSr-D1 {11411}. 7DL {11412, 11417}. **v:** Canthatch CTH-K RL5451 {11411}; Columbus {11417}; Katepwa {11417}. Other Canadian Thatcher derivatives {11417}. **ma:** Localised to a 1.3 cM genetic interval flanked by *Xkwh239* and *Xkwh281* {11412}. **c:** *TraesCS7D01G526100*. Encodes a mutant form of *TaMed15b.D*, a subunit of the Medicator complex {11412}.

3.21. Reaction to *Puccinia striiformis* Westend.

Disease: Stripe rust, yellow rust.

3.21.1. Designated genes for resistance to stripe rust

YR1

Yr1 {851}. [*L* {1622}]. 2AL {940}. 2A {1610}, {877}. **bin:** 2AL1-0.85-1.00 {10564}. **i:** AVS+Yr1 {970}. **v:** Chinese 166 {851}; Corin {230}; Dalee {83}; Durin {1459}; E2025 {1267}; E7700 {1267}; E8594 {1267}; Feng-Kang 13 {1610}; Heines 110 {604}; Maris Ranger {1459}; Maris Templar {1459}; Odra {73}; Ritmo {10038}. **v2:** Argent *Yr3a Yr4a Yr6* {1067}; Avocet (UK) *Yr2 Yr6* {1459}; Bounty *Yr13* {1459}; Fenman *Yr2* {1459}; Galahad *Yr2* {heterogeneous} *Yr14* {1459}; Galahad *Yr14* {83}; Kraka *Yr32* {10038}; Ibis *Yr2* {604}; Longbow *Yr2 Yr6* {83}; Mardler *Yr2 Yr3a*

Yr4a Yr13 {1459}, {604}; Maris Templar *Yr3a Yr4a* {604}; Marksman {heterogeneous} *Yr2 Yr13* {1459}; Mithras *Yr2 Yr6* {1459}; Nudif TP1 *Yr3a* {1431}; Nudif TP3 *Yr3c* {1431}; Nudif TP250 *Yr6* {1431}; Regina *Yr2* {73}; Rothwell Perdix *Yr2* {604}; Savannah *Yr2 Yr3 Yr9 Yr32* {10032}; Sportsman *Yr13* {1459}; Stetson *Yr9* {83}; Sylvia *Yr2* {1430}; Tadorna *Yr2* {1431}; Virtue *Yr13* {1459,83}. **ma:** *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* – 16.5 cM – *Sr48* {10564}.
A report {1267} that Kalyansona and Nadadores carried *Yr1* is not correct.

YR2

Yr2 {851}. Recessive {1351}. [*U* {1622}]. 7B {184}, {746}, {186}. **v:** Derius {230}; Flevina {1431}; Hana; HD2329 {1352}; Kalyansona {1352, 1351}; Laketch {50}; Leda {1430}; Manella {1431}; Merlin {1622}; Odra {71}; PBW54 {1352}; PBW120 {1352}; Slavia {71,73}; Soissonais Desprez {851}; WG377 {1352}; WH147 {1352}; WL711 {1352}; WL1562 {1352}. **v2:** Avocet (U.K.) *Yr1 Yr6* {1459}; Brigand *Yr14* {83}; Cleo *Yr3c* {1457}; Cleo *Yr3c Yr14* {1431}; Fenman *Yr1* {1459}; Flamingo *Yr6* {1430}; Flevina *Yr7* {1430}; Galahad (heterogeneous) *Yr1 Yr14* {1459}; Garant *Yr7* {230}; Hardi *Yr7* {230}; Heines Kolben *Yr6* {611}; Heines Peko *Yr6 Yr25* {746}; Heines VII *Yr25* {851}; Ibis *Yr1* {604}; Lely *Yr7* {1430}; Liberator *Yr3c* {1431}; Longbow *Yr1 Yr6* {83}; Mardler *Yr1 Yr3a Yr4a Yr13* {1459}; Maris Beacon *Yr3b Yr4b* {1459}; Maris Huntsman *Yr3a Yr4a Yr13* {604}; Maris Nimrod *Yr13* {1459}; Marksman *Yr1* (heterogeneous) *Yr13* {1459}; Mithras *Yr1 Yr6* {1459}; Nautica *Yr9* {1430}; Norman *Yr6* {83}; Rapier *Yr4* {83}; Rothwell Perdix *Yr1* {604}; Sonalika *YrA* {1352}; Stella *Yr3* {1430}; Sylvia *Yr1* {1430}; Tadorna *Yr1* {1431}; Viginta *Yr3a Yr4a* {71,73}; Wizard (heterogeneous) *Yr14* {1459}; Yamhill *Yr3a Yr4a*; Zdar *Yr4a* {73}.
Yr2 originally referred to a gene in Heines VII conferring resistance to European pathotypes. However, Heines VII possesses at least additional resistance gene, *Yr25* {1351} that can be detected with a geographically wider range of pathogen isolates. *Yr2* is present in Kalyansona {1351} and a range of spring wheats distributed by CIMMYT.

YR3

Yr3a {851}. 1B {184}, {185}. 2B {10370}. 5BL {11235}. **i:** Taichung 29*6/Vilmorin 23 {10370}. **v:** Bon Fermier {1431}; Nudif TP1 {1431}; Stephens {184,182}; Vilmorin 23 {10370}. **v2:** Argent *Yr1 Yr4a Yr6* {1067}; Cappelle-Desprez *Yr4a* {851}; Druchamp *Yr4a*; Hobbit *Yr4a Yr14* {604}; Kinsman *Yr4a Yr6* {604}; Mardler *Yr1 Yr2 Yr4a Yr13* {1459}; Maris Huntsman *Yr2 Yr4a Yr13* {604}; Maris Freeman *Yr4a Yr6* {604}; Maris Ranger *Yr4a Yr6* {604}; Nord Desprez *Yr4a* {184}, {182}; Top *Yr4a* {230}; Viginta *Yr2 Yr4a*; Yamhill *Yr2 Yr4a* {182}; Zdar *Yr4a*{71, 73}. **ma:** *Yr3 (YrV23)* – *Xwmc356-2B*, 9.4 cM {10370}.

Yr3b {851}. Chen and Line {182} found that a second gene in Hybrid 46 - presumably this gene was not located at the *Yr3* locus. **v2:** Hybrid 46 *Yr4b* {851}.

Yr3c {851}. 1B {184}. **v:** Minister {184}, {182}, {851}. **v2:** Cleo *Yr2* {1430}; Maris Beacon *Yr2 Yr4b* {1459}.

Undesignated allele. **v:** Enkoy {50}; Vilmorin 23; Staring {1430}. **v2:** Minister *Yr2* {1430}; Savannah *Yr1 Yr2 Yr9 Yr32* {10016}; Senat *Yr32* {10016}; Stella *Yr2* {1430}.

YR4

Yr4.

Yr4a {851}. 6B {184}, {185}. **v:** Vilmorin 23 {184}. **v2:** Argent *Yr1 Yr3a Yr6* {1067}; Cappelle-Desprez *Yr3a* {851}; Druchamp *Yr3a* {182}; Hobbit *Yr3a Yr14* {604}; Huntsman *Yr2 Yr3a Yr13* {604}; Kinsman *Yr3a Yr6* {604}; Maris Ranger *Yr3a Yr6* {604}; Maris Freeman *Yr3a Yr6* {604}; Mardler *Yr1 Yr2 Yr3a Yr13* {1459}; Nord Desprez *Yr3a* {182}; Top *Yr3a* {230}; Viginta *Yr2 Yr3a* {71,73}; Yamhill *Yr2 Yr3a*; Zdar *Yr3a* {71}, {73}.

Yr4b {851}. 6B {184}. **v:** Avalon {1160}; Opal {1431}; Staring {1430}. **v2:** Hybrid 46 *Yr3b*; Maris Beacon *Yr2 Yr3b* {1459, 1160}; Nudif TP12 *Yr3c* {1431}; Stella *Yr2* {1430}. Undesignated allele. [*YrRub* {10720}]. 3BS {10720}.

bin: 3BS3-0.87-1.00 {10720}. **v:** Avalon {10720}; Bolac; Emu S {10720}; Kenya Kubangu {50}; Rubric AUS33333 {10720}. **v2:** Avalon *Yr14* {83}; Rapier *Yr2 Yr14* {83}. **ma:** *Yr4* – 2.9 cM – *Xcfb3530-3B* – 2.4 cM – *Xbarc75-3B* {10720}.
The conclusion that *YrRub* is *Yr4* is based on specificity similarities and the presence of the *Xcfb3530*$_{150}$ and *Xbarc75*$_{132}$ alleles in the five genotypes listed above. The 3BS location is not consistent with that listed for *Yr4a and Yr4b*.

YR5

Allelism with *YR7* and *YRSP* (*Sr5b*) is reported in {10759} but cloning indicated that *YR5* and *YrSP* are not allelic with *Yr7* {11351}.

Yr5a [{11351}]. [*Yr5* {877}.] Allelic with *Yr7* and *YrSp* {10759} 2BL {34}. **i:** AVS+Yr5 {970}; Lemhi+Yr5 {11153}. **v:** By 33 {3102}; E5557 {1267}; E8510 {1267}; *T. spelta album* {877}; Seven spelt accessions from Europe and Iran {640}. **ma:** *Yr5* – 10.5 & 13.3 cM – *Xgwm501-2B* {3102}; Completely linked to Resistance Gene-Analog Polymorphism (GRAP) markers *Xwgp17-2B, Xwgp19-2B* and *Xwgp26-2B* {10096}; *Xwgp17-2B* was later converted into a simpler Cleaved Amplified Polymorphic Sequence (CAPS) PCR marker {10097}; Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310 {10435}; *Xwmc175-2B* – 1.1 cM – *YrSTS-7/8* – 0.3 cM – *Yr5* – 0.4 cM – *Xbarc349-2B*{10826}; *Xwmc175-2B* – 4.6 cM – *YR5/ TaAffrx.65234.1.S2-at/Ta.28038* – 0.7 cM – *S23M41-310/STS:S23M41-275* {11153}. Accurate prediction of *Yr5a* was achieved with markers *IWA4096, IWA 6121* and *IWA7850* for which primer sequences are available in Cereals DB {11286}. **c:** *Yr5a* (Genbank MN273772) along with *Yr7* and *Yr5b* has a BED-LRR structure lacking a CC-domain {11351}.

Yr5b [{11351}]. [*YrSP*{10018}, *YrSp* {10352}, *YrSp*]. 2B {10018, 10352}. **bin:** 2BL-C-0.5. **i:** Cx1 = Avocet S*4/Spaldings Prolific {10018}; Taichung*6/Spaldings Prolific {10352}. **v2:** Spaldings Prolific *Yr25* {10018, 10352}. **ma:** *YrSp* – *Xwmc-2B*, 12.1 cM{10352}; *IWA638* – 0.6 cM – *YrSP* – 1.5 cM –

dp269-2 – 1.9 cM – *Xwmc332-2B* {11091}. **c:** (Genbank MN273773) along with *Yr5* and *Yr7* has a BED-LRR structure lacking a CC-domain {11351}. *Yr5b* is a truncated form of *Yr5* but confers a different specificity {11351}.

YR6

Yr6 {877}. [*B* {1622}]. 7B {746}. 7BS {331}. **i:** AVS+Yr6 {970}. **v:** Austerlitz {230}; Fielder {181}; Heines Kolben {1622}; Koga II {746}; Maris Dove {604}; Recital {230}; Takari {368}. **v2:** Argent *Yr1 Yr3a Yr4a* {1067}; Avocet (UK) *Yr1 Yr2* {1459}; Cadenza *Yr7* {11187}; Flamingo *Yr2* {1430}; Heines Peko *Yr2*{746, 877}; Kinsman *Yr3a Yr4a* {604}; Kolben *Yr2* {611}; Longbow *Yr1 Yr2* {1459, 83}; Maris Freeman *Yr3a Yr4a* {604}; Maris Ranger *Yr3a Yr4a* {604}; Mithras *Yr1 Yr2* {1459}; Norman *Yr2* {1459, 83}; Nudif TP241 *Yr7* {1431}; Nudif TP250 *Yr1* {1431}; Orca *Yr3c* {1431}; Pavon 76 *Yr7* {284}; Penjamo 62 (heterogeneous) *Yr18* {1562}. **tv:** Duilio {192}; Latino {192}; Norba {192}; Quadruro {192}; Rodeo (heterogeneous) {192}. **ma:** *Xgwm577-7B* – *Yr6* , <0.4 cM {11187}; Narrowed to an ~60 kb region including *Xgwm577* {11188}; Given the location of *Xgwm577* the gene location should be 7BL.

YR7 TraesCS2B01G488000

Allelism with *YR5a* and *YRSP* is reported in {10759} but cloning indicated that *YR7* is not allelic with *YR5a* and *YrSP* (*Sr5b*) {11351}.

Yr7 {877}. Allelic with *Yr5a* and *YrSp* {10759} 2B {1429}, {612}. 2BL {965}. **i:** AVS+Yr7 {970}; Taichung 29*6/Lee {10371}. **v:** Present in many hexaploid wheats with *Sr9g* – see {965}; Brock {83}; Lee {877}; Nudif TP257 {1431}; PBW12 {1352}; Paragon {11351}. Prinqual {230}; Renard {83}; Talent {230}; Tango {230}; Tommy {83}; WL2265 {1352}. **v2:** Cadenza *Yr6* {11187}; Donata *Yr9* {1430}; Flevina *Yr2* {1431}; Garant *Yr2* {230}; Hardi *Yr2* {230}; Lely *Yr2* {1430}; Nudif TP241 *Yr6* {1431}; Pakistan 81 = Veery#5 *Yr9* {284}; Pavon 76 *Yr6* {284}; Reichersberg 42 *Yr25* {10}; Thatcher {965}. **tv:** Iumillo {965}; but not present Acme and Kubanka which also carry *Sr9g* {965}. **ma:** *Yr7* – *Xgwm526-2B*, 5.3 cM {10371}; *Xwmc175A-2B* – *Yr7*, <0.4 cM {11187}. **c:** *Yr7* (Genbank MN273771) along with *Yr5a* and *YrSP* has a BED-LRR structure lacking a CC-domain {11351}.

YR8

Yr8 {1217, 1218}. Derived from *Ae. comosa*. 2D = T2D-2M {1218} = T2DS-2M#1L.2M#1S {389}. **i:** AVS+Yr8 {970}. **tr:** Chromosome 2D-2M translocations in Hobbit Sib and Maris Widgeon {1016}; Compair {1217, 1218}; CS 3D/2M 3/8 {967}; See also *Sr34* and {967}.
2A = 2A-2M = T2AS-2M#1L.2M#1S {389} CS 2A/2M 4/2 {967}.
2M-1. **su:** CS 2M#1(2A) {967}.

YR9

Yr9 {878}. Derived from *S. cereale*. See also Reaction to *P. graminis, Sr31*: Reaction to *P. triticina Lr26* 1B=1BL.1RS. **i:** AVS+Yr9 {970}. **v:** Almus {998}; Aurora {1623}.

Chromosome status not specified Baron {83}; Benno {998}; Bezostaya II {998}; Branka {71}; Clement {1532, 1430}; Cougar {0267}; Danubia {68}; GR876 {753}; Hammer {83}; Iris {68}; Kavkaz {1623}; Kromerzhizhskaya {1149}; Lyutestsens 15 {1149}; Lovrin 10 {998}; Lovrin 13 {998}; Mildress {1027}; Perseus {998}; Predgornaya {998}; Rawhide (heterogeneous) {0267}; Riebesel 47/51{878, 1623}; Roxana {68}; Sabina {68}; Salmon {998}; Sarhad 82 {284}; Selekta {68}; Shtorm {1149}; Skorospelka 35 {998}; Sleipner {10038}; Solaris {68}; St 2153/63 {997}; Stuart {83}; Veery {986}; Weique {1627}; Winnetou {998}; Weihenstephan 1007/53 {1623}. **v2:** Agra *Yr3* {71,68}; Brigadier *Yr17* {10785}; Donata *Yr7* {1430}; Haven *Yr6* {10038}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 *Yr18 Yr27* {10160}; Lynx *Yr6 Yr17* {10038}; Nautica *Yr2* {1430}; Pakistan 81 = Veery#5 *Yr7* {284}; Savannah *Yr1 Yr2 Yr3 Yr17* {10016}; Stetson *Yr1* {83}; Sparta *Yr3* {71}. **tv:** Cando*2/Veery, KS91WGRC14 {381}.
1R(1B) {1623, 997} **su:** Burgas 2 {998}; Clement {1160}; Lovrin 13 {998}; Mildress {998}; Mironovskaja 10 {998}; Neuzucht {1623}; Orlando {1623}; Roseana {68}; Saladin {997}; Salzmunder Bartweizen {1623}; St 14/44 {998}; Weique {1627}; Wentzel W {1623}; Winnetou {1027}; Zorba {998}; See also {50}. **ma:** Several markers tightly linked with *Yr9* were identified in {377}; *Yr9* – 3.7 cM – *Xgwm582-1BL* {10365}.
Stripe rust resistant wheat - *S. africanum* derivatives G17 (substitution line with 1R^{a}), L9-15 (1BL, 1RS^{a} and L2-20 (putative cryptic translocations) are reported in {10596}.

YR10 *TraesCS1B03G0003500*, *TraesCS1B03G0003600* (CS RefSeq 2.1)

Yr10 {878}. [*YrVav* {0262}]. 1BS {1002}. 1B {641}. **i:** AVS+Yr10 {970}. **v:** AC Radiant {11167}; Crest {11304}; Jacmar {11145}; Moro {878}; PI 178383 {878}; QLD709 = Janz*2/*T. vavilovii* {0262}; *T. spelta* 415 {641}; *T. vavilovii* AUS 22498 {0262}; 10 Chinese cultivars {11304}. **ma:** A SCAR marker was described in {0261}; QLD709 and *T. spelta* 415, both with white glumes, failed to amplify the SCAR sequence, but both carried unique alleles at the *Gli-B1* and *Xpsp3000-1B* loci {0262}. These differed from the Moro source of *Yr10*. *Yr10* – 1.5 cM – *Gli-B1* – 1.1 cM – *Xpsp3000-1B* {0261}; *Yr10* – 1.2 cM – *Xpsp3000* – 4.0 cM – *Gli-B1*{321}; Cosegregation between a RGA marker *RgaYr10a* and *Yr10* was reported in {0376}. *Yr10/Xsdauw79* – 0.2 cM – *Xsdauw78* – 1.0 cM – $Yr10_{CG}$ – 2.1 cM – *Xsdauw75* – 0.5 cM – *Xpsp3000-1B* {11304}. **c:** *Yr10* has a CC-NBS-LRR structure. GenBank AF149112 {11145}. AF149112 ($Yr10_{CG}$), TraesCS1B03G0000200, shown not to be the candidate gene {11304}.
YrNAM {11692}. **c:** A gene named *YrNAM* located 1.2 cM from 'Yr_{CG}', the original allegedly claimed *Yr10*, but with common specificity, encoded an NLR with 5' NAM and 3' ZNF0BED domains {11692}. Yr_{CG} was confirmed as *Yr10* {11763). GenBank OP490604.

YR11

Yr11. Adult plant resistance. [*R11* {1157}]. **v:** Joss Cambier {606}. **v2:** Heines VII *Yr2 Yr25* see {970}.

YR12

Yr12. Adult plant resistance. [*R12* {1157}]. **v:** Fleurus {1158}; Frontier {1159}; Pride {1157}. **v2:** Armada *Yr3a Yr4a* {81, 1160}; Mega *Yr3a Yr4a* {1160, 1157}. **v:** Waggoner *Yr3a Yr4a Yr6* {1158}.

YR13

Yr13. Adult plant resistance. [*R13* {1157}]. **v2:** Bounty *Yr1 Yr3a Yr4a* {1459}; Brigand *Yr2 Yr3a Yr4a Yr14* {609}; Copain *Yr3a Yr4a* {1158}; Gawain *Yr2 Yr3a Yr4a Yr14* {81}; Guardian *Yr2* {82}; Hustler *Yr1 Yr2 Yr3a Yr4a* {1459, 83}; Kinsman *Yr3a Yr4a Yr6* {1459}; Mardler *Yr1 Yr2 Yr3a Yr4a* {1459}; Maris Huntsman *Yr2 Yr3a Yr4a* {1459, 83, 604}; Maris Nimrod *Yr2 Yr3a Yr4a*{1459, 607, 1157}; Marksman *Yr1* {heterogeneous} *Yr2 Yr3a Yr4a* {1459}; Pageant *Yr2 Yr3a Yr4a* {82}; Professor Marchal *Yr2 Yr3a Yr4a* {607}; Sportsman *Yr1 Yr3a Yr4a* {1459}; Virtue *Yr1 Yr3a Yr4a* {1158, 1459, 83}.

YR14

Yr14. Adult plant resistance. [*R14* {1157}]. **v:** Kador {1158}; Score {1157}; Wembley {610}. **v2:** Avalon *Yr3b Yr4b* {1459, 83}; Brigand *Yr2 Yr3a Yr4a Yr13* {1459, 83, 609}; Galahad *Yr1 Yr2* (heterogeneous) *Yr3a Yr4a* {1459, 83}; Gawain *Yr2 Yr3a Yr4a Yr13* {81}; Hobbit *Yr3a Yr4a* {1459, 1157}; Maris Bilbo *Yr3a Yr4a* 1459, 1157}; Moulin *Yr6* {83}; Rapier *Yr2 Yr3b Yr4b* {83}; Wizard *Yr2* (heterogeneous) *Yr3b Yr4b* {1459, 83}.

YR15

Yr15 {432}, {969}. 1BS {939}, {969|, {0003}. *YrH52* {0003}, *YrG303* {11429}, *Wtk1* {11392}. **i:** AVS+Yr15 {970}. **v:** Agrestis {330}; Boston {330}; Clearwhite 515 {11392}; Cortez {330}; Expresso {11392}; Legron {330}; Ochre {11240}; Patwin 515 {11392}; Seahawk {11392}. Hexaploid derivatives of *T. dicoccoides* G-25 {466, 432}; *T. dicoccoides* H52 {0003, 11429}; *T. dicoccodes* G303 {11429}; V763-2312 {969}; V763-254 {969}. **tv:** *T. dicoccoides* G-25 {466, 432, 431}; ; D447 derivatives B1, B2, B9, B10 {1434}. **ma:** *Xgwm33-1B* – 5 cM – *Yr15* {9904}; *Xgwm33-1B* – 4.5 cM – *Yr15* – 5.6 cM – *UBC199200* – 5.6 cM – *Nor-B1* {110}; Gene order *Yr15 – Yr24 – Xgwm11-1B* {10112}; *OPB131420* – 27.1 cM – *Yr15* – 11.0 cM – *Nor-B 1*{1434}; *Xwmc128/Xgwm273/Xgwm582-1B* – 0.4 cM – *Yr15/Xwgp34/Xgwm413/Xbarc8*{10826}; *Xbarc8-1B* – 3.9 cM – *Yr15* – 2.5 cM – *Xgwm413-1BS* {11173}. *Xbarc8-1B* – 0.26 cM – *R11/R5* – 0.51 cM – *Yr15* – 0.26 cM – *Xgwm413-1B/R8* {11240}; *Xbarc-8-1B* – 4.2 cM – *Yr15* – 3.5 cM – *Xgwm413-1B* {11348}; *Xbarc8-1B* – 4.1 cM – *Yr15* – 2.5 cM – *Xuhw-1B* – 0.5 cM – *Xgwm413-1B* {11348}. *Yr15* is proximal to *Yr64*; recombinant lines are reported in {11349}; *Xwhu300-1B* – 0.013 cM – *Xwhu273-1B* {11392}; distal ...*Yr15* – 9.6 cM – *YrH52* – 1.4 cM – *Nor-B1* – 0.8 cM – *Xgwm264a* – 0.6 cM – *Xgwm18*{3}; *Xgmw273a* – 2.7 cM – *YrH52* – 1.3 cM – *Xgwm413/Nor1*...centromere {108}; A line combing combining *Yr15 and Yr64* is reported in {11618}: gene order *Xbarc8*$_{239}$ – *YR15* – *Xgwm413*$_{102}$ – *YR64* – *Xgwm273*$_{196}$. **c:** Encodes a putative kinase-pseudokinase protein designated as wheat tandom kinase 1 (TPK1), g-DNA 4,655 bp, 665 amino acids. GenBank MG649384, MG674157 {11392}, MK188918 (*YrH52*) {11429}, and MG18819 (*YrG303*).

YR16

Yr16 {1598}. Adult plant resistance. 2D {1598}. **v:** Bersee {1604}; Cappelle-Desprez {1598}.

YR17

Yr17 {62}. 2AS-6M^{v}.2AS {62}. 6M^{v} = 2MS-6MS.6ML or 2MS-6ML.6MS {0009}. *YrHy1* {11308}, *YrMm58* {11308}. **i:** AVS+Yr17 {970}. **v:** Apache {10554}; See *Lr37* (Reaction to *P. triticina*) and *Sr38* (Reaction to *P. graminis*); Arche {0044}; Balthazar {0044}; Bill {10554}; Brigadier {0044}; Caphorn {10554}; CDS Stanley {11579}; Clever {10554}; Clarus {10554}; Cordial {0044}; Corsaire {10554}; Eureka {44}; Hussar {0044}; Huaiyang 1 {11308}; Jagger {10973, 11328}; Kris {10283}; Kochu {11267}; Mace {11579}; Mengmai 58 {11308}; Milan {11267}; Mutus {11267}; Pernel {44}; Rapsodia {10554}; Renan {10554, 0044}; Rheia {10554}; RL 6081 {939}; SY Mattis {11579}. Genotype list in {02105}. **v2:** Brigadier *Yr9* {10785}; Lynx *Yr6 Yr9*; Savannah *Yr1 Yr2 Yr2 Yr32*{ 10016}. **ma:** *Yr17* was closely linked to the SCAR marker SC-Y15, developed from RAPD marker OP-Y15$_{580}$, and to *Xpsr150-2N*^{v} {0044}; Characterized by null alleles for *Xwmc382-2A* and *Xwmc407-2A* {10283}; SCAR markers SC-372 and SC-385 were developed in {10796}.
Although *Yr17* was reported as a seedling-effective gene {62} some researchers report problems in obtaining repeatable seedling responses and prefer to treat this gene as conferring adult plant resistance {11221}.The 2NS translocated segment carrying *Yr17* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}.
Mundt {11340} noted that many genotypes containing *Yr17* continued to have adult plant resistance to races virulent on the seedlings. These cultivars included Renan, Apache, Jagger, Bobtail and Madsen. However, it was unclear as to whether this represented additional resistance gene(s) in the introduced segment or APR genes at other loci.
The 2N^{V}S segment carries a second high-temperature adult plant resistance gene designated *YrM1225* in AvS+Yr17 mutant M1225 {11706}. Presumably the same gene was mapped to the proximal 19.36 – 33 MB region of the translocation in the Jagger reference genome and two candidate genes were predicted {11760}.

YR18. TraesCS7D03G0183600

Yr18 1362}. 7DS {324}. 7D {1362}. **i:** AVS+Yr18 {970}; Thatcher (*Yr7*) near-isogenic lines with *Lr34* including the 13 2-gene combinations reported in {434, 937}. **v:** Jupateco 73R; Lerma Rojo 64 {1375}; Libellula {11139}; Nacazari 76 {1375}; Strampelli {11139}; Tesia F 79 {1375}; Tonichi S 81 {1375}; Wheaton 1375}. **v2:** Parula *Yr29* {10281}; Penjamo 62 *Yr6* (heterogeneous) {1375}; Saar *Yr29* {10481}; Wheats with *Lr34* (See *Lr34*); Others {1376}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Bascribey 95, Seyhan 95 *Yr9 Yr27* {10160}. **ma:** Complete linkage with *Lr34*{937,1362}; *Ltn*{1361}; and *Bdv1*{1363}; *Xgwm120-7D* – 0.9 cM – *Yr18* – 0.7 cM – *Xgwm295-7D* {10259}. **c:** See *Lr34*; Putative ABC transporter {10648}. This gene is identical to *Lr34, Pm38* and *Ltn* and confers stem rust resistance in some genetic backgrounds. Some AVS NILs also have *Yr18*. Forty-three Chinese land varieties predicted to have *Yr18* based on markers had high rust severities. Genetic analyses of four of these landrace (Sichuanyonggang 2, Baikemai, Youmai and Zhangsihuang) indicated the presence of an independent suppressor {11101}. Libellula had an additional 4 QTL and Strampelli had an additional 3 QTL {11139}.

Yr18 conferred seedling resistance to leaf rust when transformed into durum wheat {M10114}.

YR19

Yr19 {183}. [*YrCom* {183}]. 5B {183}. **v2:** Compair *Yr8* {183}.

YR20

Yr20 {183}. [*YrFie* {181}]. 6D {183}. **v2:** Fielder *Yr6* {183}.

YR21

Yr21 {183}. [*YrLem* {181}]. 1B {183,10450}. **v:** Lemhi {183}.
A closely linked gene, also in Lemhi, conferred resistance to *P. s. hordei* {10450}. Both genes were mapped relative to RGAP markers. *Yr21 – YrRpsLem*, 0.3 cM {10450}.

YR22

Yr22 {183}. [*YrLe1*{183}]. 4D{183}. **v2:** Lee *Yr7 Yr23*{183}.

YR23

Yr23 {183}. [*YrLe2* {183}]. 6D {183}. **v2:** Lee *Yr7 Yr22* {183}.

YR24
Identical to *YR26*.

Yr24 {952}. [*YrCH42*]. 1BS {952}. **i:** AVS+Yr24 {970}. **v:** Chuanmai 42 {10339}; Meering*3/K733/*Ae. tauschii* AUS18911 {952}; Neimai 836 {11259}. Synthetic 769 {10339}. **tv:** Decoy 1 {10339}; K733 {952}. **ma:** Gene order *Yr15 – Yr24 – Xgwm11-1B* {10112}; *Xbarc187-1B* – 2.3 cM – *Yr24* – 1.6 cM – *Xgwm498-1B* {10339}.
Yr24 is identical to *Yr26* {10339, 11391}.

YR25

Yr25 {158}. 1D {158}. **v:** Carina {0010}; Hugenout {0010}; Strubes Dickkopf; TP1295 {158}; TP981 {158}; Tugela {314}; Tugela-DN {0010, 314}. **v2:** Carstens V *Yr32* {10016}; Heines Peko *Yr2 Yr6* {0010}; Reichersberg 42 *Yr7* {0010}; Spaldings Prolific *YrSP* {10016}.
Yr25 was predicted to be present in Strubes Dickkopf, Heines VII *Yr2*, Heines Peko *Yr2 Yr6*, Reichersberg 42 *Yr7* and Clement *Yr9* {158}. This prediction was confirmed for Heines VII, Heines Peko and Reichersberg 42 but the pathogen culture used in {0010} was not virulent on Clement (*Yr9*) or on Strubes Dickkopf where another, or a different gene, must be present.

YR26*. Identical to *YR24 {10339, 11391}.

Yr26 {617}. The earlier location of 6AS (6AL.6VS) {617} is not corect.1BS {0285}. 1BL{10544}. **bin:** C-1BL-6-0.32 {10544}. **i:** AVS+Yr26 {970}. **v:** Guinong 22 {11098}; Nannong 9918 {10544}; Nei 2938 {10544}; Nei 4221 {10544}; Neimai 9 {10544}; Lines R43, R55, R64 and R77 {0285}. **tv:** *T. turgidum* Gamma 80-1. **tr:** Yangmai-5 {617}. **ma:** *Yr26* – 1.9 cM – *Xgwm11-1B/Xgwm18-1B* {0285}; *Xgwm11/18-1B* – 1.1 cM – *Xwe171/202/210-1B* – 0.4 cM – *Xwe177/201-1B* – 0.3 cM – *Xwe173-1B* – 1.4 cM – *Yr26* – 6.7 cM – *Xbarc181-1BL* – 3.0 cM – *Xwmc419-1BL*{10544}; *Xgwm11-1B* – 0.9 cM – *Yr26* – 6.3 cM – *Xbarc181* {11350}. Located between KASP markers *WRS435* and *WRS312* in an interval of 0.4 cM {11350}.
According to {10554} the markers most closely associated with *Yr26* are actually located in chromosome 1BL.

YR27. *TraesKAR2B01G0121530LC. TraesCSB02G182800.*

Yr27 {928}. [*YrSk* {928}; *QYr.sgi-2B.1* {10184, 11232}.]. 2BS {928}. **i:** AVS+Yr27 {970}. **v:** Avocet 2B (= AvocetS + *QYr.sgi-2B.1*) {11593}. Ciano 79 {928}; Inquilab 91 {928}; Kauz {928}; McMurachy {928}; Opata 85 {928}; PWB343 {928}; Selkirk {928}; Webster {928}. **v2:** Attila *Yr27* {928}; Kariega *Yr18* {11593}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 *Yr9 Yr18* {10160}. **ma:** When analysed as a QTL, variation associated with the *Yr27* locus was associated with RFLP markers *Xcdo152-2B* and *Xcdo405-2B* {928}. A *Yr27*-specific molecular marker was based on Asn 895 found only in *Yr27* {11593}.
Many CIMMYT wheat lines {953}. Recombination *Yr31* – *Yr27*, 0.148, *Yr31* – *Lr23*, 0.295 {0325}. **c:** *Yr27* is an allele at the *LR13/NE2* locus {11593}.

YR28

Yr28 {1377}. [*YrAS2388* {10822, 11438}]; *YrAet672* {11664}. 4DS {1377}. **v:** Synthetic = Altar 84/*Ae. tauschii* W-219. Synthetic/Opata 85 SSD population. Genotype lists: {970}, {1325}. **dv:** *Ae. tauschii* W-219 {1377}; CPI 110672 {11664}. **ma:** Close association with *Xmwg634-4DS* {1377}. **c:** *Yr28* has a CC-NBS-LRR structure, alternative splicing in the NBS region and duplicated 3' UTR {11438}. GenBank MK73661 – MK73666 {11438}.
Yr28 was present in all tested accessions of *Ae. tauschii* ssp. *strangulata* and some accessions of ssp. *tauschii* {11438}. Often suppressed in synthetic and derived wheat backgrounds.
Yr22 was also reported for chromosome 4D, but in the absence of an appropriate single gene stock and the unavailability of avirulent cultures in most laboratories, tests of linkage with *Yr28* are unlikely in the foreseeable future. Partial suppression of resistance in synthetic wheat derivatives carrying *Yr28* was associated with reduced transcript accumulation {11664}.

YR29

Yr29 {119}. Adult plant resistance {0119}. 1BL{0119}. **s:** Lalbahadur(Parula 1B) {10281}. **v:** Druchamp {11235}; Kundan {11248}. **v2:** Attila *Yr27* {10281}; Parula *Yr18* {10281}; Pavon F76 *Yr6 Yr7 Yr30* {119}; Quaiu3 *Yr30* {10943}; Saar *Yr18* {10481}; *Yr29* is completely linked with *Lr46*. See

Lr46 {119}. **tv:** Stewart {11542}. **ma:** *Xwmc44-1B* – 1.4 cM – *Xbac24prot* – 9.5 cM – *Yr29* 2.9 cM – *Xbac17R* .....*Xgwm140-1B*{10281}; *Xgwm44-1B* – 3.6 cM – *Yr29* – 2.1 cM – *XtG818/XBac17R*.....*Xgwm140-1B* {10281}; Associated with *Ltn2* and *Lr46*; *QYr.ucw-1BL* was mapped to a 0.24 cM region (332 kb IWGSC RefSeq v1.0 between *ucw.k31* and *csLV46G22* {11386}.
Yr29 is a frequent gene in durum wheat ({11542}and references therein).

YR30

Yr30 {0120}. Adult plant resistance {0120}. 3BS {0120}. **v:** Opata 85 {0120}; Parula {0120}. **v2:** Inia 66 *YrA* {0120}; Pavon F76 *Yr6 Yr7 Yr29* {0120}; Quaiu3 *Yr29* {10943}; *Yr30* is closely linked with *Sr2* and *Lr27* {0120}.
According to {11773} *Yr30* is present in Yaco S, Zhou8425b, Napo 63 and Orofen.

YR31

Yr31 {0325}. 2BS. **v:** Pastor {0325}. **ma:** Recombination values: *Yr31* – *Yr27*, 0.148; *Yr31* – *Lr23*, 0.295; *Yr27* – *Lr23*, 0.131{0325}; *Yr31* maps between *Lr12* and *Lr23* {10928}.

YR32

Yr32 {10016}. [*YrCV* {1430}, *YrCv* {939}]. 2AL {10016}. **i:** Avocet S*4/Carstens V {970}; Cook*6/Carstens V {970}; CRW380 = Carstens V/3*Avocet S {10016}; Tres/6*/Avocet S {10016}. **v:** Anouska {1430}; Caribo {1430}; Consort {10021, 10023}; Cyrano {1430}; Danis {10023}; Deben {10283}; Hereward {10021, 10022}; Okapi {1430}; Oxbow {10021}; Senat {10016}; Solist {10016}; Stakado {10016}; Toisondor {11144}; Tres {10016}; Vivant {10023}; Wasmo {10016}. **v2:** Carstens V *Yr25* {10016}; Felix *Yr3* {1430}; Kraka *Yr1* {10021, 10038}; Savannah *Yr1 Yr2 Yr3 Yr4 Yr17* {10016}; Senat *Yr3* {10016}; Zdar *Yr3a Yr4a* {67}. **ma:** *Xwmc198-2A* – 2 cM – *Yr32* {10016}; *Yr32* was coincident with one AFLP marker {10016}.

YR33

Yr33 {10039}. More readily detected in seedling tests at elevated temperatures {10336}. 7DL {10039}. **v:** Batavia {10039}; EGA Gregory; Strezecki. **ma:** Linkage with *Xgwm111-7D* and *Xgwm437-7D* {10039}.

YR34

Yr34 {10040}. [Syn. *Yr48* {11266}]. 5AL {10040}. **v:** AUSC {10040}; UC1110/PI610750 RIL#143 {11266}; AUS27492 {11720}; WAWHT2046 = AUS91389 {10040}. **ma:** *Xgwm410.2-5A* – 8.2 cM – *B1* – 12.2 cM – *Yr34* {10040}; *Xgwm291-5A* – 0.5 cM – *B1* – 1.5 cM – *Yr34/Xgwm410.2-5A/Xcfa2149-5A/KASP_109/KASP_6988/*etc. {11266}; *Xgwm291-5A* – 2.3 cM – *B1* – 0.7 cM – *Yr34/Xgwm410.2-5A/Xcfa2149-5A/KASP_109/KASP_6988/*etc. {11266}. *Yr34* is in a 5AS.5AL-5A^{m}L translocation segment that is present in genotypes Arina*LrFor* and SY Mattis in the Wheat10+ Genome panel {11602}. Associated with 5 markers {11720}.
This gene confers a weak seedling resistance (IT 2C to 3C) and a strong adult plant resistance (0 to 10R)

{10040} to Australian pathotype 134E16A+, but is not effective against Australian pathotype 110E143A+ {10040}.
Yr34 is <1cM from the awn inhibitor *B1* {11266}.

YR35

Yr35 {10203}. [*YrS8* {10204}]. 6BS {10203}; $6^S S.6^S L$-6BL {11778}. **v:** 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS {10204}. **tv:** According to {11778} *Yr35* originated from *Ae. longissima* or *Ae. sharonensis*. *T. dicoccoides* 479 {10204}. **ma:** *Xgwm191-6B* – 18.9 cM –*Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B* {10780}.
Genetically associated with *Lr53*.

Yr36

Yr36 {10138, 10272}. Adult plant resistance. 6BS {10138}. **i:** Yecora Rojo NIL PI 638740 {10138}. **v:** Burnside {11044}; Glencross {11044}; Glupro {10138}; Lilian {11044}; Shumai 1701 {11258}; Somerset {11044}; UC1041+Yr36 {10649}. **itv:** UC1113 NIL PI 638741 {10138}. **tv:** RSL#65 {623, 10138, 10649}; *T. dicoccoides* FA-15 {10138}; *T. dicoccum* PI 415152 {M10058}. **ma:** *Yr36* is between *Xucw74-6B* and *Xucw77-6B* and 3-7 cM proximal to *Nor-B2* {10138}; *Yr36* is closely linked to the high grain protein locus of *T. turgidum* var. *dicoccoides* FA-15 {10138}; *Nor-B2 ....Xucw68-6B – Xucw69-6B/Xbarc101-6B/Yr36 – Xucw66-6B*{10272}; *Yr36* is 2 - 4 cM proximal to *Gpc-B1* {10272}. **c:** ACF33182; *Yr36* encodes wheat kinase-START-1 protein {10649}; WKS1 is absent in almost all modern tetraploid and common wheats {10649}; Sr36 was shown to reduce the ability of the thylakoidassociated ascorbate peroxidase to detoxify reactive oxygen species {11128}.
Although originally described as conferring high temperature adult plant resistance. This gene confers partial resistance in both juvenile and adult plants at temperatures less than 18C {11277}.

YR37

Yr37 {10139}. Derived from *Ae. kotschyi*. 2DL {10139}. **v:** Line S14 {10139}. **ad:** Line 8078 {10139}. **al:** *Ae. kotschyi* 617 {10139}.

YR38

Yr38 {10224}. [*YrS12* {10204}]. 6A ($6AL-6L^{sh}.6S^{sh}$) {10224}. **v:** nong = *Ae. sharonensis*-174/9*CS//3*W84-17/3/CS/4/W84-17 {10224}; Recombinants with shorter segments - 07M4-39, 07M4-157 and 07M4-175 are reported in {10691}. **al:** *Ae. sharonensis*-174 {10224}.

YR39

Yr39 {10416}. HTAP resistance 7BL {10416}. **v:** Alpowa {10416}. **ma:** Closely linked to several RGAP markers {10416}.

YR40

Yr40 {10328}. Derived from *Ae. geniculata*. 5DS(5DL.5DS-T5MS^G {10328}. **v:** TA 5602 {10328}; TA 5603 {10328}; TA56501 {11553}. **ad:** TA7659 {11553}. **al:** *Ae. geniculata* (=*ovata*) (U^{s}U^{s}M^{g}MM^g) TA10437 {10328}. **ma:** Completely linked with distinctive alleles of *Gsp, Xfbb276* and *Xbcd873* {10328}; Completely linkd with *Lr57* {10328}; CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.
Line TA5601 carries an estimated 5% of 5M^g; and TA5602, 20% {11553}. Genetic analysis of the segment in TA5602 indicated terminal replacement of 9.4 Mb in chromosome 5D and that *Yr40* is 12.4 cM proximal to *Lr57* {11553}.

YR41

Yr41 {10502}. [*YrCN19* {10228}]. 2BS {10228, 10502}. **v:** AIM {10228}; AIM6 {10228}; Chuannong 19 {10228, 10502}. **ma:** Complete linkage to a 391 bp allele of *Xgwm410-2BS*{10228}; *Xgwm410-2B* – 0.3 cM – *Yr41* {10502}.

YR42

Yr42 {10537}. Derived from *Ae. neglecta*. 6A = 6AL-6^{Aen}L.6^{Aen}S {10537}. **v:** Line 03M119-71A {10537}. **al:** *Ae. neglecta* 155 {10537}.
Associated with *Lr62* {10537}.

YR43

Yr43 {10673}. 2BL {10673}. **v:** IDO377s = PI 591045 {10673}; Lolo {10673}; many IDO377s derivatives {10673}. **ma:** *Xwms501-2B* – 11.6 cM – *Xwgp110-2B* – 4.4 cM – *Yr43* – 5.5 cM – *Xwgp103-2B* – 12.8 cM – *Xbarc139-2B* {10673}.

YR44

Yr44 {10673}. [*YrZak* {10674}]. 2BL {10674}. **v:** Zak = PI 607839 {10674}. **ma:** *XSTS7/8/Yr5* – 12.7 cM – *Yr44* – 3.9 cM – *Xwgp100* – 1.1 cM – *Xgwm501-2B*{10674}.

YR45

Yr45 {10677}. 3DL {10677}. **v:** PI 181434 {10677}; PI 660056 {11024}. **ma:** *Xbarc6-3D* – 0.9 cM – *Xwmc656-3D* – 6.9 cM – *Xwpl18-3D* – 4.8 cM – *Yr45* – 5.8 cM – *Xwp115-3D* {10677}.
This gene is highly effective and confers resistance to all North American *Pst* pathotypes.

YR46

Yr46 {10678}. Adult plant resistance. 4DL {10678}. **bin:** Distal to 0.56. **i:** RL6077 = Thatcher*6/PI 250413 {10678}. **v:** Chapingo 48 {11070}; PI 250413 {10678}. **ma:** *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices

{11070}.
Pleiotropic or closely linked with *Sr55* and *Lr67*

YR47

Yr47 {10679}. 5BS {10679}. **bin:** 5BS6-0.81-1.00. **v:** AUS28183 = V336 {10679}; AUS28187 {10679}. **ma:** *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xcfb309-5B* – *Xsun480/Xmag705/Xfcp552-5B* – 0.4 cM – *Yr47* – 4.3 cM – *icg16c008/Xgwm234-5B* {11200}; *Xsun180* – 0.4 cM – *Lr52* – 0.2 cM – *Yr47* – 1.4 cM – *Xgwm234-5B* {11200}.
This is a seedling resistance gene (IT 1CN), effective against the main Australian groups of *Pst*. V336 is the original source of *Lr52.*

YR48

Yr48 {10705}. [Syn. *Yr34* {11266}]. Adult plant resistance. [*Qyr.ucw-5AL* {10705}]. 5AL {10705}. **bin:** 5AL23 0.87-1.00. **v:** UC1110 (MR)/PI 610750 (MR): RIL4 GSTR 13504 {10705}; RIL167 GSTR 13618 {10705}; UC1110/PI610750 RIL#143 {11266}. **ma:** Co-segregated with *Vrn2*, *BE495011*, *Xcfa2149-5AL, Xgpw2181a-5AL, Xwmc74-5AL,* and *Xwmc410-5AL*{10705}; *Xwmc727-5AL* – 4.4 cM – *Yr48* – 0.3 cM – *Xwms291-5AL* {10705}.
PI 610750 = Synthetic 205 ((Croc 1 / *Ae. tauschii*)/Kauz) {10705}.

YR49

Yr49 {10746}. Adult plant resistance. 3DS {10746}. **bin:** 3DS6-0.55-1.00). **v:** AvocetS*3 / Chuanmai 18 AUS91433 {10746}. **v2:** Chuanmai 18 *Yr18* {10746}. **ma:** *Xgps7321-3D/Yr49* – 1 cM – *Xgwm161-3D* {10746}.

YR50

Yr50 {10849}. Derived from *Th. intermedium*. 4BL {10849}. **v:** CH233{10849}. **ma:** cent...*Xbarc1096-4B* – 8.0 cM – *Yr50* – 7.2 cM – *Xbarc-4B* {10849}.
The genetic distance between *Yr50* and *Yr62* was estimated to be 27.1±8.6 cM {11023}.

YR51

Yr51 {10850}. [*YrAW1*{10850}]. 4AL {10850}. **bin:** 4AL4-0.80-1.00. **v:** Line 5515 AUS 91456 {10850}. **v2:** AUS 278589 *Yr57* {10850}. **ma:** *Xowm45F3R304A* – 1.2 cM – *Yr51* – 2.5 cM – *Xsun104-4A* – 1.8 cM – *Xgwm160-4A* {10850}.

YR52

Yr52 {10852}. Adult plant resistance. 7BL {10852}. **bin:** 7BL3-0.86-1.00. **v:** PI 183527 {10852}; PI 660057 = Avocet S/PI 183527 F4-41 {10853}. **ma:** *Xbarc182-7B* – 1.2 cM – *Yr52* – 1.1 cM – *Xwgp5258* – 5.7 cM – *Xcfa2040-7B* {10852}.

YR53

Yr53 {10854}. 2BL {10854}. **bin:** 2BL3-0-0.35. **tv:** PI 480148 {10854}. **v:** Avocet S/PI 480148 F5-128 {10854}. **ma:** *Xwmc441-2B* – 5.6 cM – *Yr53* – 2.7 cM – *XLRRrev/NLRRrev*$_{350}$ – 6.5 cM – *Xwmc149-2B* {10853}; *Yr53* was estimated to be 35 cM distal to *Yr5* based on an F2 allelism test, but on an integrated map this distance was about 20 cM.

YR54

Yr54 {10944}. Adult plant resistance. 2DL {10944}. **v:** *Yr54* RIL GID6032209 {10944}; *Yr54* RIL GID6032334 {10944}. **v2:** Quaiu3*Yr29 Yr30* {10943, 10944}. **ma:** *Yr54* – 0.4 cM – *Xgwm301-2D* {10944}.
Yr54 could be the same as *Qyr.tam-2D* in Alcedo {10945}.

YR55

Yr55 {10953}. 2DL {10953}. **v:** Frelon *Yr17* AUS 38882 {10953}. **ma:** *Xmag4089-2D* – 11.4 cM – *Yr55* – 8.4 cM – *Xmag3385-2D* {10953}.

YR56

Yr56 {10955}. [*Qyr.sun-2A* {10955}]. 2AS {10955}. **bin:** Tentatively 2AS5-0.78-1.00 {10955}. **tv:** AUS 91575 {10955}; Wollaroi (AUS 99174) {10955}. **ma:** *Xbarc212-2A* – 3.7 cM – *Xbarc124-2A* – 2.1 cM – *Xsun167-2A* – 5.7 cM – *Yr56* – 7.6 cM – *Xsun168-2A* – 5.0 cM – *Xsun169-2A* – 8.0 cM – *Xgwm512-2A* {10955}.
Wollaroi has additional APR QTL {10955}.

YR57

Yr57 {10963}. [*YrAW2* {10963}]. 3BS {10963}. **bin:** 3BS8-0.78-1.00. **v:** AUS 91463 {10963}. **v2:** AUS 27858 *Yr51*{10963}. **ma:** *sts3B15* – 4.5 cM – *BS00062676* – 2.3 cM – *Yr57* – 2.0 cM – *Xgwm389-3B* – 2.0 cM – *Xbarc75-3B* {10963}; *Bs0006276* – 0.3 cM – *Yr57* – 1.3 cm – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B* {11480}.

YR58

Yr58 {10964}. Adult plant resistance. [*QYr.sun-3BS* {10964}] 3BS {10964}. **bin:** 3BS7-0.87-1.00. **v:** Sonora W195 AUS 19292 *Yr46* {10964. **ma:** *1121669/3023704* – 3.9 cM – *Yr58* – 4.6 cM – *100016328/123392* {10964}.

YR59

Yr59 {10966}. Adult plant resistance. 7BL {10966}. **bin:** 7BL-0.86-1.00. **v:** Avocet S/PI 178759 F_4-158 {10967}; PI 660061; PI 178759 {10966}. **ma:** *Xwmc557-7B* – 2.2 cM – *Xwgp5175* – 2.1 cM – *Yr59* – 1.1 cM – *Xbarc32* – 0.5 cM – *Xbarc182-7B* {10966}. *Yr59* can be detected in high temperature seedling tests {10966, 10967}. *Yr59* is a highly effective HTAP resistance gene. Crosses with lines possessing *Yr39, Yr52* or *YrZH84* previously reported on chromosome 7BL segregated, indicating that they are at different loci. However, the allelism test data were based on F_2 phenotypes only. The linkage order of these genes is (proximal) *Yr39* – 31.2 cM – *Yr52* – 5.4 cM – *YrPI178759* – 6.0 cM – *YrZH84* (distal).

YR60

Yr60 {10968}. 4AL {10968}. **v:** Almop, Avocet*3//Lalbmono 1B*4/Pavon GID 5934039 {10968}. **v2:** LB(Pavon1B) *Yr29* {10968}. **ma:** *Xwmc313/Xwmc219-4A* – 0.51 cM – *Yr60/Xwmc776-4A* {10968}.
Yr60 was estimated to be about 10 cM distal to *Yr51*

YR61

Yr61 {10970}. [*Yrpd34* {10970}]. 7AS {10970}. **v:** Pindong 34 {10970}. **ma:** *Xwgp5765b* – 3.9 cM – *Yr61* – 1.9 cM – *Xwp5467* – 12.5 cM – *Xcfa2174* {10970}.

YR62

Yr62 {11023}. Adult plant resistance. 4BL {11023}. **bin:** 4BL5-0.86-1.00. **v:** PI 192252 {11023}; PI 660060 = Avocet S/PI 192252 F4-103 {11024}. **ma:** *IWA3611-4B* – 0.8 cM – *IWA4041-4B* – 0.8 cM – *IWA2171-4B* – 0.7 cM – *IWA99-4B* – 1.0 cM – *IWA1923-4B* – 1.2 cM – *Xgwm251-4B* – 3.3 cM – *Yr62* – 2.0 cM – *Xgwm192-* – 0.6 cM – *Xgwm495-4B* – 0.7 cM – *Xgwm513-4B* {11023}.
The genetic distance between *Yr62* and *Yr50* was estimated to be 27.1±8.6 cM {11023}.

YR63

Yr63 {11027}. 7BS {11027}. **bin:** 7BS1-0.27-1.00. **v:** AUS 27955 {11027}. **ma:** *IWB33120* – 0.9 cM – *Yr63* – 1.5 cM – *IWB52844* – 10.5 cM – *Xwmc606-7B* {11027}. *sun_KASP401* (0.6 Mb, CS RefSeq 2.1) – 2.1 cM – *sunCS_Yr63* – 2.1 cM – *sunKASP_406* (7.4 Mb) {11733}.

YR64

Yr64 {11030}. 1BS {11030}. **bin:** 1BS9-0.84-1.00. **v:** PI 660064 = Avocet S/PI 331260 {10967}. **tv:** PI 331260 {11030}. **ma:** *Xbarc8-1B* – 0.6 cM – *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 3.5 cM – *Yr64* – 2.0 cM – *Xgdm33-1B* – 5.0 cM – *Xgwm498-1B* – 3.9 cM – *Xcfd59-* – 0.4 cM – *Xgwm273-1B* – 3.9 cM – *Xgwm18-1B* – 2.6 cM – *Xbarc137-1B* – centromere {11030}; *Yr64* is distal to *Yr15*; recombinant lines are reported in {11349}. A line combing combining *Yr15 and Yr64* is reported in {11618}: gene order *Xbarc8*$_{239}$ – *YR15* – *Xgwm413*$_{102}$ – *YR64* – *Xgwm273*$_{196}$.

YR65

Yr65 {11030}. 1BS {11030}. **bin:** 1BS10-0.5-centromere. **v:** AvS/PI 480016 F_7-12 {11030}. **tv:** PI 480016 {11030}. **ma:** *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 5.5 cM – *Xgdm33-1B* – 4.6 cM –

Xgwm498-1B – 3.5 cM – *Xbarc187-1B* – 2.8 cM – *Xgwm273-1B* – 3.7 cM – *Xgwm18-1B* – 1.2 cM – *Yr65* – 2.1 cM – *Xgwm11-1B* – 2.1 cM – *Xbarc137-1B* – centromere {11030}.

YR66

Yr66 {11032}. [*YrVL1* {11032}]. 3DS {11032}. **bin:** 3DS6-0.55-1.00. **v:** AGG91584WHWA = MSP4543.1 {11032}. **v2:** VL Gehun 892 = AGG91586WHEA *Yr67* {11032}. **ma:** *KASP_18087* (3.550 Mb) – 2.1 cM – *Yr66* – 0.6 vM – *KASP_48179* {11032}.

YR67

Yr67 {11032}. [*YrC591* {11033}, *YrVL2* {11032}]. 7BL {11032, 11033}. **bin:** 7BL10-0.78-1.00. **v:** AGG91585WHEA = MSP4543.4 {11032}; C306 {11032}; C591 {11032, 11033}. **v2:** VL Gehun 892 = AGG91586WHEA *Yr66* {11032}. **ma:** *Xbarc32-7B* – 2.2 cM – *Xcfa2040-7B* – 8.0 cM – *Yr67* – 11.7 cM – *SC-P35M48* {11033}; *KASP_37096* (7.170 Mb) – 1.2 cM – *Yr67* – 3.6 CM – *KASP_2239* 7.211 MB) {11032}.

YR68 **CURATOR'S NOTE:** publication could not be located.

Yr68 {11051}. Adult plant resistance. 4BL {11051}. **bin:** 4BL1-0.86-1.00. **i:** AGG91587WHEA1 = csAvYr4BL = Avocet S*5/Undesignated International Nursery ex New Zealand Entry 03.25 {11051}. **v:** Undesignated International Nursery ex New Zealand 03.25 {11051}. **ma:** *IWB74301* – 0.5 cM – *Yr68/IWA4640* – 0.5 cM – *IWB28394* {11051}.

Yr69

Yr69 {11052}. Derived from *Thinopyrum ponticum* partial amphiploid Xiaoyan 7430. [*YrCH86* {11052}]. 2AS {11052}. **bin:** 2AS5-0.78-1.00. **v:** CH7086 {11052}. **ma:** *Xwmc25-2A* – 2.7 cM – *X2AS33* – 1.9 cM – *Yr69* – 3.2 cM – *Xmag3807-2A* {11052}.
Linked with *Yr17*: (F_2 seedling test) 30.0 cM {11052}. No positive evidence for a *Th. Ponticum* origin was prested.

YR70

Yr70 {11055}. Derived from *Ae. geniculata* [*YrUmb* {11055}]. 5DS {11055}. **v:** IL393-4, *T. durum* cv. WH890 / *Ae. umbellulata* Pau 3732 // CS Ph^I/3/2*WL711{11055}. **al:** *Ae. umbellulata* Pau 3732 {11055}. **ma:** *Yr70* – 7.6 cM – *Xgwm190-5D* {11055}; A co-segregating 450 bp *Lr57*-*Yr40*-CAPS16 marker was present in IL393-4, but not in many Australian wheat cultivars {11055}.
Yr70 behaves as an allele of *Yr40* derived from *Ae. geniculata*. The low infection types are also different. The introgression carrying the *Ae. umbellulata* segment replacing terminal chromosome arm 5DS was 9.47 Mb with the break point between *TraesCS5D02G1600* and *TraesCS5G02G20010* {11552}. Independent mutations indicated that *Yr70* differed from *Lr76* {11552}.

YR71

Yr71 {11056}. Adult plant resistance. [*YrSA3* {11056}]. 3DL {11056}. **v:** AGG91588WHEA, Sunco/Avocet S RIL4667.153.11.1 {11056}. **v2:** Sunco *Yr18* {11056}. **ma:** *Yr71* – 1.6 cM – *IWB17207/IWB10438/IWB23615/IWB63653* – 0.5 cM – *IWB57983* – 0.9 cM – *IWB23518* – 2.4 cM – *Xgwm114b-3D* – 5.6 cM – *Sr24/Lr24* {11056}.

YR72

Yr72 {11059}. [*YrAW4* {11059}]. 2BL {11059}. **bin:** 2BL5-0.59-0.89. **v:** AUS27506 {11059}; AUS27894 {11059}. **ma:** *Xsun481-2BL* (*wPt-665550*) – 1.8 cM – *Yr72* – 1.2 cM – *IWB12294* – 1.5 cM – *Xsun482-2BL* (*wPt-7161*) – 1.5 cM – *IWB69000* {11059}.

YR73

Yr73 {11062}. Complementary gene involved in the *Yr* specificity. 3DL {11064, 11062}. **v2:** Avocet R *Yr74* {11063}; Anza = WW15 *Yr74* {11062}; Banks R *Yr74* {11063}; Condor R *Yr74* {11063}; Egret R *Yr74* {11063}; Funo *Yr74* {11062}; Jupateco 73 *Yr74* {11062}; Lerma Rojo-64 *Yr74* {11062}. **ma:** Located and mapped by DarT-Seq markers {11062}.

YR74

Yr74 {11062}. Complementary gene involved in the *YrA* specificity. 5BL {11062}. **v2:** Avocet R *Yr73* {11063}; Anza = WW15 *Yr73* {11062}; Banks R *Yr73* {11063}; Condor R *Yr73* {11063}; Egret R *Yr73* {11063}; Funo *Yr73* {11062}; Jupateco 73 *Yr73* {11062}; Lerma Rojo-64 *Yr73* {11062}. **ma:** Located and mapped by DarT-Seq markers {11062}.

The cross Avocet R/Teal used to map *Yr73* and *Yr74* included a 5BL-7BL reciprocal translocation. Susceptible lines carrying the individual genes will be permanently accessioned after screening candidate lines for the Avocet R = Chinese Spring chromosome configuration. The translocated chromosomes are present in Teal and do not involve *Yr74*.

Yr75

Yr75 {11065}. Adult plant resistance. [*YrAxe* {11065}]. 7AL {11065}. **bin:** 7AL16-0.86-0.90. **v:** Axe/Nyabing-3 RIL#5 {11065}. **v2:** Axe *Yr29* {11065}. **ma:** *Xcfa2016-7A* – 1.0 cM – *Yr75* – 0.3 cM – *IWB36240* {11065}. *sunKASP_429*/*_428* – 0.1 cM – *sunKASP-427* – 0.4 cM – *Yr75* – 0.3 cM – *sunKASP_430* {11670}.

YR76

Yr76 {11067}. [*YrTye* {186}]. 3AS {11067}. 6D {186}. **bin:** 3AS4-0.45-1.00 {11067}. **i:** AvS*4/Tyee{11067}. **v:** Tyee Citr 17773 {11067}. **v2:** ARS-Amber {11067}; Cara {11067}; Chukar {11067}); Hyak *Yr17* (based on flanking markers) {11067}. **ma:** *Xbarc321-6D* – 6.2 cM – *Xbarc57-6D* – 4.3 cM – *Xwmc11-6D* – 2.6 cM – *Yr76* – 3.4 cM – *Xwmc532-6D* – 6.9 cM – *Xgwm369-6D* – 2.6 cM – *Xbarc12-6D* {11067}.

YR77

Yr77 {11174}. Adult plant resistance. [*Qyr.ucw-6D* {11174}]. 6DS {11174}. **v:** PI 322118 {11174}; PI 164377 {11174}; PI 388095 {11174}; PI 520350 {11174}; PI 623378 {11174}. **ma:** *Yr77* was strongly associated with IWA167 in the region *Xbarc54-6D* (6DS) – 15.2 cM – *IWA167* (6DS) – 3.9 cM – *Xcfd188-6D* (6DL){11174}.

Among the listed accessions two were from India, one from Pakistan, one from Iran, and one from the USA.

YR78

Yr78 {11174}. Adult plant resistance. [*Qyr.ucw-6B* {11174}]. 6BS {11174}. **v:** Cadenza {11591}; Lancer {11591}; PI 519805 {11174}; Spelt PI 190962 {11591}; Nine others {11174}. **ma:** The *Yr78* peak fell within a 4.3 cM interval, *IWA7257* – *Xwmc737-6B* {11174}. *Yr78* was mapped to a 0.05 cM interval including the un-assembled *NOR-B2* locus on chromosome 6BS (RefSeq v1.1 0 region between 101,735,482 and 112,897,900 bp) {11591}.

According to {11174} *Yr78* is identical to *QYr.wgp-6BS.1* in Stephens {10602} and *QYr.sun-6B* in Janz {10751}.

YR79

Yr79 {11222}. 7BS {11222}. **bin**: 7BL-0.40-0.45. **v:** PI 182103 {11222}; PI 679609, Avocet S / PI 679609 RIL#195 {11222}. **ma**: *IWA220* – 2.9 cM – *Yr79* – *Xwmc335-7B* – 0.9 cM – *Xbarc72-7B* – 1.7 cM – *Xgwm297-7B*) – 1.6 cM – *Xgwm333* {11222}.

YR80

Yr80 {11261}. Adult plant resistance. *YrAW11* {11261}. 3BL {11261}. **bin:** 3BL2-C-0.22. **v:** AUS27284 {11261}. **ma:** *Xgwm3763B* – 15.2 cM – *KASP_5392/KASP_65624* – 3.0 cM – *Yr80* – 4.9 cM – *KASP_53113* {11261}.

YR81

Yr81 {11262}. Adult plant resistance. *YrAW5* {11262}. 6AS {11262}. **v:** Aus27430/AvS RIL#16 {11262}. **v2:** AUS27430 *Yr29* {11262}. **ma:** *KASP_3077* – 2.7 cM – *Yr81* – 6.4 cM – *Xgwm459-6A* – 1.0 cM – *KASP_11315* {11262}.

YR82

Yr82 {11322}. 3BL {11322}. **bin:** 3BL7-0.63-1.00. **v2:** AUS27969 = JI 1190592 *Yr29* {11322}. **ma:** *KASP_13376/sunKASP_301* – 0.4 cM – *sunKASP_300* – 2.0 cM – *Yr82* – 2.0 cM – *KASP_8775* {11322}.

YR83

Yr83 {11396}. 6A (T6AL·6RL {11396}. **tr:** T6AL·6RL C19.3 {11396}. **ad:** Wheat + 6R {11396}; Wheat + 6RL {11396}. **su:** CS + 6R(6D) {11396}. **al:** Triticale accession T-701 {11396}. **ma:** Deletion mapping indicated that *Yr83* was located in 6RL bin FL 0.73-1.00 containing PCR markers

KU.86, TNAC1823, TNAC1826, and TNAC1844 {11396}.
The only previously designated *Yr* gene derived from *Secale cereale* is *Yr9* from chromosome 1RS.

YR84

Yr84{11585}. *YrPI487260* {11585}. 1BS {11585}. AvocetS + Yr84 {11777}. **v:** Ruta*2 / PI 487260 {11585}. **tv:** *T. dicoccoides* PI 487260 {11585}. **ma:** Located at 9.65 – 11.99 Mb *YR84* is proximal to *YR10* (0-1.4 Mb) and distal to *YR15* (98 Mb) {11585} in the Zavitan v2 assembly (11585). Reduced to a 0.5 cM interval (975 Kb, Zavitan seq. v2). **c:** *Yr84* mutations were identified in closely linked head-to-head CNL (GenBank PP841907) and NL (NB-ARC-LR) (GenBank PP841906) genes, both of which were required for resistance {11777}.
Yr84 confers resistance to all *Pst* pathotypes thus far tested and is described as incompletely dominant. Other named *YR* loci in chr. 1B are proximal to *YR15* or located in arm 1BL. The low infection type is ; (fleck) to ;1 on a 0-4 scale. *Yr84* varies from other permanently named *Yr* genes in the region by location, specificity and dominance.

YR85

Yr85 {11616}. *YrTr1* {181}. 1BS {11616}. **bin**: 1BS18 (0.5). **i:** AvSYrTr1NIL {11616}. **v:** Tres CI 017917 {11616}. **ma**: *IWA406* – 3.0 cM – *IWA63* – 1.6 cM – *IWA5370* – 2.2 cM – *IWA4349* – 2.0 cM – *IWA2583* – 1.8 cM – *YR85* – 1.3 cM – *IWA7480* – 3.0 cM – *Xbarc8* – 5.1 cM – *IWA2197* – 3.1 cM – *Xgwm413* – 7.4 cM – *Xbarc137* – 4.6 cM– *Xwmc626* {11616}; *Rg1* – 1.4 cM – *Yr10* – 7.4 cM – *YR85* {11616}; *Yr10*/*Xsdauw79* (1.519 Mb, 0-1.4 Mb[a]) – *Yr84* (9.65 – 11.99 Mb[a]) – *IWA2583* (30.675 Mb) – *YR85* – *IWA7480* (60.382 Mb) – *Yr15*/*uhw264* (67.695 Mb, 98 Mb[a]) {11616}. [a]Values from the Zavitan v2 assembly {11585}.

YR86

Yr86 {11641}. Adult plant resistance. *YrZM895* {11641}; *QYr.caas-2AL.2* {11641}. 2AL {11641}. **v:** Liken 4 = Shaaken 4 {11641}; Zhongmai 895 {11641}. **ma:** Flanked by *Ax-111584166* (703.7 Mb) and *Ax-110429464* (715.3 Mb) {11641}. KASP markers developed in {11641}. Located to a 0.15 cM, 710.3 – 712.6 Mb, interval in a Jimai 22 / Zhongmai 895 F_2 population; however, recombination was suppressed in crosses of Zhongmai 895 with Emai 580 and Avocet S due to a 4.1 Mb inversion in the region {11730}.

YR87

Yr87 {11712}. 6B (6B-6S^{sh}) {11683, 11684, 11712}. **v:** Line 6B-RY-32-3-14 {11683} = Line 42 {11684} = D42 {11712} = **Genebank accession number to be advised**. **al:** *Ae. longissima* AEG-6782-2 {11712}; *Ae. sharonensis* AEG-548-4 {11712}. **c:** The same NLR gene with a distinctive coiled-coil (CC) domain was cloned from each alien diploid accession {11712}.
Development of lines with shortened 6S^{sh} segments is described in {11684}.
All 16 EMS-induced mutants in Line D42 were susceptible to both stripe rust and leaf rust {11712}.

Sources of additional genes for seedling (designated “12”) and adult resistances (“13”, “14”, “15”) are listed in {1430}.
Genotype lists: Chinese common wheats {10369}. European wheats {10579}. U.K. wheats {10697}.

3.21.2. Temporarily designated genes for resistance to stripe rust

North American workers {181, 186, 184} allocated a number of temporary designations to uncatalogued genes detected with North American *P. striiformis* accessions. Druchamp, Yamhill and Stephens were reported to carry ‘*Yr3a* or *Yr4a*’ because these genes could not be distinguished with the cultures that were used.

Yr041133 {11675}. 7BL {11675}. **v:** Line 041133 {11675}. **ma:** *Xicst23* (608.9 Mb, CS RefSeq 1.0) – 0.6 cM – *Yr041133* – *Xicst338* (609.7 Mb) {11675}.

YrA. Refers to a phenotype specificity that appears to be controlled by complementary genes {1563}. **v:** Avocet* {*= heterogeneous}; Anza = Karamu = Mexicani =T4 = WW15; Banks*; Condor*; Cocamba; Egret*; Inia 66; Lerma Rojo 64; Lerma Rojo 64A; Nainari 60; Nuri 70; Sanda 73; Sonalika; Zaminder 80. **v2:** Condor selection P44 *Yr6**; Pari 73 *Yr6*; Saric 70 *Yr6*; Yecora 70 *Yr6*{1563}. The complementary genes are now named *Yr73* and *Yr74*.

YrAc {11613}. 5DS {11613}. **v:** *Ae. caudata* derivative PAU16060 {11613}. **al:** *Ae. caudata* PAU3556 {11613}.

YrAlp {10416}. 1BS {10416}. **v2:** Alpowa *Yr39* {10416}. **ma:** *YrAlp* – 15.2 cM – *Xgwm18-1B* – 1.1 cM – *Xgwm11-1B* {10416}; and more closely linked to RGAP markers {10416}.

YrAS1676 {11672}. 1AL {11672}. **v:** Undesignated selection.**v2:** AS1676 *Yr18* {11672}. **ma:** Located to a 1.7 cM region – 485.3 – 490.2 Mb where it co-segregated with 6 KASP markers {11672}. May be the same as *YrXH-1AL* in Xiaohemai based on common markers {11672}.

YrAS2388 {10822}. [*Yr28* {11438}; NLR_{4D-1} {11438}]. **v:** KS91WGRC11 {11599}. **dv:** *Ae. tauschii* AS2388 {10822}; *Ae. tauschii* accessions Clae9 {11438}; PI 5111383 {11438}; PI 511384 {11438}. **ma:** *Xwmc617-4DS* – 34.6 cM – *YrAS2388* – 1.7 cM – *Xwmc285-4DS* {10822}. KASP markers were developed in {11566}. **c:** *Yr28* has a CC-NBS-LRR structure, alternative splicing in the NBS region and duplicated 3’ UTR {11438}. GenBank MK73661 – MK73666 {11438}.

YrAvS {11007}. **v:** Avocet R {11007}; Avocet S {11007}.
This designation was used to describe an assumed resistance gene in both Avocet R and Avocet S, the latter being the genetic background of the Avocet S near-isogenic lines. AvS NILs with *Yr6*, *Yr7* and *Yr9*, as well as Avocet R, were susceptible to the variant of *Pst* race 6 E0 {11007}.

YrC142 {10667}. 1BS {10667}. **v:** Synthetic CI142 = Gaza/Boy//*Ae. tauschii* 271 {10667}. **ma:** Located in the *Yr24/Yr26* region close to *Xbarc187-1B* and *Xgwm273-1B* {10667}.
Although postulated to be unique this gene is likely *Yr24/Yr26*.

YrC591 {10606}. *Yr67*. 7BL {10606}. **bin:** 7BL3-0.85.1.00. **v:** C591 {10606}; Zhongzhi 1 {10606}. **ma:** *Xcfa20-40-7B* – 8.0 cM – *YrC591* – 11.7 cM – *SCP35M48* {10606}; *Xmag1714-7B* – 1.2 cM – – 0.4 cM – *Xbarc182-7B* {11099}. This gene is *Yr67* {11032}.

YrCf75 {11646}. Recessive. 2AL {11646}. **v:** Changfeng 75 {11646}. **ma:** Located in interval 577-638 Mb (CS RefSeq v1.0, flanked by *AX-1110060462* and *AX-111004763* {11646}.

YrCle {186}. 4B {186}. **v2:** Clement *Yr9* {186}.

YrCK {10221, 10220}. Temperature sensitive {10219}. 2DS {10220}. **v:** Cook *Yr34* {10221, 10219, 10220}; Sunco *Yr34* {10220}.

YrCN17 {10562, 10686}. Derived from *S. cereale*. 1B, 1BL, 1RS {10562, 10686}. **v:** Chuannong 17 {10686}; CN12 {10562}; CN17 {10562}; CN18 {10562}. **dv:** *S. cereale* R14 {10686}. **al:** *S. cereale* L155 {10562}.

YrD {185}. 6A {185}. **v:** Druchamp {185}.

YrDa1 {186}. 1A {186}. **v2:** Daws *YrDa2* {186}.

YrDa2 {186}. 5D {186}. **v2:** Daws *YrDa1* {186}.

YrDru {184, 185}. 6B {185}. 5B {184}. **v:** Druchamp {184, 185}.

YrDru2 {184}. 6A {184}. **v:** Druchamp {184}.

YrExp1 {10601}. 1BL {10601}. **v2:** Express *YrExp2* {10601}. **ma:** *Xwgp78-1B* – 4.2 cM – *YrExp1* – 3.4 cM – *Xwmc631-1B* {10601}.

YrExp2 {10601}. 5BL {10601}. **v2:** Express *YrExp1* {10601}. **ma:** *Xgwm639-5B* – 9.2 cM – *Xwgp81-5B* – 1 cM – *YrExp2* – 0.7 cM – *Xwgp82-5B* {10601}.
Based on the presence of the nearest flanking markers *YrExp2* was postulated in Expresso, Blanca Grande, Buck Pronto and Jeff/Pronto {10601}.

YrF {11156}. 2B {11218}. 2BS {11219}. **v2:** Francolin#1 *Yr29* {11156, 11218, 11219}. **ma:** *Xgwm374-2B* – 2.0 cM – *YrF* – 1.8 cM – *Xwmc474-2B* {11219}.
Francolin#1 is also released under the names Ufam and BARI Gom 27 {11156}.

YrF {11781}. 5AS {11781}. **bin:** 5AS-0.4-0.98 {11781}. **v:** Flanders {11781}. **ma:** *Xbarc56-5A* 2.0 cM – *YrF* – 0.6 cM – *AX108925494* {11781}.

YrHA {11100}. 1AL {11100}. **v:** H901414-121-5-5-9 {11100}. **ma:** *Xwmc469-1A* – 3.4 cM – *YrHA* – 4.6 cM – *Xgwm497-1A* {11100}.

YrH46 {184}. 6A {184}. **v2:** Hybrid 46 *Yr4b* {184}.
Not the same gene as *YrDru2* {184}.

YrHu {11229}. Derived from *Psathyrostachys huashanica*. 3AS {11229}. **bin:** H9020-17-25-6-4 {11229}. **ma:** *Xcfd79-3A* – 7.2 cM – *YrHu* – 0.7 cM – *BG604577* {11229}.

YrH62 {11303}. 1B {11303}. **v:** Line 03031-1-5 (ex CIMMYT) {11303}. **ma:** *Xgwm273-1B* – 3.7 cM – *Ax-109871410/Ax-109472792/Ax109352427* – 0.3 cM – *YrH62* – 0.8 cM – *Ax-109862469* – 2.1 cM *Xbarc137-1B* {11303}.

YrH9020 {10979}. Derived from *Psathyrostachys huashanica*. 2DS {10979}. **v:** H9020-1-6-8-3 {10979}. **al:** *Psathyrostachys huashanica* 0503383 {10979}. **ma:** *Xgwm102-2D* – 3.8 cM – *Xgwm455-2D* – 5.8 cM – *YrH9020* – 4.4 cM – *Xgwm261-2D* – 2.3 cM – *Xwmc503-2D* – 0.6 cM – *Xcfd53-2D* {10979}.

YrHVII {186}. 4A {186}. **v2:** Heines VII *Yr2 Yr25* {186}.

YrJ22 {11195}. 2AL {11195}. **v:** Jimai 22 {11195}. **ma:** *Xgwm382-2AL* – 1.0 cM – *YrJ22* – 7.3 cM – *IWA1348* {11195}; The mapped region was reduced to 0.3 Mb corresponding to 340.5 kb; *H736* – *J22/HJ732* – *H400* (768.7 – 769.0 Mb) {11679}.

YrJ44 {11696}. *QYr.nwafu-6AL* {11696}. 6AL {11696}. **v2:** Jimai 44 *Yr29* {11696}. **ma:** Mapped to a 3.5 cM interval flanked by AQP markers *AX-109373479 and AX-109563479* {11696}.

YrKK {11034}. Adult plant resistance. 2BS {11034}. **bin:** 2BS-1. **v:** Kenya Kuku {11034}. **ma:** *Xgwm148-2BS* – 3.2 cM – *YrKK* – 1.8 cM – *Xwmc474-3B* {11034}. Resistance conferred by *YrKK* at the adult stage approached immunity. A slight effect was observed on seedling response {11034}.

YrLk {11252}. 7BL {11252}. **v:** Lankao 5 {11252}. *Xbrac267-7B* – 4.4 cM – *YrLk* – 3.3 cM – *Xwmc396-7B* {11252}.

YrLM168a {11284}. Adult plant resistance. 6BL {11284}. **v:** *Xwmc756-6B* – 4.6 cM – *YrLM168a* – 4.6 cM – *Xbarc146-6B* {11284}. **ma:** *Xwmc756-6B* – 4.6 cM – *YrLM168a* – 4.6 cM – *Xbarc146-6B* {11284}. LM168a and LM168b are derivatives of Milan {11284}.

YrMin. 4A {184}. **v:** Minister {184}.

YrMor {186}. 4B {186}. **v2:** Moro *Yr10* {186}. **ma:** The development of an STS marker, derived from an AFLP fragment, that co-segregates with *YrMor* was reported in {357}.

YrMY37. *yrMY37* [{11282}]. Recessive. 7BL {11282}. **v:** Mianmai 37 {11282}. **ma:** *Xwmc476-7B* – 1.57 cM – *Xgwm297-7B* – 0.79 cM – *YrMY37* – 0.38 cM – *Xbarc267-7B* {11282}.

YrMY41 {11271}. 1B {11271}. **v:** Mianmai 41 {11271}.
A cross with AvS+Yr26 failed to segregate. Although claimed to be a possible allele of *Yr24/Yr26* the gene identified is likely to be the same.

YrND. 4A {184}. **v2:** Nord Desprez *Yr3a Yr4a* {184}.
May be the same as *YrMin* {184}.

Yrns-B1 {33}. 3BS {33}. **v:** Lgst.79-74 {33}. **ma:** *Xgwm493* (distal) - 21 cM – *Yrns-B1* {33}; As a QTL, *Yrns-B1* was located in a 3 cM interval between *Xgwm493-3B* and *Xgwm1329-3B* {10383}.

YrP {11614}. 5DS {11614}. **v:** *Ae. peregrina* derivative PAU16058 {11614}. **al:** *Ae. peregrina* PAU3519 {11614}.

YrP81 {10696}. 2BS {10696}. **v:** P81{10696}; Xu29 {10696}. **ma:** *Xgwm429-2B* – 1.8 cM – *YrP81* – 4.1 cM – *Xwmc770-2B* {10696}.

YrPak {11543}. 5BS {11543}. **v:** PI 1388231 {11543}. **ma:** *sunKASP_338* – 3.3 cM – *YrPak* – 3.5 cM – *sumKASP_341* {11543}.
PI 1388231 also carried two genes for adult plant resistance, one of which was positive with *Lr46* marker *Lr46_SNP1G22* {11543}.

YrR61 {10914}. [*QYr.uga-2AS* {10914}]. 2AS {10914}. **v:** Pioneer 26R61 = PI 612056 {10914}.

YrR212 {10562}. Derived from *S. cereale* 1B, 1BL.1RS {10562}. **v:** R185 {10562}; R205 {10562}; R212 {10562}. **al:** *S. cereale* R212 {10562}.

YrS {185}. 3B {185}. **v:** Stephens {185}.

YrS2199{10618}. 2BL{10618}. **bin:** 2BL0.89-1.00{10618}. **v:** S2199{10618}. **ma:** *Xgwm120-3B* – 11.0 cM – *YrS2199* – 0.7 cM – *Xdp269-2B*{10618}.

YrSte {184}. 2B {184}. **v:** Stephens {184}.

YrSte2. Stephens {184} 3B {184}.

YrSD {11085}. 5BL. **i:** Taichung 29*6/Strubes Dickkopf {11085}. **v:** Strubes Dickkopf {11085}. **ma:** *Xwmc640-5B* – 3.6 cM – *YrSD* – 2.4 cM – *Xbarc59-5B* – 3.0 cM – *Xwmc783-5B* {11085}.
The authors concluded that this gene was different from *Yr25*, which was located in chromosome 1D {158}.

YrSP {10018}. 2BS {10018}. **bin:** 2BL-C-0.5. **i:** Cx1 = Avocet S*4/Spaldings Prolific {10018}. **v2:** Spaldings Prolific *Yr25* {10018}. **ma:** *IWA638* – 0.6 cM – *YrSP* – 1.5 cM – *dp269-2* – 1.9 cM – *Xwmc332-2B* {11091}.MOVE TO YR5

YrSp {10352}. Allelic with *Yr5* and *Yr7* {10759} [*YrSP* {10018}]. 2B {10018, 10352}. Probably 2BL. **i:** Avocet*3/Spaldings Prolific {10018}; Taichung*6/Spaldings Prolific {10352}. **v:** Spaldings Prolific {10018, 10352}. **ma:** *YrSp* – *Xwmc-2B*, 12.1 cM{10352}. MOVE TO YR5

YrTr1 {186}. 6D {186}. **v2:** Tres *YrTr2* {186}.

YrTr2 {186}. 3A {186}. **v2:** Tres *YrTr1* {186}.

YrTye {186}. 6D {186}. **v:** Tyee {186}.

Yru1 {11494}. *TuG1812G0500003718*. 5AL {11494}. **bin:** 5AL10-0.57-0.78. **dv:** *T. urartu* PI 428309 {11494}. **ma:** *Xgwm186-5A* – 30.5 cM – *Yru1* – 10.8 cM – *Xgpw7007-5A*, then fine mapped with 82 additional polymorphic markers {11494}. **c:** *Yru1* has as NBS-LRR structure with N-terminal ankyrin and C-terminal WRKY repeats {11494}. GenBank MT018453.
The *Yru* resistance allele was present in a number of *T. urartu* accessions, but not in G1812 {11494}.

YrV23 {10370}. Presumed to be *Yr3a*. 2B {184}. **v:** Vilmorin 23 {10370}; Vilmorin {184}.
Allelic but not the same as *YrSte* {184}.

Yrwh2 {11150}. Recessive. 3BS {11150}. **v:** Wuhan 2 {11150}. **ma:** *Xwmc540-3B* – 5.9 cM – *Yrwh2* – 10 cM – *Xgwm566-3B* {11150}.

YrXH [{11729}]. *YrXH-1AL* {11729}. 1AL {11729}. **v:** Xiaohemai ZM004745 {11729}. **ma:** Located to a 1.5 cM interval – 484.33 – 490.09 Mb, CS RefSeq 1.0 {11729}.
May be the same as *YrXH-1AL* {11672} based on common markers with {11729}.

Yrxy1 {10829}. High temperature resistance. **v:** Mingxian 169/Xiaoyan 54 F_3-4-14 {10829}. **v2:** Xiaoyan 54 *Yrxy2* {10829}. **ma:** *Xbarc49-7AS* – 15.8 cM – *Yrxy1* with closer flanking RGA markers {10829}.

Yrxy2 {10829}. High temperature resistance. **v:** Mingxian 169/Xiaoyan 54 F_3-4-30 {10829}. **v2:** Xiaoyan 54 *Yrxy1* {10829}. **ma:** *Xwmc794-2AS* – 4.0 cM – *Yrxy2* – 6.4 cM – *Xbarc5-2AL* {10829}.

YrYam {184, 185}. 4B {185}. **v2:** Yamhill *Yr2 Yr3a Yr4a* {185}.

YrZH22 {11563}. 4BL {11563}. **v:** Zhoumai 22 {11563}. **ma:** *XWGGB133* – 3.29 cM – *YrGH22* – 2.63 cM – *XWGGB146* {11563}.
YrZH22 could not be distinguished from *Yr50* based on map location.

YrZH84 {10331}. 7BL {10331}. **v:** Annong 7959 {10331}; Zhoumai 11 {10331}; Zhoumai 12 {10331}. **v2:** Zhou 8425B *Yr9* {10331}. **ma:** *Xwmc276-7B* – 0.6 cM – *Xcfa2040-* – *YrZH84* – 4.8 cM – *Xbarc32-7B* {10331}.

3.21.3. Stripe rust QTL

Alcedo (R) / Brigadier (S): DH population: Two major QTLs *QPst.jic-2DL* (R^2 up to 0.36) and *QPst.jic-4BL* (R^2 up to 0.29) for percent infection contributed be Alcedo {10785}. A seedling-expressed QTL was located at the same position in 2DL {10774}.

Avocet S / AUS27482. AUS 27482 was shown to have *Yr34* (*YrAW6*) and a second novel gene (*YrAW7*) on chromosome 2B linked to *IWB71684* {11720}.

Avocet S / Attila: QTLs were located on chromosomes 2BS (probably *Yr27*), 2BL (a race-specific effect) and 7BL (*XP32/M59 - Xgwm344-7B* {10586}.

Avocet (S) / Chapio (I): F_6RIL population: In Mexico QTLs were located in chromosomes 2BS (*Yr31*), 3BS(*Yr30*) and 7DS(*Yr18*); only the last two were effective in 2009. In China QTLs were located in chromosomes 3BS, 5BL and 7DS. A 3DS QTL was effective in Mexico in 2009 and in China in 2013 {11020}.

Avocet R (S) / Chilero: *Lr46/Yr29*, *QLr.cim-5DS/QYr.cim-5DS*, *QYr.cim.6BS* and *QYr.cim-7BL* from Chilero, and *QLR.cim-1DL/QYr.cim-1DL* from Avocet R {11306}.

Avocet S (S) / Eltan (MR): RIL population: Three QTL for seedling reaction located on chromosome arms 2BS, 4AL and 5BS (minor) and two addition QTL for APR identified on chromosome arms 6AS and 7BL {11560}. A significant increase in the disease response of Eltan was associated with races virulent on Eltan seedlings**.**

Avocet (S) / Kundan (R): *Yr29* plus *QYr.cim-2AL* flanked by *3064488_30:T>G* ($R^2 = 0.05 – 0.09$), *QYr.cim-3DS* flanked by *3021242* and *224356* ($R^2 = 0.04$} and *QYr.cim-5AS* flanked by *3025355_10:T>C* and *1067590* ($R^2 = 0.04 – 0.05$) {11248}.

Avocet S (S) / Napo 63 (R): *Qyrnap.nwafu-2BS* (11283}. 2BS {11283}. **bin:** 2BS-1-0.53. **ma:** Mapped to a 5.46 cM interval flanked by KASP markers *90K-AN34* and *90K-AN36*; and by *Xbarc55-2B* and *Xgwm374-2B* {11283 }.

Avocet (S) / Pastor (I): RIL population: QTL mapped on 1BL (*Yr29*), 2BS(*Yr31*), 5A, 6B and 7AL plus minor QTLs on 1AL, 1B, 3A, 3B, 4D, 6A, 7AS and 7AL {10928}.

Avocet S/Pavon 76: QTL identified in 1BL (*Xgwm259*), 3BS (PstAATMseCAC2), 4BL (*Xgwm495*), 6AL (*Xgwm617*), 6BL (PstAAGGMseCGA1) {10443}.

Avocet S / PI 182103 (R): RIL population: QTL detected on chromosomes 2AS and 3AL for seedling resistance and 4DL, 5BS and 7BL for APR; *QyrPI182103.wgp-4DL* was designated as *Yr79* {11222}.

Avocet S (S) / Qinnong 142 (R): RIL population: Two QTL for seedling resistance to race CYR23 on chromosome arms 1DL and 4AL. These genes were not effective against races used in the field where APR was controlled by QTL on chromosome arms 1BL (*QYrqin.nwafu-1BL*: probably *Yr29*), 6BS (*QYrqin.nwafu-6BS*, possibly *Yr78*); 2AL *QYrqin.nwafu-2AL*) and 2BL (*QYrqin.nwafu-2BL*) {11559}.

Avocet S (S) / Qinnong 142 (R): RIL population: Adult plant resistance: *QYrqin.nwafu-1BL – AX-95133868 – AX-94522424*, $R^2 = 0.16 – 0.20$, likely *Yr29*; *QYrqin.nwafu-2AL*, *AX-94655393 – AX-9489521*, $R^2 = 0.08 – 0.20$; *QYrqin.nwafu-2BL*, *AX-94507002 – AX-94562871*, $R^2 = 0.18 – 0.39$; *QYrqin.nwafu-6BS* $R^2 = 0.14 – 0.31$ {11377}.
Seedling resistance in Qinnong 142 to race CYR23 was attributed to genes on chromosomes 1DS and 4AL {11377}.

Camp Remy/Michigan Amber: Two QTLs were located on chromosome 2BL (*QYR1,* LOD score 12) and 2AL (*QYR2*, LOD 2.2) {0287}. Four QTLs were scored in the ITMI population. The most effective (*QYR3*, LOD 7.4) on chromosome 2BS was probably *Yr27*, the others were located in 7DS (*QYR4,* LOD 3.4), 5A (*QYR5,* LOD 2.8), 3D (*QYR6,* LOD 2.8) and 6DL(*QYR7,* LOD 2.4) {0287}.

Camp Remy/Recital: 217 RILs. Six QTLs for APR were detected over 4 years. *QYr.inra-2BL* (R^2=0.42-0.61) corresponded largely to seedling resistance gene *Rsp* and possibly *Yr7*. The other genes were *Qyr.inra-2AL, QYr.inra-2BL, QYr.inra-2DS* (perhaps *Yr16*), *QYr.inra-5BL.1* and *QYr.inra-5BL.2* {10279}. Differential reactions of RILs possessing different QTL occurred between old and new *P. striiformis* races {11144}.

Capo (R) / Arina (S) and **Capo (R) / Furore (S)**: Four QTL on chromosomes 2AL, 2BL, 3BS and 5A were from Capo and one on chromosome 3AS was from Arina; the QTL on 2AL, 2BL and 3BS were co-located with QTL for resistance to leaf rust {11449}.Claire / Lemhi: DH population: 4 QTLs for APR:*Qyr.niab-2D.1* (at or near *Yr16*, R^2=0.1-0.25, *Qyr.niab2DL.2* (R^2=0.14-0.32), *Qyr.niab-2BL*, and *Qyr.niab-7B* (R^2=0.11-0.13) {10962}. An unknown seedling resistance gene was located in chromosome 3BL {10962}.

Chuanmai 42 (variable) / Chuanmai 55 (R): RIL population: Two QTL on chr. 1B and 2A were derived from CH55 and a less effective QTL on Chr 7B was from CH42 {11558}. The chr 1B QTL was postulated to be *Yr29*. CH42 carries *Yr24* and CH55 carries the 1BL.1RS (*Yr9*) translocation and 5B.7B reciprocal translocation– neither gene was effective in this study {11558}.

Coker 9835 (S) / VA96W-270 RIL population: Adult plant resistance was conferred by *QYr.ar-3BS* (nearest markers *Xbarc147, ger9-3p, IWA6092*) and *QYr.ar-4BL* (nearest markers *Xbarc163, Xcfd39* and several *IWA* markers {11175}. Cultivar Pat had the same haplotype {11175}. USG 3555 / Neuse: Three QTL on chromosomes 1AS, 4BL and 7D (not *Yr18*) were derived from USG 3555 and one QTL on chromosome 3A was from Neuse {11142}.

Express / Avocet S: RIL population: Relative AUDPC for high temperature APR was controlled by *QYrex.wgp-6AS*, R^2=0.326, interval *Xgwm334-6A - Xgwp56-6A*; *QYrex.wgp-3BS*, R^2=0.274, interval *Xgwm299-3B - Xwgp66-3B, QYrex.wgp.1BL*, R^2=0.094, interval *Xwmc631-1B - Xwgp78-1B* {10672}. When rust phenotyping was based on infection type only the 6S and 3BL QTLs were evident {10672}.

Druchamp (R) / Michigan Amber (S): Eight QTL for high-temperature adult plant resistance: QTL in chromosomes 1BL (nearest marker *Xgwm131-1B*), 2BL (*IWA7583*), and 5BL (2, *IWA2558* and *IWA6383*) were stable across environments, whereas genes in chromosomes 1BL (*IWA8581*, probably *Yr29*), 1DS (*IWA22668*), 3AL (*IWA6834*) and 6BL {*IWA6420*) were not {11284}. In addition three QTL for all stage resistance were detected on chromosomes 5B (probably *Yr3*, *IWA6271*), 5DL (*IWA8331*) and 6BL (*IWA3297*).

Fukuhokomugi/Oligoculm: Seven QTLs were identified for stripe rust severity in a joint analysis of five datasets from a doubled haploid population {10060}. Their location, associated marker, percentage variation explained, and genotype contributing to enhanced resistance at that locus, are listed as: 3BS; *Xgwm389-3B*; 0.2-4.9%; Oligoculm {10060}. 4BL; *Xgwm538-4B*; 1.8-12.3%; Oligoculm {10060}. 4DL; *Xwmc399-4D*; 2.5-8.0%; Oligoculm {10060.} 5BL; *Xwmc415-5B*; 2.4-16.1%; Oligoculm {10060}. 6BS(centromeric); *Xgwm935-6B*; 0.5-3.8%; Oligoculm {10060}. 7BS; *Xgwm935-7B*; 1-5.2%; Oligoculm {10060}. 7DS; *Xgwm295-7D*; 10.7-23.7%; Fukuho {10060}; the 7DS QTL was probably *Yr18* {10060}.

Four QTLs were identified for stripe rust infection in a joint analysis of three datasets from a Fukuhokomugi/Oligoculm doubled haploid population {10060}. Their location, associated marker, percentage variation explained and parent contributing to enhanced resistance at that locus are listed as:. 2DL; *Xgwm349-2D*; 6.5-9.6%; Fukuho {10060}. 3BS; *Xgwm389-3B*; 15.1-24.5%; Oligoculm{10060}. The 3BS QTL may be *Yr30* {10060}. 5BL; *Xwmc415-5B*; 6.4-12.7%; Oligoculm {10060}. 7BL; *Xwmc166-7B*; 2.5-9%; Oligoculm {10060}.

Flinor (R) / Mingxian 169 (S): Two independent QTLs for high temperature (24/18C) seedling resistance located in chromosome 5BL, designated *QYr-tem-5B.1* (*Xbarc89 - Xgwm67*) and *QYr-tem-5B.2* (*Xbarc140n - Xwmc235*) and R^2 = 0.37 and 0.33, respectively {10797}.

Guanggtoumai (R) / Avocet S (S): RIL population. *QYr.GTM-5DL* accounted for 22 – 44% of the phenotypic variation across three sites (11562).

Guardian / Avocet S: F3 lines. One major QTL, *QPst.jic-1BL* (*Xgwm818-1 - Xgwm259-1B*, R^2 up to 0.45), and two minor resistance QTLs on chromosomes 2D and 4B originating from Guardian {10589}. The major QTL was in the region of *Yr29*.

Jagger (MR) / 2174 (MS): RIL population: *Qyr.osu-2A (Yr17)* and *Qyr.osu-5A* (in *Xgwm156-5A* - centromere region) from Jagger and *Yr18* from 2174 (but only in tests in China) {10973}. According to 11393 *Qyr.osu-5A* is an orthologue of *OsXA21* and confers resistance to multiple pathogens/pests.

Kariega/Avocet S: DH population: Two QTLs *QYr.sgi-7D* (probably *Yr18*) and *QYr.sgi.2B.1* accounted for 29 and 30%, respectively, of the phenotypic variation for stripe rust response. The nearest marker to the latter was *Xgwm148-2B* {10184}. These locations were confirmed in a subsequent study; *QYr.sgi-2B.1a* was located within the *wPt5556 – wPt6278* segment {11232}.

Kukri (MR) / Janz (MR): DH population: Tested with pre- and post-2003 Australian *Pst* races in several environments. *QYr.sun-7B* (Kukri) and *Qyr.sun-7D (=Yr18))* (Janz) were consistent over environments; *QYr.sun-1B, -5B* and *-6B* were detected in most environments and *QYr.sun-3B* was identified in only one season. Two genes, *QYR.sun-1A* from Janz and *QYr.sun-2A* from Kukri, were detected only with pre- and post-2003 races, respectively, and likely contributed to differential responses of these cultivars to the two groups of races {10751}.

Luke (R) /Aquileja (R): Two QTLs for high-temperature adult plan resistance, *QYRlu.cau-2BS.1* (distal, flanked by *Xwmc154-2B* and *Xgwm148-2B*, R^2 = 0.366) and *QYrl.cau-2BS.2* (proximal, flanked by *Xgwm148-2B* and *Xbarc167-2B*, R^2 = 0.415) from Luke, and *QYraq.cau-2BL* (flanked by *Xwmc175-2B* and *Xwmc332-2B*, R^2 = 0.615) in Aquileja for stripe number {10582}.

Luke (MR) / AQ24788-83 (APR): RIL population: *QYr.cau-2AL* near *IWB4475* (R^2 = 23-40%) from AQ24788-83 and *Yr18* (R^2 = 11.0-14.7%) from Luke (11393).

Mianyang351-15 (R) / Zhengzhou 5389 (R): RIL population: Seven QTL were located on chromosome arms 1BL (*Yr29*), 2AS (*Yr17* or another gene), 2DS, 3AS, 3DS, and 7BL (possibly associated with *Lr68*) {11545}.

Mingxian 169 (S) / Centrum (R): RIL population: QTL detected on chromosomes 7BL (*QYrcen.nwafu-7BL*, R^2 = 23.4%, *AX-94556751 - AX-110366788*), 1AL (*QYrcen.nwafu-1AL* (R^2 = 11.2%, *AX-94488258 – AX-94458040*) and 4AL (*QYrcen.nwafu-4BL*, R^2 = 12.6%, *AX-94695204 – AX-94996273* {11365}.

Mingxian 169 (S) / Chakwal 86 (R): RIL population: QTL on chromosomes 1BL (*Yr29*), 3BS (not *Yr30*) and 6BS (*QYrcw.nwafu-6BS*) contributed to the high level of APR in Chakwal 86 {11371}.

Mingxian (S) / P1057: RIL population, and Avocet S (S) /P10057 and Zhengmai 9023 (S) / P10057 F_2:F_3 populations: Two strong QTL located in clustered QTL regions: *Qlrlov.nwafu-2BS* identified by *IAW5377, IWA2674, IWA5830*, and *Qyrlov.nwafu-3BS* identified by *IWB57990* and *IWB6491* {11279}.

Mingxian (S) / P9936 (R): RIL population: *QYr.nwafu-3BS* (probably *Yr30*) and *QYr.nwafu-7BL* flanked by *AX-108819274* and *AX*-11040708 (R^2 = 36.0 – 38.9%; a KASP marker was developed for the latter {11373}.

Mingxian 169 / P10090: *QYr.nwafu*-6A (syn *YrP10090* for adult plant resistance reduced stripe rust severity by a mean 14.8%. Located in the chr. 6A centromeric region and flanked by *Ax94460938* and*Ax710585473*, a 3.5 cM region corresponding to physical interval 107.1 – 446.5 Mb {11555}.

Mingxian 169 (S) / Qing Shumai (R): RIL population: APR QTL *QYr.cau.6DL*, *Xbarc1121-6D – Xgpw4005-6D* region: positive interaction with *Yr18* {11323}.
Mingxian 169 (S) / Toni (R): RIL population: *QYrto.swust-3AS*, *AX-95240191 – AX-9482889091*, R^2 = 0.22 – 0.56: *QYrto.swust-3BS*, *AX-994509749 – AX-94998050*, R^2 = 0.23 – 0.55 {11379}.

Otane (R) / Tiritea (S): DH population: QTL in 7DS (probably *Yr18*), 5DL (from Otane) and 7BL (Tiritea) {10150}. Interval mapping of 7DS indicated that the presumed *Yr18* was 7 cM from *Xgwm44-7D* {10150}.

Pingyuan 50 (R) / Mingxian 169 (S): DH population: APR: *QYrcaas-2BS* (*Xbarc13-2BS) - Xbarc230-2BS*, R^2=0.05-0.09), *QYr.caas-5AL*(*Xwmc410-5AL - Xbarc261-5AL*, R^2=0.05-0.2), *QYrcaas-6BS*(*Xgwm361-6BS - Xbarc136-6BS*, R^2=0.05-0.08) {10693}.

Pioneer 26R61(R) / AGS2000(S): RIL population: Two QTLs, *QYr.uga-2AS* (R^2=0.56) flanked by *Xbarc124-2A* and *Xgwm359-2A* (also named *YrR61*) and *QYr.uga-6AS* (R^2=0.06) {10914}. Minor QTLs were also on other chromosomes

Renan (R) / Recital (S): RIL population: Tested for AUDPC in 1995/6 and 2005/6 with pathogen isolates avirulent and virulent, respectively, for *Yr17*:*QYr.inra-2AS.2,* (=*Yr17*), R^2=0.45, 1995/6; *QYr.inra-2AS.1*, R^2=0.9, 2005/6; *QYr.inra-2BS*, R^2=0.11 & 0.13, *QYr.inra-3Bcent*, R^2=0.06 in 2005/6; *QYr.inra-6B*, R^2=0.04 & 0.06; from Renan; and *QYr.inra-2AS.1*, R^2=0.09; *QYr.inra-3DS*, R^2=0.08 & 0.12 from Recital. Other QTLs were effective only at certain growth stages {10689}.

Soru#1 (R) / Naxos (MR): RIL population: Seedling and field tests detected two moderately effective QTL that were likely *Yr24* and *Yr28* derived from Soru#1 {11368}. A KASP marker was developed for *Yr28*.

Stephens / Michigan Amber: Two QTLs for high temperature APR were located in chromosome 6BS; *QYrst.wgp-6BS.1* located in a 3.9 cM region flanked by *Xbarc101-6B* and *Xbarc136-6B* and *QYrst.wgp-6BS.2* located in a 17.5 cM region flanked by *Xgwm132-6B* and *Xgdm113-6B* {10602}.

Stephens (I) / Platte (S): RIL population: 13 QTLs were identified across several environments; significant QTL x environment interactions suggested that plant stage specificity, pathogen genotype and temperature as well as host genotype were important in determining rust response {10890}.

Stewart (R) / Bansi: Durum, F_5 and F_7 populations: *Yr29* and *QYr-3BL* ($r^2 = 0.045$); the latter was in the vicinity of *Yr80* with *kIWA6221* as the nearest marker {11542}.

Svevo (R) / Zavitan (MS): Tetraploid, RIL population tested in Israel and China. Nine QTL for APR; 8 from Svevo and one from Zavitan, the most effective of which was *QYrsv.swust-1BL.1* {11557}. This QTL overlapped the *Yr29* region and Svevo was positive for the *Yr29* marker.

Thatcher (S) / Hong Qimai (APR): RIL population: *QYr.cau-2AL* near *Xgwm311-2A* and *IWB4475* (R^2 = 47-52%), *Qyr.cau*-4AL (R^2 = 5-7%) and *Qyr.cau-7AL* (R^2 = 9-10%) derived from Hong Mai {11366}.

***T. monococcum* PAU14087 (R) / *T. boeoticum* PAU5088 (R):** RIL population: One adult plant resistance QTL identified in each parent and named *QYrtm.pau-2A* (in a 3.6 cM interval between *Xwmc407-2A* and *Xwmc170-2A*; $R^2 = 0.14$) and *QYrtb.pau-5A* (in a 8.9 cM interval between *Xbarc151-5A* and *Xcfd12-5A*; $R^2 = 0.24$) {10518}.

UC1110 (MR) / PI 610750 (MR): RIL population: *QYr.ucw-3BS* ex UC1110, R^2=0.22, associated with *Xgwm522-3B.1*. This marker differs from *Xgwm533-3B.2* that is associated with *Yr30* {10705}; *QYr.ucw-5AL*, R^2=0.1, ex PI 61075 - syn. *Yr48* {10705}; *QYr.ucw-2BS*, R^2=0.045, ex UC1110, located in the centromeric region near *Xwmc474-2BS* {10705}, *Qyr.ucw-2AS*, R^2=0.023, ex PI 61725, near *wPt-5839* {10705}.

Yaco S (R) / Mingxian 169 (R): Adult plant resistance. *Qyryac.nwafu-2BS* located within a 1.3 cM region flanked by KASP markers *BS00022657_51* and *IACX6411.BobWhite_22503_605* within the 10.4 cM *Xgwm148-2B – Xbarc55-2B* region {11241}.

Yibinzhuermai (AS1591) / Taichung 29: RIL population: QTL in chromosome arms 5BL, 6AL and 7DS (Yr18) derived from Yibinzhuermai; *QYr.YBZR-6AL* was considered new (11759}.

Yr16DH70 (Cappelle Desprez / 2*Palmiet Selection) / Palmiet: DH population: One major effect QTL, *Qyr.ufs-2A*, and three less effective QTLs in 2D (possibly *Yr16*), 5B and 6D were from Yr16DH70, and a minor effect QTL on 4B was from Palmiet {10933}.

Four QTLs were detected in a multiple cross analysis {10283}: Chromosome 2AL (probably *Yr32* in Deben, Kris and Soloist), 2AS (probably *Yr17* in Kris), 2BL (*Xwmc149-2B – Xwmc317a-2B* in Deben) and 6BL (*Xwmc397-6B - Xwmc105b-6B* in Soloist and Kris).A summary of published QTL locations is provided in {11089}; 49 chromosome regions on 20 of the 21 wheat chromosomes were covered. Markers associated with many stripe rust resistance genes are summarized in {11254}.

Tetraploid wheat

Kofa (S) / W9262-260D3 (MR): DH population: QTL were identified on chromosomes 5B (APR) and 7B (seedling resistance and APR) in the region of Yr67 {11689}. Full resistance required the presence of both QTL. The 5B QTL was not detected in field trials in Mexico {11689}.

3.21.4. Spike response to stripe rust

Bouvet et al. {11658} identified five QTL controlling stripe rust response in spikes in a UK Magic population; three (on chromosomes 2D, 4D and 5A (possibly *Yr34*)) co-located with previously identified QTL and two (chromosomes 2D and 4A) associated with flowering time. Heritability was lower than that for leaf response.

3.22. Reaction to *Puccinia triticina*

Disease: Brown rust, leaf rust.

3.22.1. Genes for resistance

LR1

Lr1 {47}. 5D {954}. 5DL {945}. 1B {1409}. **i:** Centenario/6*Thatcher {317}; Malakoff/6*Prelude {317}; Wichita*4/Malakoff {613}. **v:** Line 87E03-S2B1 {10561}; Centenario {317}; Chicora 'S' {143}; Daws (heterogeneous) {1019}; Dirkwin {1019}; Glenlea {976, 1255}; Halle 9H37 {74}; Hyslop {1019}; Luke {heterogeneous}{1019}; Malakoff {47}; McDermid {1019}; Mexico 120 {933}; Newton {1023}, {1024}, {143}; Norco {1019}; Shabati Sonora {842}; Sonora 64 {842}; Tarsa {842}; Uruguay {954}; Walliday {1019}. **v2:** Blueboy *Lr10* {143}; Blueboy II *Lr10 Lr24* {143}; Erythrospermum 142 and 953 *Lr3* {74}; Laura *Lr10 Lr34* {712}; Norka *Lr20* {1552}; Plainsman V *Lr3* {1024}; Suneca *Lr13* {485}. **dv:** Several *Ae. tauschii* accessions {10191}. **ma:** Co-seg. with *Xpsr567-5D* and *Xglk621-5D* in a Frisal/*Lr1* resistant line. pTAG621 was converted to a diagnostic STS{354}; Terminally located{10189}; In *Ae. tauschii* recombination in the region was 5-10X that in common wheat, gene order *Xpsr567-5D - Lr1 - Xabc718-5D*{10191}; Mapped to a 0.7 cM interval in *Ae. tauschii* and a 0.075 cM interval in wheat {10408}; A candidate gene for *Lr1, Lr1RGA1*, encoding a CC-NBS-LRR protein, cosegregated with *Lr1*{10408}; Co-segregation with RGA567-5{10561}. **c:** *Lr1* is a member of a multigene family (PSR567), has a CC-NBS-LRR structure, and produces a protein of 1,344 aa, EF567063 {10561}.

LR2. 1B {1409}. 2DS {942, 843}.

Lr2a {320}. [*Lr2* {47}]. **i:** Prelude*6/Webster {320}; Red Bobs*6/Webster {320}; Webster/6*Thatcher RL6016 {306}; Wichita*4/Webster {613}. **v:** EurekRRa CI 17738 {143}; Festiguay {843}; Webster CI 3780 {47}; Common in the Canadian Western Spring Wheat (CWSW) cultivars {11700}. **v2:** Alex *Lr10* {976}; Ck 9835 *Lr9* {10146}; Ck 9663 *Lr2 Lr10* {10146}; Guard *Lr10c* {976}; James *Lr10* {976}; Len *Lr10* {976}; Marshall *Lr10* {976}; Mediterranean W1728 *Lr3* {1369}; Shield *Lr3 Lr10* {198}; Waldron *Lr10* {143}. **ma:** Flanked by KASP markers *kwm1620* (64.455 Mb, CS REFSeq 2.1.) and *kwm1623* (64.760 Mb) {11700}.

Lr2b {320}. [*Lr2*^{2} {1409}]. **i:** Prelude*6/Carina {320}; Red Bobs*6/Carina {320}; Thatcher*6/Carina {320}; Wichita/4*Carina {613}. **v:** Carina {613}.

Lr2c {320}. [*Lr2*^{3} {1409}]. **i:** Prelude*5/Brevit {320}; Prelude*6/Loros {320}; Red Bobs*6/Brevit {320}; Red Bobs*6/Loros {320}; Thatcher*4/Brevit {320}; Thatcher*6/Loros {320}; Wichita*4/Brevit {613}; Wichita*4/Loros {613}. **v:** Brevit {613}; Loros {1257, 317}.

LR3 {47}.

Because *Lr3* appears to be a complex locus {486} Democrat and Democrat/6* Thatcher should be accepted as standards. There is evidence to suggest that the allele in Mentana, and therefore many derivatives, is *Lr3b* {939}. If this is correct, many genotypes listed under *Lr3a* are likely to be *Lr3b*. Durum cv. Storlom likely carries *Lr3a* or *Lr3b* {10469}. Cv. Camayo was considered to have a closely linked gene, or *Lr3* allele {10469}. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B*. All three Thatcher NILs with named *Lr3* alleles carried the STS marker {10469}.

Lr3a {10028}. [*Lr3* {47}]. 6B {549}. 6BL {939}. **i:** Democrat/6*Thatcher {318}; Wichita*4/ Mediterranean {613}. **v:** Belocerkovskaja 289 {74}; Bennett {1024}; Democrat {47}; Fertodi 293 {74}; Gage {1024}; Hana {68}; Homestead {1024}; Ilyitchovka {75}; Juna {75}; Jubilejne {68}; Kawvale {143}; Lancota {1024}; Mara {68}; Mediterranean {47}; Mediterranean W3732 {1369}; Mentana {842}; Mironovskaya 264 & 808 {74}; Odra {75}; Osetinskaya {74}; Ottawa {143}; Pawnee {1408}; Ponca {143}; Rannaja 12 {74}; Shawnee {143}; Shirahada {842}; Sinvalocho MA {10929}; Skorospelka 3b {74}; Sledkovicova K1004 {74}; Viginta {68}; Warrior {1024, 143}; Yubileynaya {75}. **v2:** Amika *Lr26* {76}; Bezostaya 1 *Lr34* {74}; Bowie *Lr14b* {319}; Erythrospermum 142 & 953 *Lr1* {74}; Istra *Lr26* {76}; Mediterranean W1728 *Lr2a* {1369}; Plainsman V *Lr1* {1024}; Shield *Lr2a Lr10* {198}; Solaris *Lr26* {76}; See also {69}. **tv:** Storlom {10469}. **ma:** Co-segregation with *Xmwg798-6B* {10469, 9921}; cDNA marker TaR16 was completely linked to *Lr3* in a population of 109 gametes {10058}; *UBC840*$_{540}$ - *Lr3a*, 6 cM {10263}.

Lr3b. [*Lr3bg* {486}]. **i:** Thatcher*6/Bage; RL6094 = Tc*6/T6 {307}. **v:** Bage {486}. **v2:** T6 *Lr16* {307}.
Durum cv. Storlom likely carries *Lr3a* or *Lr3b* {10469}. Cv. Camayo was considered to have a closely linked gene, or *Lr3* allele {10469}. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B*. All three Thatcher NILs with named *Lr3* alleles carried the STS marker {10469}.

Lr3c. [*Lr3ka* {486}]. **i:** Tc*6/Klein Aniversario. **v:** Blava {10345}; CI 13227 {11021}; Klein Aniversario {486}.

Lr3d {11054}. **i:** RL6062, Thatcher*6/PI 268316 {11054}. **v:** PI 268316 {11054}.

LR4, LR5, LR6, LR7, LR8 {365}. **v:** Purdue Selection 3369-61-1-10 = Waban{365}; Not available as separate single-gene lines. Therefore, alleles at these predicted loci were never characterized.

LR9

Lr9 {1408}. Derived from *Ae. umbellulata*. 6BL = T6BS.6BL-6U#1L {389}. 6B{1299}, {1296}, {954}. **i:** T47 = Transfer = CS + *Lr9* {1408}; Thatcher*6/Transfer; Wichita*4/ Transfer {613}; Lines listed in {10244}. **v:** Abe {143}; Arthur 71 {1024, 1320}; Clemson 201 {465}; McNair 701 & 2203 {143}; PI 468940 {1439}; Riley 67 {1024, 1320}; Sullivan {1110}; Transfer {1296}. **v2:** Ck 9835 *Lr2a* {10146}; Ck 9663 *Lr2a Lr10* {10146}; Lockett *Lr24* {10146}; Oasis *Lr1* {1109}. **al:** *Ae. umbellulata* TA1851 {11630}. **ma:** Co-seg with *XksuD27-6B* {48}; co-seg with *Xmwg684-6B* and STS *Xsfr1* {1272}; *Lr9* – 8 cM – *Xpsr546-6B* {1272}; SCAR markers were developed in {10244}. **c:** Encodes a 1,167-aa protein with an N-terminal tandem kinase domain followed by a von Willebrand factor type A (vWA) domain in the C-terminus {11630}. The ~28.4 Mb translocation at 725.61 Mb replaces a 5.58 Mb wheat segment containing 87 high confidence genes {11630}.
Lr9 has the identical sequence and translocation breakpoint to *Lr58* {11630}.
The structures of additional translocations are given in {389}.

LR10

Lr10 {199}. [*LrL* {31}]. 1A {312}, {546}. 1AS {939}. **i:** Exchange/6*Thatcher {306}; Gabo/6*Thatcher {306}; Lee/6*Thatcher {306}; Selkirk/6*Thatcher {306}; Timstein/6*Thatcher{306}. **s:** CS*5/Timstein 1A {939}; CS/7*Kenya Farmer 1A {939}. **v:** Centurk {1024}; Centurk 78 {1024}; Concho {143}; Federation {939}; Mayo 52 {31}; Mayo 54 {31}; Parker {546, 1024}; Rocky {1024}; Scout 66 {2101}; Sinton {1256}; Tascosa {143}; TAM-105 {55}; Unknown accessions {208}; See also {337}. **v2:** Alex *Lr2a* {976}; Blueboy *Lr1* {143}; Blueboy II *Lr1 Lr24* {143}; Ck 9663 *Lr2a Lr9* {10146}; Era *Lr13* {143}; Exchange *Lr12 Lr16* {31}; Gabo *Lr23* {31}; Guard *Lr2a* {976}; James *Lr2a* {976}; Kenya Farmer *Lr23* {939}; Laura *Lr1 Lr34* {712}; Lee *Lr23* {31}; Len *Lr2a* {976}; Marshall *Lr2a* {976}; Parker 76 *Lr24* {143}; Selkirk *Lr14a Lr16* {31,199}; Shield *Lr2a Lr3* {198}; Timstein *Lr23* {31}; Waldron *Lr2a* {143}; Warden *Lr16* {31}. **tv:** Altar 82 {10760}; Russello {10760}. **ma:** *Xcdo426-1A* – 5.1 cM – *Lr10*{1058}; *Lr10* – 8 cM – *Glu-A3* {355}; cosegregation with *Xsfr1(Lrk10-1A)* and *Xsfrp1(Lrk10-1A)* {1270}; complete linkage with *Xsfr1(Lrk10-1A)*, which encodes a protein kinase {639}. **c:** *Lr10* was cloned - it has a CC-NBS-LRR structure, syn, *T10rga1* GenBank AY270157 {10442}; A second CC-NBS-LRR gene, *RGA2*, is required for expression of *Lr10* in tetraploid and hexaploid wheats {10760}.

Lrk10. A receptor-like kinase. The locus *Xsfr1(Lrk10)-1A*, detected by the probe Lrk10, is completely linked with *Lr10* in chromosome 1AS {356}. The gene encodes a receptor-like kinase with extracellular and kinase domains {0297}. Using probe pLrk10-A, developed from the extracellular domain, 6 homologues were found in chromosomes 1A (1), 1B (3) and 1D (2) as well as group 1 chromosomes of *T. monococcum*, *Ae. tauschii* and barley {0296, 0294}. Probes based on the kinase domain identified further homologues in chromosomes 3AS and 3BS as well as the corresponding regions in rice and maize {0294}. Both orthologous and paralogous evolution were suggested.

LR11

Lr11 {1409}. [*LrBP2* {11074}]. 2DS {11074}. 2A {1409}. **i:** Thatcher*6/Hussar {306}; Wichita*4/Hussar {613}. **v:** Bulgaria 88 {142}; Hart {1024}; Hazen {49}; Hussar {1409}; Panola {10830}; Pioneer 2850; Pocahontas {10146}; Saluda {10699, 10146}. **v2:** Buck Poncho *Lr10* {11074}; Ck9803 *Lr18* {10595}; FFR 524 *Lr18* {10595}; Jamestown *Lr18* {10830}; Karl 92 *Lr3 Lr10* {2101}; Oasis *Lr9* {143}; Pioneer 2684 *Lr18* {10595}; SS520 *Lr18* {10595}. **ma:** *Lr11* – 0.3 cM – *SCAR32/35* – 1.6 cM – *Xgwm614-2D* {11074}.

LR12

Lr12 {326}. Adult plant reaction. 4B {312}. 4BL {10951}. **bin:** 4BL5-0.86-1.00. **i:** Exchange/6*Thatcher {306}. **v:** Opal {306}. **v2:** AC Domain *Lr10 Lr34* {228}; Caldwell *Lr14a* {10787}; Chinese Spring *Lr34* {301}; Exchange *Lr10 Lr16* {326}; Sturdy *Lr13* {301}; Unknown accessions {208}. **ma:** *Xgwm251-4B* – 0.9 cM – *Lr12* – 1.9 cM – *Xgwm149-4B* {10951}. Possible commonality with *Lr31*.

LR13 *TraesCS2B01G182800* {11530, 11531}; also predicted in {11529}.

Lr13 {326}. Although originally described as a gene for adult plant reaction {032}, {326}, *Lr13* can be detected at the seedling stage especially at high temperatures {939, 1156}. [*LrZH22* {11467, 11468}; *LrLC10* {11468}]. 2BS {939}. **i:** Tc*7/Frontana = RL4031 {306}; fifteen Thatcher lines with 2-gene combinations {711}. **bin:** 2BS1-0.35-0.75. **v:** This gene is very widespread {939}; Hereward {288}; Hustler {608}; Kinsman {608}; Kenya Plume {1370}; Liaochen 10 {11468, 11530}; Manitou {326}; Mardler {608}; Maris Huntsman {608}; Moulin {288}; Napayo {70}; Neepawa {143}; Norman {608}; Pastiche {288}; Polk {143}; Virtue {608}; Zhoumai 22 {11467, 11468, 11531}. **v2:** AC Barrie *Lr6* {10178}; Beaver *Lr26* {1032}; BH1146 *Lr34* {268}; Biggar *Lr14a* {712}; Chris *Lr34*; Columbus *Lr16* {1258}; Cumpas 88 *Lr26* {1373}; Era *Lr1 0* {143}; Frontana *Lr34* {32}, {1374}, {326}; Genesis *Lr14a* {712}; Hartog *Lr1 Lr46* {127}; Hobbit *Lr17a* {608}; Hobbit Sib *Lr17a* {1350}; Inia 66 *Lr14a Lr17* {1373}; Klein Aniversario *Lr3ka* {32}; Kenyon *Lr16* {300}; Lerma Rojo 64 *Lr17a Lr34* {1373}; Oasis 86 *Lr19* {1373}; Parula *Lr34 Lr46* {1374}; Suneca *Lr1* {485}; Yecora *Lr1* {1374}. **ma:** *Xpsr912-2B* – 9.1 cM – *Lr13* – 7.9 cM – *Xbcd1709-2B* – 9.8 cM – Cent. {88}; *Lr13* – 10.7 and 10.3 cM – *Xgwm630-2BS* {10463}; *Xbarc163-2B* – 5.1 cM – *Lr13* – 8.7 cM – *Xstm773b-2B* {329}; *Xbarc55-2B* – 1.1 cM – *Xkwh37* – 4.9 cM – *Lr13* – 5.8 cM – *Xgpw1109* – 3.7 cM – *Xbarc18-2B*{11068}; *Xbarc55-2B* – 2.4 cM – *LrZH22* – 4.8 cM – *Xgwm374-2B* {11467}; *Xbarc55-2B* – 2.2 cM – *XCAUT163* – 1.10 cM – *LrLC10* – 0.55 cM – *Lseq22* – 6.05 cM – *Xbarc18-2B* {11468}. **c:** Encodes a CC-NBS-LRR protein {11531; 11532} that is identical to that produced by one of the *Ne2m* haplotypes {11531}.

GenBank MW756036 {11532}. *Lr13* is an allele of the *YR27/NE2* locus {11593}.
Pleiotropic with the specific *Ne2m* allele at the *NE2* locus.

LR14.

Lr14a {964, 319}. [*LrLla* {10520}]. 7B{964}. 7BL {770}. **bin:** 7BL10-0.78-1.00. **i:** Selkirk/6*Thatcher {319}; Arina LrFor {11549}. **s:** CS*6/Hope 7B {964}. **v:** Aotea {964}; Brigand {608}; Gala {964}; Glenwari {964}; Hofed {964}; Hope {964}; H-44 {964}; Lawrence {964}; Redman {964}; Regent {964}; Renown {964}; Spica {964}. **v2:** Biggar *Lr13* {712}; Brambling *Lr23 Lr34* {10563}; Caldwell *Lr12* {10787}; Genesis *Lr13* {712}; Inia 66 *Lr13 Lr17a* {939}; Selkirk *Lr10 Lr16* {319}. **tv:** Arcangelo {11015}; Bicre {11015}; Creso {11015}; Colosseo {11015}; Italo {11015}; Lloreta INIA {10520}; Plinio {11015}; Somateria {10520}. **v2:** Forno *Lr34 Lr75* {11549}. **ma:** *Xwmc273-7B* – 13 cM – *Lr14a* – 10 cM – *Xgwm344-7B* {10520}; *Xwmc10/Xgwm344/wPt1085-7B* – 1.1 cM – *wPt4038-HRM* – 0.1 cM – *Lr14a* – 1.0 cM – *wPt4140-HRM* {11015}.
The *Lr14* region in tetraploid wheat harbours *Qlr.ubo-7B.2*, a gene that confers durable resistance in durums {10734, 10736} and that is present in many Italian, CIMMYT and ICARDA durum cultivars {10736}. The relationship of this gene described as *Lr14c* (reference genotype Creso) in {10735} remains to be determined. Reasons for considering *Lr14c* as a unique allele are given in {10735} but according to {11518} the gene sequence in Creso is identical to that of *Lr14a*. In association mapping the presence of *QLr.ubo-7B.2* was predicted with 96% accuracy based on appropriate alleles of *Xcfa2257.2, Xgwm344.2* and *Xwmc10* in the distal region of chromosome 7BL {10736}. **c:** *Lr14a* encodes a membrane-localized protein with 12 ankyrin repeats and structural similarity to Ca^{2+}-permeable non-selective cation channels {11549}. GenBank MT 123593.
Based on sequence *Lr14a* was identified in a few spelt (e.g. PI 190962) and a few wild emmer accessions {11549}.

Lr14b {319}. **i:** Maria Escobar/6*Thatcher {319}. **v:** Weebill 1 {10571}. **v2:** Bowie *Lr3*; CI 13227 *Lr68* {10817}; Maria Escobar *Lr17* {319}; Rafaela *Lr17* {314}.
Most accessions with *Lr14b*, including the Tc NILs probably carry APR gene *Lr68* {10817} which could be the same as *QLr.osu-7BL* {10817}. A marker based on the *Lr14a* sequence failed to amplify a product in the Tc+14b NIL {11549}.

Lr14ab. **i:** Lr14a/6*Thatcher//Lr14b/6*Thatcher Seln {319}.

LR15

Lr15 {843}. 2DS {942}, {843}. **i:** Thatcher*6/Kenya W1483 {306}. **bin:** 2DS1-0.33-0.47. **v:** Kenya W1483 {843}. **ma:** *Xgwm4562-2D* – 3.1 cM – *Lr15* – 9.3 cM – *Xgwm102-2D* {11234}; *Xwmc764-2B* – 9.4 cM – *Lr16* – 1.4 cM – *Xwmc661-2B* {11219}.
Probably allelic with *Lr2*.

LR16

Lr16 {318}. The following chromosome locations are consistant with the finding that the first location was based on the use of a Rescue monosomic series. Rescue differs from CS by a 2B-4B translocation {939}. *Lr16* is always asociated with *Sr23*. [*LrE* {31}]. 4B {312}. 2BS. **i:** Exchange/6*Thatcher {306}; RL6096 = Tc*6/T6 {307}. **v:** AC Domain {10170}; AC Foremost {10170}; Arapahoe {2101}; Brule {2101}; Ciano 79 {1373}; Etoile de Choisy {74}; Imuris 79 {1373}; McKenzie {10170}; Millenium {2101}; Papago 86 {1373}; Redland {2101}; Vista {2101}; Waxwing {11267}. **v2:** AC Barrie *Lr13* {10178}; Columbus (heterogeneous) *Lr13* {1258}; Exchange *Lr10 Lr12* {31}; Kenyon *Lr13* {300}; Francolin#1 *Lr46* {11219}; Selkirk *Lr10 Lr14a* {31}; T6 *Lr3bg* {307}; Warden *Lr10* {31}. **ma:** Distally located: *Lr16* – *Xwmc764-2*, 1, 9 and 3 cM, respectively, in crosses RL4452/AC Domain, BW278/AC Foremost and HY644/McKenzie {10189, 10170}.

A recessive gene *LrCH1539* in accession CH1539, flanked by markers *scau2BS81* (6.227 Mb, CS RefSeq 1.0) and *scau2BS47* (7.006 Mb) was located at the same position as *Lr16* {11680|.

LR17

Lr17a. [*Lr17*]. 2A {314}. 2AS {62}. **bin:** 2AS-5 {10572}. **i:** Klein Lucero/6*Prelude {318}; Klein Lucero/6*Thatcher {318}; Maria Escobar/4*Thatcher {318}. **v:** CDS Stanley {11579}; EAP 26127{314}; Jagger {10346}, {338}, {10146}; Jupateco {939}; Klein Lucero {318}; Mace {11579}; Santa Fe {10830}; TAM111 {10595}; SY Mattis {11579}; Trego {10572}. **v2:** Fuller *Lr39* {10699}; Inia 66 *Lr13 Lr14a*; Jagger *Lr37* {11328}; Lerma Rojo 64 *Lr13 Lr34* {1373}; Maria Escobar *Lr14b* {318}; Rafaela *Lr14b* {314}. **ma:** *Xbarc123-2A* – 4.8 cM – *Xgwm636-2A* – 4.0 cM – *Lr17a*{10571}; *Xgwm614-2A* – 0.7 cM – *Lr17a* – *Xwmc407-2A*{10572}; *Lr17a* – 3.7 cM – *Xbarc212-2a* {10795}.

Lr17b {1350}. [*WBR2* {615}, *LrH* {970}]. 2A {1350}. **v:** Brock {260}; Harrier {1350}; Maris Fundin {1350}; Norin 10-Brevor, 14 {1350}; Norman {1350}. **v2:** Contra *Lr13* {10345}; Hobbit Sib = Dwarf A *Lr13* {1350}; Kalasz *Lr13* {10345}; Riband *Lr13* {10345}; Sarka *Lr13* {10345}; Tarso *Lr26* {229}.

LR18

Lr18 {318}. Derived from *T. timopheevii*. Independently derived lines with *Lr18* possess a unique N band terminally located in chromosome 5BL {1614}. Low seedling responses conferred by *Lr18* are most effective at 15-18C. With increasing temperatures the response becomes less effective and ineffective at 25-27C {935}, see also, {1614}. 5BL {935} = T5BS.5BL-5G#1L {389}. **i:** Africa 43/7*Thatcher {318}; Red Egyptian PI 170925/6*Thatcher {318}. **v:** Africa 43 {318}; Red Egyptian PI 170925 {318}; Red Egyptian PI 17016-2c {318}; Sabikei 12 {935}; Timvera {935}; Timvera Derivative {935}; Certain WYR accessions {935}; FTF {1614}; Several Sabikei lines including Sabikei 12 {1614}. **v2:** Ck9803 *Lr11* {10595}; FFR 524 *Lr11* {10595}; Jamestown *Lr11* {10830}; Pioneer 2684 *Lr11* {10595}; SS520 *Lr11* {10595}.

A resistance gene, *LrTt2*, in line 842-2 was located on chromosome 5BL in a similar region to *Lr18*. The claim that *Lr18* and *LrTt2* were different was based on low seedling infection types, but the genetic backgrounds were different {10752}.

LR19

Lr19 {140}. Derived from *Th. elongatum*.
7DL = T7DS.7DL-7Ae#1L {1323}, {389}, {388}, {657}, {291}, {956} **i:** Agatha = T4 = TC + *Lr19* {1323}, {956}; Sears transfer 7D-7Ag no. 1 {10255}. **v:** Dobrynya{ 10821}; Ekada 6 {10821}; L503 {1346}; L505 {10821}; L513{1346}; Mutant 28 {598}; Samsar {108}; Sunnan {684}; Pallada {11161}; Volgouralskaya {10821}; See *Sr25*.
7AL Lines I-22 and I-23 {10255}. **v2:** Kinelskaya Niva *Lr23* {10821}; Oasis 86 *Lr13* {1373}.
7AL **tv:** This translocation was transferred to durum wheat and engineered to produce normally inherited secondary recombinants with smaller alien segments, such as R5-2-10, and tertiary recombinants such as R1 {10633}. **ma:** Located in the *Xwg420-7Ag – Xmwg2062-7Ag* interval {10255}; RAPD, SCAR and SSR markers co-inciding with, or flanking, *Lr19* in a derivative of Knott's Agatha Mutant 28 (C80.1) were reported in {10379}. **ma:** *Xbg262436 – LR19 – Xbarc76-7E – PSY-E1*n-*XBE445653* {11699}. **c:** A candidate sequence, AG15, with a 1,258 amino acid sequence and a CC-NBS-LRR structure was reported in {10575}. The chromosome with *Lr19* in Indis is probably identical to that in Agatha {1162}. 7DL = T7DS.7DL-7Ae#1-7DL {388}. **v:** Mutant 235 {681}. 7AL = T7A-7Ae#1 {330}. **v:** Sears' 7A-7Ag No.12 {330} 7BL {1163}. **v:** 88M22-149 {1163}; 4 further derivatives of 88M22-149 {0232}.
7AgL {1304} = 7Ae#1L. **su:** Agrus. **ma:** Co-seg with 8 RFLP markers {048}; *Ep-D1c* – 0.33 cM – *Lr19* {1587}; cosegregation with *Ep-D1d* {974}; Prins *et al* {1162} studied 29 deletion mutants in Indis and determined the gene order: *Sd-1 – Xpsr105-7D – Xpsr129-7D – Lr19 – Wsp-D1 – Sr25 – Y*; The following gene order for the *Thinopyrum* segment is given in {0101}; Cent – *Sd1 – Xpsr165-7D – Xpsr105-7D – Xpsr129-7D – XcslH81-1 – Xwg380-7D – Xmwg2062-7D – Lr19 – Wsp-D1 – Sr25/Y*; An STS marker closely linked and distal to *Lr19* was developed from an AFLP {0273}.
Although *Lr19* is usually associated with *Sr25*. Sears' transfer 7D-7Ag No. 11 carries neither *Lr19* nor *Sr25*. See *Lr29*.
Knott {681} obtained two mutants (28 and 235) of Agatha possessing *Lr19*, but with reduced levels of yellow pigment in the flour. Marais {890, 892} obtained mutants and recombined lines with intermediate levels of, or no, yellow pigment. It was shown that recombinant line 88M22-149 lacked yellow pigment {1163}.
Secondary translocation line I-96 derived from Sears' 7D-7Ag no.1 involved *Lr19* being located in an intercalary segment with low yellow pigment and lacking *Sd1* {10255}.
Two T7DS.7DL-7EL-7DL lines: 1-40 lacked *PSE-E1* whereas 9-80 carried it {11699}.
Lr19 in lines I-22 and I-23 retaining yellow pigment but lacking *Sd1* was transferred to durum chromosome 7BL {10255}. One of the lines with the shortest 7Ag segment, *Lr19*-I49-299, was used in a further cycle of recombination {10278}.

LR20

Lr20 {140}. 7AL {1305, 1554}. **i:** Thatcher+Lr20. **s:** CS*5/Axminster 7A {1293}. **v:** Axminster {1175}, {1305}, {348}; Birdproof {1554}; Bonus {1554}; Converse {1554}; Festival {1554}; Kenora {1554}; Kenya W744 {1554}; Maris Halberd {608}; Normandie {1554, 348}; Sappo {608}; Sicco

{310}; Thew {140, 1552}; Timmo {608}. **v2:** Norka *Lr1* {1554}; See *Pm1* (Reaction to *Blumeria graminis*) & *Sr15* (Reaction to *Puccinia graminis*) with which *Lr20* is always associated. *Lr20* in Sicco appears to differ from that in Sappo, Timmo and Maris Halberd {310}; *Lr20* in Norka (*Lr1+Lr20*) may differ from that in Thew {939}. **ma:** Complete cosegregation of several markers including *Xcdo347-7A, Xpsr121-7A, Xpsr680-7A, Xpsr687-7A, Xbzh232(Tha)-7A, Xrgc607-7A* and *Xsts638-7A* with *Pm1* and *Lr20* was reported in {323}; *Lr20 – STS638*, 7.1 cM {10263}.

LR21

Lr21 {1241}. [*Lr40* {10415, 1200}]. 1DL {1241}. 1D {650}. 1DS {448}. **i:** Thatcher*6/Tetra Canthatch/*Ae. tauschii* var. *meyeri* RL 5289 {306}. **v:** Barlow {11093}; Faller {11093}; Tetra Canthatch/*Ae. tauschii* var. *meyeri* RL 5289, RL 5406 {648}; Lovitt {10766}; McKenzie {228, 10766}; Prosper {11093}; WGRC2 = TA1649/3* Wichita {299}; WGRC7 = Wichita/TA1649//2*Wichita {299}. **v2:** AC Cora *Lr13* {713}; WGRC16 = TAM107*3/*Ae. tauschii* TA 2460 *Lr39* {10415}, {220}. **dv:** *Ae. tauschii* accessions: RL5289 = TA1599{1241}; *Ae. tauschii* TA2460 *Lr39* {10415}, {220}; TA1649 {299}; TA1691 {299}; TA2378 {299}; TA2470 {299}; TA2483 {299}; TA2495 {299}; TA2527 {299}; TA2528 {299}. **ma:** All members of the *Lr21* family carry a STS derivative of *XksuD14-1D* that has a resistance gene analogue structure {299}; *XksuD14-1D* was reported to map 1.8 cM proximal to *Lr21* in{375}; *Lr21* – 0 cM – *rgaYr10b* – 0.6 cM – *Xgdm33-1D* {360}; *Xksu-1D* is part of *Lr21* {10420}. **c:** *Lr21* was cloned and shown to have a NBS-LRR structure {10420}. *Lr21*-mediated resistance requires expression of *RAR1, SGT1* and *HSP90* {11274}.
A reconstituted effective *Lr21* allele (designated *Lr21-b*) was obtained as a rare (1/5,872) recombinant (accession TA4446) between *Lr21* pseudogenes in common wheat cultivars Fielder and Wichita {10620}. Further haplotype analyses are reported in {10766}.
A further spontaneous allele designated *Lr21-tbk* with 'several mutations in exons 2 and 3' leading to three amino acid changes was identified cv. Tobak {11762}.

LR22

Lr22a {1241}. Adult plant reaction. 2DS {1241}. **i:** Neepawa*6/RL5404, RL4495 {10467}; Thatcher*3//Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271 {306}; Thatcher*7//Tetra-Canthatch/RL5271, RL 6044 {10467}; CH Campala Lr22a {11209}. **v:** Line 98B34-T4B {10467}; Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404 {311}. **v2:** AC Minto *Lr11 Lr13* {713}. **dv:** *Ae. squarrosa* var. *strangulata* RL 5271. **ma:** *Xgwm296-2DS* – 2.0 cM – *Lr22a* {10446}; *Xgwm455-2D* – 1.5 cM – *Lr22a* – 2.9 cM – *Xgwm296-2D* {10467}; *Xgwm455-2D* **–** 0.39 cM **–** *Lr22a* – 1.1 cM **–** *Xgwm296-2D* {11209}. **c:** GenBank KY064064; NBS-LRR structure encoding an intracellular immune receptor homologous to the *Arabidopsis thaliana* RPM1 protein {11209}.

Lr22b{298}. Adult plant reaction. **v:** Canthatch {298}; Marquis {970}; Thatcher {298}.
This gene will be present in near-isogenic lines based on Thatcher.

LR23

Lr23 {948}. [*LrG* {951}]. 2BS {948}. **i:** Lee FL 310/6*Thatcher {948}. **s:** CS*7/Kenya Farmer 2B {948}; CS*6/Timstein 2B {948}. **v:** BT-Schomburhk {11601}; Cranbrook; Crim {1091}; Hope/Timstein {1091}; I 310678 {1091}; I 310685 {1091}; I 349162 {1091}; IWP94 {10569}; K 45973 {1091}; K 51070 {1091}; Rocta {1091}. **v2:** Gamenya *Lr3* {1552}; Gabo *Lr10* {1552}; Kenya Farmer *Lr10* {1552}; Lee *Lr10* {1552}; Pastor *Lr46* {10928}; Timstein *Lr10* {1552}; Brambling *Lr14a Lr34* {10563}. **tv:** Altar 84 {1058}: Gaza {11601}; Tamoroi {11601}. **ma:** Associated with *Xksu904(Per2)-2B* {90}; SSR and KASP markers were developed in {11601}.
A QTL, which is likely to correspond to *Lr23*, was identified in the Opata 85/W-7984 (ITMI) RIL mapping population. The resistance was contributed by W-7974 {0090}.

LR24

Lr24. Derived from *Thin. elongatum*.
Always present with *Sr24* {956}. See *Sr24* (Reaction to *P. graminis*). [*LrAg* {141}]. 3DL {1389, 956}. **i:** Tc+Lr24 (ex Agent). **v:** Cody {1284}; Cutter {10595}; Jagalene {10595}; McCormick {10595}; Ogallala {10595}; Osage {143}; Payne {1390, 1024}; SST 23 {1324}; SST 44 = T4R {1324}; Timpaw {1255}; Torres {128}; Wanken {1255}; Australian genotypes {340}. **v2:** Blueboy II *Lr1 Lr10* {141}; Fox *Lr10* {141}; Lockett *Lr9* {10146}; Parker 76 *Lr10* {1024, 143}; Siouxland *Lr26* {1283}. **ma:** Co-seg of *Lr24* in Agent with 8 RFLP markers; segment in Sears' 3D-3Ag#1 is shorter than in Agent {48}; Tagged with *Xpsr1203-6B* {1271}; cosegregation with RAPD marker that was converted to a SCAR {231}; Linked with SCAR marker SCS73$_{719}$ earlier thought to tag *Lr19* {10147}.
Australian white seeded cultivars with *Lr24* were recombinants derived from Sears' translocation lines 3Ag#3 and 3Ag#14.
1BL {185} = T1BL.1BS-3Ae#1L {600} **v:** Amigo {1463}, {185}, {600}; Teewon {600}. **ma:** SCAR markers were developed in {10368}. A PCR marker, Sr24#12, was confirmed across all sources of *Lr24* {10257}.
This source of *Lr24* is also not associated with red seed colour.

LR25

Lr25. Derived from *S. cereale* cv. Rosen. 4BS{389}, {271}, {270}, {380}. Revised to T4BS.4BL-5RL {543} and later to T4BS.4BL-2R#1L. **i:** Tc+Lr25 *Lr48* {10738}. **v:** Transec {273}; Transfed {269}; Always present with *Pm7*. **ma:** Cosegregation with a RAPD {1165}.
LR25 is closely linked with *LR48* {10738}.

LR26

Lr26. Derived from *S. cereale*. See also Reaction to *P. graminis, Sr31*; Reaction to *P. striiformis, Lr26.* T1BL.1RS.1R (1B). **i:** MA1 and MA2 four breakpoint double translocation lines 1RS-1BS-1RS-1BS.1BL in Pavon {84}. **v:** AGS 2000 {10595}; Derivatives of Petkus rye - see *Yr9* (Reaction to *P. striifromis*) & *Sr31* (Reaction to *P. graminis*); Bacanora 88 {1373}; Cougar {267}; Pioneer 26R61 {10595}; Rawhide (heterogeneous) {267}; GR876 {753}; Iris {75}; Sabina {75}. **v2:** Beaver *Lr13* {10687}; Cumpas 88 *Lr13* {1373}; Istra *Lr3* {76}; Siouxland *Lr24* {1283}; Solaris *Lr3* {76}; Many

wheats with *Lr26* also carry *Lr3*. Amika {heterogeneous} *Lr3* {76}; See also {310}. **tv:** Cando*2/Veery, KS91WGRC14 {381}. **ma:** Several markers tightly linked with *Lr26* were identified in {377}.
1BS/1RS recombinants 4.4 cM proximal to *Gli-B1/Glu-B3* {0084}. Hanusova *et al.* {492} identified 127 wheats with *Lr26* but only 16 of them were listed.

LR27

Lr27 {1367}. One of two complementary genes; the second gene, *Lr31*, is located in chromosome 4BS {1367}. The following wheats have both *Lr27* and *Lr31*.
Lr27 is present in wheats with *Sr2*, but is not expressed in the absence of the complementary factor {1366}. [*LrGt* {1366}, *A* {1058, 1366}]. 3BS {1367}. **s:** CS*6/Ciano 3B {1366}; CS*6/Ciano 5B {1366}; CS*6/Hope 3B {1366}. **v:** Gatcher {1366}; Ocoroni 86 {1373}. **v2:** Anhuac *Lr13 Lr17* {1361}; Cocoraque 75 *Lr13 Lr17a Lr34* {1361}; Jupateco 73S *Lr17a* {1361}; SUN 27A *Lr1 Lr2a* {1366}; Timgalen *Lr3* {heterogeneous} *Lr10*{1366}. **tv:** Benimichi C2004 {10585}; Jupare C2001 {10585}. **ma:** Positive association with *XksuG53-3B* {1058}.

LR28

Lr28 {967}. Derived from *Ae. speltoides*. 4AL {967} = T4AS.4AL-7S#2S {389}. **i:** CS 2A/2M 4/2 {967}; CS 2D/2M 3/8 {967}. **v:** Sunland {11069}; Tobak {11717}. **ma:** *Lr28* was tagged using STS primer OPJ-01$_{378}$ {1052}; A linked RAPD marker, S421$_{640}$ was converted to a TPSCAR, SCS421$_{570}$ {10236}; *Xbarc219-4A* – 2.2 cM – *Xwmc219-4A* {11069}.

LR29

Lr29 {939}. Derived from *Th. elongatum*. 7DS {939} = T7DL-7Ae#1S {389}. **i:** Sears' CS 7D/*Ag*#11 {1300, 939}; RL6080 = Tc*6/Sears' 7D/Ag#11 {316}. **ma:** Co-segregation with two RAPDs {1165}.

LR30

Lr30 {315}. Recessive {315}. [*LrT*]. 4AL {315}. **i:** RL 6049 = Thatcher*6/Terenzio {315}. **v2:** Terenzio Lr34 {315}.

LR31

Lr31 {1367}. One of two complementary genes, the second gene is *Lr27*. [*B* {1058, 1366}]. 4BL {1367}. **v:** Ocoroni 86 {1373}. **v2:** Chinese Spring *Lr12 Lr34* {1367}; See *Lr27* for list of wheats with *Lr27* +*Lr31*. **tv:** Benimichi C2004 {10585}; Jupare C2001 {10585}. **ma:** A positive association with *XksuG10-4B* {1058}.
Possible commonality with *Lr12*.

LR32

Lr32. 3D {644}. 3DS {645}. **i:** RL6086 = Tc*7/RL5713/Marquis K {10874}; BW196 = Katepwa*6/RL5713/2*Marquis K {10874}. **v:** Tetra Canthatch/*Ae. tauschii* RL5497-1, RL5713, RL5713/Marquis-K {644}. **dv:** *Ae. tauschii* RL5497-1 {644}. **ma:** *Xbcd1278-3D* – 3.6 cM – *Lr32* {48}; *Xcdo395-3D* – 6.9 cM – *Lr32*{48}; *Xbarc128-3D* – 9.1 cM – *Lr32* – *Xwmc43/Xbarc235-3D* {10874}.

LR33

Lr33 {325}. 1BL {325}. **i:** RL6057 = Tc*6/PI 58548 {325, 297, 321}. **v:** PI 268454a {297}; PI 58548 {325, 297}. **v2:** KU168-2 *Lr34* {11687}; PI 268316 *Lr2c Lr34* {297}; Others {1322}. **ma:** KASP markers flanking *Lr33* in the centromeric region were identified in {11687}.

LR34 *TraesCS7D03G0183600*

Lr34 {299, 297}. In addition to conferring seedling and adult plant resistance, *Lr34* responds in a complementary manner when combined with either *Lr33* or *LrT3* {321}. In the Thatcher background, *Lr34* is associated with increased resistance to stem rust {299}, {321}.
Although the resistance gene in the near-isogenic Thatcher line, RL6077, was considered to be *Lr34* on the basis of disease response, leaf tip necrosis and its association with resistance to stripe rust, a cross with RL6058 segregated for two genes. A translocation to another chromosome was suggested {324}. [*LrT2* {321}]. 7DS {1058}, {324}. 7D {299}. **i:** Arina + Lr34 {10648}; Lalbahudar + Lr34 {10648}; Line 897 {321}; Line 920 {321}; Selections Jupateco 73R *Lr17a Lr27* + *Lr31* and Jupateco 73S *Lr17a Lr27* + *Lr31* and Cocoraque 75 *Lr13 Lr17a Lr27* + *Lr31* and Anhuac 75 *Lr13 Lr17a Lr27* + *Lr31*, can be considered near-isogenic for the presence and absence, respectively, of *Lr34*{1361}. **v:** Ardito {10648}; Arina*3/Forno {10380}; Bezostaya {10387, 10648}; Condor {10387, 10648}; Cook {10387}; Forno {10066, 10387, 10380}; Fukuho-Komugi {10387, 10648}; Kavkaz {10648}; Lantian 12 {10682}; Libellula {10682}; Otane {10387}; Pegaso {10648}; Penjamo 62 {10648}; RL6058 = Tc*6/PI 58548 {297}; PI 268454 {297}; Strampelli {10682}; Westphal 12 {268}; Others {1322}, {1376}, {299}, {321}; See {1362}; 2174 {10888}; List of U.S. hard wheats in {10888}; Pedigree charts showing the presence of *Lr34* in various Canadian wheat classes are given in {10889}. **v2:** Anza = WW15 *Lr13* heterogeneous {10648}; Brambling *Lr14a Lr23* {10563}; BH1146 *Lr13*; Chinese Spring *Lr12 Lr31* {301, 10648}; Chris *Lr13* {10648}; Frontana *Lr13* {1374}; Glenlea *Lr1* {327}, {10648}; Jupateco R *Lr17a, Lr27* + *Lr31* {10648}; Lageadinho *LrT3* {321}; Laura *Lr1 Lr10* {712}; Mentana *Lr3b* {10493, 10648}; Parula *Lr13 Lr46* {1374}; PI 58548 *Lr33* {297}, {321}; RL 6059 = Tc*6/Terenzio *Lr33* {297}; RL 6069 = Tc*6/Lageadinho *LrT3* {321}; RL6070 = Tc*5/PI 321999 *LrT3* {321}; RL6050 = Tc*6/Terenzio *LrT3* {321}; Saar *Lr46* {10481}; Sturdy *Lr12 Lr13* {301}; Terenzio *Lr3 Lr30 LrT3* {321}; Thirteen Thatcher lines with 2-gene combinations{434}. **ma:** Complete linkage with *Ltn* (leaf tip necrosis) {1361}, *Yr18* (Reaction to *P. striiformis*) {1362, 937} and *Bdv1* (Reaction to barley yellow dwarf virus) and *Pm38* (Reaction to *B. graminis*) {0090}; association with *Xwg834-7D* {268}; *Xgwm120-7D* – 0.9 cM – *Lr34* – 2.7 cM – *Xgwm295-7D* {10259}; *Lr34* .....*XsfrBF473324* – 0.5 cM – *Xsfr.cdo475-7D* – 0.7 cM – *Xswm10-7D* {10387}; A 150 bp allele (b) of STS *csLV34*, derived from wEST *BQ788742* was identified in most wheats with *Lr34; CsLV34a* – 0.4 cM – *Lr34* {10387}; STS marker csLV34 was used to confirm or postulate the presence of *Lr34* in Australian cultivars {10493} and Hungarian materials {10701}; Further markers for *Lr34* and various marker-positive haplotypes that lack leaf rust resistance are described in {10888, 10887}; A gene based (3 bp indel in in exon 11), dominant HRM

marker is reported in {11669}. **c:** *Lr34* spans 11,805 bp and produces a 1,401 aa protein that belongs to the drug resistance subfamily of ABC reporters {10648}; GenBank FJ436983 {10648}; Further confirmation of the ABC transporter is provided in {10887}.
A QTL, which is likely to correspond to *Lr34*, was identified in the Opata 85/W-7984 (ITMI) RI mapping population. The resistance was contributed by Opata 85 {0090}.
On the basis of leaf tip necrosis and lack of segregation in a diallel, cv. Saar, Simogh, Homa, Parastoo and Cocnoos were considered to have *Lr34*, but each also possessed 2 or 3 additional adult plant resistance factors {10110}. This gene is identical to *Yr18, Pm38* and *Ltn* and confers stem rust resistance in some genetic backgrounds.
Lr34 conferred seedling resistance to leaf rust when transformed into durum wheat {11314}.
Diagnostic markers based on the gene sequence are reported in {10713}; AC Domain, Cappelle Desprez, H-45, Jagger, Newton, RL 6077, and H-45 do not carry *Lr34* {10713}.

LR35

Lr35 {651}. Derived from *Ae. speltoides*{651}. Adult plant resistance {651}. 2B {651} = 2BL-2SL-2SS#2.2SL#2 {11037}. **i:** RL6082 = Thatcher*7/RL5711 {11037}. **v:** RL5711 {651}. **ma:** A. SCAR marker was developed {9923}.
Complete cosegregation between *Lr35* and RFLP loci *Xwg996-2B*, *Xpsr540-2B* and *Xbcd260-2B* was observed. The RFLP probe BCD260 was converted to a CAPS and STS marker {0045}. Lines with shortened alien segments are reported in {10741}.
Lines with shortened alien segments bearing *Lr35* are described in {10741}.

LR36

Lr36. Derived from *Ae. speltoides*. 6BS {292}. **v:** CDC Bounty {11253}; Line 2-9-2 {292}; Line E84018 {292}. **al:** *Ae. speltoides* Popn. 2 {292}. **ma:** *Xcfd13-6* – 5.2 cM – *Lr36* – 3.8 cM – *Xgwm88-6B* {11588}. Since *Lr36* is located in an alien segment these markers likely map the boundaries.

LR37

Lr37 {62}. Derived from *Ae. ventricosa*. Recessive {667}.
Lr37 can be detected in seedlings at low temperatures (17°C) and is effective in adult plants under field conditions. See also *Sr38* (Reaction to *P. graminis*) and *Yr17* (Reaction to *P. striiformis*) 2AS {62}. $6M^v$ = 2MS-6MS.6ML or 2MS-6ML.6MS {0009}.
VPM1 and derivatives: 2AS {62} = 2AL.2AS-$2N^v$S{0213} **i:** RL 6081 = Tc^*/VPM1{939}; RL6081 = Tc^*8/VPM1 {316}; Various NILs listed in {0213}. **v:** Hyak {21}; Madsen {20}; Rendezvous {62}; VPM1 {62}; VPM1 derivatives {939}; see also Reaction to *P. striiformis tritici Yr17*. Moisson derivatives: *Lr* {113}. 2AS = 2AL.2AS-$2N^v$S {113}. **ad:** Moisson + $6N^v$ = $6N^v$S.$6N^v$L-$2N^v$S or $6N^v$L.$6N^v$S-$2N^v$S {0009}. **v:** Mx12 {0213}; Mx22 {0213}. **ma:** (relevant to both groups of derivatives) PCR primers designed from marker *csVrga1D3* {0183} producing a 383 bp product allows detection of the $2N^v$S segment {0213}; see also: See also *Sr38* (Reaction to *P. graminis*) and *Yr17* (Reaction to *P. striiformis*.

A resistance gene analog containing an NBS-LRR R gene sequence was isolated from the *Ae. ventricosa* segment carrying *Lr37* {0183}.
The 2NS translocated segment carrying *Lr37* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH-9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}. SCAR markers SC-372 and SC-385 were developed in {10796}.

LR38

Lr38 {392}. Derived from *Th. Intermedium*.
1DL = T1DS.1DL-7Ai#2L {389}, {390}. **v:** T25 {390}.
2AL = 2AS.2AL-7Ai#2L {389}, {392}. **v:** W49 {392} = T33 {390}.
3DS = 3DL.3DS-7Ai#2L{389}, {390}. **v:** T4 {390}.
5AS = 5AL.5AS-7Ai#2L{389}, {390}. **v** T24 {390}.
6DL = 6DS.6DL-7Ai#2L{389}, {390}. **i:** RL6097 = Thatcher*6/T7 {307}. **v:** T7{390}, {307}; 7Ai#2(7D) {389}, {392}; 7Ai#2(7A) {390}. **su:** W52 {389}, {390}.

LR39

Lr39 {1200, 2100}. Derived from *Ae. tauschii* {02100}. *Lr41* {215}. *LrT* {11207}. 2DS{10731, 02100}. **i:** TC*4 / Overley, GSTR 447 {11498}. **v:** Amour {11086}; Bullet {11086}; Fuller {10595}; KS90WGRC10 = TAM107*3/*Ae. tauschii* TA2460 {220}; Overley {10595, 10699}; Postrack {10830}; PostRock {11093}; PBW114 /*Ae. tauschii* PAU14195 // 4*WH542 backcross selections {11207}; TAM112 {11086; TA4186 = TA1675*2/Wichita {02100}; Thunderbolt{02100}; Winterhawk {11086}. **v2:** Fuller *Lr17a* {10699}; WGRC16=TAM107*3/*Ae. tauschii* TA 2460 {220}. **dv:** *Ae. tauschi* PAU14195 {11207}; *Ae. tauschii* TA 1675 {2100}; *Ae. tauschii* TA2460 *Lr21* {10415, 220}; *Lr21*{10415,220}. **ma:** 10.7 cM distal to *Xgwm210-2D*{02100}; Four markers, *Xbarc124-2D, Xgwm210-2D, Xgdm35-2D* and *Xcfd36-2D* were closely linked with the terminally located *Lr39* (formerly *Lr41*), but the gene order was inconsistent and no specific allele was associated with it {10731}; *Xcau96-2D* – 1.6 cM – *LrT* (*Lr39*) – 0.6 cM – *Xbarc124-2D* – 0.3 cM – *Xte6-2D* – *IwT* – 4.1 cM – *Xgdm35-2D* {11207}. **c:** Predicted to encode a wheat tandom kinase (WTK) – two amino acid changes relative to *T. tauschii* AL8/78 {11685}.

LR40 **Deleted,** see *LR21*.

Lr40 {10415, 1200}.

LR41 **Deleted**, see *LR39*.

Lr41 {215}.

LR42. *AET1Gv20040300*.

Lr42 {218}. 1D {218}. **i:** TC*4 / Century, GSTR 448 {11498}; Tc + Lr42 PI 701841 {J. Kolmer pers. com Feb 2023}. **v:** AR93005 {10840}; Fannin {10595}; KS93U50 {M22059}. **v2:** KS91WGRC11

Lr24 {10840}, {218}; Quaiu 3 *Lr46* {10943}. **dv:** TA2450 {218}. **v:** KS93U50 {11599}. **ma:** *Lr42* – 0.8 cM – *Xwmc432-1D* – 1.6 cM – *Xcfd-D1* {10840}. Flanked by *pC43* and pC50 at 8.65 Mb and 8.77 Mb, respectively (Aet 4.0) {11599}. **c:** CC-NB-ARC protein with 920 amono acids{11599}. Marker *Pc50*, 46 kb from *LR42* was recommended for MAS although additional gene-based markers were identified {11599}.
According to {11599} *Lr42* was present in >1,000 CIMMYT lines.

***lr42*.** **c:** The *lr42* allele has fewer LRR repeats {11599}.

LR43 **Deleted,** wrongly based on a gene combination.

Lr43 {218}.

LR44

Lr44 {322}. 1B {322}. **i:** RL6147 = Thatcher*6/*T. spelta* 7831 {322}. **v:** *T. spelta* 7831 {322}; *T. spelta* 7839 {322}.

LR45

Lr45 {958}. Derived from *Secale cereale*. 2A = T2AS-2R#3S.2R#3L {389}, {958}. **i:** RL6144 = Thatcher*7/ST-1 {958}. **v:** ST-1 {958}; Various Australian backcross derivatives {958}.

LR46

Lr46 {1364}. Completely linked with *Yr29* {0119}. Adult plant resistance. 1B{1346}. 1BL{0119}. **s:** Lalbahadur(Pavon 1B) *Lr1* {1364}; Lalbahadur(Parula 1B) {10281}. **v:** Attila {10281}; Kundan {11248}; Siete Cerros {10817}. **v2:** CI 13227 *Lr3c*; Frontana *Lr13 Lr14b Lr34 Lr68* {10817}; Pavon F76 *Lr1 Lr10 Lr13* {1364, 119}; Parula *Lr13 Lr34* {10281}; Parula *Lr3b Lr13 Lr14b Lr34 Lr68* {10817}; Quaiu 3 *Lr42* {10943}; Saar *Lr34* {10481}. **tv:** Present in the following tetraploid wheats in combination with other genes/QTL: Bairds {11600}; Dunkler {M23032}; Heller#1 {M23032}. **ma:** An RFLP marker associated with *Lr46* with a recombination value of about 10% was identified in{0119}; *Xwmc44-1B* – 1.4 cM – *Xbac24prot* – 9.5 cM – *Lr46* – 2.9 cM – *Xbac17R.......Xgwm140-1B* {10281}; *Xwmc44-1B* – 3.6 cM – *Lr46* 2.1 cM – *XtG818/Xbac17R......Xgwm140-1B* {10281}; *XSTS1BL2* – 2.2 cM – *Lr46/XSTS1BL9* – 2.2 cM – *XSTS1BL17* {10326}. Associated with *Ltn2* and *Yr29*.

LR47

Lr47 {9901}. Derived from *Ae. speltoides* {9901}.
7AS = Ti7AS-7S#1S-7AS.7AL {9901}. **v:** Bionta 2004 {10737}. Pavon derivative PI 603918 {9901}. Backsross derivatives based on Express, Kern, RS15, Yecora Rojo and UC1041 {0126, 11721}. Recombinants with reduced 7S#1 segments {11721}. **c:** *Lr47* was identified as a CNL, which was also present *Ae. speltoides* accessions T2140002, Y162 and Y397 {11721}.
7A = T7AS-7S#1S.7S#1L {389}. **v:** CI 17882, CI 17884, CI 17885, KS 90H450 {9901}.
7AL = Ti7AS.7AL-7S#1L-7AL. Pavon derivative PI 603919 {9901}. **ma:** *Lr47* was located in the

distal one-third of 7AS, 2-10 cM from the centromere and within a 20-30 cM segment {9901}. Complete linkage with several RFLP markers {9901} and PCR specific markers {0126}.
KASP markers for detection of *Lr47* are reported in {11544}.

LR48

Lr48 {0085}. Adult plant resistance {0085}. Recessive {0085}. 2BS {10842, 329}. 4BS {10738}. **i:** CSP44 / 5*Lal Bahadur AUS91421 {0329}. **v2:** CSP44 *Lr34*{0085}; Dove *Lr34*{0329}. **ma:** *Xgwm429b-2B* – 6.1 cM – *Lr48* – 7.3 cM – *Xbarc7-2B* {329}; RAPD markers flanking *Lr48* at 2.7 and 8.6 cM are reported in {10738}; *Xwmc175-2B* – 10.3 cM – *Lr48* – 2.5 cM – *Xwmc332-2B* {10842}; Centromere – 27.5 cM – *Lr48* (est.) {10842}; *Xgwm429b-2B* – 4.2 cM – *Sun563/Sun497* – 0.6 cM – *IWB31002/IWB39834/IWB3432/IWB72894/Lr48* – 0.3 cM – *IWB70147* – 2.0 cM – *Xbarc67-2B* {11112}; *Xsun563/Xsun497* – 0.6 cM – 5 SNP markers/*Lr48* – 0.3 cM – *IWB70147* – 2.0 cM – *XBARC0-7-2B* – 9.4 cM – *Lr13* {11172}.
Lr48 is closely linked with *Lr25* {10738}. Based on haplotype analysis *Lr48* was postulated in 13 Australian Condor relatives {11112}. The suggestion that this gene is present in 13 Australian varieties carrying *Lr48* markers and hence *Lr48* {11172} needs verification.

LR49

Lr49 {0085}. Adult plant resistance {0085}. 2AS {0329}. 4BL{0329}. **i:** VL404 / 5*Lal Bahadur *Lr34* {0329}. **v2:** Tonichi *Lr34* {0329}; VL404 *Lr34* {0085}. **ma:** *Xbarc163-4B* – 8.1 cM – *Lr49* – 10.1 cM – *Xwmc349-4B* {0329}; *Xgwm251-4B* – 8.6 cM – *XsunKASP_21* – 0.4 cM – *Lr49* – 0.6 cM – *XsunKASP_24* – 8.1 cM – *Xwmc349-4B* {11484}.

LR50

Lr50 {0221}. Based on linkage with SSR markers. 2BL {0221}. **v:** KS96WGRC36 = TAM*3/TA870 {0221}; U2657 = Karl 92*4/TA674 {0221}; U3067 = TAM107*4/TA874 {0221}; U3193 = TAM107*4/TA874 {0221}. **tv:** *T. armeniacum* TA870 {0221}; *T. armeniacum* TA145; TA874 {0221}; TA870 {0221}; TA895 {0221}. **ma:** Linked with *Xgwm382-2B* (6.7 cM) and *Xgdm87-2B* (9.4 cM) {0221}.

LR51

Lr51 {308}. 1BL {0308}. **i:** Express*7/T1 {0308}; Koln*7/T1 {308}; UC1037*7/T2 {0308}. **v:** Neepawa*6/*Ae. speltoides* F-7, selections 3 and 12 {306}; Interstitial translocations T1AS.1AL-1S#F7-12L-1AL {0308} = T1; T1BS.1BL-1S#F7L-1BL {0306}. **al:** *Ae. speltoides* F-7 selections 3 and 12 {0306}. **ma:** Linked with RFLP markers *Xmwg710-1B* and *Xaga7-1B* {0308}; A CAPS marker was developed from *XAga7-1B* {0308}.

LR52

Lr52 {10035}. [*LrW* {309}]. 5BS {10035}. **bin:** 5BS6-0.81-1.00. **v:** AUS28183 = V336 {10679}; AUS18187 {10679}; Tc-LrW = RL6107 {10035}. **v2:** V618 *Lr33* {309}; V336 *Lr33 LrB* {309}. **ma:**

Xgwm234-5B – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xcfb309-5B* – *Xsun480/Xmag705/Xfcp552-5B* – 0.4 cM – *Yr47* – 4.3 cM –*icg16c008/Xgwm234-5B* {11200}; *Xsun180* – 0.4 cM – *Lr52* – 0.2 cM – *Yr47* – 1.4 cM – *Xgwm234-5B* {11200}.

LR53

Lr53{10203}. [*LrS8* {10204}]. 6BS {10203}; According to {11778} *Lr53* originated from *Ae. longissima* or *Ae. sharonensis*; 6^{S}S.6^{S}L-6BL {117787}. **v:** 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS {10204}. Yangmai 21 derivative C580 with a reduced alien segment (<6.03 MB). **tv:** *T. dicoccoides* 479 {10204}. **ma:** *Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B* {10780}. *Lr53* was genetically independent of *Lr36* {10780}.
Genetically associated with *Yr35*.

LR54

Lr54 {10139}. Derived from *Ae. kotschyi*. 2DL {10139}. **v:** Line S14 {10139}. **ad:** Line 8078 {10139}. **al:** *Ae. kotschyi* 617 {10139}.

LR55

Lr55 {10180}. Derived from *Elymus trachycaulis* {10180}. 1B (1BL.1H^{t}S {10180}. **ad:** CS + 1H^{t} {10180}. **v:** KS04WGRC45 = Heyne*3/TA5586.

LR56

Lr56 {10224}. [*LrS12* {10204}]. 6A (6AL-6S^{sh}L.6S^{sh}S) {10224}. **v:** Line 0352 = *Ae. sharonensis*-174/9*CS//3*W84-17/3/CS/4/W84-17 {10224}; Recombinants with shorter segments - 07M4-39, 07M4-157 and 07M4-175 - are reported in {10691}. **al:** *Ae. sharonensis*-174 {10224}.

LR57

Lr57 {10328}. Derived from *Ae. geniculata*. 5DS (5DL.5DS-T5MS^{G} {10328}. **v:** TA5601 {11553}; TA5602 {10328}; TA5603 {10328}; Since TA5602 and TA5603 are fourth backcross selections to WL711, they likely also carry *Lr13*. **al:** *Ae. geniculata* (=*ovata*) (U^{S}U^{S}M^{G}M^{G} TA10437) {10328}. **ma:** Completely linked with distinctive alleles of *Gsp, Xfbb276* and *Xbcd873* {10328}; Completely linked with *Yr40* {10328}; CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.
Line TA5601 carries an estimated 5% of 5M^{g}; and TA5602, 20% {11553}. Genetic analysis of the segment in TA5602 indicated terminal replacement of 9.4 Mb in chr 5D and that *Lr57* is 12.4 cM distal to *Yr40* {11553}.

LR58

Lr58 {10375}. Derived from *Ae. triuncialis* = T2BS.2BL-2^{t}L(0.95). 2BL {10375}. **v:** TA5605 = WL711*4/*Ae. triuncialis* TA10438 *Lr13* {10375}. **al:** *Ae. triuncialis* TA10438 {10375}. **ma:** TA5605 possesses *Ae. triuncialis* alleles of RFLP markers *XksuH16, XksuF11* and *Xbg123* and SSR marker

Xcfd50 in the terminal region of chromosome 2BL {10375}; A codominant STS marker *Xncw-Lr58-1* was based on the sequence of *XksuH16* {10819}.
Identical in sequence to *Lr9* {11630}. The differing chromosome location was attributed to radiation treatment {11630}.

LR59

Lr59 {10399}. Derived from *Ae. triuncialis*. 1A, probably 1AS alien centric fusion {10399}. **v:** Line 0306 {10399} = *Ae. peregrina*-680/2*CS//5*W84-17 {10399}. **al:** *Ae. peregrina* (UUSS, 2n=28) 680 {10399}.
Problems in recovering balanced recombinants are reported in {10762}.
Further study of this translocation (Lr59-Full) identified a 1AS.1L^{P}-6S^{P}-6BS structure. Another round of recombination identified the following types: 1AS.1L^{P}-1AL; 1AS.1L^{P}-6S^{P}-6BS; and 1AS.1AL-1L^{P}-6S^{P}-6BS (Line Lr59-151 had the shortest alien segment). Recombinants with 6BS retained the wheat *GLI-B2* locus {11499}.

LR60

Lr60 {10400}. [*LrW2* {0305}]. 1DS {10400}. **v:** RL6172 {0305} = Thatcher*3/V860. **ma:** *Lr60* – 8.4 cM – *Xbarc149-1D/Lr21*{10400}; *Lr60* – 13 cM – *Lr21* {10400}.

LR61

Lr61 {10485}. [*LrAW2* {11223}]. 6BS {10485}. **tv:** AUS 26579 {11224}; AUS 26582 {11224}; Guayacan 2 {10485}; Guayacan INIA {10485}; PI 244061 {11280}. **ma:** *Lr61* – 2.2 cM – *P81/M70*$_{269}$/P87/M75$_{131}$ – 4.6 cM – *P87/M76*$_{149}$ – 21.7 cM – *Xwmc487-6B* {10485}; *sun682* – 0.7 cM – *Lr61/sun683/sun684* – 0.2 cM – *sunKASP_60* {11223}; *sun682* – 0.6 cM – *Lr61/sun684* – 0.6 cm – *sunKASP_59* {11223}.
The designation *LrAW2* was also used for *Lr82*.

LR62

Lr62 {10537}. Derived from *Ae. neglecta* 6A = 6AL-6^{Aen}L.6^{Aen}S {10537}. **v:** Line 03M119-71A {10537}. **al:** *Ae. neglecta* 155 {10537}.
Associated with *Yr42* {10537}.

LR63

Lr63 {10875}. Derived from *T. monococcum* 3AS {10875}. **i:** RL6137 = Thatcher*6/TMR5-J14-12-24 {10646, 10875}. **v:** TMR5-J14-12-24{10646}. **dv:** *T. monococcum* {10646}. **ma:** *Xbarc321/Xbarc57-3A* – 2.9 cM – *Lr63* {10875}.

LR64

Lr64 {10550}. 6AL {10550}. **i:** RL 6149 = Thatcher*6/*T. dicoccoides* 8404 *LrX* {10550}. **v:** Tc/RL6149-RIL13, GSTR 451{11399, 11498}. **tv:** *T. dicoccoides* 8404 {10550}. **ma:** *Xbarc104-6A* – 13.9 cM – *Lr64* – 21.9 cM – *Xgwm427-6A* {10550}; *K-IWB38521* – 1.0 cM – *Lr64/K-IWB59855* – 2.9 cM – *K-IWB72197* – 10 cM – *K-IWB73609* {11399}.
The second recessive gene (*LrX*) in RL6149 was located in chromosome 1DS: *K-IWB577* – 11.2 cM – *LrX/IWB38437* {11399}.

LR65

Lr65 {10848}. [*LrAlt* {10739}]. 2AS {10739, 10848}. **v:** Selection ARK 0; {10848}. **v2:** *T. spelta* Altgold Rotkorn *Lr71* {10739, 10848}. **ma:** *Lr65* – 1.8 cM – *Xbarc212-2A/Xwmc382-2A* – 2 cM – *Xgwm636*{10739}; *XE41M57-165* – 3 cM – *Lr65* – 2 cM – *Xbarc124/Xbarc222/Xgwm614-2A* {10848}; *LR65* – 0.5 cM – *Alt-64* – 0.05 cM – *Alt-21* – 1.7 cM – *Xbarc212-2A* {11536}; *AltID-11* – 0.7 cM – *Lr65* – 0.02 cM – *Alt-64* – 1.1 cM – *Alt21* {11536}. *TraesCS2A02G001500* was predicted as the candidate position for *LR65* {11536}. *LR65* was estimated to be about 10 cM from *LR17* {10848}.
Some plants of Altgold Rotkorn possess *Lr71* conferring IT 12C {10848}.

LR66

Lr66 {10591}. *LrS13* {10592}. 3A {10591}. 3A = 3A-3S^{S}. **v:** Line 07M127-3 = *Ae. speltoides* / 5*CS // 2*CSph1b mutant /3/2* W84-17/4/CSN3AT3B {10591}. **al:** *Ae. speltoides* Accession 691{10591}. **ma:** Most user-friendly marker, SCAR S15-t3 {10591}.

LR67

Lr67 {10675}. Adult plant resistance. 4DL {10675}. **bin:** C-0.53 {10675}; Distal to 0.56 {10678}. **i:** RL6077 = Thatcher*6/PI 250413 {10675}. **v:** Chapingo 48 {11070}; PI 250413 {10676}; Yaqui 53 {11070}. **v2** NP876 *Lr46* {11441}; Sujata *Lr46* {11440, 11442}. **ma:** *Xcfd71-4D* – 1.5 cM – *Lr67* {10675}; Pleiotrophic with *Yr46*; Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of *Lr67/Yr46* {10678}; *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}; GenBank: coding sequence KR604817.2, 1,545 bp; protein sequence ALL26331.2, 514 amino acids. *Lr67* was predicted in 51 accessions mainly collected in the Indian subcontinent {11448} using the gene-specific marker *SNP1-TM4* {11070}.
Lr67 is pleiotropic or closely linked with *Sr55*, *Yr46*, *Pm46* and *Ltn3*.

LR68

Lr68 {10817}. Adult plant resistance. 7BL {10817}. **v:** Arula 1 CIMMYT GID 1847450 {10817}; Arula 2 CIMMYT GID 1847422 {10817}. **v2:** Arula 1 *Lr14b* CIMMYT GID 1847450 {10817}; Arula 2 *Lr14b* CIMMYT GID 1847422 {10817}; Frontana *Lr13 Lr14b Lr34 Lr46* {10817}; Parula *Lr3b Lr13 Lr14b Lr34 Lr46* {10817}; Rayon F89 *Lr14b* {10817}; Sujata *Lr46 Lr67* {11442}; Weebill *Lr14b* {10817}. **ma:** Close linkage with several markers in chromosome arm 7BL and *Lr14b* in the Apav x

Arula population. Flanking markers are *Xpsy1-1* and *Xgwm146-7BL* at 0.4 and 0.6 cM. Gamma-irradiation induced deletion stocks of Arula 1 that lack *LrP* but have *Lr14b* were identified showing that the two genes are located at different closely linked loci {10817}; *Xwmc232-2B* – 0.2 cM – *Xcfa2257-2B* – 1.1 cM – Cs7BLNLRR – 0.3 cM – *Psy1-1* – 0.5 cM – *Lr68* – 0.6 cM – *Xgwm146-2B* {10817}; Gamma-irradiation induced deletion stocks of Arula 1 lacked *Lr68* but had *Lr14b* showing that the two genes are located at different closely linked loci {10817}.

LR69

Lr69 {10903}. 3DL {10903}. **v:** Toropi-6.3 {10903}.

LR70

Lr70 {10904}. 5DS {10904}. **v:** Yet to be named selection of cross or backcross to Tc {10904}. **v2:** KU3198 *Lrk1* {10904}. **ma:** *Lr70* – 5.6 cM – *Xbarc130-5D* – 1.7 cM – *Xwmc233-5D* {10904}.
Lrk1 is possibly *Lr52* {10904}.

LR71

Lr71 {10911}. [*LrAK12c* {10910}]. 1B centromere region not resolved {10911}. **bin:** Markers flanking *Lr71* mapped to 1BS10-0.5-cent and 1BL6-cent-0.32. **v:** LrARK12c = *T. spelta* Altgold Rotkorn selection {10910}; Common wheat reference line under increase {10911}. **v2:** *T. spelta* Altgold Rotkorn (heterogeneous) *Lr65* {10911, 10910}. **ma:** *Xgwm11-1B* – 3.3 cM – *Xgwm18-1B* – 1.0 cM – *Lr71* – 1.3 cM – *Xbarc187-1B* – 0.5 cM – *Xbarc137-1B* {10911}.

LR72

Lr72 {10947}. 7BS {10947}. **tv:** Altar C84 GID 30374 {10947}; Atil C2000 GID 6719128. **tv2:** Storlom *Lr3a* {10947}; Llareta INIA *Lr14a*{10947}; Jupare *Lr27* + *Lr31* {10947}. **ma:** *Lr72* – 5.5 cM – *Xwmc606-7B* {10947}.

LR73

Lr73 {10969}. 2BS {10969}. **v:** Morocco {10969}; Several Australian cultivars {10969}. **v2:** Federation *LR10* {10969}; **ma:** *wPt8760* – 4 cM – *Lr73* – 1.4 cM – *wPt8235* {10969}.

LR74

Lr74 {11031}. Adult plant resistance 3BS {11031}. **bin:** 3BS8-0.78-0.87. **v:** AGG91583WHEA=BT-Schomburgk Selection {11031}; Spark {11031}. **ma:** *Xcfb5006-3B* – 1.9 cM – *Lr74* – 2.2 cM – *BS00009992* – 2.7 cM – *Xgwm533-3B* {11031}.
Tc*3 / Caldwell population: a gene for adult plant resistance derived from Caldwell was identified with closest marker *Xcfb5006-3B*; the Tc*2 / Caldwell 24-1 parent shared the same T allele at KASP marker *IWB44132* as Spark and BT-Schomburgk Selection {11281}.

LR75

Lr75 {11053}. Adult plant resistance. [*Qlr.sfr-1BS* {10066}]. 1BS {10066, 11053}. **bin:** 1BS10-0.5-1.00. **v:** ArinaLr75, Arina*2//Forno/Arina#F7NIL85 {11053}; C14.20 {11053}. **v2:** Forno *Lr14a Lr34* {11053}. **ma:** *Xgwm604-1B 1.6* – cM – *Lr75* – 2.70 cM – *swm271* – 0.14 cM – *Xgwm11-1B/Xgwm18-1B/swm294/swm278/swm275* {11053}.

LR76

Lr76 {11055}. Derived from *Ae. umbellulata*. [*LrUmb* {11055}]. 5DS {11055}. **v:** IL 393-4 {11055}; *T. durum* cV. WH890/ *Ae. umbellulata* Pau 3732 // CS Ph^I/3/2*WL711, C14.21 {11055}. **al:** *Ae. umbellulata* Pau 3732 {11055}. **ma:** *Lr76* – 7.6 cM – *Xgwm190-5D* {11055}. *Lr76* behaves as an allele of *Lr57* derived from *Ae. geniculata*. The low infection types are also different. A co-segregating 450 bp *Lr57-Yr40*-CAPS16 marker was present in IL 393-4, but not in many Australian wheat cultivars {11055}. The introgression carrying the *Ae. umbellulata* segment replacing terminal Chr. 5DS was 9.47 Mb with the break point between *TraesCS5D02G1600* and *TraesCS5G02G20010* {11552}. Independent mutations indicated that *Lr76* and *Yr70* were different genes {11552}.

LR77

Lr77 {11164}. Adult plant resistance. 3BL {11164}. **v:** Tc*2 / Santa Fe 8-1C.9 {11164}; Tc*2 / Toropi GSTR 449 {11164} **v2:** Duster *Lr3a Lr11 Lr34* PI 639233 {11164}; Santa Fe *Lr3a Lr37* PI 641772 {11164}. **ma:** *IWB2531* – 3.5 cM – *IWB32805* – 3.5 cM – *Lr77/IWB10344* – 0.9 cM – IWB73555 – 5.3 cM – IWB12260 {11164}.

LR78

Lr78 {11212}. Adult plant resistance. [*QLr.cdl.5D* {11212}]. 5DS {11212}. **bin:** According to {10125} *Xbarc130* is in bin 5DS2-0.78-1.00 and *Xcfd189* is in bin 5DS1-C-0.63. **v:** Tc *2 / Santa Fe GSTR 450 {11498}. Tc*3 / Toropi 4A212A {11212}. **v2:** Toropi PI 344200 {11212}. **ma:** *Xcfd189-5D* – 13.2 cM – *IWA2689* – 2.2 cM – *Lr78* – 8.0 cM – *Xcfa2104-5D* {11212}. }.

A second selection Tc*2 / 3A12A crossed with Tc segregated for multiple QTL in chromosome arms 1BL (possibly *LR46*), 3BS and 4BS {11212}.

LR79

Lr79 {11224}. [*LrAW3* {11224}]. 3BL {11224}. **bin:** 3BL-0.63-0.90. **tv:** 242/Bansi#149, C18.15 {11224}. **tv2:** AUS26582 *Lr61* {11223, 11224}. **ma:** *KASP_31457* – 8.1 cM – *sun770* – 2.9 cM – *Lr79* – 1.8 cM – *sun786* {11224}.

Lr79 conferred resistance to Australian common wheat *Pt* races, but not to durum-specific Ethiopian and Californian races {11224}.

LR80

Lr80 {11464}. [*LrH2* {11464}]. 2DS {11464}. **v:** Hango-2, FLW6-Selection AGG95499WHEA {11464}. **ma:** *Xgdm35-2D* – 7.5 cM – *Xcau96-2D* – 0.4 cM – *Lr80* – 0.2 cM – *Xbarc124-2D* – 13.2 cM – *Xgwm296-2D* {11464}. *Xcau96-2D* – 4.0 cM – *KASP_17425* – 0.2 cM – *Lr80* – 0.4 cM – *KASP_17148* – 1.0 cM – *Xbarc124-2D* {11464}.

LR81

Lr81 {11583}. *Lr470121* {11583}. 2AS {11583}. **bin:** 2AS-0.78-1.00. **v:** RIL 92 PI 700925 {11583}. **v2:** PI 470121 *Lr34* {11583}. **ma:** *Xwmc827-2A* – 9.4 cM – *Xstars-KASP320* – 0.5 cM – *LR81* – 0.2 cM – *Xstars-KASP323* – 5.3 cM – *Xwmc296-2A* {11583}.

LR82

Lr82 {11586}. *LrAW2* {11586}. Recessive. 2BL {11586}. **v:** Aus27352 {11586}. **ma:** *KASP_22131* – 0.8 cM – *Lr82* – 1.2 cM – *KASP_11333* {11586}.
The designation *LrAW2* was also used for *Lr61*.

LR83

Lr83 {11638}. *LrX* {11399}. Recessive. 1DS {11399; 11638}. **v:** PI 701502 {11638}. **v2:** RL6149 *Lr60* {11399; 11638}. **ma:** *K-IWB38437* – 1 cM – *LR83* – 8.6 cM – 1D_9037237 – 4.7 cM – *K-IWB577* {11638}. *LR83/IWB38437* – 11.2 cM – *K-IWB577* {11399}. Locus order: *LR83* – *LR60* – *LR42* – *LR21* {11638}.

LR84. *TRITD6Bv1G225630* (Svevo).

Lr84 {11640}. *QLr.cim-6BL*) {11600}; *QLr.hzau-6BL* {11640}; *TtRPM1-630* {11640}. Adult plant resistance. 6BL {11600, 11639}. **tv:** Atred#2+6BL {11640}; Atred#2 / Bairds RIL 397 GID 7013103 {11600, 11640}. **tv2:** Bairds {M11600, 11640}; Dunkler {11639, 11640}; Heller#1 {11639, 11640}; Planeta {11640}. **ma:** *IWB8763* – *LRXX* – *IWB10767* (0.9 cM. 131.6 Kb) {11640}. **c:** NBL-LRR structure annotated as an *RPM1*-like gene {11640}.

LR85

Lr85 {11712}. 6B (6B-6S^{sh}) {11683, 11684, 11712}. **v:** Line 6B-RY-32-3-14 {11683} = Line 42 {11684} = D42 {11712} = **Genebank accession number to be advised**. **al:** *Ae. longissima* AEG-6782-2 {11712}; *Ae. sharonensis* AEG-548-4 {11683; 11712}. **c:** The same NLR gene with a distinctive coiled-coil (CC) domain was cloned from each alien diploid accession {11712}.
Development of lines with shortened 6S^{sh} segments is described in {11684}.
All 16 EMS-induced mutants in Line D42 were susceptible to both leaf rust and stripe rust {11712}.

3.22.2 Temporary designations

LrAc {11613}. Adult plant resistance. 5DS {11613}. **v:** *Ae. caudata* derivative PAU16060 {11613}. **al:** *Ae. caudata* PAU3556 {11613}.

LrAp {11698}. 6BL = 6BS.6BL-$6U^P$ {11698}. **v:** WL711 derivative ILpau16061 {11698}. **al:** *Ae peregrina* pau3519 {11698}.

LrBi16 {11042}. 7BL {11042}. **bin:** 7BL-10. **v:** Bimai 16 {11042}. **ma:** *Zcfa2257-7B* – 2.8 cM – *LrBi16* – 2.6 cM – *Xgwm344-7B* {11042}; *Xcfa2257-7B* – 2.8 cM – *LrBi16* – 2.5 cM – *Xgwm344-7B* {11082}; A closer AFLP marker could not be converted to a STS/SCAR marker{11082}.
Bimai 16 also carries *Lr26* and *LrZH84* {11042}. Allelic with *Lr14c*, but showed different reaction patterns compared to lines with *Lr14c* and *LrFun* {11082}.

LrFun {11038}. 7BL {11038}. **bin:** 7BL-10. **v:** Fundulea 90 {11038}. **ma:** *Xgwm344-7B* – 4.4 cM – *LrFun* – 5.7 cM – *Xwmc70-7B* {11038}.

LrGam6 {10929}. 2BL {10929}. **v2:** Sinvalocho MA *Lr3 LrSV1 LrSV2* {10929}. **ma:** *Xbarc-2B* – 0.6 cM – *Xgwm382-2B* – 0.6 cM – *LrGam6* – 17.9 cM – *Xgwm528-2B* {10929}.

LrK1 {10904}. 5BS {10904}. **v2:** Ku3198 *Lr70* {10904}. **ma:** *LrK1* – 0.6 cM – *Xcfd20/Xgwm234-5B* {10904}. *LrK1* could be *Lr52* or an allele {10904}.

LrKr1 {10233}. **v:** Thatcher {10233}. **v2:** Kanred *LrKr2* {10233}.

LrKr2 {10233}. **v2:** Kanred *LrKr1* {10233}.

LrMq1 {10233}. **v:** Marquis {10233}.

LrNJ97 {11043}. 2BL {11043}. **v:** Neijiang 977671 {11043}. **ma:** *Xwmc317-2B* – 4.2 cM – *LrNJ97* – 2.2 cM – *Xbarc159-2B* – 2.3 cM – *Xwmc356-2B* {11043}.

LrP {11614}. 5DS {11614}. **v:** *Ae. peregrina* derivative PAU16058 {11614}. **al:** *Ae. peregrina* PAU3519 {11614}.

LrPI244061 {11280}. 2BS {11280}. **tv:** PI 244061 {11280}. **ma**: *LrPI144061* – 11.5 cM – *KASP_2BS_IWB6117* {11280}.
This gene might be *Lr13* {11280}.

LrPI287263 {11280}. 6BL {11280}. **tv:** PI 287263 {11280}. **ma**: *LrPI287263* – 2.8 cM – *KASP_6BL_IWB44753* – 2.8 cM – *Xdupw217* {11280}.

LrPI209274 {11218}. 6BS {11280}. **tv:** PI 209274 {11280}. **ma:** *KASP_6BS_IWB39456* – 3.7 cM – *LrPI209274* – 1.0 cM – *KASP_6BS_IWB6117* – 8.1 cM – *Xdupw217-2B* {11280}.
This gene may be *Lr53* {11280}.

LrSV1 {10929}. Adult plant resistance. 2DS {10929}. **v2:** Sinvalocho MA *Lr3 LrGam6 LrSV2* {10929}. **ma:** *Xgwm296-2D* – 1.4 cM – *LrSV1* – 7.1 cM – *Xgwm261-2D* {10929}.

LrSV2 {10929}. Adult plant resistance. 3BS {10929}. **v2:** Sinvalocho MA *Lr3 LrGam6 LrSV1* {10929}. **ma:** *Xgwm389-3B* – 3.0 cM – *LrSV2/Xgwm533-3B* – 4.2 cM – *Xgwm49-3B* {10929}.

According to {11334} *LrSV2* acted in a complementary way with *Lrc*-SV2 on chromosome 4BL. These complementary genes were closely linked to the locations of *Lr27* and *Lr31* but were considered to be different genes.

LrTb {820}. Adult plant resistance {820}. **v2:** AC Taber *Lr13 Lr14a* {820}.

LrTm {277}. **dv:** *T. monococcum*. **ma:** Linked to microsatellite locus *Xgwm136* {277}.

LrTr {227}. **v:** *Ae. triuncialis* derivatives {227}. **ad:** WL711 BC2F5 addition lines {227}. **al:** *Ae. triuncalis* Acc. 3549 {227}. **ma:** Lines with *LtTr* possessed a homologue of *Xgwm368-4B* {227}.

LrTt1 {10031}. Reccessive {10031}. [*lrTt1* {10031}]. 2A {10031}. **v:** Line 842 = Saratovskaya*2/*T. timopheevii* spp. *viticulosum* {10031}. **ma:** *Xgwm812-2A* – 1.5 cM – *LrTt1* {10031}.

LrVPM {1603}. 7DL {1603}. GERMPLASM?

LrW2 {305}. A gene, identified only as *Lr*, was transferred to wheat chromosome 2AS from $6M^v$ {113}: cosegregating markers were *Xpsr933-2A* and *Xpsr150-2A*. GERMPLASM

LrWo {10747}. 5B {10747}. **tv:** Wollaroi AUS99174 {10747}. **ma:** *Xgwm234-5B* – 7.2 cM – *LrWo* – 20.3 cM – *wPT-1420* {10747}.
The relationship of *LrWo* to *Lr52* was not established.

LrZH84 {10581}. 1BL {10581}. **v:** Guizhou 98-18 {11042}; Tian 95HF2; Xinong 1183-4 {11042}; Zhoumai 11 {10682}. **v2:** Predgornaia 2 *Lr26* {10581}; Zhou 8425B *Lr26* {10581}. **ma:** *Xbarc8-1B* (cent) – 5.2 cM – *LrZh84* – 3.9 cM – *Xgwm582-1B* {10581}.

Lr64i#2 {11079}. [*6Ai#2* {11079}]. **v:** Tulaikoskaya 5 {11079}; Tulaikoskaya 10 {11079}; Tulaikoskaya 100 {11079}.

A series of temporary designations for seedling and adult plant resistance genes in six durums is given in {1648}.
A potentially novel resistance gene was located in chromosome 5BS of Iranian landrace PI 289824. *Xgwm234-5B* – 8.9 cM – *Lr* – 2.3 cM – STS $Xtxw_{200}$ {10253}.

Complex genotypes
AC Domain: *Lr10 Lr16 Lr34* {820}.
AC Splendor: *Lr1 Lr16 Lr34* {10179}
AC Teal: *Lr1 Lr13 Lr16* {821}
Alsen: *Lr2a Lr19 Lr13 Lr23 Lr34* {10152}
Alsen: *Lr2a Lr10 Lr13 Lr23 Lr34* {10223}.
Benito: *Lr1 Lr2a Lr12 Lr13* {1256}.
Buck Manantial: *Lr3 Lr13 Lr16 Lr17 Lr34?* {300}.
Carberry: *Lr21 Lr16 Lr23 Lr34 Lr46* {11567}.
Coker 9663: *Lr9 Lr10 Lr14a* {10742}.
Duster: *Lr34 Lr46 Lr77* {11369}.

Estanzuela Benteveo: *Lr13 Lr26 Lr34* {10980}.
Estanzuela Pelon: *Lr1 Lr17a Lr26 Lr34* {10980}.
Estanzuela Tarariras: *Lr3bg Lr13 Lr34* {10980}.
Era: *Lr10 Lr13 Lr34* {342}.
Grandin: *Lr2a Lr3 Lr10 Lr13 Lr34* {821}.
INIA Boyero: *Lr13 Lr26 Lr34* {10980}.
INIA Churrinche: *Lr10 Lr24* {10980}.
INIA Tero: *Lr17a Lr24* {10980}.
Mango: *Lr1 Lr13 Lr26 Lr34* {1374}.
MN7529: *Lr1 Lr2a Lr10 Lr16* {976}.
Norm: *Lr1 Lr10 Lr13 Lr16 Lr23 Lr34* {10152, 10223}
Opata 85: *Lr10 Lr27+Lr31 Lr34* {1058}.
Pasqua: *Lr11 Lr13 Lr14b Lr30 Lr34* {304}.
Pioneer 26R61: *Lr13 Lr14b Lr26* {10742}.
Prospect: *Lr1 Lr2a Lr10 Lr13* {197}.
Roblin: *Lr1 Lr10 Lr13 Lr34* {303}, {713}.
Trap: *Lr1 Lr3 Lr10 Lr13 Lr34* {1374}.
Genotype lists: Australian cultivars {0288}; Chinese cultivars {0013, 10682, 11310}; Combinations with *Lr34* {1361}; Cultivars from the former USSR {1380}; Czechoslovakian/Czech cultivars{855}, {0102}, {11717}; European cultivars {0229, 0260, 0288, 0337,10345, 10794}; Indian cultivars {1365, 1345}; Indian Subcontinent {1365}; Mexican cultivars {1373}; U.S.A. cultivars {1219}, {978}, {0334}, {10111}, {10146}, {10152}, French cultivars {10792}, Croatian cultivars {11135}. Kazakhstan cultivars {11161}, see also {970}. See {11178} for review and analysis of leaf rust resistance genes in six durum wheats.

3.22.3. Suppressor of genes for resistance to *P. triticina*

SULR23

SuLr23 {1058}. Suppressing allele. 2DS {1058}. **v:** Altar 84/*Ae. tauschii* 219 {1058}.

suLr23 {1058}. Non-suppressing allele. **v:** Opata 85 {1058}.
See also evidence for specific suppression in {948}.

3.22.4. QTLs for reaction to *P. triticina*

Two QTLs, located distally on chromosome arm 1BL and on chromosome 7DS, were mapped for leaf rust severity in a Fukuho-komugi/Oligoculm doubled haploid population {10060}. The resistance on 1BL was contributed by Oligoculm and explained 15% of the variation. The 1BL QTL may correspond to *Lr46* and was associated with marker *Xwmc44-1B* {0460}. The resistance on 7DS was contributed by Fukuho-komugi and explained 41% of the variation. The 7DS QTL corresponds to *Lr34* and was associated with marker *Xgwm295-7D* {10060}. Two major QTL, located on chromosomes 7D and 1BS, for leaf rust resistance were mapped in an Arina/Forno RIL population {10066}. The resistance on 7D

was contributed by Forno and explained 32% of the variation. This QTL most likely corresponds to *Lr34* {10066}. The resistance on 1BS (*QLr.sfr-1BS*) was associated with *Xgwm604-1B* and was contributed by Forno {10066}. Additional minor QTLs were identified on chromosome arms 2DL, 3DL, 4BS and 5AL {10066}.QTLs for leaf rust resistance were identified in {0050} and were named by the catalogue curators as follows:
QLr.pser.1BL {10743}. 1BL {10743}. **bin:** 1BL6-0.32 {10743}. **ma:** Proximal to *Xgwm264.1-1BL* {10743}. Associated with *lm* producing a lesion mimic phenotype in the absence of disease {10743}.
QLr.sfr-1B {0050}. 1BS {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno {0050}. **ma:** Associated with *Xpsr949-1B* and *Xgwm18-1B* {0050}.
QLr.sfr-2B {0050}. 2B {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0050}. **ma:** Associated with *Xpsr924-2B* and *Xglk699-2B* {0050}.
QLr.sfr-3A {0050}. 3A {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xpsr570-3A* and *Xpsr543-3A* {0050}.
QLr.sfr-4B {0050}. 4B {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno {0050}. **ma:** Associated with *Xpsr921-4B* and *Xpsr593-4B* {0050}.
QLr.sfr-4D {0050}. 4DL {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno {0050}. **ma:** Associated with *Xglk302-4D* and *Xpsr1101-4D* {0050}.
QLr.sfr-5D {0050}. 5DL {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer {0050}. **ma:** Associated with *Xpsr906-5D* and *Xpsr580-5D* {0050}.
QLr.sfr-7B.1 {0050}. 7B {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno {0050}. **ma:** Associated with *Xpsr593-7B* and *Xpsr129-7B* {0050}.
QLr.sfr-7B.2 {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno {0050}. **ma:** Associated with *Xglk750-7B* and *Xmwg710-7B* {0050}.

AGS 2038 (R) / UG111729 (MR): RIL population. Seedling and adult plant resistance was controlled by several QTL, the most important of which was designated *QLr.ags-1AL* spanned by *IWB20487* and *IWA4022* {11507}.

Avocet S / Attila: At least two additive genes for slow rusting {10586}. In addition to *Lr46* there were small effects on chromosomes 2BS, 2BL and 7BL {10586}.

Avocet R (S) / Chilero: *Lr46/Yr29* and *QLr.cim-5DS/QYr.cim-5DS*, from Chilero, and *QLR.cim-1DL/QYr.cim-1DL* from Avocet R {11306}.

Avocet / Kundan: RIL population: *Lr29* (flanked by *10902272* and *02414*, R^2 = 0.5 -0.65), *QLR.cim-2BL* flanked by *1237388* and *1081780_35C>T* from Avocet and *QLr.cim-2DS* flanked by *1237388* and *1081780_35C>T* from Kundan {11248}.

Avocet / Pastor: RIL population: QTLs mapped on 1BL (*Lr46*, 2BS, 5A, 6B and 7BL plus minor QTLs on 1B, 2A and 2D {10928}.

Avocet S / Pavon 76: QTL identified included: 1BL (*PstAFAMseCAC1&2*), 4BL (*Xgwm368*), 6AL (*Xgwm617*), 6BL (*PstAGGMseCGA1*) {10443}.

Beaver / Soissons: DH population: QTL for resistance to Australian pathotypes were located on 4-6 chromosomes over 3 years; the most consistent being 1B(1BL.1RS), 4BS (proximal to *Xbarc20-4B*) and 5AS (*QTLBvr5AS*, proximal to *Xbarc10-5A*) and in the vicinity of *wPt-8756* and *wPt-1931* {10687}.

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chr. 2AL, 2BL, 2BS and 3BS, were from Capo and one on 5BLwas from Arina; the QTL on 2AL, 2BL and 3BS were co-located with QTL for resistance to stripe rust {11449}.

CI 13227 (R) / Lakin (MS): DH population: Adult plant resistance conferred by *QLR.hwwg-2DS* (R^2 = 0.11 – 0.26), *QLr,hwwg-7BL* (R^2 = 0.08-0.19, likely *Lr68*), and *QLr.hwwg-7AL* from CI 13227, and *QLr.hwwg-3BS* from Lakin {11311}.

CI 13227 (R) / Suwon (S): SSD population {10211}. Two QTLs for slow leaf rusting, located on chromosomes 2B and 7BL, were mapped for final severity, area under disease progress curve, and infection rate in a ***QLr.osu-2B*** was associated with microsatellite markers *Xbarc18-2B* and *Xbarc167-2B* (R^2 = 9-18%). ***QLr.osu-7BL*** was associated with microsatellite marker *Xbarc182-7B* (R^2 = 12-15%) {10211}. CI 13227 constributed the resistant alleles for both QTLs. ***QLrid.ocu-2D***, linked to *Xgwm261-2D*, affected the duration of infection {10211}. However, Thatcher backcross derivatives of CI 13227 appeared to have *Lr3c* and *Lr46* {11021}.

Libellula / Huixianhong: RIL population: Six QTL on chromosome arms 1AS, 1AL, 1BL (*Lr34*), 3AL, 4BL and 7DL were detected in a least two of seven environments, the most effective of which was identified as *Lr34* {11757}.

Mianyang351-15 (R) / Zhengzhou 5389 (R): RIL population: four QTL were located on chromosome arms 1BL (*Lr46*), 2AS (*Yr37*), 2DS, and 7BL (*Lr68*) {11545}.

Ning7840 / Clark: RIL population: *QLr.hwwg-5AS* from Ning 7840; *QLr.hwwg-6AS* from Clark, flanked by *barc23-6A* and *IWA3321*; *Qlr.hwwg3BS.1* from Clark, flanked by *IWA4654* and *IWA1702*; possibly *Lr74*; and *QLr.hwwg-7DS/Lr34* from Ning 7840 {11278}.

TA 4152-60 (MR) / ND495 (MR): DH population: Five QTLs for APR were identified in the field, viz. *QLr.fcu-3AL* (R^2 = 0.18), *QLr.fcu-3BL* (R^2 = 0.19), *QLr.fcu-5BL* (R = 0.07), and *QLr.fcu-6BL* (R^2 = 0.12) from TA 4152-60 and *QLr.fcu-4DL* (R^2 = 0.13) from ND495 {10757}. The 3AL gene also conferred seedling resistance to some races and the 3BL gene conferred resistance to race MFPS {10757}.

Thatcher*3 / Americano 44d: RIL population: QTL for adult plant resistance identified on chromosomes 3AS (*QLr.cdl-3A*), 3DS (*QLr.cdl-3DS*) and 6DS (*QLr.cdl-6D*); both the 3AS and 3DS QTLs were required for expression of resistance {11296}.

26R61 (S) / AGS 2000 (R): RIL population. A single QTL (*QLr.uga-2BS*) flanked by *wPt-666389* and *wPt-2600* on chromosome arm 2BS was designated *LrA2K* {11507}. *LrA2K* – 2.9 cM – *Xwmc770-2B* {11507}.

Review of QTL in hexaploid wheat {11442}.

Tetraploid wheat:

Atred#1 / Dunkler: RIL population: Four QTL for APR, including *Lr46*, *QLr.cim-5BL* and *QLR.cim-6BL* from Dunkler and *QLr.cim-2Bc* from Atred#1 {11639}.

Atred#1 / Heller#1: RIL population: Four QTL for APR, including *Lr46*, *QLr.cim-5BL* and *QLR.cim-6BL* from Dunkler and *QLr.cim-2Bc* from Atred#1 {11639}.

Bairds (R) / Atred#1: RIL population: Four QTL for APR, including *Lr46*, *QLr.cim-5BL* and *QLR.cim-6BL* from Bairds and *QLr.cim-2Bc* from Atred#1 {11600}.

Colosseo / Lloyd: A major QTL, *QLr.ubo-7B.2*, for seedling and adult plant resistance from Colosseo, was located between *Xgwm344.2-7B* and DART 378059, **bin:** 7BL 10-0.78-1.00 {10600}.

TA4152-60 / ND 495: DH population: Four QTLs for APR, *QLr.fcu-3AL*(*Xcfa2183-3AL – Xgwm666-3AL*, R^2=0.18), *Qlr.fcu-3BL*(*Xbarc164-3BL – Xfcp544-3BL*, R^2=0.19), *Qlr.fcu5BL*, and *Qlr.fcu-6BL*(*Xbarc5-6BL – Xgwm469.2-6BL*, R^2=0.12) were from TA4152-60 and *Xlr.fcu-4DL* (*Xgdm61-4DL – Xcfa2173-4DL*, R^2=0.13) was from ND495 {10717}. The 3AL QTL conferred seedling resistance to all 3 races, and the 3BL gene gave race-specific seedling resistance to one race. *Xlr.fcu-3BL* was effective only in the presence of an allele associated with *Xgwm359-5DS* {10717}.

Association mapping in durum wheat indicated genomic regions affecting leaf rust response in chromosomes 1A, 1B, 2A, 2B (*Lr13, Lr23* region), 3B, 5A, 5B, 6B, 7A, and 7B (see *Lr14* {10736}.

Historical review of leaf rust work in Canada {18053}.

3.23. Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici*-repentis)

Disease: Tan spot, yellow leaf spot. Virulence in the pathogen is mediated by host-specific toxins and host resistance is characterized at least in part by insensitivity to those toxins. Three toxins, Ptr ToxA, Ptr ToxB and Ptr ToxC have been identified (see {10153}). Toxin sensitivity determined by use of toxins extracted from pathogen strains and resistance determined by infection experiments are treated as different traits, although common genes may be involved. A review is provided in {10690}. Introgressions of genes for insensitivity to Ptr ToxA and Ptr ToxB are outlined in {10153}.

Batavia (S) / Ernie (R): DH population tested over three years. Four (1A(Ernie), 7A, 2BS, 3BS (Batavia)), five (2BS, 5BL(E), 3D, 6A, 7D(B)) and four (2BS, 5BL(E), 1A, 6A(B),) QTL accounted for most of the variation in each year. The greatest effect across years was the QTL on chromosome 2BS (R^2=0.382, 0.298 and 0.362, respectively). This QTL was validated in four additional populations {10782}.

Grandin (S) / BR34 (R): RIL population: QTL in 1BS, *QTs.fcu-1BS*, (13-29% of variation depending on race) and 3BL, (13-41%) were involved in resistance to 4 races. Five other QTL showed race specific responses {10248}.

TA4152-60 (R) / ND495 (S): DH population: Five QTLs for resistance, all from TA4152-60 {10580}, viz., *QTs.fcu-2AS* and *QTs.fcu-5BL.1* conferring resistance to all races used, *QTs.fcu-5AL* conferring resistance to races 1, 2 and 5, *QTs.fcu-5B.2* conferring resistance to races 1 and 2, and *QTs.fcu-4AL* conferring resistance to race 3.

WH542 (R) / HD29 (S): RIL population: SIM indicated QTL on chromosomes 1B, 3AS, 3BL, 5B and 6BS, but only two were confirmed by CIM, *Qts.ksu-3AS* flanked by *Xbarc45-3A* and *Xbarc86-3A* (LOD 5,4, $R^2 = 0.23$) and *Qts.ksu-5BL* (probably *Tsn1*) flanked by *Xgwm499-5B* and *Xest.stsbe968-5B* (LOD 6,5, $R^2 = 0.27$) {10552}.

Wangshuibai / Ning 7840: RIL population: Race 1: *QTs.ksu-1AS*, R^2=0.39 (nearest marker *Xcfa2153-1A* and *QTs.ksu-2BS*, R^2=0.04) (nearest marker *Xbarc2-2B* {10753}.

3.23.1. Insensitivity to tan spot toxin (necrosis)

TSN1

tsn1 {10207}, {346}. Insensitivity (disease resistance) is recessive {346}. *Tsr1* {10508}, see Resistance to tanspot. 5BL {346}. **v:** AC Barrie {10153}; AC Cadillac {10153}; AC Elsa {10153}; Atlas 66 {10458}; BR34 {10458, 0007}; CEP17 {0007}; Chinese Spring {10458,0007}; Erik {10458, 10030, 7}; IA807 {0007}; IA905 {7}; Laura {10153}; ND688 {10458}; Opata 85 {10458}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122 {10458}, {10207}, {346}; Synthetic W-7984 = Altar 84/*Ae. tauschii* CI 18 {10458,0007}. **tv:** Altar 84 {0007}; D87450 {0007}; *T. dicoccoides* Israel A {10506}. **ma:** *Xbcd1030-5B* – 5.7 cM – *tsn1* – 16.5 cM – *Xwg583-5B*{346}; *tsn1* – 3.7 cM – *Xbcd1030-5B*{0007}; *Xfgcg7-5B* – 0.4 cM – *Tsn1/Xfcg17-5B* – 0.2 cM – *Xfcg9-5B* {10207}; *Xfcg17-5B* – 0.2 cM – *Tsn1* – 0.6 cM – *Xfcg9-5B* {10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM {10337}; *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1/XBE425878/Xfcc1/XBE443610* {10413}.
According to {10376} the same dominant allele, presumably *tsn1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN 2137 in crosses with 6B-365.

Tsn1. Sensitive to Ptr ToxA. **v:** Bobwhite {10458}; Cheyenne {10458, 0007}; Glenlea {10458}; Grandin {10458}; Hope {10458, 0007}; Jagger {0007}; Katepwa {10458}; ND2709 {10458}; ND495 {0007}; Sumai 3 {10458}; Timstein {10458, 0007}. **v2:** Kulm *Tsc1* {10458}, {10030}, {346}; Trenton *Tsc1* {0315}. **dv:** Two *Ae. speltoides* accessions {10756}. **tv:** Langdon {10458}; Some *T. dicoccoides* accessions {10756}. **ma:** *Xbcd183-5B* – 1.2 cM – *Tsn1/Xbcd1030-5B* – 2.4 cM – *Xrz575-5B* {10688}. **c:** *Tsn1* has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA {10756}. Tsn-ToxA interaction has a major role in SNB development in both common and durum wheat whereas it has a variable role in tanspot development in bread wheat and is not a significant factor for tanspot development in durum wheat {11204}..
In Kulm/Erik, toxin response accounted for 24% of the variation in disease response, which was affected

by 4-5 genes {10030}.
Ptr ToxA is functionally identical to *S. nodorum* ToxA but has two predicted amino acid differences {10459}. See Reaction to *Phaeosphaeria nodorum*.
Australian cultivars with *tsn1* and *Tsn1* are listed in {10540}.

TSN2

Tsn2 {10344}. Conditions resistance to race 3 {10344} 3BL {10344}. **sutv:** LDN(DIC-3B) {10344}. **tv:** *T. turgidum* no. 283, PI 352519 {10344}; *T. dicoccoides* Israel-A {10344}. **ma:** Identified as a QTL in region *Xgwm285-3B* – *Xwmc366.2-3B* (R^2=91%) {10344}; Also classified as a single gene: *Xgwm285-3B* – 2.1 cM – *tsn2* –.2 cM – *Xwmc366.2-3B* {10344}.

3.23.2. Insensitivity to tan spot toxin (chlorosis)

TSC1

Tsc1 {344}. Sensitivity to Ptr ToxC {344}. 1AS {344}. **v:** 6B365 {0315}; Louise {11751}; LMPG-6 {11751}; Opata 85 {344}. **v2:** Kulm *Tsn1* {0315}; Trenton *Tsn1* {0315}. **ma:** *Gli-A1* – 5.7 cM – *Tsc1* – 11.7 cM – *XksuD14-1A*{0315}; Mapped to a 2.4 cM region spanning184 kb (CS RefSeq 2.1) in the Penawawa / PI626523 RIL population **{**11751}.
According to {10376} the same allele, presumably *tsc1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN2137 in crosses with 6B-365.
tsc1 {344}. Insensitivity is recessive. *QTsc.ndsu-1A* {9924}. **v:** Chinese Spring {11751}; Katepwa {315}; Opata 85 {344}; Penawawa {11751}; PI 62673 {11751}; Synthetic W-7984 {315}.

TSC2

Tsc2. Sensitive to Ptr ToxB {10015}. 2BS {10015}. **bin:** 2BS3-0.84-1.00. **v:** Aronde {11750}; Katepwa {10871}; Maris Dove {11750}; Synthetic W-7984 {10015}; Thatcher {11750}. **tv:** Altar 84 {11750}.
tv: Altar 84 {11750}.

tsc2. Insensitivity allele {10015} **v:** Chinese Spring {11750}; Lynx {11750}. Opata 85; Salamouni {10871}. **tv:** Altar 84 {10871; Langdon {11750}. **ma:** *Xmag681-2B/XTC339813* – 2.7 cM – *Tsc/XBE444541* – 0.6 cM – *XBE517745*{10871}; An XBE444541 EST-STS co-segregating marker for *Tsc2* was developed and lines with *tsc2* produced a 505 bp fragment whereas those with *Tsc2* produced a 340 bp band {10871}. Mapped to a 1.921 Mb region (23.106 – 25.027 Mb) {11750}

QTL

QTsc.ndsu-1A {9924}. Resistance is likely recessive {344} [*Tsc1* {344}]. 1AS {344}. **v:** Synthetic W7984 {344}. **ma:** Association with *Gli-A1* {0264}, {0040}, {344}.
QTsc.ndsu-1A, or a closely associated gene, confers insensitivity to Ptr ToxC, see {0315}. Inoculation with purified toxin Ptr ToxC was used to map this locus. *QTsc.ndsu-1A* confers resistance in both seedlings and adult plants.

QTsc.ndsu-4A. 4AL {0090}. **v:** Opata 85/Synthetic W-7984 (ITMI) RI mapping population; resistance was contributed by W-7984 {0090}; In W-7976/Trenton resistance was contributed by W-7976 {0264}. **ma:** Association with *Xksu916(Oxo2)-4A* and *Xksu915(14-3-3a)-4A* {0090}; In W-7976/Trenton there was association with *Xwg622-4A* {0264}; Minor QTLs in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants {0264}.

QTL

'ITMI population': In addition to *tsc2* which accounted for 69% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL (*Xksu916(Oxo)-4AS*, W-7948) accounted for 20% of the phenotypic variation {10015}.

Salamouni / Katepwa: RIL population: variation at the *Tsc2* locus explained 54% of the variation in response to race DW5 {10871}.

QTL analyses of durum crosses infected with various isolates of race 4 (lacking in Ptr Tox 1, 2 and 3) detected QTL on chromosomes 1A (2 QTL), 4B (3 QTL) and 5A (1 QTL) {11649}.

3.23.2. Insensitivity to tan spot toxin (chlorosis)*TSR1*

Tsr1. [*tsn1* See: Insensitivity to tanspot toxin]. Resistance is recessive. 5BL. **v:** Genetic stocks that do not have *Tsn1* and other genes that respond to toxins produced by the pathogen.
The gene in Erik was allellic with resistance in a diverse set of genotypes including spelt and durum derivatives {10557}.

TSR2

Tsr2. Resistance is recessive. Confers resistance to race 3 {10344}. [*tsn2* {10344}]. 3BL {10344}. **sutv:** LDN (DIC-3B) {10344}. **tv:** *T. dicoccoides* Israel-A {10344}. **tv2:** *T. turgidum* no. 283, PI 352519 *Tsr5* {10344}. **ma:** Identified as a QTL in region *Xgwm285-3B* – *Xwmc366.2-3B* ($R^2 = 91\%$) {10344}; also classified as a single gene: *Xgwm285-3B* – 2.1 cM – *tsr2* – 15.2 cM – *Xwmc366.2-3B* {10344}.

TSR3

Tsr3. [*tsn3* {10394}]. 3D {10394}. 3DS {10419}. **v:** XX41 = [Langdon/*Ae. tauschii* CI 00017] {10394}; XX45 {10394}; XX110 {10394}. **dv:** *Ae. tauschii* CI 00017 {10394}. **ma:** *Xgwm2a* – *tsn3*, 15.3 cM, 14.4 cM and 9.5 cM in CS/XX41, CS/XX45 and CS/XX110, respectively {10419}.
Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant - all three were hemizygous-effective {10394}. The genes were given different temporary designations {10394, 10419}, but all will be considered to have a common gene until they are shown to be different.

TSR4

Tsr4. Resistance is recessive. Resistance to race 1 (culture ASC1a) {10350}. [*tsn4* {10350}]. 3A {10350}. **v:** Salamouni {10350}.

TSR5

Tsr5. [*tsn* {10509}]. 3BL {10509}. **tv2:** *T. turgidum* no. 283, PI 352519 *Tsr2* {10509}. **ma:** *Tsr5* – 8.3 cM – *Xgwm285-3B* – 2.7 cM – *Tsr2* {10509}.

TSR6

Tsr6 {10668}. Resistance is recessive. 2BS {10668}. **v:** ND-735 {10668}. **ma:** *Xwmc382-2B* – 15.3 cM – *wPt-0289* – 4.6 cM – *Tsr6* – 18.7 cM – *Xwmc-2B* {10668}. According to {10668} *Tsr6* should be identical to *tsc2* (see Insensitivity to tan spot toxin (chlorosis)).

TSR7

Tsr7 {11363}. Dominant. *QTs.zhl-3B* {11362}. 3BL {11362, 11363}. **v:** Br34 {11363}; Penawawa {11363}. **sutv:** Linked STARP markers were developed {11363}. **ma:** Linked STARP markers were developed {11363}.
Tsr7 conferred resistance to race 1 (isolate Pti2), race 2 (isolate 86-124), race 3 (isolate 331-9), and race 5 (isolate DW5) {11362}.

Temporary designations

TsrAri {10765}. Recessive 3A {10765}. **v:** Arina {10765}; Heines VII {10765}; Zenith {10765}.

TsrHar {10590}. 3B {10590}. **v:** Dashen {10590}; HAR 604 {10590}; HAR 2562 {10590}. Effective against races ASC1a (race 1) and DW-16 {10590}.

QTL

Louise / Penawawa: RIL population: *QTs.zhl-1A*, located at interval 0-6.0 cM and likely *Tsc1*; *QTs.zhl-2D*, located at 144.0-152.0 cM; *QTs.zhl-3B*, located at 72.0-78.0; and *QTs.zhl-5A* located at 154-160 cM {11362}.

A QTL analysis of 4 durum crosses identified 12 QTL on chromosomes 1B, 2B (2), 3A (3), 5A (5) and 7A {11481}.

3.24. Reaction to *Rhizoctonia* spp.

Cause of Rhizoctonia root rot.

ROT1

Rot1 {10761}. **v:** Scarlet-Rz1 {10761}.
Scarlet-Rz1 was produced by mutagenesis {10761}.

3.25. Reaction to *Sitobion avenae*

English grain aphid.

SA1

Sa1 {10877}. [*RA-1* {10877}]. 6AL {10877}. **tv:** C273 {10877}. **ma:** *Xwmc179-6A* – 3.37 cM – *Sa1* – 4.73 cM – *Xwmc580-6A* {10877}.

3.26. Reaction to *Sitodiplosis mosellana* (Gehin)

Insect pest: Orange blossum wheat midge, Wheat midge. This pest should not be confused with *Contarinia tritici*, the yellow blossom wheat midge.

SM1

Sm1 {218}. 2B {218}. **v:** Augusta {218, 11137}; Blueboy {218}; Caldwell {218}; CDC Landmark {11579}; Clark {218}; FL302 {218}; Glencross {11044}; Goodeye {11044}; Howell {218}; Knox 62 {218}; Mono {218}; Paragon {11579}; Robigus{11137}; Seneca {218}; Skalmeje {11137}. Unity {11579}. **ma:** Linked to a SCAR marker{223}; *Sm1* was mapped to a 2.5 cM interval on chromosome 2BS flanked proximally by AFLP-derived SCAR marker *WM1* and distally by SSR *Xgwm210-2B*{ 10291}; A combination of *2BS-5344126_kwm707* and *2BS-6229175_kwm693* appeared to be predictive of *Sm1* but there was variation between sources {11137}. KASP marker developed in {11579}. **c:** Gene candidate with NB-ARC-LRR-kinase-MSP structure {11579}.

QTL

Henong 215 (R) / Yanyou (S) and **6218 (S) / Jimai 24 (R):** selected RIL populations: Several QTL identified: *QSm.hbau-4A.2* with LOD scores 5.58 – 29.22 and PVE 24.4 – 44.8% were mapped to a 4.9 Mb interval; nearest markers *AX-109543456, AX-108942696* and *AX-110928325* {11425}.

Reeder I/Conan: RIL population: *QSm.mst-1A*, flanked by *Xwmc59-1A* and *Xbarc1022-1A* was the most effective and constant QTL for reduced larval infection over two years (R^2=0.17 and 0.34) {10841}. RILs with this QTL in three genetic backgrounds had reduced infestations of 42% {10841}.

3.27. Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Insect pest: Greenbug

GB1

Gb1 {1514}. Recessive. [*gb1* {222}]. 1AS {11731}. CI 9058 {222}; Dickinson Selection 28A {222}. Located in the region 13.3 – 14.2 Mb {11731}.

GB2

Gb2 {1514, 1313}. Derived from *Secale cereale*. 1A {554} = T1AL.1R#2S {389}. **v:** Amigo CI 17609 {1313}; Century {0008}; TAM107 {0008}; TAM200 {0008}; TAM202 {8}. **ma:** 2.7 cM proximal to *Sec1* in 1RS, but co-segregated with *Sec-1P*{10167}; Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.

GB3

Gb3 {1514, 624}. Resistance in Largo and derivatives was controlled by multiallelic complementary genes {783}. *Gb3* was postulated to be one of the loci concerned. 7D {554}. 7DL {0319}. **bin:** 7DL3 0.82-1.00. **v:** Largo CI 17895 {622}; TAM110 {0319}; TAM112 {194, 10764}; TXGBE373 {0319}. **al:** Insave rye. **tv:** *Ae. tauschii* PI268210 {10907}. **ma:** Completely associated with 2AFLP markers {0319}. These were also present in germplasm line KS89WGRC4, implying the likely presence of *Gb3* or a closely linked resistance gene {0319}; *Xgwm037-7D* – 0.4 cM – *Gb3/Xwmc634-7D* – 0.8 cM – *Xbarc76-7D* {10169}; *H1067J6-R* – 0.7 cM – *Gb3* – 0.4 cM – *H1009B3-F*{10907}. *Gb3* – *Gb8* 15+-1.35 cM {11378}.

GB4

Gb4 {523, 1514}. 7DL {10267}. **v:** CI 17959 {903}.
Gb4 is either closely linked or allelic to *Gb3* {10267}.

GB5

Gb5 {1515, 1514}. 7S#1L(7A) {391}; T7S#1L.7S#1S-7S {389}. tr: CI 17883; CI 17884; CI 17885 {1515}; UCRBW98-1 and UCRBW98-2 (PI 603919 has a shortened alien segment {11515}. ma: KASP markers are reported in {11516}.

GB6

Gb6. Derived from *Secale cereale*. 1A = T1AL.1R#2S {1151}. **v:** GRS1201{1152}; GRS1202 {1152}; GRS1203 {1152}; GRS1204 {1152}; GRS1205 {1152}; N96L9970 {10764}; see also *Pm17* (Reaction to *Blumeria graminis*). **su:** Tx4386 {1150}. **ad:** Tx4333 {1150}. **al:** Insave rye. **ma:** Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.

GB7

Gb7 {10169}. 7DL {10169}. **v:** Synthetic W7984 {10169}. **tv:** *Ae. tauschii* TA1651 {10169}. **ma:** *Xwg420-7D* – 2.1 cM – *Gb7* – 13.4 cM – *Xwmc671-7D* {10169}. KASP markers developed {M23026}; KASP markers developed {11633}.

GB8

Gb8 {11378}. [*Gb595379-1* {11378}.]. 7DL {11378}. **bin:** 7DL3-0.82-1.00. **v:** PI 595379-1 {11378}. **ma:** *Xbarc11-7D* – 10.41 cM – *Gb8/Xstars508* (596.4 Mb) – 7.4 cM – *Xwmc824-7D* – 4.8 cM – *Xgwm428-7D* {11378}. *Gb3* – *Gb8* 15+-1.35 cM {11378}.

GB9

Gb9 {11726}. *Gb76364*{11726}. 7DL {11726}. **v:** PI 703387, CWI 76364 {11726}. **dv:** *Ae. tauschii* Wx1027 (CIMMYT) {11726}. **ma:** Mapped to a 0.6 Mb interval - *Stars-KASP872* (599.8 Mb; CS RefSeq 2.1) 0.6 cM – *Gb9* – 0.5 cM and *Stars-KASP881* (600.5 Mb) {11726}. *Gb9* – *Gb3*, 14.9 cM {11726}. *Gb9* – *Gb8*, 16.3 cM {11726}.

Temporary designations

Gba {10267}. 7DL {10267}. **v:** TA4152L94 = CETA/*Ae. tauschii* Wx1027 {10267}. **ma:** *Xwmc671-7D* – 34.3 cM – *Gba* – 20.7 cM – *Xbarc53-7D* {10267}.

Gbb {10267}. 7DL {10267}. **v:** TA452L24 = CROC 1/*Ae. tauschii* Wx224 {10267}. **ma:** *Xwmc671-7D* – 5.4 cM – *Gbb* – 20.2 cM – *Xbarc53-7D* {10267}.

Gbc {10267}. 7DL {10267}. **v:** TA4063.1 = 68111/Rugby//Ward//*Ae. tauschii* TA2477 {10289}. **ma:** *Xgwm671-7D* – 13.7 cM – *Gbc* – 17.9 cM – *Xgdm150-7D* {10267}.

Gbd {10267}. **v:** TA4064.1 = Altar 84/*Ae. tauschii* TA2841 {10267}. **ma:** *Xgwm671-7D* – 7.9 cM – *Gbd* – 1.9 cM – *Xwmc157-7D* {10267}.

Gbx1 {10267}. [*Gbx* {10267}]. 7DL {10267}. **v:** KS89WGRC4 = Wichita/TA1695//2*Wichita {10267}. **dv:** *Ae. Tauschii* TA1695 {10267}. **ma:** *Xwmc157-7D* – 2.7 cM – *Xgdm150-7D* {10267}.

Gbx2 {10267}. [*Gbx* {10267}]. **v:** W7984 {10267}. **ma:** *Gbx2* was located 8.8 cM from *Gb3* {10267}.

Gby {10192}. 7A {10192}. **v:** Sando's Selection 4040 {10192}. **ma:** *Xpsr119-7A/Xbcd98-7A* – 5.8 cM – *Gby* – 3.8 cM – *Xpr1B-7°* {10192}.

Gbz {10171}. 7DL {10171}. **v:** KSU97-85-3 {10171}. **tv:** *Ae. tauschii* TA1675 {10171}. **ma:** *Xgdm46-7DL* – 9.5 cM – *Xwmc157-7D/Gb3/Gbz* – 5.1 cM – *Xbarc53-7D* {10171}; *Xwmc671-7D* – 3.9 cM – *Gbz/Xwmc157-7D* – 5.1 cM – *Xbarc53* {10267}.

QTL

QGb.unlp.6A for antixenosis was associated with *Xgwm1009-6A* and *Xgwm1185-6A* in a CS/CS(Synthetic 6A) DH population {10216}.

Antibiosis was associated with several markers, including *Rc3* (7DS) in chromosome 7D {10167}.

3.28. Reaction to Soil-Borne Cereal Mosaic Virus

Syn.: Soilborne wheat mosaic. Vectored to the roots by the fungus, *Polymyxa graminis*

SBM1

Sbm1 {10614}. [*SbmCz1* {10132}]. 5DL {10614}. **v:** Cadenza {10132}; Claire {11138}; Moulin {11138}; Tonic {10614}; Tremie {11138}. **v2:** Cadenza *Sbm2* {11500}. **ma:** *Xbarc110-5D* – 14.7 cM – *Sbm1* – 2.1 cM – *Xwmc765-5D* – 3.1 cM – *Xbarc144-5D/Xwmc443-5D/RRES01-5D* {10614}; Caps marker RRESO1 was developed from an AFLP fragment{10614}; *E37M49* – 9.0 cM – *Sbm1* – 1.0 cM – *Xgwm469-5D* – 2.0 cM – *Xwmc765-5D*. Resistant varieties carried 152 or 154 bp alleles at *Xgwm469-5D* {11138}; all susceptible genotypes had a null allele {11138}.
Sbm1 was identified in a DH population of Avalon (S)/Cadenza (R) {10132}.

SBM2

Sbm2 {11500}. 2BS {11500}. **v:** Xi19 {11500}. **v2:** Cadenza *Sbm1* {11500}.

Temporary designations

SbmTmr1 {10683}. 5D {10683}. **v:** TAM 107-R7 {10683}.

Sbmwm1 {11435}. **v:** Heyne {11435}. 5D {11435}. **ma:** *Xgwm272-5D* – 20.2 cM – *Sbwm1* – 2.2 cM – *wsnp_CAP11_c209_198467* – 0.7 cM – *wsnp_JD_c4438_5568170* – 8.7 cM – *Xgwm469* {11435}. *Sbm1* and *Sbmwm1* are likely the same gene.

SBWMV {10685}. 5D {10685}. **v:** KS96WGRC40 {10685}. **dv:** *Ae. tauschii* TA2397 {10685}. **ma:** *Xcfd010-5DL* – 9.5 cM – *SBWMV* – 11.1 cM – *Xbarc144-5D* {10685}.

QSbv.ksu-5D, (R^2=0.38) was found in Karl 92*2/TA4152-4 {10273}; the resistance was contributed by Karl 92.

3.29. Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides* (Fron) Deighton)

Disease: eyespot, strawbreaker footrot.

PCH1

Pch1. [*Pch* {261}]. 7DL {708}, {1603}.
7D {591, 592}. **s:** Courtot*/Roazon 7D {592}; Hobbit Sib*/VPM1 7D {591}. **v:** *Ae ventricosa* derivative {261}; Coda {10513}; H-93-70 {1521, 236}; Hyak {21}; Madsen {20}; Rendezvous {1603}; Roazon {591}; 5L 219 {1521}.
7A {0224}. **tv:** Five recombinant lines{0224}. **al:** *Ae. ventricosa* {261}. **ma:** *Pch1* was linked to *Ep-D1* and mapped 2 cM from microsatellite marker *XustSSR2001-7D* {10070}; *Ep-d1b* was a more reliable marker than the STS for selecting *Pch1* {10238}; Leonard et al. {10513} predicted that *Ep-D1* might encode an oligopeptidase B, and by comparative genetics, developed primers to a wheat oligopeptidase B-encoding wheat EST *BU1003257*. Complete linkage occurred for a derived STS marker *Xorw1* and *Pch1* in a Coda/Brundage RIL population and the marker identified the presence or absence of *Pch1* among 44 wheat accessions {10513}. *Pch1* is closely linked with *Ep-V1* {973}. Delibes *et al.* {236} concluded that

Pch1 was not located in chromosome 7D whereas Law *et al.* {776} found that H-93-70 possessed a unique allele, *Ep-D1b*, in common with VPM1 and its derivatives. Eyespot resistance and *Ep-A1b* in chromosome 7A were genetically associated {704}.

PCH2

Pch2 {228}. 7A {704}. 7AL {228}, {229}. **s:** CS*/Cappelle Desprez 7A {704}, {228}. **v:** Cappelle Desprez {704}, {228}. **ma:** *Xcdo347-7A* (distal) – 11 cM – *Pch2* – 18.8 cM – *Xwg380-7A* (proximal) {229}.
According to {0380}, this gene is not effective at the adult plant stage. Instead, the adult resistance of Cappelle-Desprez was controlled by a gene on chromosome 5A with the possibility of two less effective genes on 1A and 2B.

PCH3

Pch3 {616}. **ad:** CS + 4V {1050}.

Temporary designation

***Pch*$_{\mathrm{Dv}}$** {618}. 4VL {618}. **ad:** Wheat + 4V {618}. **su:** Wheat 4VL (4D), Yangmai 5 {618}. **ma:** Distally located; Cent...*Xcdo949-4V* – 16 cM – *Pch*$_{\mathrm{Dv}}$ – 17 cM – *Xbcd588-4V* {618}.

QTL

QPch.jic-5A {10771}. **bin:** 5AL-6 0.68-0.78. **ma:** Closely associated with *Xgwm639-5AL* {10771}.

3.30. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*Disease: Bunt, dwarf smut, stinking smut.

BT1

Bt1. [*M1* {135}]. 2B {1310}. **s:** CS*7/White Federation 38 {1304}. **v:** Albit {129}; Banner Berkeley {129}; Federation 41 {137}; Regal {129}; Sherman {137}; White Federation 38 {1166}; White Odessa {137}. **v2:** Columbia *Bt6* {1005}; Hussar *Bt2* {135}; Hyslop *Bt4* {733}; Martin *Bt7* {135}; McDermid *Bt4* {734}; Odessa *Bt7* {137}; Tyee *Bt4* {22}.

BT2

Bt2. [*H* {129}]. **v:** Canus {137}; Seln 1102 {11693}; Seln 2092 {11693}; Selection PS60-1-1075 {551}; Selection 1403 {137}. **v2:** Hussar *Bt1* {135}.

BT3

Bt3. **v:** Florence {202}, {203}; Ridit {1395}, {1000}, {152}.

BT4

Bt4. [*T* {136}]. 1B {1274, 1285, 1005}. **v:** Bison {1285}; CI15588 {11693}; Kaw {1285}; Nebred {1285}; Omaha {1285}; Oveson {1235}; Tres {heterogeneous} {23}; Turkey 1558 {137}; Turkey 2578 {137}. **v2:** Hyslop *Bt1* {733}; McDermid *Bt1* {734}; Oro *Bt7* {137}; Turkey 3055 *Bt7* {137}; Tyee *Bt1* {22}. Since *Bt4* and *Bt6* are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of *Bt4*, and Rio should be used as the source of *Bt6*

BT5

Bt5. 1B {1001}. **v:** Hohenheimer{397}; Selection R60-3432 {551}.

BT6

Bt6. [*R* {1418}]. 1B {1005}. **v:** Rio {1418}; Turkey 10095 & 10097 {53}. **v2:** Columbia *Bt1* {1005}.

Since *Bt4* and *Bt6* are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of *Bt4*, and Rio should be used as the source of *Bt6*. [T{136}].

BT7

Bt7. [*M2* {1275}]. 2D {1000}. **s:** CS*7/Cheyenne 2D {1000}. **v:** Baart {1275}; Cheyenne {1000}; Federation {1275}; Gallipoli {1000}; Onas {1275}; Ranee {1000}; Selection 1833 {556}; Seln500-77 {11693}. **v2:** CI 7090 *Bt9* {1000}; Martin *Bt1* {137}; Odessa *Bt1* {137}; Oro *Bt4* {1000}; Turkey 3055 *Bt4* {1000}.

BT8

Bt8 {1558}. **v:** HY476 {10181}; M822161 {11693}; PI 178210 {1558}; Yayla 305 {1558}.

BT9

Bt9 {1006}. 6DL {11299}. **v:** PI 166910 {1006}; PI 166921 {1006}; PI 167822 {1006}; PI 554099 {11299}; Selection M69-2073 {551}; M90387 {11693}. **v2:** CI 7090 *Bt7* {1000}; Jeff *Bt10* {1436}; PI 178383 *Bt10* {1006}; Ranger *Bt10* {1438}.

Not clearly differentiated from *Bt11* {11693}.

BT10

Bt10 {1004}. [*QCbt.spa-6D* {M11298}]. 6DS {10721}. **i:** BW553 = Neepawa*6//Red Bobs/PI 178383 {10475}. **v:** AC2000 {10181}; AC Cadillac {10181}; AC Carma {10181}; AC Crystal {10181}; AC Foremost {10181}; AC Taber {10181}; AC Vista {10181}; Fairview {1183}; M822102 {11693}; PI 116301 {1004}; PI 116306 {1004}; PI 554118 {11299}; Selection M69-2094 {551}. **v2:** Jeff *Bt9* {1436}; PI 178383 *Bt9* {1000}; Ranger *Bt9* {1438}; Others {128, 239}. **ma:** *Bt10* was completely linked with a 590 bp fragment produced by UBC primer 196 {239}; RAPD – 1.5 cM – *Bt10* {763};

Bt10/FSD_RSA – 19.3 cM – *Xgwm469-6D* – 1.8 cM – *Xwmc749-6D*. The RAPD fragment was sequenced and converted to a diagnostic PCR marker for *Bt10* in {0128}.
Present in lines with *SrCad* {10733}.

BT11

Bt11 {10997}. *QBt.ifa-6DL* {11693}. 3B {11297}; 6DL {11693}. **v:** M822123 = PI 554119 {10997, 11693}; Elgin/PI 166910 {10997, 11693}. **ma:** May be associated with *Xbarc180*, *Xwmc623*, *Xwmc808* and *Xgwm285* {11297}; Located between 492.6 and 495.2 Mbp, CS RefSeq 2.1 {11693}.
Not clearly differentiated from *Bt9* {11693}.

BT12

Bt12 {10997}. [*QBt.ifa-7DS* {11469}]. 7DS {11469}. **v:** PI 119333 {10997}. **ma:** Associated with 13 markers in a distally located physical region of ~4.3 Mbp {11469}. Validated KASP markers were derived from *IWB61302* and *IWB50978* {11469}. Although appearing to be proximal to *QDB.ui*-7DS {11182} the genes were not clearly distinguished.

BT13

Bt13 {10997}. **v:** Thule III {10997}; PI 181463 {10997}.

BT14

Bt14 {10997}. **tv:** Doubbi CI 13711 {10997}.

BT15

Bt15 {10997}. **tv:** Carleton CI 12064 {10997}.

Temporary desisgnation

Btp {10997}. **v:** PI 173437 {10997}.

QTL

Blizard (R) / 8405-JC3C (S): DH population. Resistance and markers *Xgwm374-1BS, Xgwm364-1BS* and *Xbarc128-1BS* were within a 3.9 cM interval {10783}.

Carberry / AC Cadillac: AC Cadillac contributed QTL *QCbt.spa-6D* (*Bt10*) on chromosome 6D (markers *XwPt-1695*, *XwPt-672044*, and *XwPt-5114*). Carberry contributed *QCbt.spa-1B* (*XwPt743523*), *QCbt.spa-4B* (*XwPt 744434 – Xwmc617*), *QCbt.spa-4D* (*XwPt-9747*), *QCbt.spa-5B* (*XtPt-3719*), and *QCbt.spa-7D* (*Xwmc273-7D*) {11298}.

Idaho 444 (R) / Rio Blanco S: RIL population: Three QTL for dwarf bunt resistance: *QDB.ui-7DS* (R^2 = 0.3-0.6), *QDB.ui-1A* (R^2 = 0.11-0.15) and *QDB.ui-2B* (R^2 = 0.06). Two PCR-based markers were developed for the wPt-2565 sequence on chromosome 7DS {11182}.

IDO835 (R) / Moreland (S): DH population: *Q.DB.ui-6DL* (PVE 0.53, *Bt9* region) and *Q.DB.ui-7AL* (PVE 0.38) {11400}.

Trintella / Piko: DH population: One major gene in the chromosome 1BS centromere region, nearest marker *Xgwm273-1B* {11003}. Smaller QTL effects were detected on chromosomes 7A, 7B and 5B in different years. Additional QTL are listed in {18099}.

3.31 Reaction to *Tilletia indica* Mitra

Disease: Karnal bunt.

KB1

Kb1 {394}. **v:** Chris {394}. **v2:** CMH77.308 *Kb2* {394}.

KB2

Kb2 {394}. **v:** PF7 113 {394}. **v** CMH77. 308 *Kb1* {394}; Shanghai #8 *Kb4* {394}.

KB3

Kb3 {394}. **v:** Amsel {394}.

KB4

Kb4 {394}. **v:** Shanghai #8 *Kb2* {394}.

KB5

Kb5 {394}. Recessive {394} **v2:** Pigeon *Kb6* {394}.

KB6

Kb6 {394}. Recessive {394} **v2:** Pigeon *Kb5* {394}.

QTL NEED TO SPECIFY GERMPLASM BELOW

Qkb.cnl-3B {9956}. **ma:** Located in the interval *XATPase-3B* – *Xcdo1164-3B*.

Qkb.cnl-5A.1 {9956}. **ma:** Located in the interval *Xmwg2112-5A* – *Xcdo20-5A*.

Qkb.cnl-5A.2 {9956}. **ma:** Located in the interval *Xabg391-5A* – *Xfba351-5A*.

Qkb.ksu-4BL.1. WL711/HD29 (R): RILs: $R^2 = 0.25$, associated with *Xgwm538-4B* {10498}. WH542/W485 (R) RILs: $R^2 = 0.15$, *Xgwm6-4BL – Xwmc349-4BL* interval {10499}.

Qkb.ksu-5BL.1. WH542/HD29 (R): RILs: $R^2 = 0.19$, *Xgdm116-5BL – Xwmc235-5BL* {10499}.

Qkb.ksu-6BS.1. WH542/HD29 (R): RILs: $R^2 = 0.13$, *Xwmc105-6BS – Xgwm88-6BS* {10499}.

3.32. Reaction to *Ustilago tritici* (Pers.) Rostrup

Disease: Loose smut.

UT1

Ut1 {1073}. **v:** Florence/Aurore {1073}; Renfrew {1073}; Red Bobs {1074}.

UT2

Ut2 {1073}. **v:** Kota {1073}; Little Club {1073}.

UT3

Ut3 {1074}. **v:** Carma {1074}.

UT4

Ut4 {1074}. [*QUt.spa-7B* {11168}]. 7B {11168}. **v:** 9340-CP {11168}; Glenlea {11168}; TD1 {11168}; Thatcher/Regent {1074}.

UT5

Ut5 {10940}. [*Ut-Fore* {10940}, *Ut-X* {11164}]. 5BL {10940}. **v:** Foremost {10940}. **ma:** *Xgpw5029* – 2.8 cM – *Ut5* – 1.3 cM – *Xbarc232-5b* {10940}. See *Ut-x*.
Race T10 was used for analysis {10940}.

UT6

Ut6 {11169}. [*QUt.spa-5B* {11168}]. 5BL {11169}. **v:** AC Foremost {11169}; AC Karma {10040}; AC Vista {11168}; Chinese Spring {11169}; Glenlea {11169}; HY320 {11169}; Oasis {11169}. **ma:** *Xgpw5029-5B* – 2.8 cM – *Ut6* – 2.8 cM – *Xbarc232-5B* {11169}.

UT7

Ut7 {11168}. [*QUt.spa.7A* {11168}]. 7A {11168}. **v:** SC8021V2 {11168}.

UT8

Ut8 {11168}. [*QUt.spa-3A* {11168}]. 3A {11168}. **v:** 9340-SP {11168}; Glenlea {11168}.

UT9

Ut9 {11168}. [*QUt.spa-6B* {11168}]. 6B {11168}. **v:** SC8021V2 {11168}.

UT10

Ut10 {11168}. [*QUt.sps-6D* {11168}]. 6D {11168}. **v:** SC80-21V2 {11168}.

UT11

Ut11 {11406}. 7BS {11406}. **v:** DH line TD14XDIA*B0075, CN 120264 {11406}; Sonop, TD-14 {11406}. **ma:** Co-segregation with *BS00022562_51, Excabibur_C3489_182* and *Kukri_rep_c71778_644* at 0.43, 1.20 and 1.25 Mbp {11406}.
Ut11 conferred resistance to race T2 but not T9 and T39; resistance to those races (and race T2) was conferred by *QUt.mrc-5B* {11406}.

Temporary designations

UtBW278 {11729}. 5BS {11729}. **v:** BW728 {11729}. **ma:** Mapped to a region close to *Utd1* {11729}.
Identified in a BW278 / AC Foremost cross with a *Ustiago teitici* isolate virelent to AC Foremost {11729}.

Utd1 {10684}. 5BS {10684}. **tv:** D93213 {10684}; P9163-BJ08*B {10684}; VIR 51658 {10684}. **ma:** SCAR – 3.2 cM – *Utd1* – 5.9 cM – *Xgwm234-5B* {10684}.

Ut-x {11164}. **v:** Biggar BSR {11164}. **ma:** *Xcrc4-2B* – 14 cM – *Ut-x* – 10 cM – *Xabc153-2B.2* {11164}; *Xcrc4-2B.2* (Syn. *Xcrc4.2*) is a SCAR.
Resistance to race 19 was associated with chromosome 6A of Cadet, Kota, Thatcher and TD18 {0208}. In the case of Cadet, resistance was localized to 6AS {0208}.

3.33. Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)

WSSMV is soil-borne and vectored by the fungus *Polymxa graminis*. This virus has some sequence similarity to Wheat Yellow Mosaic virus {10285}. Wheat streak mosaic disease can also be caused by Triticum mosaic virus, which is also known as High Plains Wheat mosaic virus. Low rates of seed borne transmission of WSSMV are reported.

WSS1

Wss1 {10271}. Derived from *Haynaldia villosa*. T4VS.4DL {10271}. 4D(4DL.4VS) {10271}. **tr:** NAU413 {10271}. **su:** Yangmai#5 4V(4D) {10271}.
A number of secondary translocations were induced, the smallest of which was NAU421 (FL 0.78-1.00) {11488}.

QTL

Geneva (R) / Augusta (S): 79% of the variation between these accessions was associated with markers *Xbcd1095-2D* and *Xcdo373-2D* located 12.4 cM apart in chromosome 2DL {0131}.

3.34. Reaction to Mosaic Virus

Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella*. See: Resistance to colonization by *Eriophyes tulipae*. According to {10226} WSMV may also be see-borne. At least some sources of resistance to WSMV are also effective against Triticum mosaic virus.

WSM1

Wsm1 {379}, {440}. Derived from *Th. intermedium*.

4D = T4DL.$4J^{S}S$ {389}, {391}; T4DL.4DS-4JSS {10788}. **i:** Karl*4/CI 17884 = PI 583794 = KS93WGRC27 {440}; Line E*6/rec213 (*Sr64*, *Wsm1*) = GSTR 527 {11644, https://npgsweb.ars-grin.gov/gringlobal/accessiondetail?id=2158211}. **v:** CA74 {10971}; CI 17766 = B-6-37-1 {1543}, {800}, {391}; CI 17884 {391}; S90H445 {391}; KS90H450 {391}; CI 17883 {389}; Mace PI 651043 {11006, 11179, 11643}; KS03HW12 {11006}; KS08WGGRC50 {10788}. **ad:** CI 17881 {391}; CI 17886 {391}. **su:** CI 15092 {391}; CI 17882 {391}; CI 17885 {391}. **ma:** *Wsm1* co-segregated with a STS amplified by the primer set STSJ15 {1456}; KASP markers developed in {11643}.
Wsm1 is located in $4J^{S}S$ (formerly 4Ai#2S). CI 17882, CI 17884, CI 17885 and KS90H445 also carry a 7S *Ae. speltoides* chromosome substituting for 7A (See Reaction to *Schizaphis graminum*).
Wsm1 also confers resistance to Triticum Mosaic Virus {10788}. *Wsm1* confers resistance at temperatures below 19C {11179}.

WSM2

Wsm2 {10898, 10802}. 3BS {10802}. **v:** Clara CL PI 1665948 {11329}; CO960293-2 {10802}; Oakley CL PI 670190 {11329}; RonL {10898}; Snowmass {10802}. **ma:** *Wsm2* – 5.2 cM – *XSTS3B-55* {10802}; *Xbarc102-3B* – 1.6 cM – *Wsm2* {10802}; *Xgwm389-3B* – 30.8 cM – *Wsm2* – 45.2 cM – *Xgwm566-3B* {10898}; *Xbarc87-3B* – 4.4 cM – *Wsm2* – 3.9 cM – *Xbarc102-3B* {10982}; Eight SNP markers were mapped within 1 cM of *Wsm2* {11329}. KASP markers were developed from some of these SNP {11330}; Mapped to a 4.0 Mb region in distal arm 3BS carrying 142 candidate genes, six of which were differentially expressed in Snowmass relative to susceptible Antero {11654}.

Wsm2 confers resistance at temperatures below 19C {10802}. Allele $Xbarc102\text{-}3B_{219}$ was the best predictor for *Wsm2* {10982}.

WSM3

Wsm3 {10775}. 7B {10775}. 7B (7BS.7S#3L) {10775}. TBS.7S#3L {10775}. **v:** KS12WGGRC59 TA5624 {10775}.
Wsm3 was also effective against Triticum mosaic virus at 18C {10775}.

For a review of WSMV see {11656}.

3.35. Reaction to *Xanthomonas campestris* pv. *undulosa*

Disease: Bacterial leaf streak

BLS1

Bls1 {244}. **v2:** Pavon *Bls2* {244}; Mochis T88 *Bls3 Bls4* {244}; Angostura F88 *Bls5* {244}.

Bls2 {244}. **v2:** Pavon *Bls1* {244}.

Bls3 {244}. **v2:** Mochis T88 *Bls1 Bls 4*{ 244}.

Bls4 {244}. **v2:** Mochis T88 *Bls1 Bls3* {244}.

Bls5 {244}. **v2:** Turnco F88 {244}; Angostura F88 *Bls1* {244}.

bls1 bls2 bls3 bls4 bls5: Alondra {244}.

3.36. Resistance to Colonization by *Eriophyes tulipae* (*Aceria tulipae*)

Mite pest: Wheat curl mite.
Eriophyes tulipae is the vector of wheat streak mosaic virus (WSMV) and the wheat spot mosaic agent (WSpM).

CMC1

Cmc1 {1467}. 6DS {1576}. **i:** Norsa*5/Cmc1 {10166}. **v:** *Ae. squarrosa* CI4/Novamichurinka (= AC PGR 16635) {1467}; Norstar derivative {222}.

CMC2

Cmc2 {1573}. Derived from *Th. elongatum*. 6A = T6AS.6Ae#2S {389}. 5B = T5BL.6Ae#2S {389}. 6D {1575} = T6DL.6Ae#2S {389}, {1575}. **i:** Norstar*5/Cmc2 {10166}. **v:** 875-94-2 {389}. **tr:** Rescue Derivative {1575}. **su:** Cadet 6Ae#2(6A) {1575}; Cadet 6Ae#2(6D) {1574}; Rescue 6Ae#2(6A) {1574}; Rescue 6Ae#2(6B) {1574}; Rescue 6Ae#2 (6D). **ad:** Cadet + mono-6Ae#2 {1574}; Rescue + 6Ae#2 {1574}.

CMC3

Cmc3 {222}. Derived from *Secale cereale.* 1A = 1AL.1RS. **i:** Norstar*5/Cmc3 {10166}. Need to confirm relationship of 1RS segment in Amigo and Salmon as this NIL was derived from KS80H4200 a Chinese Spring Salmon line {10166}. **v:** Amigo; TAM107 {222}. **v2:** KS96GRC40 *Cmc4* {222}. **ma:** Wheat lines with the 1RS segment and hence *Cmc3* can be selected with the rye-specific SSR *Xscm09-1R* {222};

CMC4

Cmc4 {222}. 6DS {222}. **v2:** KS96WRC40 *Cmc3* {222}. **v:** TAM112 {11612}; TAM115 {11612}; TAM204 {11612}. **dv:** *Ae. tauschii* accession {222}; *Ae. tauschii* TA1618 (11612}. **ma:** *XksuG8-6D* – 6.4 cM – *Cmc4* – 4.1 cM – *Xgdm141-6D* {222}.

3.37. Reaction to Wheat Yellow Mosaic Virus

WYMV is soil-borne and vectored by the fungus *Polymixa graminis*. This virus has some sequence similarity to Wheat Spindle Streak Mosaic {10258}, another bymovirus.

Temporary designations

YmIb {10750}. 2DL {10750}. **v:** Ibis {10750}; Jagger {10750}; KS 831957 {10750}; Madsen {10750}; Yumechikara {10750}. **ma:** *Xwmc181-2D* – 12.4 cM – *YmIb* – 2.0 cM – *Xcfd16-2D* – 2.0 cM – *Xwmc41-2D* – 3.1 cM – *Xcfd168-2D* {10750}.
The relationship of *YmIb* to a previously mapped gene in 2DL for resistance to WYMV and WSSMV in Yangfu 9311 {10258} and a Geneva derivative {0131} was not established.

YmYF {10258}. 2DL {10258}. **v:** Yangfu 931 {10258}. **ma:** *Xpsp3039-2D/Xwmc181-2D* – 0.7 cM – *Xwmc41-3D* – 8.1 cM – *Xgwm349-2D* {10258}.

QYm.nau-2D {11186}. *Q.Ymym* {11660}. 2DL {11186}. **bin:** 2DL9-0.76-1.00. **v:** Fielder {11645}; Yining Xiaomai {11186}. **ma:** *Xwmc41-2D* – 3.7 cM – *2SNP86.2* – 0.4 cM – *QYm.nau-2D* – 1.0 cM – *2EST784* {11186}.

According to {11645} *QYm.nau-2D* is a natural alien translocation from an *Aegilops* species and several subsequent wheat haplotypes arose from rare recombination events. This QTL is present in a wide range of cultivars from Europe, USA, Japan, and China {11645}.

QTL

Xifeng(R) / Zhen 9523(S): RIL population: Three QTLs, *Qym.njuy5A.1* (R^2 = 0.26-0.54), *Ym.njau-3B.1* (R^2 = 0.03-0.01) and *QYm.njau-7B.1* (R^2 = 0.03-0.05 in some trials). The chromosome 5A gene was closely associated with *Xwmc415.1*, *CINAU152* and *CINAU153* and was phenotyped as a single Mendelian gene {11073}.

Wheat Gene Catalogue – 4. References

1.	Ackerman A 1943 (Experiments to increase the yield from spring wheat, I. Crosses with Brunt Schlanstedter [Brown Schlanstedter] spring wheat with a description of Svalofs Progress spring wheat). Sveriges Utsadesforenings Tidskrift 53: 51-66. *Cited* Plant Breeding Abstracts 14: 173, p.42.
2.	Ackerman A & MacKey J 1949 (Attempts to improve the yield of spring wheat II. Crosses between spring and winter wheat. Descriptions of Svalov's Ella spring wheat). Sveriges Utsadesforenings Tidskrift 59: 105-117. *Cited* Plant Breeding Abstracts 20: 197, p.65.
3.	Acosta AC 1963 The transfer of stem rust resistance from rye to wheat. Dissertation Abstracts 23: 34-35.
4.	Ahn SN & Tanksley SD 1993 Comparative linkage maps of the rice and maize genomes. Proceedings of the National Academy of Sciences, USA 90: 7980-7984.
5.	Ainsworth C 1995 Personal communication.
6.	Ainsworth CC 1983 The genetic control of hexokinase isozymes in wheat. Genetical Research, Cambridge 42: 219-227.
7.	Ainsworth CC, Doherty P, Edwards KGK, Martienssen RA & Gale MD 1985 Allelic variation at a-amylase loci in hexaploid wheat. Theoretical and Applied Genetics 70: 400-406.
8.	Ainsworth CC, Gale MD & Baird S 1983 The genetics of beta-amylase isozymes in wheat. Allelic variation among hexaploid varieties and intrachromosomal gene locations. Theoretical and Applied Genetics 66: 39-49.
9.	Ainsworth CC, Gale MD & Baird S 1984 The genetic control of grain esterases in hexaploid wheat. Theoretical and Applied Genetics 68: 219-226.
10.	Ainsworth CC, Gale MD & Miller TE 1986 Genetic control of grain esterases in hexaploid wheat II. Homoeologous loci in related species. Theoretical and Applied Genetics 72: 219-225.
11.	Ainsworth CC, Hosein F, Tarvis M, Weir F, Burrell M, Devos KM & Gale MD 1995 Adenosine diphosphate glucose pyrophosphorylase genes in wheat: differential expression and gene mapping. Planta 197: 1-10.
12.	Ainsworth CC, Johnson HM, Jackson EA, Miller TE & Gale MD 1984 The chromosomal locations of leaf peroxidase genes in hexaploid wheat, rye and barley. Theoretical and Applied Genetics 69: 205-210.
13.	Ainsworth CC, Miller TE & Gale MD 1987 a-amylase and beta-amylase homoeoloci in species related to wheat. Genetical Research, Cambridge 49: 93-103.
14.	Aliev EB, Musaev AD & Maystrenko OI 1982 (Identification of the gene *R2* controlling grain colour in the spring bread wheat variety Diamant 2). Izv. SO AN SSSR. Ser. Bio. N. (1981) 15: 75-79. *In*: Referativnyi Zhurnal (1982) 5.65.107; *Cited* Plant Breeding Abstracts 54: 798, p.799.
15.	Allan RE 1970 Differentiating between two Norin 10/Brevor 14 semi-dwarf genes in a common genetic background. Seiken Ziho 22: 83-90.
16.	Allan RE & Vogel OA 1960 F1 monosomic analysis involving a smooth-awn durum wheat. Wheat Information Service 11: 3-4.
17.	Allan RE & Vogel OA 1965 Monosomic analysis of red seed colour in wheat. Crop Science 5: 475.
18.	Allan RE, Heyne EG & Jones ET 1956 Relationship of sources of Hessian fly and leaf rust resistance in several wheat crosses involving a white winter wheat Abstracts of the Annual

	Meeting of the American Society of Agronomy Cincinatti, Ohio. P.I. 119344-9. *Cited* Plant Breeding Abstracts1307, p. 224.
19.	Allan RE, Heyne EG, Jones ET & Johnston CO 1959 Genetic analysis of ten sources of Hessian fly resistance, their interrelationships and association with leaf rust reaction in wheat. Kansas Agricultutal Experiment Station Technical Bulletin 104: 51pp.
20.	Allan RE, Petersen CJ Jr, Rubenthaler GL, Line RF & Roberts DE 1989 Registration of 'Madsen' wheat. Crop Science 29: 1575-1576.
21.	Allan RE, Petersen CJ Jr, Rubenthaler GL, Line RF & Roberts DE 1990 Registration of 'Hyak' wheat. Crop Science 30: 234.
22.	Allan RE, Peterson CJ, Line RF, George DW & Rubenthaler GL 1980 Registration of 'Tyee' wheat. Crop Science 20: 829-830.
23.	Allan RE, Peterson CJ, Rubenthaller GL, Line RF & Morrison KJ 1986 Registration of 'Tres' wheat. Crop Science 26: 203-204.
24.	Allan RE, Vogel OA & Peterson CJ 1968 Inheritance and differentiation of semi-dwarf culm length of wheat. Crop Science 8: 701-704.
25.	Amri A, Cox TS, Gill BS & Hatchett JH 1990 Chromosomal location of the Hessian fly resistance gene *H20* in 'Jori' durum wheat. Journal of Heredity 81: 71-72.
26.	Amri A, Cox TS, Hatchett JH & Gill BS 1990 Complementary action of genes for Hessian fly resistance in wheat cultivar 'Seneca'. Journal of Heredity 81: 224-226.
27.	Anderson JA & Maan SS 1995 Interspecific nuclear-cytoplasmic compatibility controlled by genes on group 1 chromosomes in durum wheat. Genome 38: 803-808.
28.	Anderson JA, Ogihara Y, Sorrells ME & Tanksley SD 1992 Development of a chromosomal arm map for wheat based on RFLP markers. Theoretical and Applied Genetics 83: 1035-1043.
29.	Anderson MK, Williams ND & Maan SS 1971 Monosomic analysis of genes for stem rust resistance derived from Marquis and Reliance wheat. Crop Science 11: 556-558.
30.	Anderson OD, Greene FC, Yip RE, Halford NG, Shewry PR & Malpica-Romero J-M 1989 Nucleotide sequence of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, *Triticum aestivum* L. cv. Cheyenne. Nucleic Acids Research 17: 461-462.
31.	Anderson RG 1961 The inheritance of leaf rust resistance in seven varieties of common wheat. Canadian Journal of Plant Science 41: 342-359.
32.	Anderson RG 1966 Studies on the inheritance of resistance to leaf rust of wheat. Proceedings of the 2nd International Wheat Genetics Symposium Lund, Sweden 1963, (Mackey J ed.) Hereditas Supplement 2: 144-155.
33.	Anonymous 1971 CIMMYT Annual Report 1969-70.
34.	Anonymous 1976 Annual Report, Plant Breeding Institute Cambridge, 1975. 109.:
35.	Anonymous 1979 Enzyme Nomenclature (1978). Recommendations of the Nomenclature Committee of the International Union of Biochemistry. Academic Press, New York.
36.	Anonymous 1984 Enzyme Nomenclature (1984). Recommendations of the Nomenclature Committee of the International Union of Biochemistry. Academic Press, New York.
37.	Appels R & Dvorak J 1982 The wheat ribosomal DNA spacer region: its structure and variation in populations and among species. Theoretical and Applied Genetics 63: 337-348.
38.	Appels R, Driscoll CJ & Peacock WJ 1978 Heterochromatin and highly repeated DNA sequences in rye (*Secale cereale*). Chromosoma 70: 67-89.

39.	Appels R, Gerlach WR, Dennis ES, Swift H & Peacock WJ 1980 Molecular and chromosomal organization of DNA sequences coding for the ribosomal RNA's in cereals. Chromosoma 78: 293-311.
40.	Arbuzova VS 1989 Development of isogenic forms of wheat Saratovskaya 29 for introducing dominant gene-markers for separate chromosomes in monosomic lines. Cytogenetics of Agricultural Plants (Shumnyi VK & Shchapova AI eds). Novosibirsk, 1989. (In Russian). pp. 147-160.
41.	Arbuzova VS 1994 Chromosome localization of genes *Pp* for purple grain pigmentation introgressed into common wheat. Genetika (Supplement) 30: 9.
42.	Arbuzova VS, Efremova TT, Laikova LI, Maystrenko OI, Popova OM & Pshenichnikova TA 1996 The development of precise genetic stocks in two wheat cultivars and their use in genetic analysis. Euphytica 89: 11-15.
43.	Artemova NV 1982 Chromosomal control of the isoenzymes of alcohol dehydrogenase, esterase, and amylase in different rye varieties. Genetika 18: 661-667.
44.	Asakura N, Nakamura C & Ohtsuka I 1997 RAPD markers lined to the nuclear gene from *Triticum timopheevii* that confers compatability with *Aegilops squarrosa* cytoplasm on alloplasmic durum wheat. Genome 40: 201-210.
45.	Aslam M 1958 Genetic studies in interspecific crosses between durum, sphaerococcum and vulgare types of wheat. Agriculture, Pakistan 9: 109-119. *Cited* Plant Breeding Abstracts 39: 2451, p.471.
46.	Athwal DS & Watson IA 1955 Inheritance of reaction to wheat stem rust in crosses involving Marquillo, Thatcher and Hochzucht. Proceedings of the Linnaean Society of New South Wales 80: 113-129.
47.	Ausemus ER, Harrington JB, Reitz LP & Worzella WW 1946 A summary of genetic studies in hexaploid and tetraploid wheats. Journal of the American Society of Agronomy 38: 1082-1099.
48.	Autrique E, Singh RP, Tanksley SD & Sorrells ME 1995 Molecular markers for four leaf rust resistance genes introgressed into wheat from wild species. Genome 38: 75-83.
49.	Bacon RK, Kelly JT & Milus EA 1996 Registration of 'Hazan' wheat. Crop Science 36: 209-210.
50.	Badebo A, Stubbs RW, van Ginkel M & Gebeyehu G 1990 Identification of resistance genes to *Puccinia striiformis* in seedlings of Ethiopian and CIMMYT bread wheat varieties and lines. Netherlands Journal of Plant Pathology 96: 199-210.
51.	Bagnara D & Rossi L 1972 A liguleless mutation radioinduced in *Triticum durum* Desf. Wheat Information Service 33-34: 1-3.
52.	Baier AC, Zeller FJ, Oppitz K & Fischbeck G 1973 Monosomenanalyse der Mehltau und Schwarzrostresistenz des Sommerweizens 'Solo'. Zeitschrift fur Pflanzenzuchtung 70: 177-194.
53.	Baker EP 1967 Inheritance of resistance to bunt in Turkey wheat selections. Proceedings of the Linnaean Society of New South Wales 90: 189-210.
54.	Baker EP, Sanghi AK, McIntosh RA & Luig NH 1970 Cytogenetical studies in wheat III. Studies of a gene conditioning resistance to stem rust strains with unusual genes for avirulence. Australian Journal of Biological Sciences 23: 369-375.
55.	Baker RJ 1977 Inheritance of kernel hardness in spring wheat. Crop Science 17: 960-962.
56.	Baker RJ 1981 Inheritance of seed coat colour in eight spring wheat cultivars. Canadian Journal of Plant Science 61: 719-721.

57.	Balzer H-J, Borysiuk L, Meyer H-M, Matzk F & Baumlein H 1996 A pollen allergen encoding gene is expressed in wheat ovaries. Plant Molecular Biology 32: 435-445.
58.	Banks PM 1996 Personal communication.
59.	Banks PM, Larkin PJ, Bariana HS, Lagudah ES, Appels R, Waterhouse PM, Brettell RIS, Chen X, Xu HJ, Xin ZY, Qian YT, Zhou XM, Cheng ZM & Zhou GH 1995 The use of cell cultures for subchromosomal introgressions of barley yellow dwarf virus resistance from *Thinopyrum imtermedium* to wheat. Genome 38: 395-405.
60.	Barber HN, Driscoll CJ, Long PM & Vickery RS 1968 Protein genetics of wheat and homoeologous relationships of chromosomes. Nature 218: 450-452.
61.	Barber HN, Driscoll CJ, Long PM & Vickery RS 1969 Gene similiarity of the Triticinae and the study of segmental interchanges. Nature 222: 897-898.
62.	Bariana HS & McIntosh RA 1993 Cytogenetic studies in wheat XV. Chromosome location of rust resistance genes in VPM1. Genome 36: 476-482.
63.	Barkardottir RB, Jensen BF, Kreiberg JD, Nielsen PS & Gausing K 1987 Expression of selected nuclear genes during leaf development in barley. Developmental Genetics 8: 495-511.
64.	Barlow KK & Driscoll CJ 1981 Linkage studies involving two chromosomal male-sterility mutants in hexaploid wheat. Genetics 98: 791-799.
65.	Bartels D & Thompson RD 1983 The characterization of cDNA clones coding for wheat storage proteins. Nucleic Acids Research 11: 2961-2977.
66.	Bartels D, Altosaar I, Harberd NP, Barker RF & Thompson RD 1986 Molecular analysis of gamma-gliadin gene families at the complex *Gli-1* locus of bread wheat (*T. aestivum* L.). Theoretical and Applied Genetics 72: 845-853.
67.	Bartos P & Kosner J 1995 Monosomic analysis of resistance to stem rust in the winter wheat cultivar Zdar (Boheme). Cereal Rusts and Powdery Mildews Bulletin 23: 1-4.
68.	Bartos P & Stuchlikova E 1986 Genes for rust resistance. Annual Wheat Newsletter 32: 65-66.
69.	Bartos P & Stuchlikova E 1988 Genes for leaf rust resistance in productive wheats. Proceedings of the 7th European and Mediterranean Cereal Rusts Conference Vienna, Austria (B. Zwatz ed.): 85-87.
70.	Bartos P & Stuchlikova E 1989 Stem rust resistance of the wheat cultivar Maris Fundin. Cereal Rusts and Powdery Mildews Bulletin 17: 10-15.
71.	Bartos P & Valkoun J 1988 Rust resistance genes in Czechoslovak wheats. Cereal Rusts and Powdery Mildews Bulletin 16: 36-40.
72.	Bartos P, Green GJ & Dyck PL 1970 Reaction to stem rust and genetics of stem rust resistance in European wheat varieties. Canadian Journal of Botany 48: 1439-1443.
73.	Bartos P, Johnson R & Stubbs RW 1987 Postulated genes for resistance to yellow rust in Czechoslavakian wheat cultivars. Cereal Rusts Bulletin 15: 79-84.
74.	Bartos P, Samborski DJ & Dyck PL 1969 Leaf rust resistance of some European varieties of wheat. Canadian Journal of Botany 47: 543-546.
75.	Bartos P, Stucklikova E & Kubova R 1984 Wheat leaf rust epidemics in Czechoslovakia in 1983. Cereal Rusts Bulletin 12: 40-41.
76.	Bartos P, Tersova R & Slovencikova V 1983 Genetics of rust resistance in Czechoslovak wheat cultivars. Tag.-Ber., Akad. Landwirtsch. -Wiss. DDR, Berlin 216: 555-560.
77.	Barulina H 1933 (Comparative genetic study of the species of *Triticum*, I. Inheritance of the ligule in wheat species with different chromosome numbers: *T. vulgare* Vill., *T.*

	compactum Host., *T. durum* Desf.). Bulletin of Applied Botany Leningrad Series 2(5): 127-165. *Cited* Plant Breeding Abstracts 4: 951, p. 291.
78.	Baulcombe DC & Bufford D 1983 Gibberellic-acid-regulated expression of a-amylase and six other genes in wheat aleurone layers. Planta 157: 493-501.
79.	Baulcombe DC, Barker RF & Jarvis MG 1987 A gibberellin response wheat gene has homology to yeast carboxypeptidase Y. Journal of Biological Chemistry 262: 13726-13735.
80.	Baulcombe DC, Huttly AK, Matienssen RA, Barker RF & Jarvis MG 1987 A novel wheat a-amylase gene (a-*Amy3*). Molecular and General Genetics 209: 33-40.
81.	Bayles RA & Herron C 1986 Yellow rust of wheat. UK Cereal Pathogen Virulence Survey, Annual Report, National Institute Agricultural Botany 15-20.
82.	Bayles RA & Priestley RH 1983 Yellow rust of wheat. UK Cereal Pathogen Virulence Survey. 1982 Annual Report, National Institute Agricultural Botany 27-36.
83.	Bayles RA & Thomas JE 1984 Yellow rust of wheat. UK Cereal Pathogen Virulence Survey. 1983 Annual Report, National Institute Agricultural Botany 23-31.
84.	Ben Amer IM, Korzun V, Worland AJ & Borner A 1997 Genetic mapping of QTL controlling tissue-culture response on chromosome 2B of wheat (*Triticum aestivum*) in relation to major genes and RFLP markers. Theoretical and Applied Genetics 94: 1047-1052.
85.	Benedettelli S & Hart GE 1987 Genetic analysis of Triticeae shikimate dehydrogenase. Biochemical Genetics 26: 287-301.
86.	Benito C & Perez de la Vega M 1979 The chromosomal location of peroxidase isozymes of the wheat kernel. Theoretical and Applied Genetics 55: 73-76.
87.	Benito C & Salinas J 1983 The chromosomal location of malate dehydrogenase isozymes in hexaploid wheat. Theoretical and Applied Genetics 64: 255-258.
88.	Benito C, Figueiras AM & Gonzalez-Jaen MT 1984 Phosphoglucomutase - a biochemical marker for group 4 chromosomes in the Triticinae. Theoretical and Applied Genetics 68: 555-557.
89.	Benito C, Figueiras AM & Gonzalez-Jaen MT 1987 Location of genes coding isozyme markers on *Aegilops umbellulata* chromosomes adds data on homoeology among Triticiae chromosomes. Theoretical and Applied Genetics 73: 581-588.
90.	Benito C, Figueiras AM, Gonzalez-Jaen MT & Salinas J 1985 Biochemical evidence of homoeology between wheat and barley chromosomes. Zeitschrift fur Pflanzenzuchtung 94: 307-320.
91.	Benito C, Gallego FJ, Frade JM & Zaragoza C 1990 Chromosomal location of adenylate kinase isozymes in Triticeae species. Theoretical and Applied Genetics 79: 157-160.
92.	Benito C, Gallego FJ, Zaragoza C, Frede JM & Figueiras AM 1991 Biochemical evidence of a translocation between 6RL/7RL chromosome arms in rye (*Secale cereale* L.). A genetic map of 6R chromosome. Theoretical and Applied Genetics 82: 27-32.
93.	Benito C, Llorente F, Henriques-Gil N, Gallego FJ, Zaragosa C, Delibes A & Figueiras AM 1994 A map of rye chromosome 4R with cytological and molecular markers. Theoretical and Applied Genetics 87: 941-946.
94.	Benito C, Perez de la Vega M & Salinas J 1980 The inheritance of wheat kernel peroxidases. Journal of Heredity 71: 416-418.
95.	Benito MC, Sanchez M, Shin JS & Blake T 1988 A map of barley chromosome 2 using isozymic and morphological markers. Biochemical Genetics 26: 387-394.
96.	Bennett FGA 1982 Personal communication.

97.	Bennett FGA 1984 Resistance to powdery mildew in wheat: a review of its use in agricuture and breeding programmes. Plant Pathology 33: 279-300.
98.	Bennett FGA & van Kints T 1983 Mildew of wheat. UK Cereal Pathogen Virulence Survey. 1983 Annual Report, National Institute Agricultural Botany 7-21.
99.	Berg LA, Gough FJ & Williams ND 1963 Inheritance of stem rust resistance in two wheat varieties, Marquis and Kota. Phytopathology 53: 904-908.
100.	Bergman JW 1972 Chromosome locations of genes controlling esterase and malate dehydrogenase isozymes in *Triticum*. PhD Dissertation, North Dakota State University, Fargo, North Dakota.
101.	Bergman JW & Williams ND 1972 Isozyme variants of esterase and malate dehydrogenase among wheat aneuploids. Agronomy Abstracts p. 23.
102.	Berkelman T, Houtchens KA & DuPont FM 1994 Two cDNA clones encoding isoforms of the B subunit of the vacuolar ATPase from barley roots. Plant Physiology 104: 287-288.
103.	Bernard M, Autran JC & Joudrier P 1977 Possibilities d'identification de certains chromosomes de seigle a l'aide de marqueurs biochimiques. Annales d'Amelioration des Plantes 27: 355-362.
104.	Bethards LA, Skadsen RW & Scandalios JG 1987 Isolation and characterization of a cDNA clone for the *Cat2* gene in maize and its homology with other catalases. Proceedings National Academy Sciences, USA 84: 6830-6834.
106.	Bhowal JG & Jha MP 1969 An inhibitor of glume pigment in wheat. Canadian Journal of Genetics and Cytology 11: 226.
107.	Bietz JA, Shepherd KW & Wall JS 1975 Cereal single-kernel analysis of glutenin: use in wheat genetics and breeding. Cereal Chemistry 52: 513-532.
108.	Bimb HP & Johnson R 1996 Expression of the gene *Pm8* for powdery mildew resistance in wheat cultivars with the 1BL/1RS translocation which carries the gene *Yr9* for yellow rust resistance. Proceedings of the 9th European & Mediterranean Cereal Rusts & Powdery Mildews Conference, Lunteren, The Netherlands (Kema GHJ, Niks RE & Daamen RA, eds.) pp247.
109.	Blanco A & Simeone R 1982 Genetic control of gibberellic acid insensitivity in semidwarf durum wheat (*Triticum durum* Desf.). Zeitschrift fur Pflanzenzuchtung 88: 185-190.
110.	Blanco A, De Giovanni C, Laddomada B, Sciancalepore A, Simeone R, Devos KM & Gale MD 1996 Quantitative trait loci influencing grain protein content in tetraploid wheats. Plant Breeding 115: 310-316.
111.	Blanco A, Resta P, Simeone R, Parmar S, Shewry PR, Sabelli PW & Lafiandra D 1991 Chromosomal location of seed storage protein genes in the genome of *Daspyrum villosum* (L.) Candargy. Theoretical and Applied Genetics 82: 358-362.
112.	Bolton FE 1968 Inheritance of blue aleurone and purple pericarp in hexaploid wheat. Dissertation Abstracts 29: 844B. *Cited* Plant Breeding Abstracts 40: 2684, p.344.
113.	Bonhomme A, Gale MD, Koebner RMD, Nicolas P, Jahier J & Bernard M 1995 RFLP analysis of an *Aegilops ventricosa* chromosome that carries a gene conferring resistance to leaf rust (*Puccinia recondita*) when transferred to hexaploid wheat. Theoretical and Applied Genetics 90: 1042-1048.
114.	Borner A & Mettin D 1988 The genetic control of giberellic acid insensitivity of the wheat variety Ai-Bian 1. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 489-492.

115.	Borner A, Lehmann CO, Mettin D, Plaschke J, Schlegel R, Schlegel G, Melz G & Thiele V 1991 GA-insensitivity of 'Ai-bian 1a'/Pleiotropic effects of isogenic *Rht*-lines. Annual Wheat Newsletter 37: 59-60.
116.	Borner A, Plaschke J, Korzun V & Worland AJ 1996 The relationship between the dwarfing genes of wheat and rye. Euphytica 89: 69-75.
117.	Borner A, Roder MS & Korzun V 1997 Comparative molecular mapping of GA insensitive *Rht* loci on chromosomes 4B and 4D of common wheat (*Triticum aestivum*). Theoretical and Applied Genetics 95: 1133-1137.
118.	Bosch A, Figueiras AM, Gonzalez-Jaen MT & Benito C 1986 Leaf peroxidases - a biochemical marker for the group 2 chromosomes in the Triticinae. Genetical Research, Cambridge 47: 103-107.
119.	Bosch A, Vega C & Benito C 1987 The peroxidase isozymes of the wheat kernel: tissue and substrate specificity and their chromosomal location. Theoretical and Applied Genetics 73: 701-706.
120.	Bougri OV, Korzun VN & Grimm B 1996 Chromosomal assignment of the genes encoding glutamyl-tRNA reductase in barley, wheat, and rye and their organization in the barley genome. Hereditas 124: 1-6.
121.	Boyd WJR & Lee JW 1967 The control of wheat gluten synthesis at the genome and chromosome level. Experientia 23: 332-333.
122.	Bozzini A 1965 Sphaerococcoid, a radiation-induced mutation in *Triticum durum* Desf. *In*, Use of Induced Mutations in Plant Breeding. Proceedings of FAO/IAEA Meeting Rome, Italy: 375-383.
123.	Bozzini A & Scarascia-Mugnozza GT 1967 The dominant short straw mutation induced by thermal neutrons in durum wheat. Wheat Information Service 23-24: 5-6.
124.	Branlard G & Le Blanc A 1985 Les sous-unites glutenines de haut poids moleculaire des bles tendres et des bles durs cultives en France. Agronomie 5: 467-477.
125.	Branlard G, Autran JC & Monneveux P 1989 High molecular weight glutenin subunit in durum wheat (*T. durum*). Theoretical and Applied Genetics 78: 353-358.
126.	Breiman A 1995 Personal communication.
127.	Brennan PS 1983 Hartog. Journal of the Australian Institute of Agricultural Science 49: 42.
128.	Brennan PS, Martin DJ, The D & McIntosh RA 1983 Torres. Journal of the Australian Institute of Agricultural Science 49: 47.
129.	Bressman EN 1931 Varietal resistance, physiologic specialization and inheritance studies in bunt of wheat. Oregon Agricultural Experiment Station Bulletin 281: 44 pp..
130.	Briggle LW 1966 Three loci in wheat involving resistance to *Erysiphe graminis* f. sp. *tritici*. Crop Science 6: 461-465.
131.	Briggle LW 1966 Transfer of resistance to *Erysiphe graminis* f. sp. *tritici* from Khapli emmer and Yuma durum to hexaploid wheat. Crop Science 6: 459-461.
132.	Briggle LW 1969 Near-isogenic lines of wheat with genes for resistance to *Erysiphe graminis* f. sp. *tritici*. Crop Science 9: 70-72.
133.	Briggle LW Personal communication.
134.	Briggle LW & Sears ER Linkage of resistance to *Erysiphe graminis* f. sp. *tritici* (*Pm3*) and hairy glume (*Hg*) on chromosome 1A of wheat. 1966 Crop Science 6: 559-561.
135.	Briggs FN 1926 Inheritance of resistance to bunt, *Tilletia tritici*, in wheat. Journal of Agricultural Research 32: 973-990.
136.	Briggs FN 1933 A third genetic factor for resistance to bunt, *Tilletia tritici*, in wheat hybrids. Journal of Genetics 27: 435-441.

137. Briggs FN & Holton CS 1950 Reaction of wheat varieties with known genes for resistance to races of bunt, *T. caries* and *T. foetida*. Agronomy Journal 42: 483-486.

138. Brinkmann H, Matinez D, Quigley F, Martin W & Cerff R 1988 Endosymbiotic origin and codon bias of the nuclear gene for chloroplast glyceraldehyde-3-phosphate dehydrogenase from maize. Journal of Molecular Evolution 26: 320-328.

139. Broglie R, Coruzzi G, Lamppa G, Kieth B & Chua N-H 1983 Structural analysis of nuclear genes coding for the precursor to the small subunit of wheat ribulose-1,5-bisphospate carboxulase. Biotechnology 1: 55-61.

140. Browder LE 1972 Designation of two genes for resistance to *Puccinia recondita* in *Triticum aestivum*. Crop Science 12: 705-706.

141. Browder LE 1973 Probable genotype of some *Triticum aestivum* 'Agent' derivatives for reaction to *Puccinia recondita* f. sp. *tritici*. Crop Science 13: 203-206.

142. Browder LE 1973 Specificity of the *Puccinia recondita* f. sp. *tritici: Triticum aestivum* 'Bulgaria 88' relationship. Phytopathology 63: 524-528.

143. Browder LE 1980 A compendium of information about named genes for low reaction to *Puccinia recondita* in wheat. Crop Science 20: 775-779.

144. Brown AHD 1980 Genetic basis of alcohol dehydrogenase polymorphism in *Hordeum spontaneum*. Journal of Heredity 70: 127-128.

145. Brown AHD 1983 Barley. Isozymes in Plant Genetics and Breeding. Elsevier Science Publishers B.V., Amsterdam (Tanksley SD & Orton TJ eds.) Part B: 57-77.

146. Brown AHD & Jacobsen JB 1982 Genetic basis and natural variations of a-amylase isozymes in barley. Genetical Research, Cambridge 40: 315-324.

147. Brown AHD & Munday J 1981 Population-genetic structure and optimal sampling of land races of barley from Iran. Genetica 58: 85-96.

148. Brown CM & Jedlinski H 1983 'Roland' wheat. Crop Science 23: 1013-1014.

149. Brown GN 1997 The inheritance and expression of leaf chlorosis associated with gene *Sr2* for adult plant resistance to wheat stem rust. Euphytica 95: 67-71.

150. Brown JWS, Kemble RJ, Law CN & Flavell RB 1979 Control of endosperm proteins in *Triticum aestivum* (var. Chinese Spring) and *Aegilops umbellulata* by homoeologous group 1 chromosomes. Genetics 93: 189-200.

151. Bryan GJ, Collins AJ, Stephenson P, Orry A, Smith JB & Gale MD 1997 Isolation and characterisation of microsatellites from hexaploid bread wheat. Theoretical and Applied Genetics 94: 557-563.

152. Bryan WE 1937 Breeding for smut resistance in Arizona-grown wheat. Arizona Agricultural Experiment Station, Technical Bulletin 66: 28 pp..

153. Busch R, Behrans R, Agiez A & Elakkad M 1989 Inheritance of tolerance to, and agronomic effects of, difenzoquet herbicide in spring wheat. Crop Science 29: 47-50.

154. Cadalen T, Boeuf C, Bernard S & Bernard M 1997 An intervarietal molecular marker map in *Triticum aestivum* L. em. Thell. and comparison with a map from a wide cross. Theoretical and Applied Genetics 94: 367-377.

155. Caldwell RM & Compton LE 1943 Complementary lethal genes in wheat. Journal of Heredity 34: 67-70.

156. Caldwell RM, Cartwright WB & Compton LE 1946 Inheritance of Hessian fly resistance derived from W38 and durum P.I.94587. Journal of the American Society of Agronomy 38: 398-409.

157.	Caldwell RM, Gallun RL & Compton LE 1966 Genetics and expression of resistance to Hessian fly, *Phytophaga destructor* (Say). Proceedings of the 2nd International Wheat Genetics Symposium Lund 1963 (MacKey J ed.): Hereditas Suppl. 2: 462-463.
158.	Calonnec A & Johnson R 1998 Chromosomal location of genes for resistance to *Puccinia striiformis* in the wheat line TP1295 selected from the cross of Soissonais-Desprez with Lemhi. European Journal of Plant Pathology 104: 835-847.
159.	Campbell AB & Czarnecki EM 1981 Benito hard red spring wheat. Canadian Journal of Plant Science 61: 145-146.
160.	Campbell AB & McGinnis RC 1958 A monosomic analysis of stem rust reaction and awn expression in Redman wheat. Canadian Journal of Plant Science 38: 184-187.
161.	Carbonero R 1992 Personal communication.
162.	Carlson SK, Patterson FL & Gallun RL 1978 Inheritance of resistance to Hessian fly derived from *Triticum turgidum* L. Crop Science 18: 1011-1014.
163.	Carrillo JM, Vazquez JF & Orellana J 1990 Linkage relationships between the loci *Sec 1* and *Sec 3* in rye. Heredity 64: 125-130.
164.	Carrillo JM, Vazquez JF & Orellana J 1992 Identification and mapping of the *Gli-R3* locus on chromosome 1R of rye (*Secale cereale* L.). Theoretical and Applied Genetics 84: 237-241.
165.	Carter MV 1954 Additional genes in *Triticum vulgare* for resistance to *Erysiphe graminis tritici*. Australian Journal of Biological Sciences 7: 411-414.
166.	Cartwright WB & Wiebe GA 1936 Inheritance of resistance to the Hessian fly in the wheat crosses Dawson x Poso and Dawson x Big Club. Journal of Agricultural Research 52: 691-695.
167.	Cassidy BG & Dvorak J 1991 Molecular characterization of a low-molecular-weight glutenin cDNA clone from *Triticum durum*. Theoretical and Applied Genetics 81: 653-660.
168.	Cauderon Y, Autran JC, Joudrier P & Kobrehel K 1978 Identification de chromosomes d' *Agropyron intermedium* impliques dans la synthese des gliadines, des beta-amylases et des peroxidases a l'aide de lignees d'addition Ble X *Agropyron*. Annales d'Amelioration des Plantes 28: 257-267.
169.	Cauderon Y, Saigne B & Dauge M 1973 The resistance to wheat rusts of *Agropyron intermedium* and its use in wheat improvement. Proceedings of the 4th International Wheat Genetics Symposium (Sears ER & Sears LMS eds.) University of Missouri, Columbia, USA: 401-407.
170.	Causse M, Fulton TM, Cho YG, Ahn SN, Chunwongse J, Wu K, Xiao J, Yu Z, Ronald PC, Harrington SB, Second GA, McCouch SR & Tanksley SD 1994 Saturated molecular map of the rice genome based on an interspecific backcross population. Genetics 138: 1251-1274.
171.	Cebert E, Ohm H, Patterson F, Ratcliff R & Cambron S 1996 Genetic analysis of Hessian fly resistance in durum wheat. Agronomy Abstracts 88: 88.
172.	Ceolini C & Galili G 1982 Chromosome arm location and mode of expression of a phosphodiesterase gene from diploid wheat *Triticum longissimum*. Cereal Research Communications 10: 151-157.
173.	Ceoloni C 1988 Personal communication.
174.	Ceoloni C, Del Signore G, Pasquini M & Testa A 1988 Transfer of mildew resistance from *Triticum longissimum* into wheat by *ph1* induced homoeologous recombination. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 221-226.
175.	Chandler P 1995 Personal communication.

176. Chandler PM, Zwar JA, Jacobsen JV, Higgins TJV & Inglis AS 1984 The effects of gibberellic acid and abscisic acid on a-amylase mRNA levels in barley aleurone layers studied using an a-amylase cDNA clone. Plant Molecular Biology 3: 407-418.

177. Chantachume Y, Rathjen AJ, Paul JG & Shepherd KW 1993 Genetic studies on boron tolerance of wheat. Focussed Plant Improvement: Towards Responsible and Sustainable Agriculture. Proceedings of the 10th Australian Plant Breeding Conference (Imrie BC & Hacker JB eds): Volume 2.: 74-75.

178. Chao S, Raines CA, Longstaff M, Sharp PJ, Gale MD & Dyer TA 1989 Chromosomal location and copy number in wheat and some of its close relatives of genes for enzymes involved in photosynthesis. Molecular and General Genetics 218: 423-430.

179. Chao S, Sharp PJ & Gale MD 1988 A linkage map of wheat group 7 chromosomes using RFLP markers. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 493-498.

180. Chao S, Sharp PJ, Worland AJ, Koebner RMD & Gale MD 1989 RFLP-based genetic maps of wheat homoeologous group 7 chromosomes. Theoretical and Applied Genetics 78: 495-504.

181. Chen XM & Line RF 1992 Identification of stripe rust resistance genes in wheat genotypes used to differentiate North American races of *Puccinia striiformis*. Phytopathology 82: 1428-1434.

182. Chen XM & Line RF 1993 Inheritance of stripe rust resistance in wheat cultivars postulated to have resistance genes at *Yr3* and *Yr4* loci. Phytopathology 83: 382-388.

183. Chen XM, Jones SS & Line RF 1995 Chromosomal location of genes for stripe rust resistance in spring wheat cultivars Compair, Fielder, Lee and Lemhi and interactions of aneuploid wheats with races of *Puccinia striiformis*. Phytopathology 85: 375-381.

184. Chen XM, Jones SS & Line RF 1996 Chromosomal location of genes for resistance to *Puccinia striiformis* in seven wheat cultivars with resistance genes at the *Yr3* and *Yr4* loci. Phytopathology 86: 1228-1233.

185. Chen XM, Line RF & Jones SS 1994 Chromosomal location of genes for resistance to *Puccinia sriiformis* in wheat cultivars Druchamp, Stephens, and Yamhill. Phytopathology 84: 1116.

186. Chen XM, Line RF & Jones SS 1995 Chromosomal location of genes for resistance to *Puccinia striiformis* in winter wheat cultivars Heines VII, Clement, Moro, Tyee, Tres and Daws. Phytopathology 85: 1362-1367.

187. Chen Z, Devey M, Tuleen NA & Hart GE 1994 Use of recombinant substitution lines in the construction of RFLP-based genetic maps of chromosomes 6A and 6B of tetraploid wheat (*Triticum turgidum* L.). Theoretical and Applied Genetics 89: 703-712.

188. Cheng CL, Dewdney J, Kleinhofs J & Goodman HM 1986 Cloning and nitrate induction of nitrate reductase mRNA. Proceedings of the National Academy of Sciences, USA 83: 6825-6828.

189. Chenicek KJ & Hart GE 1987 Identification and chromosomal locations of aconitase gene loci in Triticeae species. Theoretical and Applied Genetics 74: 261-268.

190. Cheung WY, Moore G, Money TA & Gale MD 1992 HpaII library indicates 'methylation-free islands' in wheat and barley. Theoretical and Applied Genetics 84: 739-746.

191. Chhabra AK & Sethi SK 1991 Inheritance of cleistogamous flowering in durum wheat (*Triticum durum*). Euphytica 55: 147-150.

192.	Chilosi G & Johnson R 1990 Resistance to races of *Puccinia striiformis* in seedlings of Italian wheats and possible presence of the *Yr6* gene in some durum cultivars. Journal of Genetics and Breeding 44: 13-20.
193.	Chin TC 1944 The inheritance of some quantitative characters in the interspecific crosses of wheat. Chinese Journal of Science and Agriculture 1: 204-217.
194.	Chinoy CN, Devos KM, Bringloe D, Gray JC, Gale MD & Dyer TA 1991 Chromosomal location of the genes for ferrodoxin in wheat, barley and rye. Theoretical and Applied Genetics 82: 1-2.
195.	Chojecki AJS & Gale MD 1982 Genetic control of glucose phosphate isomerase in wheat and related species. Heredity 49: 339-349.
196.	Chojecki AJS, Gale MD, Holt LM & Payne PI 1983 The intrachromosomal mapping of a glucose phosphate isomerase structural gene, using allelic variation among stocks of Chinese Spring wheat. Genetical Research, Cambridge 41: 221-226.
197.	Cholick FA, Buchenau GW & Sellers KM 1990 Registration of 'Prospect' wheat. Crop Science 30: 233-234.
198.	Cholick FA, Hatchett JH, Steiger DK, Buchanan GW & Sellers KM 1988 Registration of 'Shield' wheat. Crop Science 28: 720-721.
199.	Choudhuri HC 1958 The inheritance of stem and leaf rust resistance in common wheat. Indian Journal of Genetics 18: 90-115.
200.	Christopher DA, Atsmon D & Feldman M 1985 Mode of inheritance and chromosomal allocation of stunting genes in commom wheat. Crop Science 25: 147-151.
201.	Chung YS & Griffey CA 1995 Powdery mildew resistance in winter wheat II. Identity of resistance genes. Crop Science 35: 383-388.
202.	Churchward JG 1931 Studies on the inheritance of resistance to bunt in a cross between Florence and Hard Federation wheats. Journal of the Royal Society of New South Wales 64: 298-319.
203.	Churchward JG 1932 Inheritance of resistance to bunt, *Tilletia tritici* (Bjerk) Winter, and other characters in certain crosses of "Florence wheat". Proceedings of the Linnaean Society of New South Wales 57: 133-147.
204.	Churchward JG 1938 Studies on physiologic specialization of the organisms causing bunt in wheat and the genetics of resistance to this and certain other wheat diseases. Part II Genetical studies. Journal of the Royal Society of New South Wales 71: 547-590.
205.	Ciaffi M, Lafiandra D, Porceddu E & Benedettelli S 1993 Storage-protein variation in wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) from Jordan and Turkey. I. Electrophoretic characterization of genotypes. Theoretical and Applied Genetics 86: 474-480.
206.	Clark JA, Quisenberry KS & Powers L 1933 Inheritance of bunt reaction and other characters in Hope wheat crosses. Journal of Agricultural Research 46: 413-425.
207.	Clarke BC, Stancombe P, Money T, Foote T & Moore G 1992 Targeting deletion (homoeologous chromosome pairing locus) or addition line single copy sequences from cereal genomes. Nucleic Acids Research 20: 1289-1292.
208.	Claude PP, Dyck PL & Evans LE 1986 An evaluation of 391 spring wheat introductions for resistance to stem rust and leaf rust. Canadian Journal of Plant Pathology 8: 132-139.
209.	Close S, Kortt AA & Chandler PM 1989 A cDNA-based comparison of dehydration-induced proteins (dehydrins) in barley and corn. Plant Molecular Biology 13: 95-108.
210.	Close TJ & Chandler PM 1990 Cereal dehydrins; serology, gene mapping and potential functional roles. Australian Journal of Plant Physiology 17: 333-334.

211.	Coe EH & Neuffer MG 1993 Gene loci and linkage map of corn (maize) (*Zea mays*) (2N=20). In: Genetic Maps 6. (O'Brien SJ ed.). Cold Spring Harbor Laboratory Press, Cold Spring Harbor: 157-189.
212.	Collinge D 1994 Personal communication.
213.	Cone KC, Burr FA & Burr B 1986 Molecular analysis of the maize anthocyanin regulatory locus C1. Proceedings of the National Academy of Sciences, USA 83: 9631-9635.
214.	Copp LGL 1965 Purple grain in hexaploid wheat. Wheat Information Service 18: 19-20.
215.	Cox TS 1991 Personal communication.
216.	Cox TS 1991 The contribution of introduced germplasm to the development of U.S. wheat cultivars. In: Use of Plant Introductions in Cultivar Development, Part I, Crop Science Society of America Special Publication No. 17: 25-47.
217.	Cox TS & Hatchett JH 1994 Resistance gene *H26* transferred from dipoid goatgrass to common wheat. Crop Science 34: 958-960.
218.	Cox TS, Raupp WJ & Gill BS 1993 Leaf rust-resistance genes *Lr41*, *Lr42* and *Lr43* transferred from *Triticum tauschii* to common wheat. Crop Science 34: 339-343.
219.	Cox TS, Sears RG & Gill BS 1991 Registration of KS87UP9, a winter wheat germplasm segregating for a dominant male sterility gene. Crop Science 31: 247.
220.	Cox TS, Sears RG & Gill BS 1992 Registration of KS90WGRC10 leaf rust-resistant red winter wheat germplasm. Crop Science 32: 506.
221.	Crosby AR 1957 Nucleolar activity of lagging chromosomes in wheat. American Journal of Botany 44: 813-822.
222.	Curtis BC, Schlehuber AM & Wood EA 1960 Genetics of greenbug (*Toxoptera graminum* Rond.) resistance in two strains of common wheat. Agronomy Journal 52: 599-602.
223.	Curtis C & Feldman M 1988 Increased proximal recombination frequency in common wheat by premeiotic colchicine treatment. Proceedings of the 7th International Wheat Genetics Symposium, IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 243-248.
224.	Curtis CA & Lukaszewski AJ 1991 Genetic linkage between C-bands and storage proteins in chromosome 1B of tetraploid wheat. Theoretical and Applied Genetics 81: 245-252.
225.	Curtis CA & Lukaszewski AJ 1993 Localization of genes in rye that restore male fertility to hexaploid wheat with *timopheevi* cytoplasm. Plant Breeding 111: 106-112.
226.	Czarnecki EM & Lukow OM 1992 Linkage of stem rust resistance gene *Sr33* and the gliadin (*Gli-D1*) locus on chromosome 1DS. Genome 35: 565-568.
227.	Dabrowska T 1983 Studies on chromosomal location of genes involved in beta-amylase isozymes in wheat kernels (*Triticum aestivum* L.). Genetica Polonica 24: 9-19.
228.	De la Pena RC, Murray TD & Jones SS 1996 Linkage relations among eyespot resistance gene *Pch2*, endopeptidase *Ep-A1b* and RFLP marker *Xpsr121* on chromosome 7A of wheat. Plant Breeding 115: 273-275.
229.	De la Pena RC, Murray TD & Jones SS 1997 Identification of an RFLP interval containing *Pch2* on chromosome 7AL in wheat. Genome 40: 249-252.
230.	De Vallavieille-Pope C, Picard-Formery H, Radulovic S & Johnson R 1990 Specific resistance factors to yellow rust in seedlings of some French varieties and races of *Puccinia striiformis* Westend in France. Agronomie 2: 103-113.
231.	Dedryver F, Jubier MF, Thouvenin J & Goyeau H 1996 Molecular markers linked to the leaf rust resistance gene *Lr24* in different wheat cultivars. Genome 39: 830-835.
232.	Delaney DE, Nasuda S, Endo TR, Gill BS & Hulbert SH 1995 Cytologically based physical maps of the group-2 chromosomes of wheat. Theoretical and Applied Genetics 91: 568-573.

233. Delaney DE, Nasuda S, Endo TR, Gill BS & Hulbert SH 1995 Cytologically based physical maps of the group 3 chromosomes of wheat. Theoretical and Applied Genetics 91: 780-782.

234. Delhaize E, Craig S, Beaton CD, Bennet RJ, Jagadish VC & Randall PJ 1993 Aluminium tolerance in wheat (*Triticum aestivum* L.) 1. Uptake and distribution of aluminum in root species. Plant Physiology 103: 685-693.

235. Delibes A, Del Morala J, Martin-Sanchez JA, Mejias A, Gallego M, Casado D, Sin E & Lopez-Brana I 1997 Hessian fly-resistance gene transferred from chromosome 4M^{v} of *Aegilops ventricosa* to *Triticum aestivum*. Theoretical and Applied Genetics 94: 858-864.

236. Delibes A, Lopez-Brana I, Mana M & Garcia-Olmedo F 1988 Present progress in the characterization of *Triticum aestivum*/*Aegilops ventricosa* transfer lines. Proceedings of the 7th International Wheat Genetics Symposium, IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 249-252.

237. Delibes A, Otero C & Garcia-Olmedo F 1981 Biochemical markers associated with two M^{v} chromosomes from *Aegilops ventricosa* in wheat - *Aegilops* addition lines. Theoretical and Applied Genetics 60: 5-10.

238. Delibes A, Romero D, Aguaded S, Duce A, Mena M, Lopez-Brana I, Andres M-F, Martin-Sanchez JA & Garcia-Olmedo F 1993 Resistance to the cereal cyst nematode (*Heterodera avenae* Woll.) transferred from the wild grass *Aegilops ventricosa* to hexaploid wheat by a "stepping-stone" procedure. Theoretical and Applied Genetics 87: 402-408.

239. Demeke T, Laroche A & Gaudet DA 1996 A DNA marker for the *Bt-10* common bunt resistance gene in wheat. Genome 39: 51-55.

240. Deng JY & Gao ZL 1982 Discovery and determination of a dominant male-sterile gene and its importance in genetics and wheat breeding. Scientia Sinica (Series B) 25: 508-516.

241. DePace C, Benedettelli S, Qualset C, Hart GE, Scarascia Mugnosa GT, Delre V & Vittori D 1988 Biochemical markers in *Triticum* x *Dasypyrum* amphiploids and derived disomic addition lines. Proceedings of the 7th International Wheat Genetics Symposium, IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 503-510.

242. DePace C, Montebone L, Delre V, Jan CC, Qualset CO & Scarascia Mugnozza GT 1988 Biochemical versatility of amphiploids derived from crossing *Dasypyrum villosum* Candargy and wheat: genetic control and phenotypical aspects. Theoretical and Applied Genetics 76: 513-529.

243. Derera NF 1982 The harmful harvest rain. Journal of the Australian Institute of Agricultural Science 48: 67-75.

244. Duveiller E, van Ginkel M & Thizssen M 1993 Genetic analysis of resistance to bacterial leaf streak caused by *Xanthomonas campestris* pv *undulosa* in bread wheat. Euphytica 66: 35-43.

245. Devey ME & Hart GE 1993 Chromosomal localization of intergenomic RFLP loci in hexaploid wheat. Genome 36: 913-918.

246. Devos KM 1996 Personal communication.

247. Devos KM & Gale MD 1993 Extended genetic maps of the homoeologous group 3 chromosomes of wheat, rye and barley. Theoretical and Applied Genetics 85: 649-652.

248. Devos KM, Atkinson MD, Chinoy CN, Guiltnan MJ, Quatrano RS & Gale MD 1991 Chromosomal location and variability in wheat, barley and rye of a wheat gene encoding a bZIP protein (*EmBP-1*). Theoretical and Applied Genetics 82: 665-667.

249. Devos KM, Atkinson MD, Chinoy CN, Harcourt RL, Koebner RMD, Liu CJ, Masojc P, Xie DX & Gale MD 1993 Chromosome rearrangements in the rye genome relative to that of wheat. Theoretical and Applied Genetics 85: 673-680.

250.	Devos KM, Atkinson MD, Chinoy CN, Liu C & Gale MD 1992 RFLP based genetic map of the homoeologous group 3 chromosomes of wheat and rye. Theoretical and Applied Genetics 83: 931-939.
251.	Devos KM, Atkinson MD, Chinoy CN, Lloyd JC, Raines CA, Dyer TA & Gale MD 1992 The coding sequence for sedoheptulose-1,7-bisphosphatase detects multiple homologues in wheat genomic DNA. Theoretical and Applied Genetics 85: 133-135.
252.	Devos KM, Bryan GJ, Collins AJ, Stephenson P & Gale MD 1995 Application of two microsatellite sequences in wheat storage proteins as molecular markers. Theoretical and Applied Genetics 90: 247-252.
253.	Devos KM, Chao S, Li QY, Simonetti MC & Gale MD 1994 Relationship between chromosome 9 of maize and wheat homoeologous group 7 chromosomes. Genetics 138: 1287-1292.
254.	Devos KM, Chinoy CN, Atkinson MD, Hansen L, von Wettstein-Knowles P & Gale MD 1991 Chromosomal location in wheat of the genes coding for the acyl carrier proteins 1 and 111. Theoretical and Applied Genetics 82: 3-5.
255.	Devos KM, Dubcovsky J, Dvorak J, Chinoy CN & Gale MD 1995 Structural evolution of wheat chromosomes 4A, 5A and 7B and its impact on recombination. Theoretical and Applied Genetics 91: 282-288.
256.	Devos KM, Millan T & Gale MD 1993 Comparative RFLP maps of the homoeologous group 2 chromosomes of wheat, rye and barley. Theoretical and Applied Genetics 85: 784-792.
257.	Dhaliwal HS, Sharma SK & Randhawa AS 1986 How to overcome hybrid necrosis in wheat. Wheat Information Service 61: 27-28.
258.	Doan NP & Fincher GB 1988 The A-and B-chains of carboxypeptidase I from germinated barley originate from a single precursor polypeptide. Journal of Biological Chemistry 263: 11106-11110.
259.	Dong H & Quick JS 1995 Inheritance and allelism of resistances to the Russian wheat aphid in seven wheat lines. Euphytica 81: 299-303.
260.	Dong H, Quick JS & Zhang Y 1997 Inheritance and allelism of Russian wheat aphid resistance in several wheat lines. Plant Breeding 116: 449-453.
261.	Doussinault G, Delibes A, Sanchez-Monge R & Garcia-Olmedo F 1983 Transfer of a dominant gene for resistance to eyespot disease from a wild grass to hexaploid wheat. Nature 303: 698-700.
262.	D'Ovidio R & Porceddu E 1996 PCR-based assay for detecting 1B-genes for low molecular weight glutenin subunits related to gluten quality properties in durum wheat. Plant Breeding 115: 413-415.
263.	D'Ovidio R, Masci S & Porceddu E 1995 Development of a set of oligonucleotide primers specific for genes at the *Glu-1* complex of wheat. Theoretical and Applied Genetics 91: 189-194.
264.	D'Ovidio R, Simeone M, Masci S & Porceddu E 1997 Molecular characterization of a LMW-GS gene located on chromosome 1B and the development of primers specific for the *Glu-B3* complex locus in durum wheat. Theoretical and Applied Genetics 95: 1119-1126.
265.	Dratewka-Kos E, Rahman S, Grzelczak ZF, Kennedy TD, Murray R & Lane BG 1989 Polypeptide structure of germin as deduced from cDNA sequencing. Journal of Biological Chemistry 264: 4896-4900.

266.	Drefahl S & Bushbeck R 1991 Gene localization of aspartate aminotransferase and endopeptidase isozymes in wheat and rye using developmental and organ-specific patterns. Plant Breeding 107: 218-225.
267.	Driscoll CJ 1966 Gene-centromere distances in wheat by aneuploid F2 observations. Genetics 54: 131-135.
268.	Driscoll CJ 1975 Cytogenetic analysis of two chromosomal male-sterility mutants in hexaploid wheat. Australian Journal of Biological Sciences 28: 413-416.
269.	Driscoll CJ Personal communication.
270.	Driscoll CJ & Anderson LM 1967 Cytogenetic studies of Transec - a wheat-rye translocation line. Canadian Journal of Genetics and Cytology 9: 375-380.
271.	Driscoll CJ & Bielig LM 1968 Mapping of the Transec wheat-rye translocation. Canadian Journal of Genetics and Cytology 10: 421-425.
272.	Driscoll CJ & Jensen NF 1964 Chromosomes associated with waxlessness, awnedness and time of maturity of common wheat. Canadian Journal of Genetics and Cytology 6: 324-333.
273.	Driscoll CJ & Jensen NF 1965 Release of a wheat-rye translocation stock involving leaf rust and powdery mildew resistances. Crop Science 5: 279-280.
274.	Driscoll CJ & Sears ER 1963 The nature of a spontaneous transfer of hairy neck from rye to wheat. Proceedings of the XI International Congress of Genetics The Hague 1: 123.
275.	Driscoll CJ & Sears ER 1965 Mapping of a wheat-rye translocation. Genetics 51: 439-443.
276.	Dubcovsky J & Dvorak J 1995 Ribosomal RNA multigene loci: nomads of the Triticeae genomes. Genetics 140: 1367-1377.
277.	Dubcovsky J, Echaide M, Giancola S, Rousset M, Luo MC, Joppa LR & Dvorak J 1997 Seed-storage-protein loci in RFLP maps of diploid, tetraploid, and hexaploid wheat. Theoretical and Applied Genetics 95: 1169-1180.
278.	Dubcovsky J, Galvez AF & Dvorak J 1994 Comparison of the genetic organization of the early salt-stress responsive wheat. Theoretical and Applied Genetics 87: 957-964.
279.	Dubcovsky J, Lijavetzky D, Appendino L, Tranquilli G & Dvorak JD 1998 Comparative RFLP mapping of *Triticum monococcum* genes controlling vernalization requirement. Theoretical and Applied Genetics 97: 968-975.
280.	Dubcovsky J, Luo M-C & Dvorak J 1995 Differentiation between homoeologous chromosomes 1A of wheat and $1A^m$ of *Triticum monococcum* and its recognition by the wheat *Ph1* locus. Proceedings of the National Academy Sciences, USA 92: 6645-6649.
281.	Dubcovsky J, Luo M-C & Dvorak J 1995 Linkage relationships among stress-induced genes in wheat. Theoretical and Applied Genetics 91: 795-801.
282.	Dubcovsky J, Luo, M-C, Zhong G-Y, Bransteitter R, Desai A, Kilian A, Kleinhofs A & Dvorak J 1996 Genetic map of diploid wheat, *Triticum monococcum* L., and its comparison with maps of *Hordeum vulgare* L. Genetics 143: 983-999.
283.	Dubcovsky J, Santa Maria G, Epstein E, Luo M-C & Dvorak J 1996 Mapping of the K+/Na+ discrimination locus *Kna1* in wheat. Theoretical and Applied Genetics 92: 448-454.
284.	Dubin HJ, Johnson R & Stubbs RW 1989 Postulated genes to stripe rust in selected CIMMYT and related wheats. Plant Disease 73: 472-475.
285.	DuPont FM 1995 Personal communication.
286.	DuToit F 1989 Inheritance of resistance in two *Triticum aestivium* lines to Russian wheat aphid (*Homoptera* : *Aphididea*). Journal of Economic Entomology 82: 1251-1253.
287.	DuToit F, Wessels WG & Marais GF 1995 The chromosome arm location of Russian wheat aphid resistance gene *Dn5*. Cereal Research Communications 23: 15-17.

288.	Dvorak J & Appels R 1986 Investigation of homoeologous crossing over and sister chromatid exchange in the wheat NOR-B2 locus coding for rRNA and GLI-B2 locus coding for gliadins. Genetics 113: 1037-1056.
289.	Dvorak J & Chen KC 1984 Distribution of nonstructural variation between wheat cultivars along chromosome arm 6Bp: evidence from the linkage map and physical map of the arm. Genetics 106: 325-333.
290.	Dvorak J & Gorham J 1992 Methodology of gene transfer by homoeologous recombination into *Triticum turgidum*: Transfer of K^+/Na^+ discrimination from *Triticum aestivum*. Genome 35: 639-646.
291.	Dvorak J & Knott DR 1977 Homoeologous chromatin exchange in a radiation-induced gene transfer. Canadian Journal of Genetics and Cytology 19: 125-131.
292.	Dvorak J & Knott DR 1990 Location of a *Triticum speltoides* chromosome segment conferring resistance to leaf rust in *Triticum aestivum*. Genome 33: 892-897.
293.	Dvorak J, Dubcovsky J, Luo MC, Devos KM & Gale MD 1995 Differentiation between wheat chromosomes 4B and 4D. Genome 38: 1139-1147.
294.	Dvorak J, Lassner MW, Kota RS & Chen KC 1984 The distribution of the ribosomal RNA genes in the *Triticum speltoides* and *Elytrigia elongata* genomes. Canadian Journal of Genetics and Cytology 26: 628-632.
295.	Dvorak J, Zhang H-B, Kota RS & Lassner M 1989 Organisation and evolution of the 5S ribosomal RNA gene family in wheat and related species. Genome 32: 1003-1016.
296.	Dweikat I, Ohm H, Paterson F & Cambron S 1997 Identification of RAPD markers for 11 Hessian fly resistance genes in wheat. Theoretical and Applied Genetics 94: 419-423.
297.	Dyck PL 1977 Genetics of leaf rust reaction in three introductions of common wheat. Canadian Journal of Genetics and Cytology 19: 711-716.
298.	Dyck PL 1979 Identification of the gene for adult-plant leaf rust resistance in Thatcher. Canadian Journal of Plant Science 59: 499-501.
299.	Dyck PL 1987 The association of a gene for leaf rust resistance with the chromosome 7D suppressor of stem rust resistance in common wheat. Genome 29: 467-469.
300.	Dyck PL 1989 The inheritance of leaf rust resistance in wheat cultivars Kenyon and Buck Manantial. Canadian Journal of Plant Science 69: 1113-1117.
301.	Dyck PL 1991 Genetics of adult plant leaf rust resistance in 'Chinese Spring' and 'Sturdy' wheats. Crop Science 24: 309-311.
302.	Dyck PL 1992 Transfer of a gene for stem rust resistance from *Triticum araraticum* to hexaploid wheat. Genome 35: 788-792.
303.	Dyck PL 1993 Inheritance of leaf rust and stem rust resistance in 'Roblin' wheat. Genome 36: 289-293.
304.	Dyck PL 1993 The inheritance of leaf rust resistance in the wheat cultivar Pasqua. Canadian Journal of Plant Science 73: 903-906.
305.	Dyck PL 1994 Genetics of leaf rust resistance in 13 accessions of the Watkins wheat collection. Euphytica 80: 151-155.
306.	Dyck PL Personal communication.
307.	Dyck PL & Friebe B 1993 Evaluation of leaf rust resistance from wheat chromosomal translocation lines. Crop Science 33: 687-690.
308.	Dyck PL & Green GJ 1970 Genetics of stem rust resistance in wheat cultivar 'Red Bobs'. Canadian Journal of Plant Science 50: 229-232.
309.	Dyck PL & Jedel PE 1989 Genetics of resistance to leaf rust in two accessions of common wheat. Canadian Journal of Plant Science 69: 531-534.

310.	Dyck PL & Johnson R 1988 Resistance to the leaf rust or brown rust pathogen (*Puccinia recondita*) due to *Lr20* and its temperature sensitivity in European spring wheats. Proceedings of the 7th European and Mediterranean Cereal Rusts Conference Vienna, Austria (Zwatz B. ed.): 91-93.
311.	Dyck PL & Kerber ER 1970 Inheritance in hexaploid wheat of adult-plant leaf rust resistance derived from *Aegilops squarrosa*. Canadian Journal of Genetics and Cytology 12: 175-180.
312.	Dyck PL & Kerber ER 1971 Chromosome location of three genes for leaf rust resistance in common wheat. Canadian Journal of Genetics and Cytology 13: 480-483.
313.	Dyck PL & Kerber ER 1977 Chromosome location of gene *Sr29* for reaction to stem rust. Canadian Journal of Genetics and Cytology 19: 371-373.
314.	Dyck PL & Kerber ER 1977 Inheritance of leaf rust resistance in wheat cultivars Rafaela and EAP 26127 and chromosome location of gene *Lr17*. Canadian Journal of Genetics and Cytology 19: 355-358.
315.	Dyck PL & Kerber ER 1981 Aneuploid analysis of a gene for leaf rust resistance derived from the common wheat cultivar Terenzio. Canadian Journal of Genetics and Cytology 23: 405-409.
316.	Dyck PL & Lukow OM 1988 The genetic analysis of two interspecific sources of leaf rust resistance and their effect on the quality of common wheat. Canadian Journal of Plant Science 68: 633-639.
317.	Dyck PL & Samborski DJ 1968 Genetics of resistance to leaf rust in the common wheat varieties Webster, Loros, Brevit, Carina, Malakoff and Centenario. Canadian Journal of Genetics and Cytology 10: 7-17.
318.	Dyck PL & Samborski DJ 1968 Host-parasite interactions involving two genes for leaf rust resistance in wheat. Proceedings of the 3rd International Wheat Genetics Symposium Australian Academy of Science, Canberra (Findlay KW & Shepherd KW eds.): 245-250.
319.	Dyck PL & Samborski DJ 1970 The genetics of two alleles for leaf rust resistance at the *Lr14* locus in wheat. Canadian Journal of Genetics and Cytology 8: 689-694.
320.	Dyck PL & Samborski DJ 1974 Inheritance of virulence in *Puccinia recondita* of alleles at the *Lr2* locus for resistance in wheat. Canadian Journal of Genetics and Cytology 16: 323-332.
321.	Dyck PL & Samborski DJ 1982 The inheritance of resistance to *Puccinia recondita* in a group of common wheat cultivars. Canadian Journal of Genetics and Cytology 24: 273-283.
322.	Dyck PL & Sykes EE 1994 Genetics of leaf-rust resistance in three spelt wheats. Canadian Journal of Plant Science 74: 231-233.
323.	Dyck PL & Sykes EE 1995 The inheritance of stem rust and leaf rust resistance in some Ethiopian wheat cultivars. Euphytica 81: 291-297.
324.	Dyck PL, Kerber ER & Aung T 1994 An interchromosomal reciprocal translocation in wheat involving leaf rust resistance gene *Lr34*. Genome 37: 556-559.
325.	Dyck PL, Kerber ER & Lukow OM 1987 Chromosome location and linkage of a new gene (*Lr33*) for reaction to *Puccinia recondita*. Genome 29: 463-466.
326.	Dyck PL, Samborski DJ & Anderson RG 1966 Inheritance of adult plant leaf rust resistance derived from the common wheat varieties Exchange and Frontana. Canadian Journal of Genetics and Cytology 8: 665-671.
327.	Dyck PL, Samborski DJ & Martens JW 1985 Inheritance of resistance to leaf rust and stem rust in the wheat cultivar Glenlea. Canadian Journal of Plant Pathology 7: 351-354.

328.	Eastwood RF, Lagudah ES & Appels R 1994 A directed search for DNA sequences, tightly linked to cereal cyst nematode resistance genes in *Triticum tauschii*. Genome 37: 311-319.
329.	Eastwood RF, Lagudah ES, Halloran GM, Brown JS, Kollmorgan JF & Appels R 1993 Resistance to cereal cyst nematode in *Triticum tauschii*. *In* Focussed Plant Improvement: Towards Responsible and Sustainable Agriculture, Proceedings of the 10th Australian Plant Breeding Conference, Gold Coast 1993 (Imrie BC and Hacker JB ed): Volume 2.: 7-18.
330.	Eizenga GC 1987 Locating the *Agropyron* segment in wheat-*Agropyron* transfer no. 12. Genome 29: 365-366.
331.	El-Bedewy R & Robbelen G 1982 Chromosomal location and change of dominance of a gene for resistance against yellow rust, *Puccinia striiformis* West., in wheat, *Triticum aestivum* L. Zeitschrift fur Pflanzenzuchtung 89: 145-157.
332.	Elkeles A, Devos KM, Graur D, Zizi M & Breiman A 1995 Multiple cDNAs of wheat voltage-dependent anion channels (VDAC): Isolation, differential expression, mapping and evolution. Plant Molecular Biology 29: 109-124.
333.	Endo TR 1979 On the *Aegilops* chromosome having gametocidal action on common wheat. Proceedings of the 5th International Wheat Genetics Symposium, New Delhi, 1978 (Ramanujam S ed.): 306-314.
334.	Endo TR 1982 Gametocidal chromosomes of three *Aegilops* species in common wheat. Canadian Journal of Genetics and Cytology 24: 201-206.
335.	Endo TR 1985 Two types of gametocidal chromosomes of *Aegilops sharonensis* and *Ae. longissima*. Japanese Journal of Genetics 60: 125-135.
336.	Endo TR 1988 Induction of chromosome structural changes by a chromosome of *Aegilops cylindrica* L. in common wheat. Journal of Heredity 79: 366-370.
337.	Endo TR & Katayama Y 1978 Finding a selectively retained chromosome of *Aegilops caudata* L. in common wheat. Wheat Information Service 47-48: 32-35.
338.	Endo TR & Tsunewaki K 1975 Sterility of common wheat with *Aegilops triuncialis* cytoplasm. Journal of Heredity 66: 13-18.
339.	Erpelding JE, Blake NK, Blake TK & Talbert LE 1996 Transfer of sequence tagged site PCR markers between wheat and barley. Genome 39: 802-810.
340.	Espelund M, Saeboe-Larssen S, Hughes DW, Galau GA, Larsen F & Jakobsen KS 1992 Late embryogenesis-abundant genes encoding proteins with different numbers of hydrophilic repeats are regulated differentially by abscisic acid and osmotic stress. The Plant Journal 2: 241-252.
341.	Everson EH, Freed RD, Zwer PK, Morrison LW, Marchetti BL, Clayton JL, Gallun RL & Yamazaki WT 1986 Registration of 'Frankenmuth' wheat. Crop Science 26: 202-203.
342.	Ezzahiri B & Roelfs AP 1989 Inheritance and expression of adult plant resistance to leaf rust in Era wheat. Plant Disease 73: 549-551.
343.	Falk DE & Kasha KJ 1983 Genetic studies on the crossability of hexaploid wheat with rye and *Hordeum bulbosum*. Theoretical and Applied Genetics 64: 303-307.
344.	Faris JD 1996 *Tsc1* for tan spot resistance. Personal communication.
345.	Faris JD 1997 Personal communication.
346.	Faris JD, Anderson JA, Francl LJ & Jordahl JG 1996 Chromosomal location of a gene conditioning insensitivity in wheat to a necrosis-inducing culture filtrate from *Pyrenophora tritici-repentis*. Phytopathology 86: 459-463.
347.	Favret EA 1979 Personal communication.

348. Favret EA & Vallega J 1954 (Genetics of resistance to *Erysiphe graminis* in wheat.). Review of Investigative Agriculture, Buenos Aires 8: 105-110. *Cited* Plant Breeding Abstracts 26: 1174, p. 203.

349. Fedak G & Yui PY 1982 Chromosomes of Chinese Spring wheat carrying genes for crossability with Betzes barley. Canadian Journal of Genetics & Cytology 24: 227-233.

350. Felix I, Martinant JP, Bernard M & Bernard S 1996 Genetic characterization of storage proteins in a set of F_1-derived haploid lines in bread wheat. Theoretical and Applied Genetics 92: 340-346.

351. Fernandez de Caleya R, Hernandez-Lucas C, Carbonera P & Garcia-Olmedo F 1976 Gene expression in alloploids: genetic control of lipopurothionins in wheat. Genetics 83: 687-699.

352. Fernandez JA & Jouve N 1987 Chromosomal location of structural genes controlling isozymes in *Hordeum chilense*.1. 6-Phosphogluconate dehydrogenase and malate dehydrogenase. Theoretical and Applied Genetics 73: 433-439.

353. Fernandez JA & Jouve N 1987 Chromosomal location of structural genes controlling isozymes in *Hordeum chilense*.3. Esterases, glutamate oxaloacetate transaminase and phosphoglucomutase. Theoretical and Applied Genetics 73: 690-698.

354. Feuillet C, Messmer M, Schachermayr G & Keller B 1995 Genetic and physical characterisation of the *Lr1* leaf rust resistance locus in wheat (*Triticum aestivum* L.). Molecular and Genetical Genetics 248: 553-562.

355. Feuillet C, Schachermayr G & Keller B 1997 Molecular cloning of a new receptor-like kinase gene encoded at the *Lr10* disease resistance locus of wheat. The Plant Journal 11: 45-52.

356. Feuillet C, Schachermayr GM & Keller B 1997 Molecular cloning of a new receptor-like kinase gene encoded at the *Lr10* disease resistance locus of wheat. The Plant Journal 11: 45-52.

357. Fick GN & Qualset CO 1973 Genes for dwarfness in wheat, *Triticum aestivum* L. Genetics 75: 531-539.

358. Fick GN & Qualset CO 1973 Inheritance and distribution of grass-dwarfing genes in short-statured wheats. Crop Science 13: 31-33.

359. Fick GN & Qualset CO 1975 Genetic control of endosperm amylase activity and gibberellic acid responses in standard-height and short-statured wheats. Proceedings of the National Academy of Sciences, USA 72: 892-895.

360. Figueiras AM, Elorrieta MA & Benito C 1991 Genetic and cytogenetic maps of chromosomes 1R, 4R and 7R in cultivated rye (*Secale cereale*). Genome 34: 681-685.

361. Figueiras AM, Gonzalez-Jaen MT & Benito C 1986 Biochemical evidence of homoeology between *Triticum aestivum* and *Agropyron intermedium* chromosomes. Theoretical and Applied Genetics 72: 826-832.

362. Figueiras AM, Zaragoza C, Gallego FJ & Benito C 1991 NADH dehydrogenase a new molecular marker for homoeology group 4 in Triticeae. A map of the 4RS chromosome arm in rye. Theoretical and Applied Genetics 83: 169-172.

363. Fincher G 1991 Personal communication.

364. Fisher J Personal communication.

365. Fitzgerald PM, Caldwell RM & Nelson OE 1957 Inheritance of resistance to certain races of leaf rust in wheat. Agronomy Journal 49: 539-543.

366. Flavell RB & O'Dell M 1976 Ribosomal RNA genes on homoeologous chromosomes of group 5 and 6 in hexaploid wheat. Heredity 37: 377-385.

367. Flavell RB & Smith DB 1974 The role of homoeologous group 1 chromosomes in the control of rRNA genes in wheat. Biochemical Genetics 12: 271-279.

368. Fletcher RJ 1983 Takari. Journal of the Australian Institute of Agricultural Science 49: 46.

369. Fletcher RJ & McIntosh RA 1971 Unpublished.

370. Flintham JE & Humphray SJ 1993 Red coat genes and wheat dormancy. Annals of Applied Biology 36: 135-141.

371. Flintham JE, Borner A, Worland AJ & Gale MD 1997 Optimising wheat grain yield: effects of *Rht* (gibberellin-insensitive) dwarfing genes. Journal of Agricultural Science 128: 11-25.

372. Forde BG, Kreis M, Williamson MS, Fry RP, Pywell J, Shewry PR, Bunce N & Miflin BJ 1985 Short tandem repeats shared by B-and C-hordein cDNAs suggest a common evolutionary origin for two groups of cereal storage protein genes. EMBO Journal 4: 9-15.

373. Forde J, Malpica JM, Halford NG, Shewry PR, Anderson OD, Greene FC & Miflin BJ 1985 The nucleotide sequence of an HMW glutenin subunit gene located on chromosome 1A of wheat (*Triticum aestivum* L.). Nucleic Acids Research 13: 6817-6832.

374. Forster BP, Reader SM, Forsyth SA, Koebner RMD, Miller TE, Gale MD & Cauderon Y 1987 An assessment of the homoeology of six *Agropyron intermedium* chromosomes added to wheat. Genetical Research, Cambridge 50: 91-97.

375. Foster JE, Gallun RL, Patterson FL & Ohm HW 1987 Registration of common wheat germplasm resistant to Hessian fly. Crop Science 27: 374.

376. Frankel OH 1950 A polymeric multiple gene change in hexaploid wheat. Heredity 4: 103-116.

377. Frankel OH & Roskams M 1975 Stability of floral differentiation in *Triticum*. Proceedings of the Royal Society of London, B. 188: 139-162.

378. Frankel OH, Shineberg B & Munday A 1969 The genetic basis of an invariant character in wheat. Heredity 24: 571-591.

379. Friebe B 1992 Personal communication.

380. Friebe B 1994 Personal communication.

381. Friebe B, Gill BS, Cox TS & Zeller FJ 1993 Registration of KS91WGRC14 stem rust and powdery mildew resistant T1BL.1RS durum wheat germplasm. Crop Science 33: 220.

382. Friebe B, Gill BS, Tuleen NA & Cox TS 1994 Registration of KS93WGRC28 powdery mildew resistant 6BS.6RL hard red winter wheat germplasm. Crop Science 35: 1237.

383. Friebe B, Hatchett JH, Sears RG & Gill BS 1990 Transfer of Hessian fly resistance from 'Chaupan' rye to hexaploid wheat via a 2BS-2RL wheat rye chromosome translocation. Theoretical and Applied Genetics 79: 385-389.

384. Friebe B, Hatchett JM, Gill BS, Mukai Y & Sebesta EE 1991 Transfer of Hessian fly resistance from rye to wheat via radiation-induced terminal and intercalary chromosomal translocations. Theoretical and Applied Genetics 83: 33-40.

385. Friebe B, Heun M & Bushuk W 1989 Cytological characterization, powdery mildew resistance and storage protein composition of tetraploid and hexaploid 1BL/1RS wheat-rye tanslocation lines. Theoretical and Applied Genetics 78: 425-432.

386. Friebe B, Heun M, Tuleen N, Zeller FJ & Gill BS 1994 Cytogenetically monitored transfer of powdery mildew resistance from rye into wheat. Crop Science 34: 621-625.

387. Friebe B, Jellen EN & Gill BS 1996 Verification of the identity of the Chinese Spring ditelosomic stocks Dt7DS and Dt7DL. Wheat Information Service 83: 31-32.

388.	Friebe B, Jiang J, Knott DR & Gill BS 1994 Compensation indices of radiation-induced wheat-*Agropyron elongatum* translocations conferring resistance to leaf rust and stem rust. Crop Science 34: 400-404.
389.	Friebe B, Jiang J, Raupp WJ, McIntosh RA & Gill BS 1996 Characterization of wheat-alien translocations conferring resistance to diseases and pests: current status. Euphytica 91: 59-87.
390.	Friebe B, Jiang JM, Gill BS & Dyck PL 1993 Radiation-induced nonhomoeologous wheat-*Agropyron intermedium* chromosomal translocations conferring resistance to leaf rust. Theoretical and Applied Genetics 86: 141-149.
391.	Friebe B, Mukai Y, Dhaliwal HS, Martin TJ & Gill BS 1991 Identification of alien chromatin specifying resistance to wheat streak mosaic and greenbug in wheat germplasm by C-banding and in situ hybridization. Theoretical and Applied Genetics 81: 381-389.
392.	Friebe B, Zeller FJ, Mukai Y, Forster BP, Bartos P & McIntosh RA 1992 Characterization of wheat-*Agropyron intermedium* derivatives carrying resistance against leaf, stripe and stem rust by C-banding, in situ hybridization and isozyme analysis. Theoretical and Applied Genetics 83: 775-782.
393.	Fu TK & Sears ER 1973 The relationships between chiasmata and crossing over in *Triticum aestivum*. Genetics 75: 231-246.
394.	Fuentes-Davila G, Rajaram S & Singh G 1995 Inheritance of resistance to Karnal bunt (*Tilletia indica* Mitra) in bread wheat (*Triticum aestivum* L.). Plant Breeding 114: 250-252.
395.	Futers TS, Vaughan TJ, Sharp PJ & Cuming AC 1990 Molecular cloning and chromosomal location of genes encoding the 'Early-methionine-labelled' (Em) polypeptide of *Triticum aestivum* L. var. Chinese Spring. Theoretical and Applied Genetics 80: 43-48.
396.	Gaines EF & Carstens A 1926 The linkage of pubescent node and beard factors as evidenced by a cross between two varieties of wheat. Journal of Agricultural Research 33: 753-755.
397.	Gaines EF & Smith WK 1933 Reaction of varieties and hybrids of wheat to physiologic forms of bunt. Journal of the American Society of Agronomy 25: 273-284.
398.	Gale MD 1983 Alpha-amylase genes in wheat. Proceedings of the Third International Symposium on Pre-harvest Sprouting in Cereals. Westview Press, Boulder, USA (Kruger JE & LaBerge DE eds.) 273-284.
399.	Gale MD 1993 Personal communication.
400.	Gale MD Personal communication.
401.	Gale MD & Flavell RB 1971 The genetic control of anthocyanin biosynthesis by homoeologous chromosomes in wheat. Genetical Research, Cambridge 18: 237-244.
402.	Gale MD & King RW 1988 Semi-dwarf genes in Australian wheats. Agricultural Science 1: 18-20.
403.	Gale MD & Law CN 1976 The identification and exploitation of Norin 10 semi-dwarfing genes. Annual Report of the Plant Breeding Institute, Cambridge 21-35.
404.	Gale MD & Marshall GA 1973 Insensitivity to gibberellin in dwarf wheats. Annals of Botany 37: 729-735.
405.	Gale MD & Marshall GA 1975 The nature and genetic control of gibberellin insensitivity in dwarf wheat grain. Heredity 35: 55-65.
406.	Gale MD & Marshall GA 1976 The chromosomal location of *Gai1* and *Rht1*, genes for gibberellin insensitivity and semi-dwarfism, in a derivative of Norin 10 wheat. Heredity 37: 283-289.

407. Gale MD & Marshall GA 1978 A classification of the Norin 10 and Tom Thumb dwarfing genes in hexaploid bread wheat. Proceedings of the 5th International Wheat Genetics Symposium New Delhi, India (Ramanujam S ed.): 995-1001.

408. Gale MD & Youssifian S 1983 Pleiotropic effects of the Norin 10 dwarfing genes *Rht1* and *Rht2* and interactions in response to chlormequat. Proceedings of the 6th International Wheat Genetics Symposium Kyoto, Japan (Sakamoto S ed.): 271-277.

410. Gale MD, Atkinson MD, Chinoy CN, Harcourt RL, Jia J, Li QY & Devos KM 1995 Genetic maps of hexaploid wheat. Proceedings 8th International Wheat Genetics Symposium (Li ZS, Xin ZY eds.). China Agricultural Scientech Press, Beijing: 29-40.

411. Gale MD, Law CN & Worland AJ 1975 The chromosomal location of a major dwarfing gene from Norin 10 in new British semi-dwarf wheats. Heredity 35: 417-421.

412. Gale MD, Law CN, Chojecki AJ & Kempton RA 1983 Genetic control of alpha-amylase production in wheat. Theoretical and Applied Genetics 64: 309-316.

413. Gale MD, Law CN, Marshall GA & Worland AJ 1975 The genetic control of gibberellic acid insensitivity and coleoptile length in a 'dwarf' wheat. Heredity 34: 393-399.

414. Gale MD, Law CN, Marshall GA, Snape JW & Worland AJ 1982 The analysis and evaluation of semi-dwarfing genes in wheat, including a major height-reducing gene in the variety "Sava". IAEA Tecdoc: Semi-dwarf Cereal Mutants and Their Use in Cross Breeding 268: 7-23.

415. Gale MD, Marshall GA & Rao MV 1981 A classification of the Norin 10 and Tom Thumb dwarfing genes in British, Mexican, Indian and other hexaploid bread wheat varieties. Euphytica 30: 355-361.

416. Gale MD, Marshall GA, Gregory RS & Quick JS 1981 Norin 10 semi-dwarfism in tetraploid wheat and associated effects on yield. Euphytica 30: 347-354.

417. Gale MD, Scott PR, Law CN, Ainsworth CC, Hollins TW & Worland AJ 1984 An alpha-amylase gene from *Aegilops ventricosa* transferred to bread wheat together with a factor for eyespot resistance. Heredity 52: 431-435.

418. Galiba G, Quarrie SA, Sutka J, Morgounov A & Snape JW 1995 RFLP mapping of the vernalization (*Vrn1*) and frost resistance (*Fr1*) genes on chromosome 5A of wheat. Theoretical and Applied Genetics 90: 1174-1179.

419. Galiba G, Quarrie SA, Sutka J, Morgunov A & Snape JW 1995 RFLP mapping of the vernalisation (*Vrn1*) and frost resistance (*Fr1*) genes on chromosome 5A of wheat. Theoretical and Applied Genetics 90: 1174-1179.

420. Galili G & Feldman M 1983 Genetic control of endosperm proteins in wheat 2. Variation in high-molecular-weight glutenin and gliadin subunits of *Triticum aestivum*. Theoretical and Applied Genetics 66: 77-86.

421. Galili G & Feldman M 1984 A deficiency of the rapidly migrating high molecular weight glutenin subunit D5 in common wheat. Cereal Research Communications 12: 259-261.

422. Galili G & Feldman M 1984 Mapping of glutenin and gliadin genes located on chromosome 1B of common wheat. Molecular and General Genetics 193: 293-298.

423. Galili S, Galili G & Feldman M 1991 Chromosomal location of genes for Rubisco small subunit and Rubisco-binding protein in common wheat. Theoretical and Applied Genetics 81: 98-104.

424. Gallagher LW, Soliman KM, Qualset CO, Huffaker RC & Rains DW 1980 Major gene control of nitrate reductase activity in common wheat. Crop Science 20: 717-721.

425. Gallun RL & Patterson FL 1977 Monosomic analysis of wheat for resistance to Hessian fly. Journal of Heredity 68: 223-226.

426.	Gallun RL & Reitz LP 1972 Wheat cultivars resistant to races of Hessian fly. United States Department of Agriculture, Agricultural Research Station., Production Research Report 134: 16pp.
427.	Garcia-Maroto F, Marana C, Montana M, Garcia-Olmedo F & Carbonero P 1990 Cloning of cDNA and chromosomal location of genes encoding the three types of subunits of the wheat tetrameric inhibitor of insect a-amylase. Plant Molecular Biology 14: 845-853.
428.	Garcia-Olmedo F 1968 Genetics of synthesis of beta-sitosterol esters in wheat and related species. Nature 220: 1144-1145.
429.	Gautier MF & Joudrier P 1998 Personal communication.
430.	Gautier MF, Alary R & Joudrier P 1990 Cloning and characterisation of a cDNA encoding the wheat (*Triticum durum* Desf.) CM16 protein. Plant Molecular Biology 14: 313-322.
431.	Gerechter-Amitai ZK & Grama A 1974 Inheritance of resistance to stripe rust (*Puccinia striiformis*) in crosses between wild emmer (*Triticum dicoccoides*) and cultivated tetraploid and hexaploid wheats, I. *Triticum durum*. Euphytica 23: 387-392.
432.	Gerechter-Amitai ZK, van Silfhout CH, Grama A & Kleitman F 1989 *Yr15*-a new gene for resistance to *Puccinia striiformis* in *Triticum dicoccoides* sel. G-25. Euphytica 43: 187-190.
433.	Gerlach WL & Bedbrook JR 1979 Cloning and characterisation of ribosomal RNA genes from wheat and barley. Nucleic Acids Research 7: 1869-1886.
434.	German SE & Kolmer JA 1992 Effect of *Lr34* in the enhancement of resistance to leaf rust of wheat. Theoretical and Applied Genetics 84: 97-105.
435.	Gfeller F & Svejda F 1960 Inheritance of post-harvest seed dormancy and kernel colour in spring wheat lines. Canadian Journal of Plant Science 40: 1-6.
436.	Gfeller F & Whiteside AGO 1961 Inheritance of quality as related to agronomic characters in advanced lines of a spring wheat cross. Canadian Journal of Plant Science 41: 604-617.
437.	Ghosh S, Sikka SM & Rao MV 1958 Inheritance studies in wheat IV. Inheritance of rust resistance and other characters. Indian Journal of Genetics 18: 142-162.
438.	Gilchrist JA & Sorrells ME 1983 Inheritance of kernel colour in 'Charcoal' wheat. Journal of Heredity 73: 457-460.
439.	Gill BS 1993 Molecular cytogenetic analysis in wheat. Crop Science 33: 902-908.
440.	Gill BS, Friebe B, Wilson DL, Martin DJ & Cox TS 1995 Registration of KS93WRC27 wheat streak mosaic virus resistant T4DL.4Ai#2S wheat germplasm. Crop Science 35: 1236-1237.
441.	Gill BS, Hatchett JH & Raupp WJ 1987 Chromosomal mapping of Hessian fly resistance gene *H13* in the D genome of wheat. Journal of Heredity 78: 97-100.
442.	Gill BS, Wilson DL, Raupp JH, Cox TS, Amri A & Sears RG 1991 Registration of KS89WGRC3 and KS89WGRC6 Hessian fly-resistant hard red winter wheat germplasm. Crop Science 31: 245.
443.	Gill KS & Gill BS 1996 A PCR-based screening assay of *Ph1*, the chromosome pairing regulator gene of wheat. Crop Science 36: 719-722.
444.	Gill KS, Gill BS & Endo TR 1993 A chromosome region-specific mapping strategy reveals gene-rich telomeric ends in wheat. Chromosoma 102: 374-381.
445.	Gill KS, Gill BS, Endo T & Taylor T 1996 Identification and high-density mapping of gene-rich regions in chromosome group 1 of wheat. Genetics 144: 1883-1891.
446.	Gill KS, Gill BS, Endo TR & Boyko EV 1996 Identification and high-density mapping of gene-rich regions in chromosome group 5 of wheat. Genetics 143: 1001-1012.
447.	Gill KS, Gill BS, Endo TR & Mukai Y 1993 Fine physical mapping of *Ph1*, a chromosome pairing regulator gene in polyploid wheat. Genetics 134: 1231-1236.

448.	Gill KS, Lubbers EL, Gill BS, Raupp WJ & Cox TS 1991 A genetic linkage map of *Triticum taushii* (DD) and its relationship to the D genome of bread wheat (AABBDD). Genome 34: 362-374.
449.	Giorgi B 1983 Origin, behaviour and utilization of a *Ph1* mutant of durum wheat, *Triticum turgidum* (L.) var. durum. Proceedings of the 6th International Wheat Genetics Symposium Kyoto, Japan (Sakamoto S ed.): 1033-1040.
450.	Giorgi B & Mosconi C 1982 Short-straw mutants and other dwarfing gene sources used for the improvement of wheats and barley in Italy. IAEA Tecdoc: Semi-dwarf Cereal Mutants and Their Use in Cross-breeding 268: 53-64.
451.	Giorgi B, Barbera F, Bitti O & Cavicchioni G 1984 Field performance of F3 progenies from a durum wheat involving two different semidwarfing genes: *Rht1* and *Sd* mutation. IAEA Tecdoc: Semi-dwarf Cereal Mutants and Their Use in Cross-breeding II 307: 91-95.
452.	Giroux MJ & Morris CF 1997 A glycine to serine change in puroindoline b is associated with wheat grain hardness and low levels of starch-surface friabilin. Theoretical and Applied Genetics 95: 857-864.
453.	Goldmark P, Curry J, Morris CG & Walker-Simmons MK 1992 Cloning and expression of an embryo-specific mRNA up-regulated in hydrated dormant seeds. Plant Molecular Biology 19: 433-441.
454.	Golenberg EM 1986 Chromosomal location of peptidase, PEPT-1, genes in *Triticum aestivum* var. Chinese Spring. Genetical Research, Cambridge 48: 19-20.
455.	Gomez L, Sanchez-Monge R & Salcedo G 1988 A family of endosperm globulins encoded by genes located in group 1 chromosomes of wheat and related species. Molecular and General Genetics 214: 541-546.
456.	Goncharov NP & Konovalov AA 1996 Inheritance of glucose phosphate isomerase, awnedness, hairy glume, and growth habit in *Aegilops speltoides* and *Aegilops aucheri*. Russian Journal of Genetics (Eng vers) 32(5): 571-576.
457.	Goncharov NP, Konovalov AA & Chikida NN 1997 Genetic variation at the *GPI-1* loci among *Aegilops* and *Triticum* genera and phylogeny of polyploid wheat. Zhurnal Obzhckei Biologii 58(2): 75-79.
458.	Goncharov NP, Konovalov AA, Gaidalenok RF, Goryachkovskaya TN, Tseveleva ON, Pel'tek SE, Litkovskaya NP & Khristov YA 1997 Genetic mapping of the short arm of chromosome 1B in common wheat cultivar Salmon. Russian Journal of Genetics (Eng vers) 33(4): 387-392.
459.	Gornicki P, Faris J, King I, Podkowinski J, Gill B & Haselkorn R 1998 Plastid-localized acetyl-CoA carboxylase of bread wheat is encoded by a single gene on each of the three ancestral chromosome sets. Proceedings of the National Academy of Sciences, USA 94: 14179-14184.
460.	Gotoh T 1979 Genetic studies on growth habit of some important spring wheat cultivars in Japan, with special reference to the identification of the spring genes involved. Japanese Journal of Breeding 29: 133-145.
461.	Gotoh T 1980 Gene analysis of the degree of vernalisation requirement in winter wheat. Japanese Journal of Breeding 30: 1-10.
462.	Graham RD 1978 Nutrient efficiency objectives in cereal breeding. Plant Nutrition Proceedings of the 8th International Colloquium on Plant Analysis and Fertilizer Problems, Auckland, 'NZ 165-170.
463.	Graham RD 1984 Breeding for nutritional characteristics in cereals. Advances in Plant Nutrition 1: 57-102.

464. Graham RD, Asher JS, Ellis PAE & Shepherd KW 1987 Transfer to wheat of the copper efficiency factor carried on rye chromosome 5RL. Plant and Soil 99: 107-114.

465. Graham WD Jr., Gambrell RH & Myers CW 1996 Registration of Clemson 201 soft red winter wheat. Crop Science 36: 468.

466. Grama A & Gerechter-Amitai ZK 1974 Inheritance of resistance to stripe rust (*Puccinia striiformis*) in crosses between wild emmer (*Triticum dicoccoides*) and cultivated tetraploid and hexaploid wheats II. *Triticum aestivum*. Euphytica 23: 393-398.

467. Graner A, Jahoor A, Schondelmaier J, Siedler H, Pillen K, Fischbeck G, Wenzel G & Herrmann RG 1991 Construction of an RFLP map of barley. Theoretical and Applied Genetics 83: 250-256.

468. Green GJ, Knott DR, Watson IA & Pugsley AT 1960 Seedling reactions to stem rust of lines of Marquis wheat with substituted genes for rust resistance. Canadian Journal of Plant Science 40: 524-538.

469. Green R 1991 Isolation and characterisation of genes induced in barley during powdery mildew infection. PhD thesis, Cambridge University.

470. Greenwell P & Schofield JD 1989 The chemical basis of grain hardness and softness. Proceedings of International Cereal Chemistry Conference, University of Helsinki, Finland: 59-72.

471. Guiltnan MJ, Marcotte WRJ & Quatrano RS 1990 A plant leucine zipper protein that recognizes an abscisic acid response element. Science 250: 267-271.

472. Gulick PJ & Dvorak J 1990 Selective enrichment of cDNAs from salt-stress-induced genes in the wheatgrass, *Lophopyrum elongatum*, by the formamide-phenol emulsion reassociation technique. Gene 95: 173-177.

473. Gulli M, Maestri E, Hartings H, Raho G, Perrotta C, Devos KM & Marmiroli N 1995 Isolation and characterization of abscisic acid inducible genes in barley seedlings and their responsiveness to environmental stress. Plant Physiology (Life Science Advances) 14: 89-96.

474. Gulyaeva JB 1984 Localization of the genes for pubesence of the glumes and coloration of the auricles in the leaf sheath in winter wheat variety Ulyanovka. Trudy po Prikladnoi Botanike, Genetikei Selektsii 85: 85-86.

475. Gupta N & Swaminathan MS 1967 An induced sphaerococcoid mutant in *Triticum dicoccum*. Current Science 36: 19.

476. Gupta RB 1989 Low-molecular-weight subunits of glutelin in wheat and related species: their characterization, genetics, and relation to bread-making quality. PhD Thesis, University of Adelaide, Australia

477. Gupta RB & Shepherd KW 1987 Interaction between genes controlling a new group of glutenin subunits in bread wheat. Theoretical and Applied Genetics 74: 459-465.

478. Gupta RB & Shepherd KW 1988 Inheritance of novel high-molecular-weight glutenin subunits in the Tunisian bread wheat BT-2288. Genome 30: 442-445.

479. Gupta RB & Shepherd KW 1988 Low-molecular weight glutenin subunits in wheat; their variation inheritance and association with bread-making quality. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 943-949.

480. Gupta RB & Shepherd KW 1990 Two-step one-dimensional SDS-PAGE analysis of LMW subunits of glutelin.2. Genetic control of the subunits in species related to wheat. Theoretical and Applied Genetics 80: 183-187.

481.	Gupta RB & Shepherd KW 1990 Two-step one-dimensionl SDS-PAGE analysis of LMW subunits of glutelin.1. Variation and genetic control of the subunits in hexaploid wheats. Theoretical and Applied Genetics 80: 65-74.
482.	Gupta RB & Shepherd KW 1993 Production of multiple wheat-rye 1RS translocation stocks and genetic analysis of LMW subunits of glutenin and gliadins in wheats using these stocks. Theoretical and Applied Genetics 85: 719-728.
483.	Gupta RB, Singh NK & Shepherd KW 1988 The cumulative effect of allelic variation in LMW and HMW glutenin subunits on dough properties in the progeny of two bread wheats. Theoretical and Applied Genetics 77: 57-64.
484.	Gyarfas J 1978 Transference of disease resistance from *Triticum timopheevii* to *Triticum aestivum*. MScAgr Thesis, University of Sydney, Australia.
485.	Gyarfas J 1983 Suneca. Journal of the Australian Institute of Agricultural Science 49: 43-44.
486.	Haggag MEA & Dyck PL 1973 The inheritance of leaf rust resistance in four common wheat varieties possessing genes at or near the *Lr3* locus. Canadian Journal of Genetics and Cytology 15: 127-134.
487.	Halloran GM & Boydell CW 1967 Wheat chromosomes with genes for photoperiodic response. Canadian Journal of Genetics and Cytology 9: 394-398.
488.	Hansen L 1987 Three cDNA clones for barley leaf acyl carrier proteins I and III. Carlsberg Research Communications 52: 381-392.
489.	Hansen L & Kauppinen S 1991 Barley Acyl carrier II: Nucleotide sequence of cDNA clones and chromosomal location of *Acl2* gene. Plant Physiology 97: 472-474.
490.	Hanson AD & Brown AHD 1984 Three alcohol dehydrogenase genes in wild and cultivated barley: Characterization of the products of variant alleles. Biochemical Genetics 22: 495-515.
491.	Hanusova R, Bartos P & Zeller FJ 1997 Characterization of the suppressor gene of powdery mildew resistance gene *Pm8* in common wheat (*Triticum aestivum* L.) cv. Regina. Journal of Applied Genetics 38: 11-17.
492.	Hanusova R, Hsam SLK, Bartos P & Zeller FJ 1996 Suppression of powdery mildew resistance gene *Pm8* in *Triticum aestivum* L. (common wheat) cultivars carrying wheat-rye translocation T 1BL.1RS. Heredity 77: 383-387.
493.	Harberd NP & Edwards KJR 1983 Further studies on the alcohol dehydrogenases in barley: Evidence for a third alcohol dehydrogenase locus and data on the effect of an alcohol dehydrogenase-1 null mutation in homozygous and in heterozygous condition. Genetical Research, Cambridge 41: 109-116.
494.	Harberd NP, Bartels D & Thompsom RD 1985 Analysis of the gliadin multigene loci in bread wheat using nullisomic-tetrasomic lines. Molecular and General Genetics 198: 234-242.
495.	Harberd NP, Bartels D & Thompson RD 1986 DNA restriction-fragment variation in the gene family encoding high-molecular-weight (HMW) glutenin subunits of wheat. Biochemical Genetics 24: 579-596.
496.	Harcourt RL 1992 PhD Thesis, Cambridge University, UK.
497.	Harcourt RL & Gale MD 1991 A chromosome-specific DNA sequence which reveals a high level of RFLP in wheat. Theoretical and Applied Genetics 81: 397-400.
498.	Hare RA 1992 Anatomical location and inheritance of variegated red seed coat colour in hexaploid wheat. Crop Science 32: 115-117.

499. Hare RA & McIntosh RA 1979 Genetic and cytogenetic studies of durable adult-plant resistances in 'Hope' and related cultivars to wheat rusts. Zeitschrift fur Pflanzenzuchtung 83: 350-367.

500. Hare RA, Du Cros DL & Barnes WC 1986 Genetic linkage between glume colour and certain gliadin proteins in durum wheat. Crop Science 26: 831-833.

501. Hart GE 1969 Genetic control of alcohol dehydrogenase isozymes in *Triticum dicoccum*. Biochemical Genetics 3: 617-625.

502. Hart GE 1970 Evidence for triplicate genes for alcohol dehydrogenase in hexaploid wheat. Proceedings of the National Academy of Sciences, USA 66: 1136-1141.

503. Hart GE 1971 Evolution of alcohol dehydrogenase isozymes in *Triticum*. Isozyme Bulletin 4: 15.

504. Hart GE 1973 Homoeologous gene evolution in hexaploid wheat. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri (Sears ER & Sears LMS eds.): 805-810.

505. Hart GE 1975 Glutamate oxaloacetate transaminase isozymes of *Triticum*: evidence for multiple systems of triplicate structural genes in hexaploid wheat. Isozymes: III. Developmental Biology, Academic Press, New York (Markert C ed.): 637-657.

506. Hart GE 1978 Chromosomal arm locations of *Adh-R1* and an acid phosphatase structural gene in Imperial rye. Cereal Research Communications 6: 123-133.

507. Hart GE 1979 Evidence for a triplicate set of glucosephosphate isomerase structural genes in hexaploid wheat. Biochemical Genetics 17: 585-598.

508. Hart GE 1983 Discovery and genetic control of hexaploid wheat NAD-dependent alcohol dehydrogenase which acts in aromatic alcohols. American Journal of Botany 70: 63.

509. Hart GE 1983 Genetics and evolution of multilocus isozymes in hexaploid wheat. *In*, Isozymes-Current Topics in Biological and Medical Research. Alan, R. Liss, Inc., New York. (Rattazzi HC, Scandalios JG & Whitt GS eds.): 10: 365-380.

510. Hart GE 1983 Hexaploid wheat (*Triticum aestivum*, L. em Thell.). *In*, Isozymes in Plant Genetics and Breeding. Elsevier Science Publishers, B.V., Amsterdam. (Tanksley SD & Orton TJ eds.): Part B: 35-36.

511. Hart GE 1984 Biochemical loci of hexaploid wheat (*Triticum aestivum*, 2n =42, Genomes AABBDD). *In*, Genetic Maps. Cold Spring Harbor Laboratory, (O'Brien SJ ed.): 3: 485-490.

512. Hart GE 1987 Genetic and biochemical studies of enzymes. *In*, Wheat and Wheat Improvement. American Society of Agronomy, Madison. (Heyne EG ed.): 199-214.

513. Hart GE 1987 Genetic control of NADH dehydrogenase-1 and aromatic alcohol dehydrogenase-2 in hexaploid wheat. Biochemical Genetics 25: 837-846.

514. Hart GE 1996 Personal communication.

515. Hart GE & Gale MD 1988 Guidelines for nomenclature of biochemical/molecular loci in wheat and related species. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 1215-1218.

516. Hart GE & Langston PJ 1977 Chromosome location and evolution of isozyme structural genes in hexaploid wheat. Heredity 39: 263-277.

517. Hart GE & Tuleen NA 1983 Characterizing and selecting alien genetic material in derivatives of wheat-alien species hybrids by analyses of isozyme variation. Proceedings of the 6th International Wheat Genetics Symposium, Kyoto, Japan (Sakamoto S ed.): 377-385.

518. Hart GE & Tuleen NA 1983 Chromosomal locations of eleven *Elytrigia elongata* (= *Agropyron elongatum*) isozyme structural genes. Genetical Research, Cambridge 41: 181-202.

519. Hart GE & Tuleen NA 1983 Introduction and characterization of alien genetic material. *In*, Isozymes in Plant Genetics and Breeding. Elsevier Science Publishers, B.V., Amsterdam, The Netherlands. (Tanksley SD & Orton TJ eds.): Part A: 339-362.

520. Hart GE, Islam AKMR & Shepherd KW 1980 Use of isozymes as chromosome markers in the isolation and characterization of wheat-barley chromosome addition lines. Genetical Research, Cambridge 36: 311-325.

521. Hart GE, McMillin DE & Sears ER 1976 Determination of the chromosomal location of a glutamate oxaloacetate transaminase structural gene using *Triticum*-*Agropyron* translocations. Genetics 83: 49-61.

522. Hartl L, Weiss H, Zeller FJ & Jahoor A 1993 Use of RFLP markers for the identification of alleles at the *Pm3* locus conferring powdery mildew resistance in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 86: 959-963.

523. Harvey TL, Martin TJ & Livers RW 1980 Resistance to biotype C greenbug in synthetic hexaploid wheats derived from *Triticum tauschii*. Journal of Economic Entomology 73: 387-389.

524. Hasm SLK & Zeller FJ 1997 Evidence of allellism between genes *Pm8* and *Pm17* and chromosomal location of powdery mildew and leaf rust resistance genes in the common wheat cultivar 'Amigo'. Plant Breeding 116: 119-122.

525. Hatchett JH, Martin TJ & Livers RW 1981 Expression and inheritance of resistance to Hessian fly in hexaploid wheats derived from *Triticum tauschii* (Coss.) Schmal. Crop Science 21: 731-734.

526. Hatfield PM, Callis J & Vierstra RD 1990 Cloning of ubiquitin activating enzyme from wheat and expression of a functional protein in *Escherichia coli*. Journal of Biological Chemistry 265: 15813-15817.

527. Hayter AM & Riley R 1967 Duplicate genetic activities affecting meiotic chromosome pairing at low temperature in *Triticum*. Nature 216: 1028-1029.

528. Hejgaard J, Bjorn SE & Nielsen G 1984 Localisation to chromosomes of structural genes for the major protease inhibitors of barley grains. Theoretical and Applied Genetics 68: 127-130.

529. Hejgaard J, Bjorn SE & Nielsen G 1984 Rye chromosomes carrying structural genes for the major grain protease inhibitors. Hereditas 101: 257-259.

530. Hermsen JG Th 1961 The symbolization of complementary necrosis genes in wheat: a proposal. Wheat Information Service 12: 22-23.

531. Hermsen JG Th 1963 Hybrid necrosis as a problem for the wheat breeder. Euphytica 12: 1-16.

532. Hermsen JG Th 1963 Sources and distribution of the complementary genes for hybrid necrosis in wheat. Euphytica 12: 147-160.

533. Hermsen JG Th 1963 The genetic basis of hybrid necrosis in wheat. Genetica 33: 445-487.

534. Hermsen JG Th 1963 The localization of two genes for dwarfing in the variety Timstein by means of substitution lines. Euphytica 12: 126-129.

535. Hermsen JG Th 1966 Hybrid necrosis and red hybrid chlorosis. Proceedings of the 2nd International Wheat Genetics Symposium Lund, Sweden 1963 (MacKey J ed.): Hereditas Supplement: 2: 439-452.

536. Hermsen JG Th 1967 Hybrid dwarfness in wheat. Euphytica 16: 134-162.

537.	Hermsen JG Th Personal communication.
538.	Hermsen JG Th & Waninge J 1972 Attempts to localize the gene *Ch1* for hybrid chlorosis in wheat. Euphytica 21: 204-208.
539.	Heun M 1988 Mapping powdery mildew resistance genes in winter wheat lines CI 15886 and CI 15887. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 823-827.
540.	Heun M & Fischbeck G 1987 Genes for powdery mildew resistance in cultivars of spring wheat. Plant Breeding 99: 282-288.
541.	Heun M & Fischbeck G 1987 Identification of wheat powdery mildew resistance genes by analysing host-pathogen interactions. Plant Breeding 98: 124-129.
542.	Heun M & Fischbeck G 1989 Inheritance of the powdery mildew resistance *Mlk* in wheat. Plant Breeding 103: 262-264.
543.	Heun M & Friebe B 1989 Introgression of powdery mildew resistance from rye into wheat. Phytopathology 80: 242-245.
544.	Heun M, Friebe B & Bushuk W 1990 Chromosomal location of the powdery mildew resistance gene of Amigo wheat. Phytopathology 80: 1129-1133.
545.	Heun M, Kennedy AE, Anderson JA, Lapitan NLV, Sorrells ME & Tanksley SD 1991 Construction of a restriction fragment length polymorphism map for barley (*Hordeum vulgare*). Genome 34: 437-447.
546.	Heyne EG Personal communication.
547.	Heyne EG & Finney KF 1968 Registration of Shawnee wheat. Crop Science 8: 512.
548.	Heyne EG & Johnston CO 1954 Inheritance of leaf rust reaction and other characters in crosses among Timstein, Pawnee and Redchief wheats. Agronomy Journal 46: 81-85.
549.	Heyne EG & Livers RW 1953 Monosomic analysis of leaf rust reaction, awnedness, winter injury and seed colour in Pawnee wheat. Agronomy Journal 45: 54-58.
550.	Heyne EG, Wiebe GA & Painter RH 1943 Complementary genes in wheat. Journal of Heredity 34: 243-245.
551.	Hoffmann JA & Metzger RJ 1976 Current status of virulence genes and pathogenic races of the wheat bunt fungi in the northwestern USA Phytopathology 66: 657-660.
552.	Hohmann U, Badaeva K, Busch W, Friebe B & Gill BS 1996 Molecular cytogenetic analysis of *Agropyron* chromatin specifying resistance to barley yellow dwarf virus in wheat. Genome 39: 336-347.
553.	Hohmann U, Endo TR, Gill KS & Gill BS 1994 Comparison of genetic and physical maps of group 7 chromosomes from *Triticum aestivum* L. Molecular and General Genetics 245: 644-653.
554.	Hollenhorst MM & Joppa LR 1983 Chromosomal location of genes for resistance to greenbug in 'Largo' and 'Amigo' wheats. Crop Science 23: 91-93.
555.	Holt LM, Austin RB & Payne PI 1981 Structural and genetic studies on the high-molecular weight subunits of wheat glutenin.2. Relative isoelectric points determined by two-dimensional fractionation in polyacrylamide gels. Theoretical and Applied Genetics 60: 237-243.
556.	Holton CS 1959 Genetic controls of host-parasite interactions in smut diseases. *In*, Plant Pathology Problems and Progress 1908-58 University of Wisconsin Press, Madison, Wisconson. 145-156.:
557.	Hoogendoorn J 1985 A reciprocal F1 monosomic analysis of the genetic control of the time of ear emergence, number of leaves and number of spikelets in wheat (*Triticum aestivum* L.). Euphytica 34: 545-558.

558.	Hovmoller MS 1989 Race specific powdery mildew resistance in 31 northwest European wheat cultivars. Plant Breeding 103: 228-234.
559.	Howes NK 1986 Linkage between the *Lr10* gene conditioning resistance to leaf rust, two endosperm proteins and hairy glumes in hexaploid wheat. Canadian Journal of Genetics and Cytology 28: 595-600.
560.	Hsam SLK & Zeller FJ 1982 Relationships of *Agropyron intermedium* chromosomes determined by chromosome pairing and alcohol dehydrogenase isozymes in common wheat background. Theoretical and Applied Genetics 63: 213-217.
561.	Hsam SLK, Cermeno MC, Friebe B & Zeller FJ 1995 Transfer of Amigo wheat powdery mildew resistance gene *Pm17* from TIAL.IRS to the T1BL.IRS wheat-rye translocated chromosome. Heredity 74: 497-501.
562.	Hsam SLK, Huang XQ, Earnst F, Hartl L & Zeller FJ 1998 Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em. Thell.). 5. Alleles at the *Pm1* locus. Theoretical and Applied Genetics 96: 1129-1134.
563.	Hu CC & Roelfs AP 1986 Postulation of genes for stem rust resistance in 13 Chinese wheat cultivars. Cereal Rusts Bulletin 14: 68-74.
564.	Hu CC & Roelfs AP 1986 Postulation of genes for stem rust resistance in 24 Chinese wheat cultivars. Cereal Rusts Bulletin 14: 61-67.
565.	Hu ML 1974 Genetic analyses of semidwarfing and insensitivity to gibberellin GA3 in hexaploid wheat (*Triticum aestivum*, L. em Thell.). PhD Thesis, Washington State University, USA.
566.	Hu ML 1980 A study of the X-ray induced semidwarfing gene in wheat (*Triticum aestivum*, L. em Thell.). Journal of the Agricultural Association of China 109: 5-16. *Cited* Plant Breeding Abstracts 52: 3671, p. 332.
567.	Hu ML & Konzak CF 1974 Genetic association of gibberellic acid insensitivity and semi-dwarfing in hexaploid wheat. Annual Wheat Newsletter 20: 184-185.
568.	Hu ML, Favret G, Favret EA, Donaldson E & Allan RE 1972 Inheritance of insensitivity to gibberellic acid GA3 in derivatives of oriental semidwarf wheats (Abstr.). Agronomy Abstracts p. 25.
569.	Hu ML, Konzak CF & Donaldson E Independent recessive inheritance of two new mutagen-induced plant height reducing factors in wheat (*Triticum aestivum*, L. em Thell.). (In preparation).
570.	Hu XY, Ohm HW & Dweikat I 1997 Identification of RAPD markers linked to the gene *Pm1* for resistance to powdery mildew in wheat. Theoretical and Applied Genetics 94: 832-840.
571.	Huang XQ, Hsam SLK & Zeller FJ 1997 Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em. Thell.) 4. Gene *Pm24* in Chinese landrace Chiyacao. Theoretical and Applied Genetics 95: 950-953.
572.	Huang XQ, Hsam SLK & Zeller FJ 1997 Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em Thell.). IX. Cultivars, landraces and breeding lines grown in China. Plant Breeding 116: 233-238.
573.	Hueros G, Gonzalez JM, Sanz JC & Ferrer E 1991 Gliadin gene location and C-banding identification of *Aegilops longissima* chromosomes added to wheat. Genome 34: 236-240.
574.	Hurd EA & McGinnis RC 1958 Notes on the location of genes for dwarfing in Redman wheat. Canadian Journal of Plant Science 38: 506.

575.	Hurkman WJ, Lane BG & Tanaka CK 1994 Nucleotide sequence of a transcript encoding a Germin-like protein that is present in salt-stressed barley roots. Plant Physiology 104: 803-904.
576.	Hussain T, Bowden RL, Gill BS & Cox TS 1994 Chromosomal location of wheat leaf rust resistance gene *Lr43* derived from *Triticum tauschii*. Phytopathology 84: 1116.
577.	Hussein T, Bowden RL, Gill BS & Cox TS 1998 Chromosome location of leaf rust resistance gene *Lr43* from *Aegilops tauschii* in common wheat. Crop Science 37: 1764-1766.
578.	Hutchinson J, Miller TE, Jahier J & Shepherd KW 1982 Comparison of the chromosomes of *Triticum timopheevi* with related wheats using the techniques of C-banding and *in situ* hybridisation. Theoretical and Applied Genetics 64: 31-40.
579.	Huttly AK, Martienssen RA & Baulcombe DC 1988 Sequence heterogeneity and differential expression of the a-*Amy2* gene family in wheat. Molecular and General Genetics 214: 232-240.
580.	Hvid D & Nielsen G 1977 Esterase isoenzyme variants in barley. Hereditas 87: 155-162.
581.	Inbal E 1982 Morphogenetic, genetic and physiologic aspects of stunting expression in wheat (*Triticum aestivum* L.). PhD Thesis, Weizmann Institute, 122 pp.
582.	Irani BN & Bhatia CR 1972 Chromosomal location of alcohol dehydrogenase gene(s) in rye, using wheat-rye addition lines. Genetica 43: 195-200.
583.	Izumi N, Sawada S & Sasakuma T 1981 A dominant gene of dwarfism located on chromosome 4D in *Triticum aestivum*, cv. "Ai-bian 1". Wheat Information Service 53: 21-24.
584.	Jaaska V 1978 NADP-dependent aromatic alcohol dehydrogenase in polyploid wheats and their relatives. On the origin and phylogeny of polyploid wheats. Theoretical and Applied Genetics 53: 209-217.
585.	Jaaska V 1980 Electrophoretic survey of seedling esterases in wheats in relation to their phylogeny. Theoretical and Applied Genetics 56: 273-284.
586.	Jaaska V 1982 Isoenzymes of superoxide dismutase in wheats and their relatives: Alloenzyme variation. Biochemical Physiological Pflanzen 177: 747-755.
587.	Jaaska V 1984 NAD-dependent aromatic alcohol dehydrogenase in wheats (*Triticum* L.) and goatgrasses (*Aegilops* L.): evolutionary genetics. Theoretical and Applied Genetics 67: 535-540.
588.	Jackson EA, Holt LM & Payne PI 1983 Characterisation of high-molecular-weight gliadin and low-molecular-weight glutenin subunits of wheat endosperm by two dimensional electrophoresis and the chromosomal localisation of their controlling genes. Theoretical and Applied Genetics 66: 29-37.
589.	Jackson EA, Holt LM & Payne PI 1986 *Glu-B2*, a storage protein locus controlling the D group of LMW glutenin subunits in bread wheat (*Triticum aestivum*). Genetical Research, Cambridge 46: 11-17.
590.	Jahier J 1992 Personal communication.
591.	Jahier J, Doussinault G, Dosba F & Bourgeois E 1979 Monosomic analysis of resistance to eyespot in the variety "Roazon". Proceedings of the 5th International Wheat Genetics Symposium New Delhi, India (S. Ramanujam ed.): 437-440.
592.	Jahier J, Tanguy AM & Doussinault G 1989 Analysis of the level of eyespot resistance due to genes transferred to wheat from *Aegilops ventricosa*. Euphytica 44: 55-59.

593.	Jampates R & Dvorak J 1986 Location of the *Ph1* locus in the metaphase chromosome map and the linkage map of the 5Bq arm of wheat. Canadian Journal of Genetics and Cytology 28: 511-519.
594.	Jan CC, Dvorak J, Qualset CO & Soliman KM 1981 Selection and identification of a spontaneous alien chromosome translocation in wheat. Genetics 98: 389-398.
595.	Jensen NF & Driscoll CJ 1962 Inheritance of the waxless character in wheat. Crop Science 2: 504-505.
596.	Jha KK 1964 The association of a gene for purple coleoptile with chromosome 7D of common wheat. Canadian Journal of Genetics and Cytology 6: 370-372.
597.	Ji FG & Deng JY 1985 Further study on the inheritance of the genic male sterile wheat of Taigu and the production of the dominant male-sterile octaploid triticale. Scientia Sinica (Series B) 28: 609-617.
598.	Jia J, Devos KM, Chao S, Miller TE, Reader SM & Gale MD 1996 RFLP-based maps of homoeologous group-6 chromosomes of wheat and their application in the tagging of *Pm12*, a powdery mildew resistance gene transferred from *Aegilops speltoides* to wheat. Theoretical and Applied Genetics 92: 559-565.
599.	Jia JZ 1993 Personal communication.
600.	Jiang J, Friebe B & Gill BS 1994 Chromosome painting of Amigo wheat. Theoretical and Applied Genetics 89: 811-813.
601.	Jiang JM & Gill BS 1994 New 18S-26S ribosomal RNA gene loci. Chromosomal landmarks for the evolution of polyploid wheats. Chromosoma 103: 179-185.
602.	Johansson E, Henriksson P, Svensson G & Heneen WK 1993 Detection, chromosomal location and evaluation of the functional value of a novel high Mr glutenin subunit found in Swedish wheats. Journal of Cereal Science 17: 237-245.
603.	Johnson DA, Richards RA & Turner NC 1983 Yield, water relations, gas exchange and surface reflectances of near-isogenic wheat lines differing in glaucousness. Crop Science 23: 318-325.
604.	Johnson R Personal communication.
605.	Johnson R & Dyck PL 1984 Resistance to yellow rust in *Triticum spelta* var. *album* and bread wheat cultivars Thatcher and Lee. Proceedings of the 6th European and Mediterranean Cereal Rusts Conference, Grignon: 71-74.
606.	Johnson R & Taylor AJ 1972 Isolates of *Puccinia striiformis* collected in England from wheat varieties 'Maris Beacon' and 'Joss Cambier'. Nature 238: 105-106.
607.	Johnson R & Taylor AJ 1976 Annual Report of the Plant Breeding Institute, Cambridge, 1975: 126-128.
608.	Johnson R, Smith GMB & Taylor AJ 1984 Brown rust of wheat. 1983 Annual Report of the Plant Breeding Institute, Cambridge 84-85.
609.	Johnson R, Taylor AJ & Smith GMB 1984 1983 Annual Report of the Plant Breeding Institute, Cambridge 82-85.
610.	Johnson R, Taylor AJ & Smith GMB 1986 Personal communication.
611.	Johnson R, Taylor AJ & Smith GMB 1986 Resistance to British races of *Puccinia striiformis* in the differential wheat cultivars Heines Kolben and Heines Peko. Cereal Rusts Bulletin 14: 20-23.
612.	Johnson R, Wolfe MS & Scott PR 1969 1968 Annual Report of the Plant Breeding Institute, Cambridge: 113-123.
613.	Johnston CO & Heyne EG 1964 Wichita wheat backcross lines for differential hosts in identifying physiologic races of *Puccinia recondita*. Phytopathology 54: 385-388.

614.	Jolly CJ, Glenn GM & Rahman S 1996 GSP-1 genes are linked to the grain hardness locus (*Ha*) on wheat chromosome 5D. Proceedings of the National Academy of Sciences, USA 93: 2408-2413.
615.	Jones ERL & Clifford BC 1996 Annual Report-U.K. Cereal Pathogen Virulence Survey.
616.	Jones SS 1995 Personal communication.
617.	Yildirim A, Jones SS, Murray TD & Line RF 2000 Evaluation of *Daspyrum villosum* populations for resistance to cereal eyespot and stripe rust pathogens. Plant Disease 84: 40-44.
618.	Yildirim A, Jones SS & Murray 1998 Mapping a gene conferring resistance to *Pseudocercosporella herpotrichoides* on chromosome 4V of *Daspyrum villosum* in a wheat background. Genome 41: 1-6.
619.	
620.	Jones SS, Dvorak J, Knott DR & Qualset CO 1991 Use of double-ditelosomic and normal chromosome 1D recombinant substitution lines to map *Sr33* on chromosome arm 1DS in wheat. Genome 34: 505-508.
621.	Joppa LR Personal communication.
622.	Joppa LR & Williams ND 1982 Registration of Largo, a greenbug resistant hexaploid wheat. Crop Science 22: 901-902.
623.	Joppa LR, Du C, Hart GE & Hareland GA 1997 Mapping gene(s) for grain protein in tetraploid wheat (*Triticum turgidum* L.) using a population of recombinant inbred chromosome lines. Crop Science 37: 1586-1589.
624.	Joppa LR, Timian RG & Williams ND 1980 Inheritance of resistance to greenbug toxicity in an amphiploid of *Triticum turgidum/T. tauschii*. Crop Science 20: 343-344.
625.	Joppa LR, Williams ND & Maan SS 1987 The chromosomal location of a gene (*msg*) affecting megasporogenesis in durum wheat. Genome 29: 578-591.
626.	Jorgensen JH & Jensen CJ 1972 Genes for resistance to wheat powdery mildew in derivatives of *Triticum timopheevi* and *T. carthlicum*. Euphytica 21: 121-128.
627.	Jorgensen JH & Jensen CJ 1973 Gene *Pm6* for resistance to powdery mildew in wheat. Euphytica 22: 423.
628.	Joudrier P & Cauderon Y 1976 Localisation chromosomique de genes controlant la synthese de certains constituants beta-amylasique du grain de Ble tendre. Comptes Rendus Ac. Sc. Paris, D. 282: 115-118.
629.	Jouve N & Diaz F 1990 Genetic control of esterase-6 isozymes in hexaploid wheat and related species. Euphytica 46: 165-169.
630.	Jung C & Lelley T 1985 Hybrid necrosis in triticale caused by gene-interaction between its wheat and rye genomes. Zeitschrift fur Pflanzenzuchtung 94: 344-347.
631.	Kadarn BS 1936 Genetics of the Bansi wheat of the Bombay-Deccan and a synthetic Khapli. Part I. Proceedings of the Indian Academy of Science 4: 357-369.
632.	Kaloshian I, Roberts PA, Waines JG & Thomason IJ 1990 Inheritance of resistance to root-knot nematodes in *Aegilops squarrosa* L. Journal of Heredity 81: 170-172.
633.	Kam-Morgan LNW, Gill BS & Muthukrishman S 1989 DNA restriction fragment length polymorphisms: a strategy for genetic mapping of D genome of wheat. Genome 32: 724-732.
634.	Kasarda DD, Bernardin JE & Qualset CO 1976 Relationship of gliadin protein components to chromosomes in hexaploid wheats (*Triticum aestivum*). Proceedings of the National Academy of Sciences, USA 73: 3646-3650.

635.	Kato K, Nakagawa K & Kuno H 1993 Chromosomal location of the genes for vernalization response, *Vrn2* and *Vrn4*, in common wheat, *Triticum aestivum* L. Wheat Information Service 76: 53.
636.	Kaveh H, Williams ND & Gough FJ 1968 Allelic and linkage relations among genes for reaction to wheat stem rust. Agronomy Abstracts p. 12.
637.	Kawahara T 1991 Further analysis of *Cs* chlorosis observed in hybrids between emmer and the *timopheevi* group of tetraploid wheats. Wheat Information Service 72: 83.
638.	Keim DL, Welsh JR & McConnell RL 1973 Inheritance of photoperiodic heading response in winter and spring cultivars of bread wheat. Canadian Journal of Plant Science 53: 247-250.
639.	Keller B, Schachermayr G & Feuillet C 1996 Molecular cloning of a new receptor-like kinase gene encoded at the *Lr10*, disease resistance locus of wheat. Proceedings of the 9th European and Mediterranean Cereal Rusts and Powdery Mildews Conference, Lunteren, The Netherlands (Kema GHJ, Niks RE & Daamen, eds.) pp.34-36.
640.	Kema GHJ 1992 Resistance in spelt wheat to yellow rust I. Formal analysis and variation for gliadin patterns. Euphytica 63: 207-217.
641.	Kema GHJ & Lange W 1992 Resistance in spelt wheat to yellow rust II. Monosomic analysis of the Iranian accession 415. Euphytica 63: 219-224.
642.	Kenaschuk EO, Anderson RG & Knott DR 1959 The inheritance of rust resistance, V. The inheritance of resistance to race 15B of stem rust in ten varieties of durum wheat. Canadian Journal of Plant Science 39: 316-328.
643.	Keppenne VD & Baenziger S 1990 Inheritance of the blue aleurone trait in diverse wheat crosses. Genome 33: 525-529.
644.	Kerber ER 1987 Resistance to leaf rust in wheat: *Lr32*, a third gene derived from *Triticum tauschii*. Crop Science 27: 204-206.
645.	Kerber ER 1988 Telocentric mapping in wheat of the gene *Lr32* for resistance to leaf rust. Crop Science 28: 178-179.
646.	Kerber ER 1991 Personal communication.
647.	Kerber ER Personal communication.
648.	Kerber ER & Dyck PL 1969 Inheritance in hexaploid wheat of leaf rust resistance and other characters derived from *Aegilops squarrosa*. Canadian Journal of Genetics and Cytology 11: 639-647.
649.	Kerber ER & Dyck PL 1973 Inheritance of stem rust resistance transferred from diploid wheat (*Triticum monococcum*) to tetraploid and hexaploid wheat and chromosome location of the gene involved. Canadian Journal of Genetics and Cytology 15: 397-409.
650.	Kerber ER & Dyck PL 1979 Resistance to stem rust and leaf rust of wheat in *Aegilops squarrosa* and transfer of a gene for stem rust resistance to hexaploid wheat. Proceedings of the 5th International Wheat Genetics Symposium New Delhi, India (Ramanujam S ed.): 358-364.
651.	Kerber ER & Dyck PL 1990 Transfer to hexaploid wheat of linked genes for adult-plant leaf rust and seedling stem rust resistance from an ampliploid of *Aegilops speltoides* x *Triticum monococcum*. Genome 33: 530-537.
652.	Kerber ER & Rowland GG 1974 Origin of the free threshing character in hexaploid wheat. Canadian Journal of Genetics and Cytology 16: 145-154.
653.	Kibirige-Sebunya I & Knott DR 1983 Transfer of stem rust resistance to wheat from an *Agropyron* chromosome having a gametocidal effect. Canadian Journal of Genetics and Cytology 25: 215-221.

654.	Kilduff T 1933 Inheritance of bunt and loose smut reaction and of certain other characters in Kota x Red Bobs and Garnet crosses. Canadian Journal of Research 8: 147-172.
655.	Kilian A, Kleinhofs A & Warner RL 1992 Localization of NAD(P)H-bispecific nitrate reductase genes to chromosomes of barley, rye, wheat and *Aegilops umbellulata*. Theoretical and Applied Genetics 85: 274-275.
656.	Kilian A, Kleinhofs A, Villand P, Thorbjornsen T, Olsen O-A & Kleczkowski L 1994 Mapping of the ADP-glucose phosphorylase genes in barley. Theoretical and Applied Genetics 87: 869-871.
657.	Kim N-S, Armstrong K & Knott DR 1993 Molecular detection of *Lophopyrum* chromatin in wheat-*Lophopyrum* recombinants and their use in the physical mapping of chromosome 7D. Theoretical and Applied Genetics 85: 561-567.
658.	Kim N-S, Kuspira J, Armstrong K & Bhambhani R 1993 Genetic and cytogenetic analyses of the A genome of *Triticum monococcum*. VII Localization of rDNAs and characterization of 5S rRNA genes. Genome 36: 77-86.
659.	Kimber G 1971 The inheritance of red grain colour in wheat. Zeitschrift fur Pflanzenzuchtung 66: 151-157.
660.	King IP 1989 Cytogenetic studies on a preferentially transmitted chromosome from *Aegilops sharonensis*. PhD Thesis, Council for National Academic Awards.
661.	King IP, Purdie KA, Rezanoor HN, Koebner RMD, Miller TE, Reader SM & Nicholson P 1993 Characterization of *Thinopyrum bessarabicum* chromosome segments in wheat using random amplified polymorphic DNAs (RAPDs) and genomic *in situ* hybridization. Theoretical and Applied Genetics 86: 895-900.
662.	King SW, Joshi CP & Nguyen HT 1992 DNA sequence of an ABA-responsive gene (*rab 15*) from water-stressed wheat roots. Plant Molecular Biology 18: 119-121.
663.	Kleinhofs A, Chao S & Sharp PJ 1988 Mapping of nitrate reductase genes in barley and wheat. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.) 541-546.
664.	Kleinhofs A, Kilian A, Saghai MA, Biyashev RM, Hayes P, Chen FQ, Lapitan N, Fenwick A, Blake TK, Kanazin V, Ananiev E, Dahleen L, Kudrna D, Bollinger J, Knapp SJ, Liu B, Sorrells M, Heun M, Franckowiak JD, Hoffman D, Skadsen R & Steffenson BJ 1993 A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theoretical and Applied Genetics 86: 705-712.
665.	Klindworth DL, Klindworth MM & Williams ND 1997 Telosomic mapping of four genetic markers of durum wheat. Journal of Heredity 88: 229-232.
666.	Klindworth DL, Williams ND & Duysen ME 1995 Genetic analysis of *chlorina* mutants of durum wheat. Crop Science 35: 431-436.
667.	Kloppers FJ & Pretorius ZA 1994 Expression and inheritance of leaf rust resistance gene *Lr37* in wheat seedlings. Cereal Research Communications 22: 91-97.
668.	Knackstedt MA 1995 Personal communication.
669.	Knott DR 1957 The inheritance of rust resistance II. The inheritance of stem rust resistance in six additional varieties of common wheat. Canadian Journal of Plant Science 37: 177-192.
670.	Knott DR 1957 The inheritance of rust resistance III. The inheritance of stem rust resistance in nine Kenya varieties of common wheat. Canadian Journal of Plant Science 37: 366-384.

671.	Knott DR 1959 The inheritance of rust resistance IV. Monosomic analysis of rust resistance and some other characters in six varieties of wheat including Gabo and Kenya Farmer. Canadian Journal of Plant Science 39: 215-228.
672.	Knott DR 1961 The inheritance of rust resistance VI. The transfer of stem rust resistance from *Agropyron elongatum* to common wheat. Canadian Journal of Plant Science 41: 109-123.
673.	Knott DR 1962 Inheritance of rust resistance VIII. Additional studies on Kenya varieties of wheat. Crop Science 2: 130-132.
674.	Knott DR 1962 The inheritance of rust resistance IX. The inheritance of resistance to races 15B and 56 of stem rust in the wheat variety Khapstein. Canadian Journal of Plant Science 42: 415-419.
675.	Knott DR 1965 A comparison of the reaction to stem rust of wheat lines backcrossed five and nine times to Marquis that carry the same resistance genes. Canadian Journal of Plant Science 45: 106-107.
676.	Knott DR 1966 The inheritance of stem rust resistance in wheat. Proceedings of the 2nd International Wheat Genetics Symposium Lund, Sweden 1963 (MacKey J ed.): Hereditas Supplement 2: 156-166.
677.	Knott DR 1968 The inheritance of resistance to stem rust races 56 and 15B-1L (Can.) in the wheat varieties Hope and H-44. Canadian Journal of Genetics and Cytology 10: 311-320.
678.	Knott DR 1971 Genes for stem rust resistance in wheat varieties Hope and H-44. Canadian Journal of Genetics and Cytology 13: 186-188.
679.	Knott DR 1972 Using race-specific resistance to manage the evolution of plant pathogens. Journal of Environmental Quality 1: 227-231.
680.	Knott DR 1983 The inheritance of resistance to stem rust races 15B-1 and 56 in "French Peace" wheat. Canadian Journal of Genetics and Cytology 25: 283-285.
681.	Knott DR 1984 The genetic nature of mutations of a gene for yellow pigment linked to *Lr19* in 'Agatha' wheat. Canadian Journal of Genetics and Cytology 26: 392-393.
682.	Knott DR 1984 The inheritance of resistance to race 56 of stem rust in 'Marquillo' wheat. Canadian Journal of Genetics and Cytology 26: 174-176.
683.	Knott DR 1989 The mode of inheritance of a type of dwarfism in common wheat. Genome 32: 932-933.
684.	Knott DR 1989 The Wheat Rusts - Breeding For Resistance. Springer-Verlag, Berlin.
685.	Knott DR 1990 Near-isogenic lines of wheat carrying genes for stem rust resistance. Crop Science 30: 901-905.
686.	Knott DR Personal communication.
687.	Knott DR & Anderson RG 1956 The inheritance of rust resistance I. The inheritance of stem rust resistance in ten varieties of common wheat. Canadian Journal of Agricultural Science 36: 174-195.
688.	Knott DR & McIntosh RA 1978 Inheritance of stem rust resistance in 'Webster' wheat. Crop Science 17: 365-369.
689.	Knott DR & Shen I 1961 The inheritance of rust resistance VII. The inheritance of resistance to races 15B and 56 of stem rust in eleven common wheat varieties of diverse origin. Canadian Journal of Plant Science 41: 587-601.
690.	Knowles PF & Harrington JB 1943 Breeding smooth-awned durum and vulgare wheats. Scientific Agriculture 23: 697-707.
691.	Koba T & Shimada T 1993 Crossability of common wheat with *Aegilops squarrosa*. Wheat Information Service 77: 7-12.

692.	Koba T & Tsunewaki K 1978 Mapping of the *s* and *Ch2* genes on chromosome 3D of common wheat. Wheat Information Service 45-46: 18-20.
693.	Koba T, Takumi S & Shimada T 1997 Isolation, identification and characterization of disomic and translocated barley chromosome addition lines of common wheat. Euphytica 96: 289-296.
694.	Kobrehel K 1978 Identification of chromosome segments controlling the synthesis of peroxidases in wheat seeds and in transfer lines with *Agropyron elongatum*. Canadian Journal of Botany 56: 1091-1094.
695.	Kobrehel K & Fiellet P 1975 Identification of genomes and chromosomes involved in peroxidase synthesis of wheat seeds. Canadian Journal of Botany 53: 2336-2344.
696.	Kochumadhavan M, Tomar SMS & Nambisan PNN 1980 Investigations on hybrid necrosis in wheat. Indian Journal of Genetics and Plant Breeding 40: 496-502. *Cited* Plant Breeding Abstracts 52: 2780, p.252.
697.	Kochumadhavan M, Tomar SMS, Nambisan PNN & Ramanujam S 1984 Hybrid necrosis and hybrid chlorosis in Indian varieties of *Triticum dicoccum* Schubl. Euphytica 33: 853-858.
698.	Kochumadhavan M, Tomar SMS, Nambisan PNN & Rao MV 1988 Hybrid necrosis and disease resistance in winter wheats. Indian Journal of Genetics 48: 85-90.
699.	Koebner RMD 1987 Genetic control of a novel series of trypsin inhibitors in wheat and its relatives. Biochemical Genetics 25: 591-602.
700.	Koebner RMD 1987 Genetic control of dipeptidase in the Triticeae. Theoretical and Applied Genetics 74: 387-390.
701.	Koebner RMD 1990 Subtilisin inhibitor - a polymorphic protein produced by a gene on the short arms of wheat homoeologous group 1 chromosomes. Journal of Genetics and Breeding 44: 49-52.
702.	Koebner RMD Personal communication.
703.	Koebner RMD & Martin PK 1989 Chromosomal control of the aminopeptidases of wheat and its close relatives. Theoretical and Applied Genetics 78: 657-664.
704.	Koebner RMD & Martin PK 1990 Association of eyespot resistance in wheat cv 'Cappelle-Desprez' with endopeptidase profile. Plant Breeding 104: 312-317.
705.	Koebner RMD & Miller TE 1986 A note on the nomenclature for translocated chromosomes in the Triticeae. Cereal Research Communications 14: 315-316.
706.	Koebner RMD & Shepherd KW 1983 Shikimate dehydrogenase - a biochemical marker for group 5 chromosomes in the Triticinae. Genetical Research, Cambridge 41: 209-213.
707.	Koebner RMD & Shepherd KW 1986 Controlled introgression to wheat of genes from rye chromosome 1RS by induction of allosyndesis. 1. Isolation of recombinants. Theoretical and Applied Genetics 73: 197-208.
708.	Koebner RMD, Miller TE, Snape JW & Law CN 1988 Wheat endopeptidase: genetic control, polymorphism, intrachromosomal gene location and alien variation. Genome 30: 186-192.
709.	Koebner RMD, Shepherd KW & Appels R 1986 Controlled introgression to wheat of genes from rye chromosome 1RS by induction of allosyndesis.2. Characterisation of recombinants. Theoretical and Applied Genetics 73: 209-217.
710.	Kolchinsky A, Kanazin V, Yakovleva E, Gazumyan A, Cole C & Ananiev E 1990 5S-RNA genes of barley are located on the second chromosome. Theoretical and Applied Genetics 80: 333-336.

711.	Kolmer JA 1992 Enhanced leaf rust resistance in wheat conditioned by resistance gene pairs with *Lr13*. Euphytica 61: 123-130.
712.	Kolmer JA 1994 Genetics of leaf rust resistance in three western Canada spring wheats. Plant Disease 78: 600-602.
713.	Kolmer JA 1997 Virulence in *Puccinia recondita* f. sp. *tritici* isolates from Canada to genes for adult plant resistance to wheat leaf rust. Plant Disease 81: 267-271.
714.	Kolster P, Kretching CF & van Gelder WMJ 1988 Variation in high molecular weight glutenin subunits of *Triticum aestivum* and *T. turgidum* ssp. *dicoccoides*. Euphytica 37: 141-145.
715.	Koluchii VT 1987 Association of gliadin allelic variance with elements of productivity of winter wheat in F_2 hybrids from crossing the varieties Pionerskaya and Mironovskaya 808. In: Molecular Mechanisms of Genetic Processes, Abstracts of Reports of the Sixth All-Union Symposium (In Russian), Moscow: p. 121.
716.	Konig S 1988 Nachweis von biochemischen markerfakorten fur chromosomen von *Hordeum vulgare* L. Biochemical Physiological Pflanzen 183: 345-349.
717.	Konzak CF 1976 A review of semidwarfing gene sources and a description of some new mutants useful for breeding short-stature wheats. Induced Mutations in Cross-breeding I.A.E.A., Vienna, Austria 79-93.
718.	Konzak CF 1987 Mutations and mutation breeding. *In*, Wheat and Wheat Improvement. 2nd Edition. American Society of Agronomy, Madison, Wisconsin (Heyne EG ed.): 428-443.
719.	Konzak CF & Joppa LR 1988 The inheritance and chromosomal location of a gene for chocolate chaff in durum wheat. Genome 30: 229-233.
720.	Konzak CF, Sadam M & Donaldson E 1973 Inheritance and linkage in durum wheats of semidwarfing genes with low response to gibberellin A3. Proceedings of the Symposium of Genetics and Breeding of Durum Wheat, Bari, Italy 29-40.
721.	Konzak CF, Wilson MR & Franks PA 1984 Progress in the evaluation, use in breeding, and genetic analysis of semidwarf mutants in wheat. IAEA Tecdoc: Semidwarf Mutants and Their Use in Cross-breeding II 307: 39-50.
722.	Koppinen E 1941 (Morphological characters of spring wheat). Maataloust Aikakausk 13: 145-164. *Cited* Plant Breeding Abstracts 19: 206, p.65.
723.	Korzun V, Balzer H-J, Balzer A, Baumlein H & Borner A 1996 Chromosomal location of three wheat sequences with homology to pollen allergen encoding, DNA replication regulating, and DNA (cytosine-5)-methyltransferase genes in wheat and rye. Genome 39: 1213-1215.
724.	Korzun V, Borner A, Worland AJ, Law CN & Roder MS 1997 Application of microsatellite markers to distinguish inter-varietal chromosome substitution lines of wheat (*Triticum aestivum* L.). Euphytica 95: 149-155.
725.	Korzun V, Malyshev S, Voylokov A & Borner A 1997 RFLP-based mapping of three mutant loci in rye (*Secale cereale* L.) and their relation to homoeologous loci within the Gramineae. Theoretical and Applied Genetics 95: 468-473.
726.	Korzun V, Roder M, Worland AJ & Borner A 1997 Intrachromosomal mapping of genes for dwarfing (*Rht12*) and vernalization response (*Vrn1*) in wheat using RFLP and microsatellite markers. Plant Breeding 116: 227-232.
727.	Korzun V, Roder MS, Ganal MW, Worland AJ & Law CN 1997 Genetic analysis of the dwarfing gene (*Rht8*) in wheat. Part I. Molecular mapping of *Rht8* on the short arm of

	chromosome 2D of bread wheat (*Triticum aestivum*). Theoretical and Applied Genetics 96: 1104-1109.
728.	Kota RS, Gill KS, Gill BS & Endo TR 1993 A cytogenetically based physical map of chromosome 1B in common wheat. Genome 36: 548-554.
729.	Koval SF 1994 Genetic analysis of isogenic lines of spring wheat variety Novosibirskaya 67: Location of the gene determining the brown colour of the glume in chromosome 1D. Genetica 30: 569-570. (English vers Russian Journal of Genetics 30: 508-509).
730.	Koval SF, Metavosky EV & Sosinov AA 1988 A series of near- isogenic spring bread wheat lines on the basis of the variety Novosibirskaya 67. Cereal Research Communications 16: 183-187.
731.	Kreis M, Williamson MS, Buxton B, Pyrell J, Hejgard J & Svendsen I 1987 Primary structure and differential expression of beta-amylase in normal and mutant barleys. European Journal of Biochemistry 169: 517-525.
732.	Kreis M, Williamson MS, Shewry PR, Sharp P & Gale MD 1987 Identification of a second locus encoding beta-amylase on chromosome 2 of barley. Genetical Research, Cambridge 51: 13-16.
733.	Kronstad WE, Foote WH, Kolding MF & Rohde CR 1972 Registration of Hyslop wheat. Crop Science 12: 398.
734.	Kronstad WE, Rohde CR, Kolding MF & Metzger RJ 1976 Registration of McDermid wheat. Crop Science 16: 745.
735.	Krugman T, Levy O, Snape JW, Rubin B, Korol A & Nevo E 1997 Comparative RFLP mapping of the chlortoluron resistance gene (*Su1*) in cultivated wheat (*Triticum aestivum*) and wild wheat (*Triticum dicoccoides*). Theoretical and Applied Genetics 94: 46-51.
736.	Krugman T, Rubin B, Levy O, Snape JW & Nevo E 1995 RFLP mapping of chlortoluron resistance gene *Su1*, in bread wheat (*Triticum aestivum*) and wild wheat (*Triticum dicoccoides*). Proceedings Herbicide Resistance Conference, Cordoba, Spain, 1994.
737.	Kudryakov NV 1987 Mapping of *EstA* and *EstB* genes controlling the synthesis of esterase isozyme in rye grains. Soviet Genetics 23: 1139-1145.
738.	Kulkarni LG 1934 Correlated inheritance with special reference to disease resistance in spring wheat. Journal of the American Society of Agronomy 26: 885-893.
739.	Kurata N, Moore G, Nagamura Y, Foote T, Yano M, Minobe Y & Gale MD 1994 Conservation of genome structure between rice and wheat. Bio/Technology 12: 276-278.
740.	Kurata N, Nagamura Y, Yamamoto K, Harushima Y, Sue N, Wu J, Antonio BA, Shomura A, Shimizu T, Lin S-Y, Inoue T, Fukuda A, Shimano T, Kuboki Y, Toyama T, Miyamoto Y, Kirihara T, Hayasaka K, Miyao A, Monna L, Zhong HS, Tamura Y, Wang Z-X, Momma T, Umehara Y 1994 A 300 kilobase interval genetic map of rice including 883 expressed sequences. Nature Genetics 8: 365-372.
741.	Kuspira J & Unrau J 1957 Genetic analysis of certain characters in common wheat using whole chromosome substitution lines. Canadian Journal of Plant Science 37: 300-326.
742.	Kuspira J & Unrau J 1958 Determination of the number and dominance relationships of genes on substituted chromosomes in common wheat *Triticum aestivum* L. Canadian Journal of Plant Science 38: 199-205.
743.	Kuspira J & Unrau J 1960 Determination of gene-chromosome associations and establishment of chromosome markers by aneuploid analysis in common wheat. I. F2 analysis of glume pubescence, spike density and culm colour. Canadian Journal of Genetics and Cytology 2: 301-310.

744.	Kuspira J, Maclagan J, Bhambhani RN, Sadasivaich RS & Kim N-S 1989 Genetic and cytogenetic analyses of the A genome of *Triticum monococcum* L. V. Inheritance and linkage relationships of genes determining the expression of 12 qualitative characters. Genome 32: 869-881.
745.	Kuspira J, Maclagan J, Kerby K & Bhambhani RN 1986 Genetic and cytogenetic analysis of the A genome of *Triticum monococcum* II. The mode of inheritance of spring versus winter growth habit. Canadian Journal of Genetics and Cytology 28: 88-95.
746.	Labrum KE 1980 The location of *Yr2* and *Yr6* genes conferring resistance to yellow rust. Proceedings of the 5th European and Mediterranean Cereal Rusts Conference Bari, Italy: 41-45.
747.	Lafever HN 1979 Registration of 'Titan' wheat. Crop Science 19: 749.
748.	Lafever HN 1985 Registration of 'Adena' wheat. Crop Science 25: 1131.
749.	Lafever HN 1988 Registration of 'Becker' wheat. Crop Science 28: 376.
750.	Lafever HN 1988 Registration of 'Cardinal' wheat. Crop Science 28: 377.
751.	Lafever HN 1988 Registration of 'GR855' wheat. Crop Science 28: 378-379.
752.	Lafever HN & Berzonsky WA 1993 Registration of 'Excel' wheat. Crop Science 33: 648.
753.	Lafever HN & Berzonsky WA 1993 Registration of 'GR876' wheat. Crop Science 33: 647-648.
754.	Lagudah ES & Halloran GM 1988 Phylogenetic relationships of *Triticum tauschii*, the D genome donor to hexaploid wheat.2. Inheritance and chromosomal mapping of the HMW subunits of glutenin and gliadin gene loci of *T. tauschii*. Theoretical and Applied Genetics 75: 599-605.
755.	Lagudah ES & Halloran GM 1988 Phylogenetic relationships of *Triticum taushii*, the D genome donor of hexaploid wheat 1. Variation in HMW subunits of glutenin and gliadins. Theoretical and Applied Genetics 75: 592-598.
756.	Lagudah ES & Halloran GM 1989 Phylogenetic relationships of *Triticum tauschii*, the D genome donor to hexaploid wheat 3. Variation in, and the genetics of, seed esterases (*Est-5*). Theoretical and Applied Genetics 77: 851-856.
757.	Lagudah ES, Appels R, Brown AHD & McNeil D 1991 The molecular genetic analysis of *Triticum tauschii*-the D genome donor to hexaploid wheat. Genome 34: 375-386.
758.	Lagudah ES, Clarke BC & Appels R 1989 Phylogenetic relationships of *Triticum tauschii*, the D-genome donor to hexaploid wheat. 4. Variation and chromosomal location of 5S DNA. Genome 32: 1017-1025.
759.	Lagudah ES, Flood RG & Halloran GM 1987 Variation in high molecular weight glutenin subunits in landraces of hexaploid wheat from Afghanistan. Euphytica 36: 3-9.
760.	Laikova LI, Maystrenko OI, Gaidalensk RF & Mischenko SV 1980 (Cytogenetic study of the series ditelosomic lines for spring common wheat cultivar Saratovskaya 29). [In Russian]. Actual Questions of Plant Genetics and Breeding, Novosibirsk, 171
761.	Lange W & Jochemsen G 1987 Inheritance of hairy leaf sheath in *Triticum dicoccoides*. Cereal Research Communications 15: 139-142.
762.	Lange W & Riley R 1973 The position on chromosome 5B of wheat of the locus determining crossability with rye. Genetical Research, Cambridge 22: 143-153.
763.	Laroche A, Demeke T & Gaudet DA 1996 Identification of a DNA fragment linked to the bunt *Bt-10* resistance gene and its utilization for marker-assisted selection in hexaploid wheat. Canadian Journal of Plant Pathology 18: 491.

764.	Larson RI & Atkinson TG 1981 Reaction of wheat to common root rot: Identification of a major gene, *Crr*, on chromosome 5B. Canadian Journal of Genetics and Cytology 23: 173-182.
765.	Larson RI & Atkinson TG 1982 Reaction of wheat to common root rot: linkage of a major gene, *Crr*, with the centromere of chromosome 5B. Canadian Journal of Genetics and Cytology 24: 19-25.
766.	Laurie DA, Pratchett N, Bezant JH & Snape JW 1994 Genetic analysis of a photoperiod response gene on the short arm of chromosome 2 (2H) of *Hordeum vulgare*. Heredity 72: 619-627.
767.	Laurie DA, Pratchett N, Bezant JH & Snape JW 1995 RFLP mapping of five major genes and eight quantitative trait loci controlling flowering time in a winter x spring barley (*Hordeum vulgare* L.) cross. Genome 38: 575-585.
768.	Law CN 1966 The location of genetic factors affecting a quantitative character in wheat. Genetics 53: 487-493.
769.	Law CN Personal communication.
770.	Law CN & Johnson R 1967 A genetic study of leaf rust resistance in wheat. Canadian Journal of Genetics and Cytology 9: 805-822.
771.	Law CN & Wolfe MS 1966 Location of genetic factors for mildew resistance and ear emergence time on chromosome 7B of wheat. Canadian Journal of Genetics and Cytology 8: 462-470.
772.	Law CN, Snape JW & Worland AJ 1981 Intra-specific chromosome manipulation. Philosophical Transactions of the Royal Society of London, B 292: 509-518.
773.	Law CN, Suarez E, Miller TE & Worland AJ 1998 The influence of the group 1 chromosomes of wheat on ear-emergence times and their involvement with vernalization and day length. Heredity 80: 83-91.
774.	Law CN, Sutka J & Worland AJ 1978 A genetic study of day-length response in wheat. Heredity 41: 185-191.
775.	Law CN, Worland AJ & Giorgi B 1975 The genetic control of ear emergence time by chromosomes 5A and 5D of wheat. Heredity 36: 49-58.
776.	Law CN, Worland AJ, Hollins TW, Koebner RMD & Scott PR 1988 The genetics of two sources of resistance to eyespot (*Pseudocercosporella herpotrichoides*) in wheat. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 835-840.
777.	Law CN, Young CF, Brown JWS, Snape JW & Worland AJ 1978 The study of grain protein control in wheat using whole chromosome substitution lines. *In*, Seed Protein Improvement by Nuclear Techniques I.A.E.A., Vienna, Austria 483-502.
778.	Lawrence GJ 1986 The high-molecular-weight glutenin subunit composition of Australian wheat cultivars. Australian Journal of Agricultural Research 37: 125-133.
779.	Lawrence GJ & Appels R 1986 Mapping the nucleolus organiser region, seed protein loci, and isozyme loci on chromosome 1R in rye. Theoretical and Applied Genetics 71: 742-749.
780.	Lawrence GJ & Shepherd KW 1980 Variation in glutenin protein subunits in wheat. Australian Journal of Biological Sciences 33: 221-233.
781.	Lawrence GJ & Shepherd KW 1981 Chromosomal locations of genes controlling seed proteins in species related to wheat. Theoretical and Applied Genetics 59: 25-31.
782.	Lawrence GJ, Macritchie F & Wrigley CW 1988 Dough and baking quality of wheat lines deficient in glutenin subunits controlled by the *Glu-A1*, *Glu-B1* and *Glu-D1* loci. Journal of Cereal Science 7: 109-112.

783.	Lazar MD, Peterson GL & Hu J 1995 Multigenic inheritance of biotype-E greenbug resistance in wheat. Plant Breeding 114: 492-496.
784.	Lazarus CM, Baulcombe DC & Martionssen RA 1985 Amylase genes of wheat are two multigene families which are differentially expressed. Plant Molecular Biology 5: 13-24.
785.	Le Roux J & Rijkenberg FHJ 1987 Pathotypes of *Puccinia graminis* f. sp. *tritici* with increased virulence for *Sr24*. Plant Disease 71: 1115-1119.
786.	Leath S & Heun M 1990 Identification of powdery mildew resistance genes in cultivars of soft red winter wheats. Plant Disease 74: 747-752.
787.	Lebsock KL & Briggle LW 1974 Gene *Pm5* for resistance to *Erysiphe graminis* f. sp. *tritici* in Hope wheat. Crop Science 14: 561-563.
788.	Lebsock KL, Joppa LR & Walsh D 1973 Effect of daylength response on agronomic and quality characteristics of durum wheat. Crop Science 13: 670-674.
789.	Leckie D, Snape JW & Parker BB 1988 Intrachromosomal mapping of the herbicide resistance gene *Dfq1* in hexaploid wheat. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 551-554.
790.	Lein A 1943 (The genetical basis of the crossability between wheat and rye.). Z. Ind. Abst. Vererbl. 81: 28-61. *Cited* Plant Breeding Abstracts 14: 1197, p. 304.
791.	Leisle D & Ausemus ER 1965 Inheritance of stem rust reaction in a Frontana-Kenya 58-Newthatch derivative. Canadian Journal of Genetics and Cytology 7: 422-429.
792.	Leisle D, Kovacs MI & Howes N 1985 Inheritance and linkage relationships of gliadin proteins and glume colour in durum wheat. Canadian Journal of Genetics and Cytology 27: 716-721.
793.	Leitch IJ & Heslop-Harris JS 1993 Physical mapping of four sites of 5S rDNA sequences and one site of the a-amylase-2 gene in barley (*Hordeum vulgare*). Genome 36: 517-523.
794.	Leitch IJ & Heslop-Harrison JS 1992 Physical mapping of the 18S-5.8S-2.6S rRNA genes in barley by *in situ* hybridization. Genome 35: 1013-1018.
795.	Levy AA & Feldman M 1987 Personal communication.
796.	Levy AA & Feldman M 1988 Ecogeographical distribution of HMW glutenin alleles in populations of the wild tetraploid wheat *Triticum turgidum* var. *dicoccoides*. Theoretical and Applied Genetics 75: 651-658.
797.	Levy AA & Feldman M 1989 Genetics of morphological traits in wild wheat, *Triticum turgidum* var. *dicoccoides*. Euphytica 40: 275-281.
798.	Levy AA, Galili G & Feldman M 1988 Polymorphism and genetic control of high molecular weight glutenin subunits in wild tetraploid wheat *Triticum turgidum* var. *dicoccoides*. Heredity 61: 63-72.
799.	Levy O, Benyamini Y, Rubin B, Krugman T & Nevo E 1996 Chlortoluron resistance identification and genetic analysis in wild emmer wheat (*Triticum dicoccoides*). Proceedings of the Second International Weed Control Congress Copenhagen, Denmark, 25-28 June, 1996: Volumes 1-4. Department of Weed Control and Pesticide Ecology, Slagelse, Denmark. Pp 523-528.
800.	Liang GH, Wang RC, Niblett CL & Heyne EG 1979 Registration of B-6-37-1 wheat germplasm. Crop Science 19: 421.
801.	Limin AE, Danyluk J, Chauvin L-P, Fowler DB & Sarhan F 1997 Chromosome mapping of low-temperature induced Wcs120 family genes and regulation of cold-tolerance expression in wheat. Molecular and General Genetics 253: 720-727.
802.	Limpert E, Felsenstein FG & Andrivon D 1987 Analysis of virulence in populations of wheat powdery mildew in Europe. Journal of Phytopathology 120: 1-8.

803.	Litts JC, Simmons CR, Karrer CF, Huang RL & Rodriguez RL 1990 The isolation and characterization of a barley 1,3-1,4-b-glucanase gene. European Journal of Biochemistry 194: 831-838.
804.	Liu B, Segal G, Vega JM, Feldman M & Abbo S 1997 Isolation and characterization of chromosome-specific DNA sequences from a chromosome arm genomic library of common wheat. The Plant Journal 11: 959-965.
805.	Liu BH 1987 Isolation of a spontaneous chromosome translocation in common wheat. Plant Breeding 98: 266-267.
806.	Liu BH & Deng JY 1986 A dominant gene for male sterility in wheat. Plant Breeding 97: 204-209.
807.	Liu BH & Deng JY 1986 Genome study and telosomic analysis of the single dominant male-sterile *Ta1* gene in common wheat. Scientia Sinica (Series B) 29: 516-526.
808.	Liu CJ 1991 Biochemical markers in wheat. PhD Thesis, Cambridge University, UK.
809.	Liu CJ & Gale MD 1988 Three new marker systems, iodine binding factor (*Ibf-1*), malic enzyme (*Mal-1*) and malate dehydrogenase (*Mdh-3*) in wheat and related species. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 555-560.
810.	Liu CJ & Gale MD 1989 Evidence for the genetic control of hexokinase isozymes by homoeologous group 3 chromosomes in wheat. Cereal Research Communications 17: 101-104.
811.	Liu CJ & Gale MD 1989 The chromosomal location of a third set of malate dehydrogenase loci, *Mdh-3*, in wheat, barley and related species. Theoretical and Applied Genetics 78: 349-352.
812.	Liu CJ & Gale MD 1990 *Est-7*, a set of genes controlling green tissue esterases in wheat and related species. Theoretical and Applied Genetics 79: 781-784.
813.	Liu CJ & Gale MD 1991 The chromosomal location of genes encoding NADH dehydrogenase isozymes in hexaploid wheat and related species. Genome 34: 44-51.
814.	Liu CJ & Gale MD 1994 The genetical control and tissue-specificity of esterase isozymes in hexaploid wheat. Theoretical and Applied Genetics 88: 796-802.
815.	Liu CJ, Atkinson MD, Chinoy CN, Devos KM & Gale MD 1992 Nonhomoeologous translocations between group 4, 5 and 7 chromosomes within wheat and rye. Theoretical and Applied Genetics 83: 305-312.
816.	Liu CJ, Chao S & Gale MD 1989 The genetical control of tissue specific peroxidases, *Per-1*, *Per-2*, *Per-3*, *Per-4*, and *Per-5* in wheat. Theoretical and Applied Genetics 79: 305-313.
817.	Liu CJ, Chao S & Gale MD 1989 *Wsp-1*, a set of genes controlling water-soluble proteins in wheat and related species. Genetical Research, Cambridge 54: 173-181.
818.	Liu CJ & Gale MD 1989 *Ibf-1* (Iodine binding factor), a highly variable marker system in the *Triticeae*. Theoretical and Applied Genetics 77: 233-240.
819.	Liu C-Y 1995 Identification of a new low-Mr glutenin subunit locus on chromosome 1B of durum wheat. Journal of Cereal Science 21: 209-213.
820.	Liu JQ & Kolmer JA 1997 Genetics of leaf rust resistance in Canadian spring wheats AC Domain and AC Taber. Plant Disease 81: 757-760.
821.	Liu JQ & Kolmer JA 1997 Inheritance of leaf rust resistance in wheat cultivars Grandin and CDC Teal. Plant Disease 81: 505-508.
822.	Liu Y-G & Tsunewaki K 1991 Restriction fragment length polymorphism (RFLP) analysis in wheat. II. Linkage maps of the RFLP sites in common wheat. Japanese Journal of Genetics 66: 617-633.

823.	Livers RW 1964 Fertility restoration and its inheritance in cytoplasmic male-sterile wheat. Science 144: 420.
824.	Livers RW 1978 Registration of Larned wheat. Crop Science 18: 917-918.
825.	Livers RW 1978 Registration of Sage wheat. Crop Science 18: 917.
826.	Loegering WQ 1975 An allele for low reaction to *Puccinia graminis tritici* in Chinese Spring wheat. Phytopathology 65: 925.
827.	Loegering WQ Personal communication.
828.	Loegering WQ & Harmon DL 1969 Wheat lines near-isogenic for reaction to *Puccinia graminis tritici*. Phytopathology 59: 456-459.
829.	Loegering WQ & Sears ER 1963 Distorted inheritance of stem rust resistance of Timstein wheat caused by a pollen-killing gene. Canadian Journal of Genetics and Cytology 5: 65-72.
830.	Loegering WQ & Sears ER 1966 Relationships among stem-rust genes on wheat chromosomes 2B, 4B and 6B. Crop Science 6: 157-160.
831.	Loegering WQ & Sears ER 1970 *Sr9d* - a gene in Hope wheat for reaction to *Puccinia graminis tritici*. Zeitschrift fur Pflanzenzuchtung 64: 335-339.
832.	Loegering WQ & Sears ER 1973 The gene for low reaction to *Puccinia graminis tritici* in the Thatcher-3B substitution line. Crop Science 13: 282.
833.	Loi L, Ahluwalia B & Fincher GB 1988 Chromosomal location of genes encoding barley (1-3,1-4)-beta-Glucan 4-Glucanohydrolases. Plant Physiology 87: 300-302.
834.	Longstaff M, Raines CA, McMorrow EM, Bradbeer JW & Dyer TA 1989 Wheat phosphoglycerate kinase: evidence for recombination between the genes for chloroplastic and cytosolic enzymes. Nucleic Acids Research 17: 6569-6580.
835.	Longwell AR & Svihla G 1960 Specific chromosomal control of the nucleolus and of the cytoplasm in wheat. Experimental Cell Research 20: 294-312.
836.	Lookhart GL, Hagman K & Kasarda DD 1993 High-molecular-weight glutenin subunits of the most commonly grown wheat cultivars in the U.S.in 1984. Plant Breeding 110: 48-62.
837.	Love HH & Craig WT 1924 The inheritance of pubescent nodes in a cross between two varieties of wheat. Journal of Agricultural Research 28: 841-844.
838.	Lowry JR, Sammons DJ, Baenziger PS & Moseman JG 1984 Identification and characterization of the gene conditioning powdery mildew resistance in 'Amigo' wheat. Crop Science 24: 129-132.
839.	Luig NH 1964 Heterogeneity in segregation data from wheat crosses. Nature 204: 260-261.
840.	Luig NH 1968 Mechanisms of differential transmission of gametes in wheat. Proceedings of the 3rd International Wheat Genetics Symposium, Australian Academy of Science, Canberra (Finlay KW & Shepherd KW eds.): 322-323.
841.	Luig NH 1983 A Survey of Virulence Genes in Wheat Stem Rust, *Puccinia graminis* f. sp. *tritici*. Paul Parey, Berlin 212pp..
842.	Luig NH Personal communication.
843.	Luig NH & McIntosh RA 1968 Location and linkage of genes on wheat chromosome 2D. Canadian Journal of Genetics and Cytology 10: 99-105.
844.	Luig NH & Watson IA 1965 Studies on the genetic nature of resistance to *Puccinia graminis* var. *tritici* in six varieties of common wheat. Proceedings of the Linnaean Society of New South Wales 90: 299-327.
845.	Luig NH & Watson IA 1967 Vernstein - a *Triticum aestivum* derivative with Vernal emmer type stem rust resistance. Crop Science 7: 31-33.
846.	Lukaszewski AJ & Curtis CA 1994 Transfer of the *Glu-D1* gene from chromosome 1D to chromosome 1A in hexaploid triticale. Plant Breeding 112: 177-182.

847.	Lukow OM, Payne PI & Tkachuk R 1989 The HMW glutenin subunit composition of Canadian wheat cultivars and their association with bread-making quality. Journal of Science Food and Agriculture 46: 451-460.
848.	Luo MC & Dvorak J 1996 Molecular mapping of an aluminum tolerance locus on chromosome 4D of Chinese Spring wheat. Euphytica 91: 31-35.
849.	Luo MC, Dubcovsky J, Goyal S & Dvorak J 1996 Engineering of interstitial foreign chromosome segments containing the K^+/Na^+ selectivity gene *Kna1* by sequential homoeologous recombination in durum wheat. Theoretical and Applied Genetics 93: 1180-1184.
850.	Luo MC, Yen C & Yang JL 1993 Crossability percentages of bread wheat landraces from Shaanxi and Henan provinces, China, with rye. Euphytica 67: 1-8.
851.	Lupton FCH & Macer RCF 1962 Inheritance of resistance to yellow rust (*Puccinia glumarum* Erikss. and Henn.) in seven varieties of wheat. Transactions of the British Mycological Society 45: 21-45.
852.	Lutz J, Hsam SLK, Limpert E & Zeller FJ 1994 Powdery mildew resistance in *Aegilops tauschii* Coss. and synthetic hexaploid wheats. Genetic Resources and Crop Evolution 41: 151-158.
853.	Lutz J, Hsam SLK, Limpert E & Zeller FJ 1995 Chromosomal location of powdery mildew resistance genes in *Triticum aestivum* L. (common wheat) 2. Genes *Pm2* and *Pm19* from *Aegilops squarrosa* L. Heredity 74: 152-156.
854.	Lutz J, Katzhammer M, Stephan U, Felsenstein FG, Oppitz K & Zeller FJ 1995 Identification of powdery-mildew-resistance genes in common wheat (*Triticum aestivum* L. em Thell.). V. Old German cultivars and cultivars released in the former GDR. Plant Breeding 114: 29-33.
855.	Lutz J, Limpert E, Bartos P & Zeller FJ 1992 Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L.) I. Czechoslovakian cultivars. Plant Breeding 108: 33-39.
856.	Ma H & Hughes GR 1993 Personal communication.
857.	Ma H & Hughes GR 1995 Genetic control and chromosomal location of *Triticum timopheevii*-derived resistance to *septoria nodorum* blotch in durum wheat. Genome 38: 332-338.
858.	Ma R, Zheng DS & Fan L 1996 The crossability percentages of 96 bread wheat landraces and cultivars from Japan and rye. Euphytica 92: 301-306.
859.	Ma ZQ 1994 Personal communication.
860.	Ma ZQ & Sorrells ME 1995 Genetic analysis of fertility restoration in wheat using restriction fragment length polymorphism. Crop Science 35: 1137-1143.
861.	Ma ZQ, Gill BS, Sorrells ME & Tanksley SD 1993 RFLP markers linked to two Hessian fly-resistance genes in wheat (*Triticum aestivum* L.) from *Triticum tauschii* (Coss.) Schmal. Theoretical and Applied Genetics 85: 750-754.
862.	Ma ZQ, Gill BS, Sorrells ME & Tanksley SD 1993 RFLP markers linked to two Hessian fly resistance genes in wheat (*Triticum aestivum* L.) from *Triticum tauschii* (Coss.) Schmal. Theoretical and Applied Genetics 85: 750-754.
863.	Ma ZQ, Saidi A, Quick JS & Lapitan NLV 1998 Genetic mapping of Russian wheat aphid resistance genes *Dn2* and *Dn4* in wheat. Genome 41: 303-306.
864.	Ma ZQ, Sorrells ME & Tanksley SD 1994 RFLP markers linked to powdery mildew resistance genes *Pm1*, *Pm2*, *Pm3* and *Pm4a* in wheat. Genome 37: 871-875.

865. Ma ZQ, Zhao ZH & Sorrells ME 1995 Inheritance and chromosomal location of a male fertility restoring gene transferred from *Aegilops umbellulata* Zhuk. to *Triticum aestivum* L. Molecular and General Genetics 247: 351-357.

866. Maan SS 1975 Exclusive preferential transmission of an alien chromosome in common wheat. Crop Science 15: 278-292.

867. Maan SS 1992 A gene for embryo-endosperm compatibility and seed viability in alloplasmic *Triticum turgidum*. Genome 35: 772-7798.

868. Maan SS 1992 Genetic analysis of male fertility restoration in wheat: IV. Fertile line without major *Rf* genes. Crop Science 32: 24-28.

869. Maan SS 1992 Transfer of a species cytoplasm specific (*scs*) gene from *Triticum timopheevi* to *T. turgidum*. Genome 35: 238-243.

870. Maan SS 1994 Interactions between the *scs* and *Vi* genes in alloplasmic durum wheat. Genome 37: 210-216.

871. Maan SS Personal communication.

872. Maan SS, Carlson KM, Williams ND & Yang T 1987 Chromosomal arm location and gene-centromere distance of a dominant gene for male sterility in wheat. Crop Science 27: 494-500.

873. Maan SS, Lucken KA & Bravo JM 1984 Genetic analyses of male fertility restoration in wheat I. Chromosome location of *Rf* genes. Crop Science 24: 17-20.

874. Maas FB, Patterson FL, Foster JE & Hatchett JH 1987 Expression and inheritance of resistance of 'Marquillo' wheat to Hessian fly. Crop Science 27: 49-52.

875. Maas FB, Patterson FL, Foster JE & Ohm HW 1989 Expression and inheritance of resistance of ELS6404-160 durum wheat to Hessian fly. Crop Science 29: 23-28.

876. MacDonald MD 1987 Registration of two winter wheat disomic whole chromosome substitution germplasm lines. Crop Science 27: 1097.

877. Macer RCF 1966 The formal and monosomic genetic analysis of stripe rust (*Puccinia striiformis*) resistance in wheat. Proceedings of the 2nd International Wheat Genetics Symposium, Lund, Sweden 1963 (MacKey J ed.): Hereditas Supplement 2: 127-142.

878. Macer RCF 1975 Plant pathology in a changing world. Transactions of the British Mycological Society 65: 351-374.

879. Macindoe SL & Walkden-Brown C 1968 Wheat Breeding in Australia. Science Bulletin, Third Edition. Division of Plant Industry, New South Wales Department of Agriculture, Australia. 76: 255pp..

880. Mackay MC 1987 Register of Cereal Cultivars in Australia; cv. Schomburgk. The Journal of the Australian Institute of Agricultural Science 53: 120-122.

881. MacKey J 1954 Neutron and x-ray experiments in wheat and a revision of the speltoid problem. Hereditas 40: 65-180.

882. Mahgoub El-S & Obenbach W 1988 Genetical analysis of wheat endosperm storage proteins using reciprocal sets of inbred backcross lines. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 571-576.

883. Maystrenko OI 1973 (Location of chromosomes carrying the genes *Vrn1* and *Vrn3* suppressing winter habit in wheat.). Tsitogentich. Issled. Aneuploidov Myagk. Pshenitsy. Novosibirsk. U.S.S.R. 745: 169-177. *Cited* Plant Breeding Abstracts 46: 8823, p. 745.

884. Maystrenko OI 1976 (Identification and location of genes controlling leaf hairiness in young plants of bread wheat). Genetika, U.S.S.R. 12: 5-15. *Cited* Plant Breeding Abstracts 47: 9205, p. 784.

885.	Maystrenko OI 1980 Cytogenetic study of the growth habit and ear-emergence time in wheat (*Triticum aestivum* L.). Well-Being of Mankind and Genetics: Proceedings of the 14th International Congress of Genetics MIR Publishers, Moscow. Vol 1, Book 2: 267-282.
886.	Maystrenko OI 1986 Personal communication.
887.	Maystrenko OI & Aliev EB 1985 Chromosomal location of genes responsible for photoperiodic reaction in a non-sensitive spring variety of common wheat, Shabati Sonora. Cereal Research Communications 13: 363-369.
888.	Mao L, Devos KM, Zhu L & Gale MD 1997 Cloning and genetic mapping of wheat telomere-associated sequences. Molecular and General Genetics 254: 584-591.
889.	Marais GF 1990 Preferential transmission in bread wheat of a chromosome segment derived from *Thinopyrum distichum* (Thunb.) Love. Plant Breeding 104: 152-159.
890.	Marais GF 1992 Gamma irradiation induced deletions in an alien chromosome segment of the wheat 'Indis' and their use in gene mapping. Genome 35: 225-229.
891.	Marais GF 1992 Genetic control of a response to the segregation allele, *Sd-1d* in the common wheat line 'Indis'. Euphytica 60: 89-95.
892.	Marais GF 1992 The modification of a common wheat-*Thinopyrum distichum* translocated chromosome with a locus homoeoalletic to *Lr19*. Theoretical and Applied Genetics 35: 73-78.
893.	Marais GF 1997 Personal communication.
894.	Marais GF, Wessels WG & Horn M 1998 Asssociation of a stem rust resistance gene (*Sr45*) and two Russian wheat aphid resistance genes (*Dn5* and *Dn7*) with mapped structural loci in wheat. South African Journal of Plants and Soil 15(2): 61-67.
895.	Marais GF & du Toit F A monosomic analysis of Russian wheat aphid resistance in the common wheat PI 294994. Plant Breeding 111: 246-248.
896.	Marais GF & Marais AS 1994 The derivation of compensating translocations involving homoeologous group 3 chromosomes of wheat and rye. Euphytica 79: 75-80.
897.	Marais GF, Potgieter GF, Roux HS & le Roux J 1994 An assessment of the variation for stem rust resistance in the progeny of a cross involving the *Triticum* species *aestivum*, *turgidum* and *tauschii*. South African Journal of Plants and Soil 11: 15-19.
898.	Marana C, Garcia-Olmedo F & Carbonero P 1988 Linked sucrose synthase genes in group-7 chromosomes in hexaploid wheat (*Triticum aestivum* L.). Gene 63: 253-260.
899.	Marchylo BA, Lukow OM & Kruger JE 1992 Quantitative variation in high molecular weight glutenin subunit 7 in some Canadian wheats. Journal of Cereal Science 15: 29-37.
900.	Marino CL, Nelson JC, Lu YH, Sorrells ME, Leroy P, Tuleen NA, Lopes CR & Hart GE 1996 Molecular genetic maps of the group 6 chromosomes of hexaploid wheat (*Triticum aestivum* L. em. Thell.). Genome 39: 359-366.
901.	Marshall D, Gardenshire JH, Gilmore EC, McDaniel ME & Erikson CA 1988 Registration of 'Collin' wheat. Crop Science 28: 868.
902.	Martienssen RA 1986 The molecular genetics of alpha-amylase gene families in wheat (*Triticum aestivum* L.). PhD Thesis, Cambridge University, UK.
903.	Martin TJ, Harvey TL & Hatchett JH 1982 Registration of greenbug and Hessian fly resistant wheat germplasm. Crop Science 22: 1089.
904.	Martin TJ, Sears RG, Hatchett JH, Wetzel DL, Shogren MD, Witt MD & Lawless JR 1988 Registration of 'Norkan' wheat. Crop Science 28: 198.
905.	Martinez I, Bernard M, Nicolas P & Bernard S 1994 Study of androgenetic performance and molecular characterisation of a set of wheat-rye addition lines. Theoretical and Applied Genetics 89: 982-990.

906.	Martini G, O'Dell M & Flavell RB 1982 Partial inactivation of wheat nucleolus organisers by the nucleolus organiser chromosomes from *Aegilops umbellulata*. Chromosoma 84: 687-700.
907.	Masojc P & Gale MD 1991 a-Amylase structural genes in rye. Theoretical and Applied Genetics 82: 771-776.
908.	Masojc P, Zawistowski J, Howes NK, Aung T & Gale MD 1993 Polymorphism and chromosomal location of an endogenous a-amylase inhibitor gene in common wheat. Theoretical and Applied Genetics 85: 1043-1048.
909.	Masua S, Liu YG, Sakamoto A, Nakajama T, Iwabuchi M & Tsunewaki K 1993 Chromosomal locations of the genes for histones and a histone gene binding protein family HBP-1 in common wheat. Plant Molecular Biology 22: 603-614.
910.	Matsumura S 1936 (Genetical studies on pentaploid wheat hybrids. II. Inheritance of the morphological characters independent of chromosome numbers in the combination of *Triticum polonicum* x *T. spelta*). Japanese Journal of Genetics 12: 289-306. *Cited* Plant Breeding Abstracts 7: 953, p.303.
911.	Matsumura S 1950 Linkage studies in *Triticum* II. *P*-linkage and the manifold effects of the *P* gene. Japanese Journal of Genetics 25: 111-118. *Cited* Plant Breeding Abstracts 23 (1953): 2557, p.555.
912.	Matsumura S 1951 Other studies on wheats. Annual Report of the National Institute of Genetics, Japan 1949-50 1: 25-27. *Cited* Plant Breeding Abstracts 23: 171, p.44.
913.	Matsumura S & Mochizuki A 1943 (Linkage studies in common wheat). Japanese Journal of Genetics 19: 104-106. *Cited* Plant Breeding Abstracts 21: 2527, p.824.
914.	Matsumura S & Mochizuki A 1943 Linkage studies in wheat, I. S-group. Seiken Ziho 2: 14-23. *Cited* Plant Breeding Abstracts 20: 1523, p.470.
915.	Mattern PJ, Morris R, Schmidt JW & Johnson VA 1973 Location of genes for kernel properties in the wheat variety 'Cheyenne' using chromosome substitution lines. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri (Sears ER & Sears LMS eds.): 703-708.
916.	May CE & Appels R 1984 Seedling lethality in wheat a novel phenotype associated with a 2RS/2BL translocation chromosome. Theoretical and Applied Genetics 68: 163-168.
917.	May CE & Appels R 1987 Variability and genetics of spacer DNA sequences between the ribosomal-RNA genes of hexaploid wheat (*Triticum aestivum*). Theoretical and Applied Genetics 74: 617-624.
918.	May CE & Appels R 1988 Allelism of the nucleolus organiser regions of hexaploid wheat. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 577-583.
919.	May CE, Vickery RS & Driscoll CJ 1973 Gene control in hexaploid wheat. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri (Sears ER & Sears LMS eds.): 843-849.
920.	Maystrenko OI 1987 Discovery of allelism in *Vrn2* locus of common wheat, its development type and its chromosome localization. Ecological Genetics of Plants and Animals. Thesis Reports, 3rd All-Union Conference. Kishinev, 'Shtiintsa' (In Russian). p. 148-149.
921.	Maystrenko OI 1992 The use of cytogenetic methods in ontogenesis study of common wheat. *In*: Ontogenetics of higher plants. Kishinev, 'Shtiintsa'. (In Russian). p. 98-114.
922.	Maystrenko OI 1993 Personal communication.

923.	Yelokhina LP 1989 Genetic control of spike coloration in the common spring wheat cv. 'Miltirum 553'. Proc Conf Sci Advanc Agric, Omsk, Russia Part 1: 13-14.
924.	Maystrenko OI 1993 Identification and chromosome localization of gene *Rg3* controlling red glume colour of the commong wheat ear. (In press). (In Russian).
925.	Maystrenko OI 1993 Personal communication.
926.	
927.	Maystrenko OI & Gamzikova OI 1993 Personal communication.
928.	McDonald D, McIntosh RA, Wellings CR, Singh RP & Nelson JC 2004 Cytogenetical Studies in Wheat XIX. Location and linkage studies on gene *Yr27* for resistance to stripe (yellow) rust. Euphytica 239-248.
929.	McIntosh RA 1972 Cytogenetical studies in wheat VI. Chromosome location and linkage studies involving *Sr13* and *Sr8* for reaction to *Puccinia graminis* f. sp. *tritici*. Australian Journal of Biological Sciences 25: 765-773.
930.	McIntosh RA 1976 Genetics of wheat and wheat rusts since Farrer. Journal of the Australian Institute of Agricultural Science 42: 203-216.
931.	McIntosh RA 1977 Nature of induced mutations affecting disease reaction in wheat. Induced Mutations against Plant Disease I.A.E.A., Vienna. 551-565.
932.	McIntosh RA 1978 Cytogenetical studies in wheat. X. Monosomic analysis and linkage studies involving genes for resistance to *Puccinia graminis* f. sp. *tritici* in cultivar Kota. Heredity 41: 71-82.
933.	McIntosh RA 1980 Chromosome location and linkage studies involving the wheat stem rust resistance gene *Sr14*. Cereal Research Communications 8: 315-320.
934.	McIntosh RA 1981 A gene for stem rust resistance in non-homoeologous chromosomes of hexaploid wheat progenitors. Proceedings XIII International Botanical Congress, Sydney, Australia. (Carr DJ ed.): 274.
935.	McIntosh RA 1983 Genetic and cytogenetic studies involving *Lr18* for resistance to *Puccinia recondita*. Proceedings of the 6th International Wheat Genetics Symposium Kyoto, Japan (Sakamota S ed.): 777-783.
936.	McIntosh RA 1988 Catalogue of gene symbols for wheat. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 2: 1225-1323.
937.	McIntosh RA 1992 Close genetic linkage of genes confering adult-plant resistance to leaf rust and stripe rust in wheat. Plant Pathology 41: 523-527.
938.	McIntosh RA 1994 Unpublished.
939.	McIntosh RA Unpublished.
940.	McIntosh RA & Arts CJ 1996 Genetic linkage of the *Yr1* and *Pm4* genes for stripe rust and powdery mildew resistances in wheat. Euphytica 89: 401-403.
941.	McIntosh RA & Baker EP 1967 Inheritance of purple pericarp in wheat. Proceedings of the Linnaean Society of New South Wales 92: 204-208.
942.	McIntosh RA & Baker EP 1968 A linkage map for chromosome 2D. Proceedings of the 3rd International Wheat Genetics Symposium, Australian Academy of Science, Canberra (Findlay KW & Shepherd KW eds.): 305-309.
943.	McIntosh RA & Baker EP 1968 Chromosome location and linkage studies involving the *Pm3* locus for powdery mildew resistance in wheat. Proceedings of the Linnaean Society of New South Wales 93: 232-238.
944.	McIntosh RA & Baker EP 1969 Telocentric mapping of a second gene for grass-clump dwarfism. Wheat Information Service 29: 6-7.

945.	McIntosh RA & Baker EP 1970 Cytogenetic studies in wheat IV.Chromosome location and linkage studies involving the *Pm2* locus for powdery mildew resistance. Euphytica 19: 71-77.
946.	McIntosh RA & Baker EP 1970 Cytogenetic studies in wheat V. Monosomic analysis of Vernstein stem rust resistance. Canadian Journal of Genetics and Cytology 12: 60-65.
947.	McIntosh RA & Bennett FGA 1978 Telocentric mapping of genes *Pm3a* and *Hg* on chromosome 1A of hexaploid wheat. Cereal Research Communications 6: 9-14.
948.	McIntosh RA & Dyck PL 1975 Cytogenetical studies in wheat VII. Gene *Lr23* for reaction to *Puccinia recondita* in Gabo and related cultivars. Australian Journal of Biological Sciences 28: 201-211.
949.	McIntosh RA & Gyarfas J 1971 *Triticum timopheevi* as a source of resistance to wheat stem rust. Zeitschrift fur Pflanzenzuchtung 66: 240-248.
950.	McIntosh RA & Luig NH 1973 Linkage of genes for reaction to *Puccinia graminis* f. sp. *tritici* and *P. recondita* in Selkirk wheat and related cultivars. Australian Journal of Biological Sciences 26: 1145-1152.
951.	McIntosh RA & Luig NH 1973 Recombination between genes for reaction to *Puccinia graminis* at or near the *Sr9* locus. Proceedings of the 4th International Wheat Genetics Symposium, Columbia, Missouri (Sears ER & Sears LMS eds.): 425-532.
952.	McIntosh RA and Lagudah ES 2000 Cytogenetical studies in wheat. XVIII. Gene Yr24 for resistance to stripe rust. Plant Breeding 119: 81-83.
953.	McIntosh RA et al 1998 Personal communication.
954.	McIntosh RA, Baker EP & Driscoll CJ 1965 Cytogenetic studies in wheat I. Monosomic analysis of leaf rust resistance in cultivars Uruguay and Transfer. Australian Journal of Biological Sciences 18: 971-977.
955.	McIntosh RA, Dyck PL & Green GJ 1974 Inheritance of reaction to stem rust and leaf rust in the wheat cultivar Etoile de Choisy. Canadian Journal of Genetics and Cytology 16: 571-577.
956.	McIntosh RA, Dyck PL & Green GJ 1977 Inheritance of leaf rust and stem rust resistances in wheat cultivars Agent and Agatha. Australian Journal of Agricultural Research 28: 37-45.
957.	McIntosh RA, Dyck PL, The TT, Cusick JE & Milne DL 1984 Cytogenetical studies in wheat XIII. *Sr35*-a third gene from *Triticum monococcum* for resistance to *Puccinia graminis tritici*. Zeitschrift fur Pflanzenzuchtung 92: 1-14.
958.	McIntosh RA, Friebe B, Jiang J, The D & Gill BS 1995 Chromosome location of a new gene for resistance to leaf rust in a Japanese wheat-rye translocation line. Euphytica 82: 141-147.
959.	McIntosh RA, Hart GE & Gale MD 1989 Catalogue of gene symbols for wheat: 1989 supplement. Annual Wheat Newsletter 35: 231-241.
960.	McIntosh RA, Hart GE & Gale MD 1991 Catalogue of gene symbols: 1991 supplement. Wheat Newsletter 37: 200-216.
961.	McIntosh RA, Hart GE & Gale MD 1995 Catalogue of gene symbols for wheat. Proceedings 8th International Wheat Genetics Symposium, Beijing, 1993 (Li ZS & Xin ZY eds.): 1333-1500.
963.	McIntosh RA, Hart GE, Devos, KM & Gale MD 1997 Catalogue of gene symbols for wheat: 1997 Supplement. Wheat Information Service 85: 56-81.
964.	McIntosh RA, Luig NH & Baker EP 1967 Genetic and cytogenetic studies of stem rust, leaf rust and powdery mildew resistances in Hope and related wheat cultivars. Australian Journal of Biological Sciences 20: 1181-1192.

965.	McIntosh RA, Luig NH, Johnson R & Hare RA 1981 Cytogenetical studies in wheat XI. *Sr9g* for reaction to *Puccinia graminis tritici*. Zeitschrift fur Pflanzenzuchtung 87: 274-289.
966.	McIntosh RA, Luig NH, Milne DL & Cusick JE 1983 Vulnerability of triticales to wheat stem rust. Canadian Journal of Plant Pathology 5: 61-69.
967.	McIntosh RA, Miller TE & Chapman V 1982 Cytogenetical studies in wheat XII. *Lr28* for resistance to *Puccinia recondita* and *Sr34* for resistance to *P. graminis tritici*. Zeitschrift fur Pflanzenzuchtung 89: 295-306.
968.	McIntosh RA, Partridge M & Hare RA 1980 Telocentric mapping of *Sr12* in wheat chromosome 3B. Cereal Research Communications 8: 321-324.
969.	McIntosh RA, Silk J & The TT 1996 Cytogenetic studies in wheat XVII. Monosomic analysis and linkage relationships of gene *Yr15* for resistance to stripe rust. Euphytica 89: 395-399.
970.	McIntosh RA, Wellings CR & Park RF 1995 Wheat Rusts: An Atlas of Resistance Genes. CSIRO Australia.
971.	McMillan JRA 1936 "Firing" - a heritable character of wheat. Journal of the Council of Science Industry and Research of Australia 9: 283-294.
972.	McMillan JRA 1937 Investigations on the occurrence and inheritance of the grass clump character in crosses between varieties of *Triticum vulgare* (Vill.). Bulletin of the Commonwealth Scientific Industry and Research Organization 104: 68pp..
973.	McMillin DE, Allan RE & Roberts DE 1986 Association of an isozyme locus and strawbreaker foot rot resistance derived from *Aegilops ventricosa* in wheat. Theoretical and Applied Genetics 72: 743-747.
974.	McMillin DE, Johnson JW & Roberts JJ 1993 Linkage between endopeptidase *Ep-Dld* and a gene conferring leaf rust resistance (*Lr19*) in wheat. Crop Science 33: 1201-1203.
975.	McNeal FH 1960 Yield components in a Lemhi x Thatcher wheat cross. Agronomy Journal 52: 348-349.
976.	McVey DV 1989 Verification of infection-type data for identification of genes for resistance to leaf rust in some hard red spring wheats. Crop Science 29: 304-307.
977.	McVey DV & Hamilton K 1985 Stem rust resistance gene from Triumph 64 identified in four other winter wheats. Plant Disease 69: 217-218.
978.	McVey DV & Long DL 1993 Genes for leaf rust resistance in hard red winter wheat cultivars and parental lines. Crop Science 33: 1373-1381.
979.	McVey DV & Roelfs AP 1975 Postulation of genes for stem rust resistance in the entries of the Fourth International Winter Wheat Performance Nursery. Crop Science 15: 335-337.
980.	McVittie JA, Gale MD, Marshall GA & Westcott B 1978 The intra-chromosomal mapping of the Norin 10 and Tom Thumb genes. Heredity 40: 67-70.
981.	Meadows JW, Hulford A, Raines CA & Robinson C 1991 Nucleotide sequence of a cDNA clone encoding the precursor of the 33 kDa protein of the oxygen-evolving complex from wheat. Plant Molecular Biology 16: 1085-1087.
982.	Mecham DK, Kasarda DD & Qualset CO 1978 Genetic aspects of wheat gliadin proteins. Biochemical Genetics 16: 831-853.
983.	Melz G & Thiele V 1990 Chromosome location of genes controlling 'purple leaf base' in rye and wheat. Euphytica 49: 155-159.
984.	Mena M, Orellana J, Lopez-Brana I, Garcia-Olmedo F & Delibes A 1989 Biochemical and cytological characterization of wheat/*Aegilops ventricosa* additions and transfer lines carrying chromosome $4M^v$. Theoretical and Applied Genetics 77: 184-188.

985.	Mena M, Orellana J, Lopez-Brana I, Garcia-Olmedo F & Delibes A 1993 Characterization of wheat/*Aegilops ventricosa* introgression and addition lines with respect to the M^v genome. Theoretical and Applied Genetics 86: 197-204.
986.	Merker A 1982 "Veery"- a CIMMYT spring wheat with the 1B/1R chromosome translocation. Cereal Research Communications 10: 105-106.
987.	Metakovsky EV 1990 Organization of gliadin-encoding genes which are genetic markers in wheat. Molecular Mechanisms of Genetic Processes, Nauka, Moscow (Sozinov AA & Schuppe NG eds.): 157-168.
988.	Metakovsky EV 1991 Gliadin allele identification in common wheat II. Catalogue of gliadin alleles in common wheat. Journal of Genetics and Breeding 45: 325-344.
989.	Metakovsky EV & Baboev SK 1992 Polymorphism and inheritance of gliadin polypeptides in *T. monococcum* L. Theoretical and Applied Genetics 84: 971-978.
990.	Metakovsky EV & Baboev SK 1992 Polymorphism of gliadin and unusual gliadin alleles in *Triticum boeoticum*. Genome 35: 1007-1012.
991.	Metakovsky EV & Branlard G 1998 Genetic diversity of French common wheat germplasm based on gliadin alleles. Theoretical and Applied Genetics 96: 209-218.
992.	Metakovsky EV & Sozinov AA 1987 Organization, variability and stability of the family of the gliadin-coding genes in wheat: genetic data. Gluten proteins. Proceedings of the 3rd International Workshop, Budapest, Hungary (Lastity R & Bekes F eds.): 30-45.
993.	Metakovsky EV, Akhmedov MG & Sozinov AA 1986 Genetic analysis of gliadin-encoding genes reveals gene clusters as well as single remote genes. Theoretical and Applied Genetics 73: 278-285.
994.	Metakovsky EV, Knezevic D & Javornik B 1991 Gliadin allele composition of Yugoslav wheat cultivars. Euphytica 54: 285-295.
995.	Metakovsky EV, Ng PKW, Chernakov VM, Pogna NE & Bushuk W 1993 Gliadin alleles in Canadian western red spring wheat cultivars: use of two different procedures of acid polyacrylamide gel electrophoresis for gliadin separation. Genome 36: 743-749.
996.	Metakovsky EV, Yu Novoselskaya A, Kopus MM, Sobko TA & Sozinov AA 1984 Blocks of gliadin components in winter wheat detected by one-dimensional polyacrylamide gel electrophoresis. Theoretical and Applied Genetics 67: 559-568.
997.	Mettin D, Bluthner WD & Schlegel G 1973 Additional evidence on spontaneous 1B/1R wheat rye substitutions and translocations. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri (Sears ER & Sears LMS eds.): 179-184.
998.	Mettin D, Bluthner WD & Weinrich M 1978 Studies on the nature and the possible origin of the spontaneously translocated 1B-1R chromosome in wheat. Wheat Information Service 47,48: 12-16.
999.	Metz AM, Timmer RT & Browning KS 1992 Isolation and sequence of a cDNA encoding the cap binding protein of wheat eukaryotic protein synthesis initiation factor 4F. Nucleic Acids Research 20: 4096.
1000.	Metzger RJ Personal communication.
1001.	Metzger RJ & Schaller CW Personal communication.
1002.	Metzger RJ & Silbaugh BA 1970 Inheritance of resistance to stripe rust and its association with brown glume colour in *Triticum aestivum* L. PI 178383. Crop Science 10: 567-568.
1003.	Metzger RJ & Silbaugh BA 1970 Location of genes for seed colour in hexaploid wheat, *Triticum aestivum* L. Crop Science 10: 495-496.
1004.	Metzger RJ & Silbaugh BA 1971 A new factor for resistance to common bunt in hexaploid wheats. Crop Science 11: 66-69.

1005. Metzger RJ, Rohde CR & Trione EJ 1963 Inheritance of genetic factors which condition resistance to the wheat variety Columbia to selected races of smut *Tilletia caries* and their association with red glumes. Agronomy Abstracts 85: *Cited* Plant Breeding Abstracts 34: 3599, p.445.

1006. Metzger RJ, Schaller CW & Rohde CR 1979 Inheritance of resistance to common bunt in wheat, CI 7090. Crop Science 19: 309-312.

1007. Meyer H 1977 (Genetic investigations in wheat, *Triticum aestivum* L. Part 1 Investigations into the localization of mildew-resistant genes using monosomic analysis.). Archiv. fur Zuchtungsforschung 7: 203-210. *Cited* Plant Breeding Abstracts 47: 11323, p. 960.

1008. Mickelson-Young L, Endo TR & Gill BS 1995 A cytogenetic ladder map of the wheat homoeologous group-4 chromosomes. Theoretical and Applied Genetics 90: 1007-1011.

1009. Miczynski K 1938 (Genetic studies on the phenol colour reaction in wheat.). Z. Zucht. A22: 564-587. *Cited* Plant Breeding Abstracts 8: 9697, p. 195.

1010. Millan T, Devos KM, Chinoy CN, Litts JL, Quatrano RS & Gale MD 1992 Chromosomal location and RFLP utility in wheat and barley of a wheat gene encoding seed storage 7S globulin. Theoretical and Applied Genetics 85: 387-388.

1011. Miller TE 1984 The homoeologous relationship between the chromosomes of rye and wheat. Current status. Canadian Journal of Genetics and Cytology 26: 578-589.

1012. Miller TE, Gerlach WL & Flavell RB 1980 Nucleolus organiser variation in wheat and rye revealed by *in situ* hybridisation. Heredity 45: 377-382.

1013. Miller TE, Hutchinson J & Chapman V 1982 Investigation of a preferentially transmitted *Aegilops sharonensis* chromosome in wheat. Theoretical and Applied Genetics 61: 27-33.

1014. Miller TE, Hutchinson J & Reader SM 1983 The identification of the nucleolar organizer chromosomes of diploid wheat. Theoretical and Applied Genetics 65: 145-147.

1015. Miller TE, Reader SM & Ainsworth CC 1985 A chromosome of *Hordeum chilense* homoeologous to group 7 of wheat. Canadian Journal of Genetics and Cytology 27: 101-104.

1016. Miller TE, Reader SM & Singh D 1988 Spontaneous non-Robertsonian transloations between wheat chromosomes and an alien chromosome. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 387-390.

1017. Miller TE, Reader SM, Ainsworth CC & Summers RW 1987 The introduction of a major gene for resistance to powdery mildew of wheat, *Erysiphe graminis* f. sp. *tritici*, from *Aegilops speltoides* into wheat, *Triticum aestivum*. *In*, Cereal Breeding Related to Integrated Cereal Production: Proceedings of the EUCARPIA Conference, Wageningen, The Netherlands (Jorna ML & Shootmaker LAJ eds.): 179-183.

1018. Miller TE, Reader SM, Mahmood A, Purdie KA & King IP 1995 Chromosome 3N of *Aegilops uniaristata* - a source of tolerance to high levels of aluminium in wheat. Proceedings 8th International Wheat Genetics Symposium, Beijing, 1993 (Li ZS & Xin ZY eds.): 1037-1042.

1019. Milus EA & Line RF 1980 Virulence of *Puccinia recondita* in the Pacific Northwest. Plant Disease 64: 78-80.

1020. Mitchell LE, Dennis ES & Peacock WJ 1989 Molecular anaysis of an alcohol dehydrogenase (*Adh*) gene from chromosome 1 of wheat. Genome 32: 349-358.

1021. Miura H, Parker BB & Snape JW 1992 The location of major genes associated with quantitative trait loci on chromosome arm 5BL of wheat. Theoretical and Applied Genetics 85: 197-204.

1022.	Miyazaki J, Juricek M, Angelis K, Schnerr KM, Kleinhofs A & Warner RL 1991 Characterization and sequence of a novel nitrate reductase from barley. Molecular and General Genetics 228: 329-334.
1023.	Modawi RS, Browder LE & Heyne EG 1985 Genes for low reaction to *Puccinia recondita* in 'Newton' hard red winter wheat. Crop Science 25: 13-16.
1024.	Modawi RS, Browder LE & Heyne EG 1985 Use of infection type data to identify genes for low reaction to *Puccinia recondita* in several winter wheat cultivars. Crop Science 25: 9-13.
1025.	Molnar-Lang M, Linc G & Sutka J 1996 Transfer of the recessive crossability allele *kr1* from Chinese Spring into the winter wheat Martonvasari 9. Euphytica 90: 301-305.
1026.	Montebove L, De Pace C, Jan CC, Scarascia Mugnozza GT & Qualset CO 1987 Chromosomal location of isozyme and seed storage protein genes in *Dasypyrum villosum* (L.) Candargy. Theoretical and Applied Genetics 73: 836-845.
1027.	Moonen JHE & Zeven AC 1984 SDS-PAGE of the high-molecular-weight subunits of wheat glutenin and the characterization of 1R(1B) substitution and 1BL/1RS translocation lines. Euphytica 33: 3-8.
1028.	Moonen JHE, Scheepstra A & Graveland A 1985 Biochemical properties of some high-molecular-weight subunits of wheat glutenin. Journal of Cereal Science 3: 17-27.
1029.	Moore K 1969 The genetical control of the grass-dwarf phenotype in *Triticum aestivum* L. Euphytica 18: 190-203.
1030.	Morgan JM 1991 A gene controlling differences in osmoregulatiion in wheat. Australian Journal of Plant Physiology 18: 249-257.
1031.	Morgan JM & Tan MK 1996 Chromosomal location of a wheat osmorgulation gene using RFLP analysis. Australian Journal of Plant Physiology 23: 803-806.
1032.	Morgunov AI, Rogers WJ, Sayers EJ & Metakovsky EV 1990 The high-molecular-weight glutenin subunit composition of Soviet varieties. Euphytica 51: 41-52.
1033.	Mori N, Liu Y-G & Tsunewaki K 1995 Wheat phylogeny determined by RFLP analysis of nuclear DNA. II. Wild tetraploid wheats. Theoretical and Applied Genetics 90: 129-134.
1034.	Mori N, Moriguchi T & Nakamura C 1997 RFLP analysis of nuclear DNA for study of phylogeny and domestication of tetraploid wheat. Genes and Genetic Systems 72: 153-161.
1035.	Giroux MJ & Morris CJ 1997 Personal communication.
1036.	Morris CF, Anderberg RJ, Goldmark PJ & Walker-Simmons M 1991 Molecular cloning and expression of abscisic acid-response genes in embryos of dormant wheat seeds. Plant Physiology 95: 814-821.
1037.	Morris LD, Raupp WJ & Gill BS 1990 Isolation of H^t genome chromosome additions from polyploid *Elymus trachycaulus* ($S^tS^tH^tH^t$) into common wheat (*Triticum aestivum*). Genome 33: 16-22.
1038.	Morris R & Sears ER 1967 The cytogenetics of wheat and its relatives. *In*, Wheat and Wheat Improvement. American Society of Agronomy, (Quisenberry KS & Reitz LP eds.): 19-87.
1039.	Morris R, Schmidt JW & Johnson VA 1970 Association of homoeologous group 6 aneuploids with leaf necrosis in hexaploid wheat varieties. Wheat Information Service 30: 6-7.
1040.	Morris R, Schmidt JW & Johnson VA 1972 Chromosomal location of a dwarfing gene in a Tom Thumb wheat derivative by monosomic analysis. Crop Science 12: 247-249.
1041.	Morrison JW 1953 Chromosome behaviour in wheat monosomics. Heredity 7: 203-217.

1042.	Mukai Y, Endo T & Gill BS 1992 Physical mapping of the 18S-5.8S-26S multigene family in common wheat: identification of a new locus. Chromosoma 100: 71-78.
1043.	Mukai Y, Endo TE & Gill BS 1990 Physical mapping of the 5S rRNA multigene family in common wheat. Journal of Heredity 81: 290-295.
1044.	Multani DS, Dhaliwal HS, Sharma SK & Gill KS 1989 Inheritance of isoproturon tolerance in *durum* wheat transferred from *Triticum monococcum*. Plant Breeding 102: 166-168.
1045.	Mundy J & Chua NH 1988 Abscisic acid and water stress induce the expression of a novel rice gene. EMBO Journal 7: 2279-2286.
1046.	Murai K 1997 Genetic analysis of fertility restoration against photoperiod-sensitive cytoplasmic male sterility in *Triticum aestivum* cv. Norin 61. Plant Breeding 116: 592-594.
1047.	Murai K & Tsunewaki K 1993 Photoperiod-sensitive cytoplasmic male sterility in wheat with *Aegilops crassa* cytoplasm. Euphytica 67: 41-48.
1048.	Muramatsu M 1963 Dosage effect of the *spelta* gene *q* of hexaploid wheat. Genetics 48: 469-482.
1049.	Muramatsu M 1986 The *vulgare* super gene, *Q*: its universality in durum wheat and its phenotypic effects in tetraploid and hexaploid wheats. Canadian Journal of Genetics and Cytology 28: 30-41.
1050.	Murray TD, de la Pena RC, Yildirim A & Jones SS 1994 A new source of resistance to *Pseudocercosporella herpotrichoides*, cause of eyespot disease of wheat, located on chromosome 4V of *Dasypyrum villosum*. Plant Breeding 113: 281-286.
1051.	Muthukrishnan S, Gill BS, Swegle M & Ram Chandra G 1984 Structural genes for a-amylases are located on barley chromosomes 1 and 6. Journal of Biological Chemistry 259: 13637-13639.
1052.	Naik S, Gill KS, Prakasa VS, Gupta VS, Tamhankar SA, Pujar S, Gill BS & Ranjekar PK 1998 Identification of a STS marker linked to the *Aegilops speltoides*-derived leaf rust resistance gene *Lr28* in wheat. Theoretical and Applied Genetics 97: 535-540.
1053.	Nakamura T, Yamamori M, Hirano H & Hidaka S 1993 Identification of three *Wx* proteins in wheat (*Triticum aestivum* L.). Biochemical Genetics 31: 75-86.
1054.	Nakamura T, Yamamori M, Hirano H & Hidaka S 1993 Decrease of waxy (Wx) protein in two common wheat cultivars with low amylase content. Journal of Plant Breeding 111: 99-105.
1055.	Neatby KW 1933 A chlorophyll mutation in wheat. Journal of Heredity 24: 159-162.
1056.	Neilsen CH 1982 Heredity of *Heterodera avenae* resistance originating from two barley cultivars and one spring wheat cultivar. EPPO Bulletin 12: 457-461.
1057.	Nelson JC 1996 Personal communication.
1058.	Nelson JC, Singh RP, Autrique JE & Sorrells ME 1997 Mapping genes conferring and suppressing leaf rust resistance in wheat. Crop Science 37: 1928-1935.
1059.	Nelson JC, Sorrells ME, Van Deynze AE, Lu YH, Atkinson MD, Bernard M, Leroy P, Faris JD & Anderson JA 1995 Molecular mapping of wheat: Major genes and rearrangements in homoeologous groups 4, 5 and 7. Genetics 141: 721-731.
1060.	Nelson JC, Van Deynze AE, Autrique E, Sorrells ME, Lu YH, Merlino M, Atkinson M & Leroy P 1995 Molecular mapping of wheat. Homoeologous group 2. Genome 38: 516-524.
1061.	Nelson JC, Van Deynze AE, Autrique E, Sorrells ME, Lu YH, Negre S, Bernard M & Leroy P 1995 Molecular mapping of wheat. Homoeologous group 3. Genome 38: 525-533.
1062.	Nelson W, Dubin HJ & Rajaram S 1980 Norin 10 dwarfing genes present in lines used in the CIMMYT wheat breeding programme. Cereal Research Communications 8: 573-574.

1063.	Netsvetaev VP 1978 Mapping of loci *Hrd* in chromosome 5 of barley with the help of reciprocal translocations. "Biologicheskie Osmovy Ratseonalnogo Ispolzovaniya Jivotnogo I Rastitelnogo Myra"" USSR. Riga ""Zinatne" 145-146.
1064.	Netting AG & Barber HN 1968 Chemical genetics of beta-diketone formation in wheat. Proceedings of the 3rd International Wheat Genetics Symposium, Australian Academy of Science, Canberra (Findlay KW & Shepherd KW eds.): 316-321.
1065.	Neuman PR & Hart GE 1983 Genetic control of shikimate dehydrogenase in hexaploid wheat. Biochemical Genetics 21: 963-968.
1066.	Neuman PR & Hart GE 1986 Genetic control of the mitochondrial form of superoxide dismutase in hexaploid wheat. Biochemical Genetics 24: 435-446.
1067.	Newton AC, Johnson R & Caten CE 1985 Virulence analysis of local populations of *Puccinia striiformis* f. sp. *tritici*. Cereal Rusts Bulletin 13: 11-15.
1068.	Ng PKW & Bushuk W 1989 Concerning the nomenclature of high molecular weight glutenin subunits. Journal of Cereal Science 9: 53-60.
1069.	Ng PKW, Pogna NE, Mellini F & Bushuk W 1989 *Glu-1* allele compositions of the wheat cultivars registered in Canada. Journal of Genetics and Breeding 43: 53-59.
1070.	Nicoloff H, Anastassoa-Kristeva M, Kunzel G & Rieger R 1977 The behaviour of nucleolus organizers in structurally changed karyotypes of barley. Chromosoma 62: 103-109.
1071.	Nielsen G & Frydenberg O 1971 Chromosome localization of the esterase loci *Est 1* and *Est 2* in barley by means of trisomics. Hereditas 67: 152-154.
1072.	Nielsen G, Johansen H & Jenson J 1983 Localisation on barley chromosome 5 of the locus *Pgd2* coding for phosphogluconate dehydrogenase. Barley Genetics Newsletter 13: 57.
1073.	Nielsen J 1977 Inheritance of virulence of loose smut of wheat, *Ustilago tritici* on the differential cultivars Renfrew, Florence x Aurore, Kota and Little Club. Canadian Journal of Botany 55: 260-263.
1074.	Nielsen J 1982 Inheritance of virulence of *Ustilago tritici* on the differential cultivars Carma, Red Bobs, and a derivative of the cross Thatcher x Regent. Canadian Journal of Botany 60: 1191-1193.
1075.	Nieto-Taladriz MT & Carrillo JM 1996 Complexity of the *Gli-A3* locus in bread wheat. Plant Breeding 115: 192-194.
1076.	Nieto-Taladriz MT, Branlard G & Dardevet M 1994 Polymorphism of omega-gliadins in durum wheat as revealed by the two-step APAGE/SDS-PAGE technique. Theoretical and Applied Genetics 87: 1001-1005.
1077.	Nieto-Taladriz MT, Pernas M, Salcedo G & Carrillo JM 1996 Linkage mapping of '25-kDa globulin' genes on homoeologous group-1 chromosomes of bread and durum wheat. Theoretical and Applied Genetics 93: 780-787.
1078.	Nieves R 1939 (Inheritance of grain colour in wheat). Journal of Agr. Vet., Buenos Aires: 129-154. *Cited* Plant Breeding Abstracts 11: 938, p. 279.
1079.	Niewoehner AS & Leath S 1998 Virulence of *Blumeria graminis* f. sp. *tritici* on winter wheat in the eastern United States. Plant Disease 82: 64-68.
1080.	Nishikawa K 1967 Identification and distribution of necrosis and chlorosis genes in tetraploid wheat. Seiken Ziho 19: 37-42.
1081.	Nishikawa K 1991 Chromosome mapping by use of aneuploids in wheat. Wheat Information Service 72: 60-63.

1082.	Nishikawa K & Nobuhara M 1971 Genetic studies of a-amylase isozymes in wheat I. Location of genes and variation in tetra- and hexaploid wheat. Japanese Journal of Genetics 46: 345-353.
1083.	Nishikawa K, Bon T & Furuta Y 1993 Telocentric mapping of a-amylase loci in wheat. Wheat Information Service 77: 39-45.
1084.	Nishikawa K, Furuta Y, Hina Y & Yamada T 1981 Genetic studies of a-amylase isozymes in wheat. IV. Genetic analyses in hexaploid wheat. Japanese Journal of Genetics 56: 385-395.
1085.	Nishikawa K, Mori T, Takanmi N & Furuta Y 1974 Mapping of progressive necrosis genes *Ne1* and *Ne2* of common wheat by the telocentric method. Japanese Journal of Breeding 24: 277-281.
1086.	Nkongolo KK, Quick JS, Limin AE & Fowler DB 1991 Sources and inheritance of resistance to Russian wheat aphid in *Triticum* species, amphiploids and *Triticum tauschii*. Canadian Journal of Plant Science 71: 703-708.
1087.	Noble WB & Suneson CA 1943 Differentiation of the two genetic factors for resistance to Hessian fly in Dawson wheat. Journal of Agricultural Research 67: 27-32.
1088.	Nyquist WE 1963 Inheritance of powdery mildew resistance in hybrids involving a common wheat strain derived from *Triticum timopheevi*. Crop Science 3: 40-43.
1089.	Obanni M, Ohm HW, Foster JE & Patterson FL 1989 Genetics of resistance of PI 422297 durum wheat to the Hessian fly. Crop Science 29: 249-252.
1090.	Obanni M, Patterson FL, Foster JE & Ohm HW 1988 Genetic analyses of resistance of durum wheat PI 428435 to the Hessian fly. Crop Science 28: 223-226.
1091.	Odintsova IG & Peusha KhO 1982 (Inheritance of resistance to brown rust in bread wheat varieties). Trudy po Prikladnoi Botanike, Genetikei Selektsii 71: 41-47. *Cited* Plant Breeding Abstracts 55: 7658, p.841.
1092.	Oellermann CM, Patterson FL & Gallun RL 1983 Inheritance of resistance in Luso wheat to Hessian fly. Crop Science 23: 221-224.
1093.	Oetmann A & Zeller FJ 1989 Distribution and origin of hybrid necrosis genes in German winter wheat (*Triticum aesivum* L.) cultivars. Plant Breeding 103: 207-211.
1094.	Ogihara Y, Shimizu H, Hasegawa K, Tsujimoto H & Sasakuma T 1994 Chromosome assignment of four photosynthetically-related genes and their variability in wheat species. Theoretical and Applied Genetics 88: 81-88.
1095.	Ohm HW 1988 Personal communication (1988a).
1096.	Ohm HW 1988 Personal communication (1988b).
1097.	Ohm HW, Ratcliffe RH, Patterson FL & Cambron S 1997 Resistance to Hessian fly conditioned by genes *H19* and proposed gene *H27* of durum wheat line PI422297. Crop Science 37: 113-115.
1098.	Ohm HW, Sharma HC, Patterson FL, Ratcliffe RH & Obanni M 1995 Linkage relationships among genes on wheat chromosome 5A that condition resistance to Hessian fly. Crop Science 35: 1603-1607.
1099.	Olive MR, Ellis RJ & Schuch WW 1989 Isolation and nucleotide sequences of cDNA clones encoding ADP-glucose pyrophosphate polypeptides from wheat leaf and endosperm. Plant Molecular Biology 12: 525-538.
1100.	Orth RA & Bushuk W 1974 Studies on glutenin VI. Chromosomal location of genes coding for subunits of glutenin of common wheat. Cereal Chemistry 51: 118-126.

1101.	Paderina EV, Hsam SLK & Zeller FJ 1995 Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em Thell.) VII. Cultivars grown in Western Siberia. Hereditas 123: 103-107.
1102.	Pan CL 1940 A genetic study of mature plant resistance in spring wheat to black stem rust, *Puccinia graminis tritici* and reaction to black chaff, *Bacterium translucens* var. *undulosum*. Journal of the American Society of Agronomy 32: 107-115.
1103.	Panin VM & Netsvetaev VP 1986 (Genetic control of gliadins and some morphological characters of spike in durum winter wheats.). [In Russian]. 'Nauchno-Tekhnicheski Bull. VSG I. Odessa 2: 31-36.
1104.	Patterson FL Personal communication.
1105.	Patterson FL & Gallun RL 1977 Linkage in wheat of the *H3* and *H6* genetic factors for resistance to Hessian fly. Journal of Heredity 68: 293-296.
1106.	Patterson FL, Foster JE & Ohm HW 1988 Gene *H16* in wheat for resistance to Hessian fly. Crop Science 28: 652-654.
1107.	Patterson FL, Maas FB, Foster JE, Ratcliffe RH, Cambron S, Safranski G, Taylor PL & Ohm HW 1994 Registration of eight Hessian fly resistant common winter wheat germplasm lines (Carol, Erin, Flynn, Iris, Joy, Karen, Lola and Molly). Crop Science 34: 315-316.
1108.	Patterson FL, Ohm HW, Shaner GE, Finney RE, Gallun RL, Roberts JJ & Foster JE 1985 Registration of 'Fillmore' wheat. Crop Science 25: 368-369.
1109.	Patterson FL, Roberts JJ, Finney RE, Shaner GE, Gallun RL & Ohm HW 1975 Registration of 'Oasis' wheat. Crop Science 15: 736-737.
1110.	Patterson FL, Shaner GE, Huber DM, Ohm HW, Finney RE, Gallun RL & Roberts JJ 1979 Registration of 'Sullivan' wheat. Crop Science 19: 297.
1111.	Paull J 1990 Personal communication.
1112.	Paull JG, Pallotta MA, Langridge P & The TT 1994 RFLP markers associated with *Sr22* and recombination between chromosome 7A of bread wheat and the diploid species *Triticum boeoticum*. Theoretical and Applied Genetics 89: 1039-1045.
1113.	Paull JG, Rathjen AJ & Cartwright B 1991 Major gene control of tolerance of bread wheat (*Triticum aestivum* L.) to high concentrations of soil boron. Euphytica 55: 217-228.
1114.	Payne PI 1989 Personal communication.
1115.	Payne PI Personal communication.
1116.	Payne PI & Lawrence GJ 1983 Catalogue of alleles for the complex gene loci, *Glu-A1*, *Glu-B1*, and *Glu-D1* which code for high molecular-weight subunits of glutenin in hexaploid wheat. Cereal Research Communications 11: 29-35.
1117.	Payne PI, Holt LM & Jackson EA 1984 Genetical analysis of wheat endosperm storage proteins. Proceedings of the 2nd International Workshop on Gluten Proteins Wageningen, The Netherlands: 111-120.
1118.	Payne PI, Holt LM & Law CN 1981 Structural and genetical studies on the high-molecular-weight subunits of wheat glutenin. Theoretical and Applied Genetics 60: 229-236.
1119.	Payne PI, Holt LM & Lister P 1988 *Gli-A3* and *Gli-B3*, two newly designated loci coding for some omega-type gliadins and D subunits of glutenins. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 999-1002.
1120.	Payne PI, Holt LM, Hutchinson J & Bennett MD 1984 Development and characterization of a line of bread wheat, *Triticum aestivum*, which lacks the short arm satellite 1B and the *Gli-B1* locus. Theoretical and Applied Genetics 68: 327-334.

1121.	Payne PI, Holt LM, Johnson R & Snape JW 1986 Linkage mapping of four gene loci, *Glu-B1*, *Gli-B1*, *Rg1* and *Yr10* on chromosome 1B of bread wheat. Genetica Agraria 40: 231-242.
1122.	Payne PI, Holt LM, Lawrence GJ & Law CN 1982 The genetics of gliadin and glutenin, the major storage proteins of the wheat ensosperm. Qualitas Plantarum; Plant Foods for Human Nutrition 31: 229-241.
1123.	Payne PI, Holt LM, Reader SM & Miller TE 1987 Chromosomal location of genes coding for endosperm proteins of *Hordeum chilense*, determined by two dimensional electrophoresis of wheat-*H. chilense* chromosome addition lines. Biochemical Genetics 25: 53-65.
1124.	Payne PI, Holt LM, Thompson RD, Bartels D, Harberd NP, Harris PA & Law CN 1983 The high-molecular-weight subunits of glutenin: classical genetics, molecular genetics and the relationship of bread-making quality. Proceedings of the 6th International Wheat Genetics Symosium Kyoto, Japan (Sakamoto S. ed.): 827-834.
1125.	Payne PI, Holt LM, Worland AJ & Law CN 1982 Structural and genetical studies on the high-molecular-weight subunits of wheat glutenin III. Telocentric mapping of the subunit genes on the long arms of the homoeologous group 1 chromosomes. Theoretical and Applied Genetics 63: 129-138.
1126.	Payne PI, Jackson EA, Holt LM & Law CN 1984 Genetic linkage between endosperm storage protein genes on each of the short arms of chromosomes 1A and 1B of wheat. Theoretical and Applied Genetics 67: 235-243.
1127.	Pedersen S, Due Tuvesson IK & Andersen SB 1990 Polymorphism for aconitase and glucosephosphate isomerase isozymes in hexaploid wheat. Hereditas 113: 1-6.
1128.	Penner GA, Clarke K, Bezte LJ & Leisle D 1995 Identification of RAPD markers linked to a gene governing cadmium uptake in durum wheat. Genome 38: 543-547.
1129.	Pepe JF & Heiner RE 1975 Influence of two different dwarfing sources on yield and protein percentage in semidwarf wheats. Crop Science 15: 637-639.
1130.	Petchey EM, Koebner RMD & Gale MD 1989 Genetic characterisation of a homoeoallelic series of grain esterase loci, *Est-6* in wheat. Theoretical and Applied Genetics 79: 294-296.
1131.	Pettigrew R & Driscoll CJ 1970 Cytogenetic studies of a chlorophyll mutant of hexaploid wheat. Heredity 25: 650-655.
1132.	Pettigrew R & Driscoll CJ Unpublished.
1133.	Pettigrew R, Driscoll CJ & Rienits KG 1969 A spontaneous chlorophyll mutant in hexaploid wheat. Heredity 24: 481-487.
1134.	Peusha H, Hsam SLK & Zeller FS 1995 Chromosomal location of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em Thell.) 3. Gene *Pm22* in cultivar Virest. Euphytica 91: 149-152.
1135.	Pfeffer A & Zeller FJ 1987 Genotypes of hybrid necrosis in 25 spring varieties of common wheat (*Triticum aestivum* L.). Plant Breeding 99: 83-84.
1136.	Philiptschenko J 1930 Again on the question of genes and the development of the form of ear in wheat. Bulletin of the Bureau of Genetics 8: 1-18. *Cited* Plant Breeding Abstracts 1: 163, p.16.
1137.	Piech J 1969 Genetic analysis of photoperiodic insensitivity in wheat. Genetica Polonica 10: 99-100.
1138.	Piech J & Evans LE 1979 Monosomic analysis of purple grain colour in hexaploid wheat. Zeitschrift fur Pflanzenzuchtung 82: 212-217.

1139.	Pietro ME & Hart GE 1985 The genetic control of triosephosphate isomerase of hexaploid wheat and other Triticeae species. Genetical Research, Cambridge 45: 127-142.
1140.	Pietro ME, Tuleen NA & Hart GE 1988 Development of wheat-*Triticum searsii* disomic chromosome addition lines. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 409-414.
1141.	Pirasteh B & Welsh JR 1975 Monosomic analysis of photoperiod response in wheat. Crop Science 15: 503-505.
1142.	Plaschke J, Borner A, Xie DX, Koebner RMD, Schlegel R & Gale MD 1993 RFLP mapping of genes affecting plant height and growth habit in rye. Theoretical and Applied Genetics 85: 1049-1054.
1143.	Plessers AG 1954 Genetic studies of stem rust reaction in crosses of Lee wheat with Chinese monosomic testers. Agricultural Institute Review 9: 37.
1144.	Pogna JC, Autran C, Mellini F, Lafiandra D & Feillet P 1990 Chromosome 1B encoded gliadins and glutenins subunits in durum wheat: genetics and relationship to gluten strength. Journal of Cereal Science 11: 15-34.
1145.	Pogna NE, Mellini F & Dalbelin Peruffo A 1987 Glutenin subunits of Italian common wheats of good bread making quality and comparative effects of high molecular weight glutenin subunits 2 and 5, 10 and 12 on flour quality. *In*, Hard Wheat:'Agronomic, Technological, Biochemical and Genetic Aspects. Commission of the European Communities, Brussels. (Borghi B ed.): 53-69.
1146.	Pogna NE, Mellini F, Beretta A & Dalbelin Deruffo A 1989 The high-molecular-weight glutenin subunits of common wheat cultivars grown in Italy. Journal of Genetics and Breeding 43: 17-24.
1147.	Pogna NE, Metakovsky EV, Redaelli R, Raineri F & Dachkevitch T 1993 Recombination mapping of *Gli-5*, a new gliadin-coding locus on chromosomes 1A and 1B in common wheat. Theoretical and Applied Genetics 87: 113-121.
1148.	Pokhriyal SC & Kohli SP 1962 Inheritance of field reaction to brown rust and other characters in inter-varietal crosses of *Triticum aestivum* L. Indian Journal of Genetics 22: 173-180.
1149.	Poperelya FA & Sozinov AA 1977 Electrophoresis of gliadin as a method for identification of wheats in which B-chromosome 1 is completely or partially replaced by R-chromosome 1. Doklady VASKLNIL 2: 2-4. [English translation].
1150.	Porter DR 1993 Personal communication.
1151.	Porter DR, Webster JA & Friebe B 1993 Inheritance of greenbug biotype G resistance in wheat. Crop Science 34: 625-628.
1152.	Porter DR, Webster JA, Burton RL, Puterka GJ & Smith EL 1991 New sources of resistance to greenbug in wheat. Crop Science 31: 1502-1504.
1153.	Powling A, Islam AKMR & Shepherd KW 1981 Isozymes in wheat-barley hybrid derivative lines. Biochemical Genetics 19: 237-254.
1154.	Prabhakara Rao MV 1996 Close linkage of the A*gropyron elongatum* gene *Sr26* for stem rust resistance to the centomere of wheat chromosome 6A. Wheat Information Service 82: 8-10.
1155.	Pratchett N & Laurie DA 1994 Genetic map location of the barley developmental mutant liguleless in relation to RFLP markers. Hereditas 120: 135-139.
1156.	Pretorius ZA, Wilcoxson RD, Long DL & Schafer JF 1984 Detecting leaf rust resistance gene *Lr13* in seedlings. Plant Disease 68: 585-586.

1157. Priestley RH 1978 Detection of increased virulence in populations of wheat yellow rust. *In*, Plant Disease Epidemiology. Blackwell Scientific Publishers, Oxford. (Scott PR & Bainbridge A eds.): 63-70.

1158. Priestley RH & Byford P 1979 Yellow rust of wheat. UK Cereal Pathogen Virulence Survey. 1978 Annual Report, National Institute of Agricultural Botany: 14-23.

1159. Priestley RH, Bayles RA & Crofts J 1982 Yellow rust of wheat. UK Cereal Pathogen Virulence Survey. 1981 Annual Report, National Institute of Agricultural Botany: 18-28.

1160. Priestley RH, Bayles RA & Ryall J 1984 Identification of specific resistances against *Puccinia striiformis* (yellow rust) in winter wheat varieties. Use of cluster analysis. Journal of the National Institute of Agricultural Botany 16: 477-485.

1161. Prins R & Marais GF 1999 A genetic study of the gametocidal effect of the *Lr19* translocation of common wheat. South African Journal of Plant and Soil 16(1): 10-14.

1162. Prins R, Marais GF, Janse BJH, Pretorius ZA & Marais AS 1996 A physical map of the *Thinopyrum*- derived *Lr19* translocation. Genome 39: 1013-1019.

1163. Prins R, Marais GF, Pretorius ZA, Janse BJH & Marais AS 1997 A study of modified forms of the *Lr19* translocation of common wheat. Theoretical and Applied Genetics 95: 424-430.

1164. Procunier JD, Knox RE, Bernier AM, Gray MA & Howes NK 1997 DNA markers linked to a T10 loose smut resistance gene in wheat (*Triticum aestivum* L.). Genome 40: 176-179.

1165. Procunier JD, Townley-Smith TF, Fox S, Prashar S, Gray M, Kim WK, Czarnecki E & Dyck PL 1995 PCR-based RAPD/DGGE markers linked to leaf rust resistance genes *Lr29* and *Lr25* in wheat (*Triticum aestivum* L.). Journal of Genetics and Breeding 49: 97-92.

1166. Pugsley AT 1949 The inheritance of resistance to three races of *Tilletia foetida* and two races of *T. caries* in a cross between White Federation 38 and Selection 1403 wheats. Journal of Genetics 49: 177-182.

1167. Pugsley AT 1956 The gene *SrKa1* in relation to the resistance of wheat to *Puccinia graminis tritici*. Empire Journal of Experimental Agriculture 24: 178-184.

1168. Pugsley AT 1961 Additional resistance in *Triticum vulgare* to *Erysiphe graminis tritici*. Australian Journal of Biological Sciences 14: 70-75.

1169. Pugsley AT 1965 Inheritance of a correlated day-length response in spring wheat. Nature 207: 108.

1170. Pugsley AT 1966 The photoperiodic sensitivity of some spring wheats with special reference to the variety Thatcher. Australian Journal of Agricultural Research 17: 591-599.

1171. Pugsley AT 1971 A genetic analysis of the spring-winter habit of growth in wheat. Australian Journal of Agricultural Research 22: 21-31.

1172. Pugsley AT 1972 Additional genes inhibiting winter habit in wheat. Euphytica 21: 547-552.

1173. Pugsley AT 1973 Control of developmental patterns in wheat through breeding. Proceedings of the 4th International Wheat Genetics Symposium, University of Missouri, Columbia (Sears ER & Sears LMS eds.): 857-859.

1174. Pugsley AT 1983 The impact of plant physiology on Australian wheat breeding. Euphytica 32: 743-748.

1175. Pugsley AT & Carter MV 1953 Resistance of twelve varieties of *Triticum vulgare* to *Erysiphe graminis tritici*. Australian Journal of Biological Sciences 6: 335-346.

1176. Qi LL, Cao MS, Chen PD, Li EL & Liu DJ 1996 Identification, mapping, and application of polymorphic DNA associated with resistance gene *Pm21* of wheat. Genome 39: 191-197.

1177.	Qi LL, Chen, PD, Liu DJ, Zhou B, Zhang SZ, Sheng BQ, Xiang QJ, Duang XY & Zhou YL 1995 The gene *Pm21* - a new source of resistance to wheat powdery mildew. Acta Agriculture Sinica 21: 257-261.
1178.	Quail P Personal communication.
1179.	Quarrie SA, Galiba G, Sutka J, Snape JW, Semikhododski A, Steed A, Gulli M & Calestani C 1994 Association of a major vernalisation gene with stress-induced abscisic acid production. Proceedings of COST 814 Workshop, Crop Adaptation to Cool Climates, Hamburg, October 1994.
1180.	Quarrie SA, Gulli M, Calestani C, Steed A & Marmiroli N 1994 Location of a gene regulating drought-induced abscisic acid production on the long arm of chromosome 5A of wheat. Theoretical and Applied Genetics 89: 794-800.
1181.	Quarrie SA, Steed A, Semikhodski A, Lebreton C, Calestani C, Clarkson DA, Tuberosa R, Sanguineti MC, Melchiorre R & Prioul J-L 1995 Identification of quantitative trait loci regulating water and nitrogen-use efficiency in wheat. *In*: Proceedings 2nd STRESSNET Conference. (Leigh RA, Blake-Kalff MMAM eds.). European Commission. Ref F.II.3-MOR/0001, Brussels: 175-180.
1182.	Quatrano RS, Litts J, Colwell G, Chakerian R & Hopkins R 1986 Regulation of gene expression in wheat embryos by abscisic acid; characterization of the cDNA clones for the Em and putative globulin proteins and localization of the lectin wheat germ agglutinin. *In*, Molecular Biology of Seed Storage Proteins and American Society of Plant Physiology (Shannon L & Chrispeels M eds.) 127-136.
1183.	Quick JS, Souza E & Sunderman DW 1993 Registration of 'Fairview' wheat. Crop Science 33: 878.
1184.	Rahman S, Abrahams S, Abbott D, Mukai Y, Samuel M, Morell MK & Appels R 1997 A complex arrangement of genes at a starch branching enzyme I locus in the D-genome of wheat. Genome 40: 465-474.
1185.	Rahman S, Jolly CJ, Skerritt JH & Wallosheck A 1994 Cloning of a wheat 15-KDa grain softness protein (GSP) - GSP is a mixture of puroindoline-like polypeptides. European Journal of Biochemistry 223: 917-925.
1186.	Raikhel NV & Wilkins TA 1987 Isolation and characterization of a cDNA clone encoding wheat germ agglutinin. Proceedings of the National Academy of Sciences, USA 84: 6745-6749.
1187.	Raines CA, Lloyd JC, Longstaff M, Bradley D & Dyer TA 1988 Chloroplast fructose-1,6-bisphosphatase: the product of a mosaic gene. Nucleic Acids Research 18: 7931-7942.
1188.	Raines CA, Lloyd JC, Willingham NM, Potts S & Dyer TA 1992 cDNA and gene sequences of wheat chloroplast sedoheptulase-1,7-bisphosphatase reveal homology with fructose-1,6-bisphosphatases. European Journal of Biochemistry 205: 1053-1059.
1189.	Raines CA, Longstaff M, Lloyd JC & Dyer TA 1989 Complete coding sequence of wheat phosphoribulokinase: Developmental and light-dependent expression of the mRNA. Molecular and General Genetics 218: 423-430.
1190.	Randhawa AS, Dhaliwal HS, Sharma SK & Multani DS 1987 Inheritance of 2,4-D tolerance in wheat. Current Science, India 56: 191-192. *Cited* Plant Breeding Abstracts 57: 7823, p.819.
1191.	Rao IN & Rao MVP 1980 Evidence for duplicate genes for 6-phosphogluconate dehydrogenase in rye. Genetical Research, Cambridge 35: 309-312.
1192.	Rao MVP 1972 Mapping of the compactum gene C on chromosome 2D of wheat. Wheat Information Service 35: 9.

1193.	Rao MVP 1973 Mapping the gene *R1* for red seed colour on chromosome 3D of wheat. Wheat Information Service 36: 9.
1194.	Rao MVP 1977 Mapping of the sphaerococcum gene 's' on chromosome 3D of wheat. Cereal Research Communications 5: 15-17.
1195.	Rao MVP 1981 Telocentric mapping of the arm inhibitor gene *Hd* on chromosome 4B of common wheat. Cereal Research Communications 9: 335-337.
1196.	Rao MVP 1983 Telocentric mapping of the squarehead (*vulgare*) gene *Q* on chromosome 5A of hexaploid wheat. Wheat Information Service 56: 12-13.
1197.	Rao MVP, Suseelan KN & Bhatia CR 1990 Telocentric mapping of the alcohol dehydrogenase structural gene *Adh-B1* on chromosome 4B of hexaploid wheat. Cereal Research Communications 18: 217-221.
1198.	Rasmussen SK, Welinder KG & Hejgaard J 1991 cDNA cloning, characterization and expression of an endosperm-specific barley peroxidase. Plant Molecular Biology 16: 317-327.
1199.	Raupp J 1991 Personal communication.
1200.	Raupp WJ, Gill BS, Wilson DL, Cox TS & Browder LE 1991 Personal communication.
1201.	Reader SM & Miller TE 1991 The introduction into bread wheat of a major gene for resistance to powdery mildew from wild emmer wheat. Euphytica 53: 57-60.
1202.	Rebmann G, Hertig C, Bull J, Mauch F & Dudler R 1991 Cloning and sequencing of cDNA's encoding a pathogen-induced putative peroxidase of wheat (*Triticum aestivum* L.). Plant Molecular Biology 16: 329-331.
1203.	Rebordinos L & Perez de la Vega M 1988 Gene duplication in the structural gene for a glutamate oxaloacetate transaminase zone (GOT1) in *Secale*. Journal of Heredity 79: 78-80.
1204.	Rebordinos L & Perez de la Vega M 1989 Extent of genetic variability of endosperm esterases in *Triticum aestivum* L. 2n=6x=42. Theoretical and Applied Genetics 78: 728-734.
1205.	Redaelli R, Pogna NE, Dachkevitch T, Cacciatori P, Biancard AM & Metakovsky EV 1992 Inheritance studies of the 1AS/1DS chromosome translocation in the bread wheat variety 'Perzivan-1'. Journal of Genetics and Breeding 46: 253-262.
1206.	Reddy P & Appels R 1989 A second locus for the 5S multigene family in *Secale* L.: sequence divergence in two lineages of the family. Genome 32: 456-467.
1207.	Reikhel, NV & Wilkes TA 1987 Differentiation between homoeologous chromosomes 1A of wheat and $1A^m$ of *Triticum monococcum* and its recognition by the wheat *Ph1* locus. Proceedings of the National Academy of Sciences, USA 92: 6745-6749.
1208.	Ren SX, McIntosh RA & Lu ZJ 1997 Genetic suppression of the cereal rye-derived gene *Pm8* in wheat. Euphytica 93: 353-360.
1209.	Ren SX, McIntosh RA, Sharp PJ & The TT 1996 A storage protein marker associated with the suppressor of *Pm8* for powdery mildew resistance in wheat. Theoretical and Applied Genetics 93: 1054-1060.
1210.	Ren ZL & Lelley T 1988 Genetics of hybrid necrosis in rye. Plant Breeding 100: 173-180.
1211.	Ren ZL & Lelley T 1990 Chromosomal localization of genes in the R genome causing hybrid necrosis in rye and triticale. Genome 33: 40-43.
1212.	Richards R 1988 Personal communication.
1213.	Riede CR & Anderson JA 1996 Linkage of RFLP markers to an aluminum tolerance gene in wheat. Crop Science 36: 905-909.
1214.	Riede CR, Williams ND & Miller JD 1995 Development of monogenic lines with resistance to stem rust from wheat cultivar 'Waldron'. Theoretical and Applied Genetics 90: 1064-1168.

1215.	Riede CR, Williams ND, Miller JD & Joppa LR 1995 Chromosomal location of genes for stem rust resistance derived from Waldron wheat. Theoretical and Applied Genetics 90: 1158-1163.
1216.	Riley R & Chapman V 1967 The inheritance in wheat of crossability with rye. Genetical Research, Cambridge 9: 259-267.
1217.	Riley R, Chapman V & Johnson R 1968 Introduction of yellow rust resistance of *Aegilops comosa* into wheat by genetically induced homoeologous recombination. Nature 217: 383-384.
1218.	Riley R, Chapman V & Johnson R 1968 The incorporation of alien disease resistance in wheat by genetic interference with the regulation of meiotic chromosome synapsis. Genetical Research, Cambridge 12: 199-219.
1219.	Rizvi SSA & Buchenau GW 1994 Tentative identification and verification of genes for leaf rust resistance in wheat cultivars of South Dakota. Plant Disease 78: 674-679.
1220.	Robe P & Doussinault G 1995 Genetic analysis of powdery-mildew resistance of a winter-wheat line, RE714, and identification of a new specific-resistance gene. Plant Breeding 114: 387-391.
1221.	Roberts DWA & Larson RI 1985 Vernalisation and photoperiod responses of selected chromosome substitution lines derived from 'Rescue', 'Cadet' and 'Cypress' wheats. Canadian Journal of Genetics and Cytology 27: 586-591.
1222.	Roberts JJ & Gallun RL 1984 Chromosome location of the *H5* gene for resistance to the Hessian fly in wheat. Journal of Heredity 75: 147-148.
1223.	Roberts JJ, Gallun RL, Patterson FL, Finney RE, Ohm HW & Shaner GE 1981 Registration of 'Downy' wheat. Crop Science 21: 350.
1224.	Robertson LD & Curtis BC 1967 Monosomic analysis of fertility-restoration in common wheat (*Triticum aestivum* L.). Crop Science 7: 493-495.
1225.	Roder MS, Korzun VN, Gill BS & Ganal MW 1998 The physical mapping of microsatellite markers in wheat. Genome 41: 278-283.
1226.	Roder MS, Plaschke J, Konig SU, Borner A, Sorrells ME, Tanksley SD & Ganal MW 1995 Abundance, variability and chromosomal location of microsatellites in wheat. Molecular and General Genetics 246: 327-333.
1227.	Rodriguez-Ouijano M & Carrillo JM 1996 Relationship between allelic variation of *Glu-1* and *Gli-1*/*Glu-3* prolamin loci and gluten strength in hexaploid wheat. Euphytica 91: 141-146.
1228.	Rodriguez-Quijano M, Nieto-Taladriz MT & Carrillo JM 1996 Linkage mapping of prolamin and isozyme genes on the 1S^l chromosome of *Aegilops longissima*. Theoretical and Applied Genetics 93: 295-299.
1229.	Rodriguez-Quijano M, Vasquez JF & Carrillo JM 1990 Variation of high-molecular-weight glutenin subunits in Spanish landraces of *Triticum aestivum* ssp. *vulgare* and ssp. *spelta*. Journal of Genetics and Breeding 44: 121-126.
1230.	Roelfs AP & McVey DV 1979 Low infection types produced by *Puccinia graminis* f. sp. *tritici* and wheat lines with designated genes for resistance. Phytopathology 69: 722-730.
1231.	Rogers WJ, Miller TE, Payne PI, Seekings JA, Sayers EJ, Holt LM & Law CN 1997 Introduction to bread wheat (*Triticum aestivum* L.) and assessment for bread-making quality of alleles from *T. boeoticum* Boiss. ssp. *thaoudar* at *Glu-A1* encoding two high-molecular subunits of glutenin. Euphytica 93: 19-29.
1232.	Rogers WJ, Payne PI, Miller TE, Holt LM, Law CN, Sayers EJ & Seekings JA 1989 Introduction to hexaploid wheat and assessment for bread-making quality of a *Glu-A1* locus

	from *Triticum thaoudar* encoding two high-molecular-weight subunits of glutenin XII. Eucarpia Congresson Science for Plant Breeding, Gottingen, Germany, Abstract No. 27-3:
1233.	Rogers WJ, Payne PI, Seekings JA & Sayers EJ 1991 Effect on bread-making quality of x-type and y-type subunits of glutenin. Journal of Cereal Science 14: 209-221.
1234.	Rognil OA, Devos KM, Chinoy CN, Harcourt RL, Atkinson MD & Gale MD 1992 RFLP mapping of rye chromosome 7R reveals a highly translocated chromosome relative to wheat. Genome 55: 1026-1031.
1235.	Rohde CR, van Wagoner KH, Kronstad WE & Rubenthaler GL 1988 Registration of 'Oveson' wheat. Crop Science 28: 1033.
1236.	Rohde W, Becker D & Salamini F 1988 Structural analysis of the waxy locus from *Hordeum vulgare*. Nucleic Acids Research 16: 7185-7186.
1237.	Rohde W, Dorr S, Salamini F & Becker D 1991 Structure of a chalcone synthase gene from *Hordeum vulgare*. Plant Molecular Biology 16: 1103-1106.
1238.	Rondon MR, Gough FJ & Williams ND 1966 Inheritance of stem rust resistance in *Triticum aestivum* ssp. *vulgare* 'Reliance' and P.I.94701 of *Triticum durum*. Crop Science 6: 177-179.
1239.	Rouve S, Boeuf C, Zwickert-Menteur S, Gautier MF, Joudrier P, Bernard M & Jestin L 1996 Locating supplementary RFLP markers on barley chromosome 7 and synteny with homoeologous wheat group 5. Plant Breeding 115: 511-513.
1240.	Rowland GG 1972 A cytogenetic study in hexaploid wheat of characters derived from *Aegilops squarrosa*. PhD Thesis, University of Manitoba, Winnipeg.
1241.	Rowland GG & Kerber ER 1974 Telocentric mapping in hexaploid wheat of genes for leaf rust resistance and other characters derived from *Aegilops squarrosa*. Canadian Journal of Genetics and Cytology 16: 137-144.
1242.	Ruiz M & Carrillo JM 1993 Linkage relationships between prolamin genes on chromosomes 1A and 1B of durum wheat. Theoretical and Applied Genetics 87: 353-360.
1243.	Rybalka AI & Sozinov AA 1979 Mapping the locus of Gld 1B which controls the biosynthesis of reserve proteins in soft wheat. Tsitologiyai Genetika 13: 276-282.
1244.	Sacco F, Tranquillo G, Gorgoschidse L & Suarez E 1991 Aminopeptidase B1: a centromere marker for chromosome 6B of wheat. Genome 35: 261-263.
1245.	Sachs L 1953 The occurrence of hybrid semi-lethals and the cytology of *Triticum macha* and *T. vavilovi*. Journal of Agricultural Science 43: 204-213.
1246.	Sadam M 1974 Inheritance of sensitivity to gibberellin and of semidwarfing in *Triticum turgidum* L. *durum* Desf. PhD Thesis, Washington State University, USA.
1247.	Sadam M 1975 Genetics of semidwarfing. Annual Wheat Newsletter 21: 158-159.
1248.	Saghai-Maroof MA, Soliman KM, Jorgensen RA & Allard RW 1984 Ribosomal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics. Proceedings of the National Academy of Sciences, USA 81: 8014-8018.
1249.	Saidi A & Quick JS 1994 Inheritance of Russian wheat aphid resistance in three winter wheats. Proceedings of the 6th Russian Wheat Aphid Conference, Fort Collins, Colorado, USA (Peairs FB, Kroening MK & Simmons CL eds.): 126-132.
1250.	Saidi A & Quick JS Inheritance and allelic relationships among Russian wheat aphid resistance genes in winter wheat. Crop Science 36: 256-258.
1251.	Salinas J & Benito C 1984 Phosphatase isozymes in rye. Characterisation, genetic control and chromosomal location. Zeitschrift fur Pflanzenzuchtung 93: 115-136.

1252.	Salinas J & Benito C 1985 Chromosomal location of malate dehydrogenase structural genes in rye (*Secale cereale* L.). Zeitschrift fur Pflanzenzuchtung 94: 208-217.
1253.	Salinas J & Benito C 1985 Chromosomal locations of phosphoglucomutase, phosphoglucose isomerase, and glutamate oxaloacetate transaminase structural genes in different rye cultivars. Canadian Journal of Genetics and Cytology 27: 105-113.
1254.	Salinas J & Benito C 1985 Esterase isozymes in rye-characterisation, genetic control, and chromosomal location. Theoretical and Applied Genetics 71: 136-140.
1255.	Samborski DJ 1973 Leaf rust of wheat in Canada in 1972. Canadian Plant Disease Survey 52: 168-170.
1256.	Samborski DJ 1980 Occurrence and virulence of *Puccinia recondita* in Canada in 1979. Canadian Journal of Plant Science 2: 246-248.
1257.	Samborski DJ & Dyck PL 1968 Inheritance of virulence in wheat leaf rust on the standard differential varieties. Canadian Journal of Genetics and Cytology 10: 24-32.
1258.	Samborski DJ & Dyck PL 1982 Enhancement of resistance to *Puccinia recondita* by interactions of resistance genes in wheat. Canadian Journal of Plant Pathology 4: 152-156.
1259.	Sanchez-Monge E & Villena LM 1951 (Smooth awned varieties among the Spanish wheats.). An. Estac. Exp. Aula. Dei 2: 210. *Cited* Plant Breeding Abstracts 21: 2552, p. 831.
1260.	Sanchez-Monge R, Barber D, Mendez E, Garcia-Olmedo F & Salcedo G 1986 Genes encoding alpha-amylase inhibitors are located in the short arms of chromosomes 3B, 3D and 6D of wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 72: 108-113.
1261.	Sanchez-Monge R, Delibes A, Hernandez-Lucas C, Carbonaro P & Garcia-Olmedo F 1979 Homoeologous chromosomal location of the genes encoding thionins in wheat and rye. Theoretical and Applied Genetics 54: 61-63.
1262.	Sanchez-Monge R, Fernandez JA & Salcedo G 1987 Subunits of tetrameric a-amylase inhibitors of *Hordeum chilense* are encoded by genes located in chromosomes $4H^{ch}$ and $7H^{ch}$. Theoretical and Applied Genetics 74: 811-816.
1263.	Sanghi AK & Baker EP 1972 Genetic bases for resistance in two common wheat cultivars to stem rust strains of unusual avirulence. Proceedings of the Linnean Society of New South Wales 97: 56-71.
1264.	Sarkisyan NS & Petrosyan AS 1972 (Descriptions of *Triticum aestivum* and *T. compactum* wheat varieties according to their necrotic genes.). Biol. Zhurnal. Armenii 25: 65-71. *Cited* Plant Breeding Abstracts 43: 5714, p. 465.
1265.	Sasaki M & Wada S 1966 Chromosomal location of genes for crossability with rye using chromosome substitution lines. Japanese Journal of Breeding 16 (Suppl. 2): 178-179.
1266.	Sasakuma T & Izumi N 1983 Genetical analysis of dwarfism in common wheat. Wheat Information Service 56: 41-42.
1267.	Sawhney RN & Luthra JK 1970 New resistance genes of wheat to Indian races of stripe rust (*Puccinia striiformis*). SABRAO Newsletter, Mishima 2: 155-156. *Cited* Plant Breeding Abstracts 41: 7312, p.935.
1268.	Scarth R & Law CN 1983 The location of the photoperiod gene *Ppd2* and an additional genetic factor for ear-emergence time on chromosome 2B of wheat. Heredity 51: 607-619.
1269.	Scarth R & Law CN 1984 The control of day-length response in wheat by the group 2 chromosomes. Zeitschrift fur Pflanzenzuchtung 92: 140-150.
1270.	Schachermayr GM, Feuillet C & Keller B 1997 Molecular markers for the detection of the wheat leaf rust resistance gene *Lr10* in diverse genetic backgrounds. Molecular Breeding 3: 65-74.

1271.	Schachermayr GM, Messmer MM, Feuillet C, Winzeler H, Winzeler M & Keller B 1995 Identification of molecular markers linked to the *Agropyron elongatum*-derived leaf rust resistance gene *Lr24* in wheat. Theoretical and Applied Genetics 90: 982-990.
1272.	Schachermayr R, Siedler H, Gale MD, Winzeler H, Winzeler M & Keller B 1994 Identification and localization of molecular markers linked to *Lr9* leaf rust resistance gene of wheat. Theoretical and Applied Genetics 88: 110-115.
1273.	Schafer JF, Caldwell RM, Patterson FL, Compton LE, Gallun RL & Roberts JJ 1968 Arthur soft red winter wheat, a breakthrough to a new yield level. Research Program Report Purdue University Agricultural Experiment Station, Lafayette, Indiana 335: 4pp..
1274.	Schaller CW & Briggs FN 1955 Linkage relationships of the Martin, Hussar, Turkey and Rio genes for bunt resistance in wheat. Agronomy Journal 47: 181-186.
1275.	Schaller CW, Holton CS & Kendrick EL 1960 Inheritance of the second factor for resistance to bunt *Tilletia caries* and *T. foetida*, in the wheat variety Martin. Agronomy Journal 52: 280-285.
1276.	Schlegel RT, Werner T & Hulgenhof E 1991 Confirmation of a 4BL.5RL wheat rye translocation line in wheat cultivar 'Viking' showing high copper efficiency. Plant Breeding 107: 226-234.
1277.	Schmalz H 1958 (Investigations on the inheritance of the spring-winter type of winter hardiness, also of morphological characters and of physiological characters connected with yield of wheat.). Kuhn-Archiv 72: 435-437. *Cited* Plant Breeding Abstracts 30: 261, p. 62.
1278.	Schmidt C-CH, Schubert V & Bluthner W-D 1993 Use of isozymes to characterize *Triticum aestivum-Aegilops markrafii* addition lines. Biochem Physiol Pflanzen 188: 385-392.
1279.	Schmidt JC & Seliger P 1982 Nachweis von multiplen formen der alkoholdehydrogenase in blattmaterial von *Triticum aestivum* L. "Carola". Biochem Physiol Pflanzen 177: 541-545.
1280.	Schmidt JC, Seliger P & Schlegel R 1984 Isoenzyme als biochemische Markerfaktoren fur Roggenchromosomen. Biochem Physiol Pflanzen 179: 197-210.
1281.	Schmidt JW & Johnson VA 1963 A sphaerococcum-like tetraploid wheat. Crop Science 3: 98-99.
1282.	Schmidt JW & Johnson VA 1966 Inheritance of the sphaerococcum effect in tetraploid wheat. Wheat Information Service 22: 5-6.
1283.	Schmidt JW, Johnson VA, Mattern PJ, Dreier AF, McVey DV & Hatchett JH 1985 Registration of 'Siouxland' wheat. Crop Science 25: 1130-1131.
1284.	Schmidt JW, Johnson VA, Nordquist PT, Mattern PJ, Dreier AF, McVey DV & Hatchett JH 1989 Registration of 'Cody' wheat. Crop Science 29: 490-491.
1285.	Schmidt JW, Morris R & Johnson VA 1969 Monosomic analysis for bunt resistance in derivatives of Turkey and Oro wheats. Crop Science 9: 286-288.
1286.	Schmidt JW, Weibel DE & Johnson VA 1963 Inheritance of an incompletely dominant character in common wheat simulating *Triticum sphaerococcum*. Crop Science 3: 261-264.
1287.	Schneider DM, Heun M & Fischbeck G 1991 Inheritance of the powdery mildew resistance gene *Pm9* in relation to *Pm1* and *Pm2* of wheat. Plant Breeding 107: 161-164.
1288.	Schroeder-Teeter S, Zematra RS, Schotzko DJ, Smith CM & Rafi M 1994 Monosomic analysis of Russian wheat aphid (*Diuraphis noxia*) resistance in *Triticum aestivum* line PI137739. Euphytica 74: 117-120.
1289.	Scoles GJ 1985 A gene for hybrid necrosis in an inbred line of rye (*Secale cereale* L.). Euphytica 34: 207-211.

1290.	Scoles GJ, Gill BS, Xin Z-Y, Clarke BC, McIntyre CL, Chapman C & Appels R 1988 Frequent duplication and deletion events in the 5SRNA genes and the associated spacer regions of the Triticeae. Plant Systematics and Evolution 160: 105-122.
1291.	Sears ER 1944 Cytogenetic studies with polyploid species of wheat. II. Additional chromosome aberrations in *Triticum vulgare*. Genetics 29: 232-246.
1292.	Sears ER 1947 The sphaerococcum gene in wheat. Genetics 32: 102-103.
1293.	Sears ER 1954 The aneuploids of common wheat. Missouri Agricultural Experiment Station Research Bulletin 572: 59pp.
1294.	Sears ER 1956 Neatby's virescent. Wheat Information Service 3: 5.
1295.	Sears ER 1957 Effects of chromosome XII and XVI on the action of Neatby's virescent. Wheat Information Service 6: 1.
1296.	Sears ER 1961 Identification of the wheat chromosome carrying leaf rust resistance from *Aegilops umbellulata*. Wheat Information Service 12: 12-13.
1297.	Sears ER 1966 Chromosome mapping with the aid of telocentrics. Proceedings of the 2nd International Wheat Genetics Symposium Lund, Sweden 1963 (MacKey J ed.): Hereditas Supplement 2: 370-381.
1298.	Sears ER 1967 Induced transfer of hairy neck from rye to wheat. Zeitschrift fur Pflanzenzuchtung 57: 4-25.
1299.	Sears ER 1972 Reduced proximal crossing-over in telocentric chromosomes of wheat. Genetica Iberia 24: 233-239.
1300.	Sears ER 1973 *Agropyron*-wheat transfers induced by homoeologous pairing. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri, USA (Sears ER & Sears LMS eds.): 191-199.
1301.	Sears ER 1977 An induced mutant with homoeologous pairing in common wheat. Canadian Journal of Genetics and Cytology 19: 585-593.
1302.	Sears ER 1982 A wheat mutant conditioning an intermediate level of homoeologous chromosome pairing. Canadian Journal of Genetics and Cytology 24: 715-719.
1303.	Sears ER 1984 Mutations in wheat that raise the level of meiotic chromosome pairing. *In* Gene Manipulation in Plant Improvement, 16th Stadler Genetics Symposium, Columbia, Missouri, USA (Gustafson JP ed.): 295-300.
1304.	Sears ER Personal communication.
1305.	Sears ER & Briggle LW 1969 Mapping the gene *Pm1* for resistance to *Erysiphe graminis* f. sp. *tritici* on chromosome 7A of wheat. Crop Science 9: 96-97.
1306.	Sears ER & Loegering WQ 1961 A pollen-killing gene in wheat. Genetics 46: 897.
1307.	Sears ER & Loegering WQ 1968 Mapping of stem rust genes *Sr9* and *Sr16* of wheat. Crop Science 8: 371-373.
1308.	Sears ER & Rodenhiser HA 1948 Nullisomic analysis of stem-rust resistance in *Triticum vulgare* var. Timstein. Genetics 33: 123-124.
1309.	Sears ER, Loegering WQ & Rodenhiser HA 1957 Identification of chromosomes carrying genes for stem rust resistance in four varieties of wheat. Agronomy Journal 49: 208-212.
1310.	Sears ER, Schaller CW & Briggs FN 1960 Identification of the chromosome carrying the Martin gene for resistance of wheat to bunt. Canadian Journal of Genetics and Cytology 2: 262-267.
1311.	Sears LMS & Sears ER 1968 The mutants chlorina-1 and Hermsen's virescent. Proceedings of the 3rd International Wheat Genetics Symposium, Australian Academy of Science, Canberra (Findlay KW & Shepherd KW eds.): 299-304.

1312.	Sears RG, Hatchett JM, Cox TS & Gill BS 1992 Registration of Hamlet Hessian fly resistant hard red winter wheat germplasm. Crop Science 32: 506.
1313.	Sebesta EE & Wood EA 1978 Transfer of greenbug resistance from rye to wheat with X-rays. Agronomy Abstracts 61-62.
1314.	Segal G, Liu B, Vega JM, Abbo S, Rodova M & Feldman M 1997 Identification of a chromosome-specific probe that maps within the *Ph1* deletions in common and durum wheat. Theoretical and Applied Genetics 94: 968-970.
1315.	Seitova AM, Metakovsky EV & Sozinov AA 1986 (Biotype composition and blocks of gliadin components in the winter bread wheat Bogarnaya 56). Tsitologiyai Genetika 20: 196-201. *Cited* Plant Breeding Abstracts 57: 122, p.14.
1316.	Shahla A & Tsuchiya T 1990 Genetic analysis in six telotrisomic lines in barley (*Hordeum vulgare* L.). Journal of Heredity 81: 127-130.
1317.	Shands RG & Cartwright WB 1953 A fifth gene conditioning Hessian fly response in common wheat. Agronomy Journal 45: 302-307.
1318.	Shaner GE, Ohm HW, Foster JE, Patterson FL, Gallun RL & Buechley GC 1985 Registration of 'Compton' wheat. Crop Science 25: 712-713.
1319.	Shaner GE, Ohm HW, Foster JE, Patterson FL, Gallun RL, Huber DM, Buechley GC, Safranski CG & Hertel JM 1986 Registration of 'Adder' wheat. Crop Science 26: 201.
1320.	Shaner GE, Roberts JJ & Finney RE 1972 A culture of *Puccinia recondita* virulent on the wheat cultivar Transfer. Plant Disease Reporter 56: 827-830.
1321.	Shang HS, Dyck PL & Martens JW 1988 Inheritance of resistance to *Puccinia graminis tritici* in eight resistant accessions of common wheat. Canadian Journal of Plant Pathology 10: 36-40.
1322.	Shang HS, Dyck PL & Samborski DJ 1986 Inheritance of resistance to *Puccinia recondita* in a group of resistant accessions of common wheat. Canadian Journal of Plant Pathology 8: 123-131.
1323.	Sharma D & Knott DR 1966 The transfer of leaf rust resistance from *Agropyron* to *Triticum* by irradiation. Canadian Journal of Genetics and Cytology 8: 137-143.
1324.	Sharma HC & Gill BS 1983 Current status of wide hybridization in wheat. Euphytica 32: 17-31.
1325.	Sharma S, Louwers JM, Karki CB & Snijders CHA 1995 Postulation of resistance genes to yellow rust in wild emmer wheat derivatives and advanced wheat lines from Nepal. Euphytica 81: 271-277.
1326.	Sharman BC 1944 'Coloured anthers' - a new monofactorial character in wheat, *T. vulgare* Host. Nature 154: 675.
1327.	Sharman BC 1958 Purple pericarp: a monofactorial dominant gene in tetraploid wheats. Nature 181: 929.
1328.	Sharp PJ & Soltes-Rak E 1988 Homoeologous relationships between wheat group 2 chromosome arms as determined by RFLP analysis. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 635-637.
1329.	Sharp PJ, Chao S, Desai S & Gale MD 1989 The isolation, characterisation and application in the Triticeae of a set of RFLP probes identifying each homoeologous chromosome arm. Theoretical and Applied Genetics 78: 342-348.
1330.	Sharp PJ, Desai S & Gale MD 1988 Isozyme variation and RFLPs at the beta-amylase loci in wheat. Theoretical and Applied Genetics 76: 691-699.

1331.	Sharp PJ, Kreis M, Shewry PR & Gale MD 1988 Location of beta-amylase sequences in wheat and its relatives. Theoretical and Applied Genetics 75: 286-290.
1332.	Sheen SJ & Snyder LA 1964 Studies on the inheritance of resistance to six stem rust cultures using chromosome substitution lines of a Marquis wheat selection. Canadian Journal of Genetics and Cytology 6: 74-82.
1333.	Shen TH 1933 (Inheritance of quantitative and qualitative characters in wheat crosses). Nanking Journal 3: 129-142. *Cited* Plant Breeding Abstracts 4: 654, p.202.
1334.	Shepherd KW 1968 Chromosomal control of endosperm proteins in wheat and rye. Proceedings of the 3rd International Wheat Genetics Symposium Australian Academy of Science, Canberra (Findlay KW & Shepherd KW eds.): 86-96.
1335.	Shepherd KW 1973 Homoeology of wheat and alien chromosomes controlling endosperm protein phenotypes. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri, USA (Sears ER & Sears LMS eds.): 745-760.
1336.	Shewry PR, Bradberry D, Franklin J & White RP 1984 The chromosomal locations and linkage relationships of the structural genes for the prolamin storage proteins (secalin) of rye. Theoretical and Applied Genetics 69: 63-69.
1337.	Shewry PR, Finch RA, Parmar S, Franklin J & Miflin BJ 1983 Chromosomal location of *Hor3*, a new locus governing storage proteins in barley. Heredity 50: 179-189.
1338.	Shewry PR, Miflin B & Kasarda DD 1983 The structural and evolutionary relationships of the prolamin storage proteins of barley, rye and wheat. Philosophical Transactions of the Royal Society of London Series B. 304: 297-308.
1339.	Shewry PR, Parmar S & Miller TE 1985 Chromosomal location of the structural genes for the Mr 75,000 gamma-secalins in *Secale montanum* Guss.: evidence for a translocation involving chromosomes 2R and 6R in cultivated rye (*Secale cereale* L.). Heredity 54: 381-383.
1340.	Shewry PR, Parmar S, Fulrath N, Kasarda DD & Miller TE 1986 Chromosomal locations of the structural gene for secalins in wild perennial rye (*Secale montanum* Guss.) and cultivated rye (*S. cereale* L.) determined by two-dimensional electrophoresis. Canadian Journal of Genetics and Cytology 28: 76-83.
1341.	Shewry PR, Pratt HM, Finch RA & Miflin BJ 1978 Genetic analysis of hordein polypeptides from single seeds of barley. Heredity 40: 463-466.
1342.	Sheybani HA & Jenkins BC 1961 The inheritance of glume pubescence in some durum varieties. Canadian Journal of Genetics and Cytology 3: 23-56.
1343.	Shi AN, Leath S & Murphy JP 1998 A major gene for powdery mildew resistance transferred to common wheat from wild einkorn wheat. Phytopathology 88: 144-147.
1344.	Shi AN, Leath S & Murphy JP 1996 Transfer of a major gene for powdery mildew resistance from wild einkorn wheat (*Triticum monococcum var. boeoticum*) to common wheat (*Triticum aestivum*). Phytopathology 86: 556.
1345.	Shiwani & Saini RG 1993 Diversity for resistance to leaf rust in *Triticum aestivum*. Plant Disease 77: 359-363.
1346.	Sibikeev SN, Kruprov VA, Voronina SA & Elesin VA 1996 First report of leaf rust pathotypes virulent on highly effective *Lr*-genes transferred from *Agropyron* species to bread wheat. Plant Breeding 115: 276-278.
1347.	Sikka SM, Jain KBL & Parmer KS 1961 Inheritance of some morphological characters in intervarietal crosses of *Triticum aestivum* L. Journal of the Indian Botanical Society 40: 217-233. *Cited* Plant Breeding Abstracts 32: 315, p.57.

1348. Sikka SM, Jha KK & Swaminathan MS 1959 Monosomic analysis in bread wheats. II. Identification of chromosomes carrying genes for awning and glume beak shape. Indian Journal of Genetics 19: 56-63.

1349. Sikka SM, Rao MV & Athluwalia M 1960 Inheritance studies in wheat. X. Inheritance of field reaction to rusts and other characters. Indian Journal of Agricultural Science 30: 223-232.

1350. Singh D, Park RF, Bariana HS & McIntosh 2001 Chromosome location and linkage studies of leaf rust resistance gene *Lr17b* in wheat cultivar Harrier. Plant Breeding 120: 7-12.

1351. Singh H & Johnson R 1988 Genetics of resistance to yellow rust in Heines VII, Soissonais and Kalyansona. Proceedings of the 7th International Wheat Genetics Symposium, IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 885-890.

1352. Singh H, Johnson R & Seth D 1990 Genes for race-specific resistance to yellow rust (*Puccinia striiformis*) in Indian wheat cultivars. Plant Pathology 39: 424-433.

1353. Singh N, Donovan GR, Carpenter HC, Skerrit JH & Langridge P 1993 Isolation and characterization of wheat triticin cDNA revealing a unique lysine-rich repetitive domain. Plant Molecular Biology 22: 227-237.

1354. Singh NK 1985 PhD Thesis, University of Adelaide, Australia.

1355. Singh NK & Shepherd KW 1984 A new appproach to studying the variation and genetic control of disulphide-linked endosperm proteins in wheat and rye. Proceedings of the 2nd International Workshop on Gluten Proteins Wageningen, The Netherlands: 129-136.

1356. Singh NK & Shepherd KW 1984 Mapping of the genes controlling high-molecular-weight glutelin subunits of rye on the long arm of chromosome 1R. Genetical Research, Cambridge 44: 117-123.

1357. Singh NK & Shepherd KW 1985 The structure and genetic control of a new class of disulphide-linked proteins in wheat endosperm. Theoretical and Applied Genetics 71: 79-92.

1358. Singh NK & Shepherd KW 1988 Linkage mapping of genes controlling endosperm storage proteins in wheat. 1. Genes on the short arms of group 1 chromosomes. Theoretical and Applied Genetics 75: 628-641.

1359. Singh NK & Shepherd KW 1988 Linkage mapping of genes controlling endosperm storage proteins in wheat. 2. Genes on the long arm of the group 1 chromosomes. Theoretical and Applied Genetics 75: 642-650.

1360. Singh NK, Shepherd KW, Langridge P, Clem-Gruen L, Skerritt JH & Wrigley CW 1988 Identification of legumin-like proteins in wheat. Plant Molecular Biology 11: 633-639.

1361. Singh RP 1992 Association between gene *Lr34* for leaf rust resistance and leaf tip necrosis in wheat. Crop Science 32: 874-878.

1362. Singh RP 1992 Genetic association of leaf rust resistance gene *Lr34* with adult plant resistance to stripe rust in bread wheat. Phytopathology 82: 835-838.

1363. Singh RP 1993 Genetic association of gene *Bdv1* for tolerance to barley yellow dwarf virus with genes *Lr34* and *Yr18* for adult plant resistance to rusts in bread wheat. Plant Disease 77: 1103-1106.

1364. Singh RP, Mujeeb-Kazi A & Huerta-Espino J 1998 *Lr46*: a gene conferring slow-rusting resistance to leaf rust in wheat. Phytopathology 88: 890-894.

1365. Singh RP & Gupta AK 1991 Genes for leaf rust resistance in Indian and Pakistani wheats tested with Mexican pathotypes of *Puccinia recondita* f. sp. *tritici*. Euphytica 57: 27-36.

1366.	Singh RP & McIntosh RA 1984 Complementary genes for resistance to *Puccinia recondita tritici* in *Triticum aestivum* I. Genetic and linkage studies. Canadian Journal of Genetics and Cytology 26: 723-735.
1367.	Singh RP & McIntosh RA 1984 Complementary genes for resistance to *Puccinia recondita tritici* in *Triticum aestivum* II. Cytogenetic studies. Canadian Journal of Genetics and Cytology 26: 736-742.
1368.	Singh RP & McIntosh RA 1985 Cytogenetical studies in wheat XIV. *Sr8b* for reaction to *Puccinia graminis tritici*. Canadian Journal of Genetics and Cytology 28: 189-197.
1369.	Singh RP & McIntosh RA 1985 Genetic basis of leaf rust resistance in wheat cultivar Mediterranean. Cereal Rusts Bulletin 13: 31-36.
1370.	Singh RP & McIntosh RA 1986 Genetics of resistance to *Puccinia graminis tritici* and *Puccinia recondita tritici* in Kenya Plume wheat. Euphytica 35: 245-256.
1371.	Singh RP & McIntosh RA 1987 Genetics of resistance to *Puccinia graminis tritici* in 'Chris' and 'W3746' wheats. Theoretical and Applied Genetics 73: 846-855.
1372.	Singh RP & McIntosh RA 1992 Genetic association of wheat stem rust resistance gene *Sr12* and leaf rust resistance gene *Lr27*. Cereal Research Communications 20: 217-220.
1373.	Singh RP & Rajaram S 1991 Resistance to *Puccinia recondita* f. sp. *tritici* in 50 Mexican bread wheat cultivars. Crop Science 31: 1472-1479.
1374.	Singh RP & Rajaram S 1992 Genetics of adult-plant resistance to leaf rust in 'Frontana' and three CIMMYT wheats. Genome 35: 24-31.
1375.	Singh RP & Rajaram S 1994 Genetics of adult plant resistance to stripe rust in ten bread wheats. Euphytica 72: 1-7.
1376.	Singh RP 1993 Resistance to leaf rust in 26 Mexican wheat cultivars. Crop Science 33: 633-637.
1377.	Singh RP, Nelson JC & Sorrells ME 1998 Mapping *Yr28* and other genes for resistance to stripe rust in wheat. Crop Science 40: 1148-1155.
1378.	Singh RP, Bechere E & Abdalla O 1992 Genetic analysis of resistance to stem rust in ten durum wheats. Phytopathology 92: 919-922.
1379.	Singh RP, Burnett PA, Albarran M & Rajaram S 1993 *Bdv1*: a gene for tolerance to barley yellow dwarf virus in bread wheats. Crop Science 33: 231-234.
1380.	Singh RP, Morgunov A & Huerta-Espino J 1995 Genes conferring low seedling reaction to Mexican pathotypes of *Puccinia recondita* f. sp. *tritici*, and adult-plant responses of recent wheat cultivars from the former USSR. Euphytica 81: 225-234.
1381.	Singh RP, Singh I & Chowdhury RK 1989 Hybrid necrosis in bread wheat III. Wheat Information Service 68: 6-8.
1382.	Singh RP, Villareal RL, Rajaram S & Deltoro E 1989 Cataloguing dwarfing genes *Rht1* and *Rht2* in germplasm used by the bread wheat breeding program at CIMMYT. Cereal Research Communications 17: 273-279.
1383.	Singh S & Sethi GS 1991 Crossability of some bread wheat landraces and improved cultivars from western Himalayas with rye. Euphytica 53: 137-141.
1384.	Singh SJ & McIntosh RA 1988 Allelism of two genes for stem rust resistance in triticale. Euphytica 38: 185-189.
1385.	Sitch LA & Snape JW 1986 Allelic variation at the crossability loci in wheat (*Triticum aestivum*). Wheat Information Service 63: 11-15.
1386.	Sitch LA & Snape JW 1989 Allelic variation at the crossability loci in wheat (*Triticum aestivum*). Wheat Information Service 68: 1-5.

1387.	Sitch LA, Snape JW & Firman SJ 1985 Intrachromosomal mapping of crossability genes in wheat (*Triticum aestivum*). Theoretical and Applied Genetics 70: 309-314.
1388.	Slootmaker LAJ, Lange W, Jochemsen G & Schepers J 1974 Monosomic analysis in bread wheat of resistance to cereal root eelworm. Euphytica 23: 497-503.
1389.	Smith EL, Schlehuber AM, Young HC & Edwards LH 1968 Registration of Agent wheat. Crop Science 8: 511-512.
1390.	Smith EL, Sebesta EE, Young HC, Pass H & Abbot DC 1981 Registration of Payne wheat. Crop Science 21: 636.
1391.	Smith GS 1957 Inheritance of stem rust reaction in tetraploid wheat hybrids I. Allelic genes in Mindum durum and Vernal emmer. Agronomy Journal 49: 134-137.
1392.	Smith JB 1998 Personal communication.
1393.	Smith L 1939 Mutants and linkage studies in *Triticum monococcum* and *T. aegilopoides*. Missouri Agricultural Experiment Station Research Bulletin 298: 26 pp..
1394.	Smith SM, Bedbrook J & Speir J 1983 Characterization of three cDNA clones encoding different mRNAs for the precursor of the small subunit of wheat ribulose bisphosphate carboxylase. Nucleic Acids Research 11: 8719-8734.
1395.	Smith WK 1933 Inheritance of reaction of wheat to physiologic forms of *T. levis* and *T. tritici*. Journal of Agricultural Research 47: 89-105.
1396.	Snape JW, Angus WJ, Parker B & Lechie D 1987 The chromosomal locations of genes conferring differential response to the wild oat herbicide, difenzoquat. Journal of Agricultural Science, Cambridge 108: 543-548.
1397.	Snape JW, Chapman V, Moss J, Blanchard CE & Miller TE 1979 The crossabilities of wheat varieties with *Hordeum bulbosum*. Heredity 42: 291-298.
1398.	Snape JW, Dubcovsky J & Laurie D 1998 Personal communication.
1399.	Snape JW, Flavell RB, O'dell M, Hughes WG & Payne PI 1985 Intra-chromosomal mapping of the nucleolar organiser region relative to three marker loci on chromosome 1B of wheat (*Triticum aestivum*). Theoretical and Applied Genetics 69: 263-270.
1400.	Snape JW, Law CN, Parker BB & Worland AJ 1985 Genetical analysis of chromosome 5A of wheat and its influence on important agronomic traits. Theoretical and Applied Genetics 71: 518-526.
1401.	Snape JW, Leckie D, Parker BB & Nevo E 1991 The genetical analysis and exploitation of differential responses to herbicides in crop species. *In*: Herbicide Resistance in Weeds and Crops. (Casely JC, Cussans G and Atkin RK eds.). Butterworth-Heinemann, Oxfordshire, England: 305-317.
1402.	Snape JW, Parker B, Leckie D, Rosati-Colarieti G & Bozorgipour R 1988 Differential responses to herbicides in wheat: uses as genetic markers and target genes for genetic manipulation. Proceedings of the International Congress of EUCARPIA: Genetic Manipulation in Plant Breeding, Biotechnology for the Breeder, Helsingar, Denmark.
1403.	Sobko TA 1984 Identification of the locus which controls the synthesis of alcohol-soluble endosperm proteins in soft winter wheat. Journal of Agricultural Science, Kiev N7320: 78-80.
1404.	Sobko TA & Poperelya FA 1983 (Linkage of the gliadin-coding locus *Gld 1A* and the gene for hairy glumes *Hg* in wheat.). Naucho-tekhnicheskii Byulleten Vsesoyuznogo Selektsionno-geneticheskogo Instituta 2: 28-33. *Cited* Plant Breeding Abstracts 54: 8716, p. 875.

1405.	Sobko TA & Sozinov AA 1993 Genetic control of morphologic traits of a spike and the relationship with allelic variation of marker loci of chromosomes 1A and 1B of winter common wheat. Tsitologiya I Genetika (Eng vers): 27(5): 15-22. Russian version: 15-22.
1406.	Sobko TA & Sozinov AA 1997 (Linkage mapping of the loci controlling spike morphological traits and seed storage proteins on the 1A chromosome in winter common wheats). Tsitologiya I Genetika 31(4): 18-26.
1407.	Sobko TA, Poperelya FA, Rybalka AI & Sozinov AA 1986 (Inheritance and mapping of genes coding for synthesis of storage proteins on chromosome 1A of bread wheat.). Tsitologiyaii Genetika 20: 372-376. *Cited* Plant Breeding Abstracts 57: 2629, p. 275.
1408.	Soliman AS, Heyne EG & Johnston CO 1963 Resistance to leaf rust in wheat derived from *Aegilops umbellulata* translocation lines. Crop Science 3: 254-256.
1409.	Soliman AS, Heyne EG & Johnston CO 1964 Genetic analysis of leaf rust resistance in the eight differential varieties of wheat. Crop Science 4: 246-248.
1410.	Somasco OC 1990 Inheritance of resistance to *Septoria tritici* blotch in wheat. M.Sc. Thesis, University of California, Davis, USA.
1411.	Sontag T, Salovara H & Payne PI 1986 The high molecular-weight glutenin subunit compositions of wheat varieties bred in Finland. Journal of Agricultural Science, Finland 58: 151-156.
1412.	Sorrells ME & Jensen NF 1987 Registration of 'Geneva' winter wheat. Crop Science 27: 1314-1315.
1413.	Sosa O & Foster JE 1976 Temperature and the expression of resistance to the Hessian fly. Environmental Entomology 5: 333-336.
1414.	Sourdille P, Perretant MR, Charmet G, Leroy P, Gautier MF, Joudrier P, Nelson JC, Sorrells ME & Bernard M 1996 Linkage between RFLP markers and genes affecting kernel hardness in wheat. Theoretical and Applied Genetics 93: 580-586.
1415.	Sozinov AA 1984 Blocks of cereal storage proteins as genetic markers. Proceedings of the 2nd International Workshop on Gluten Proteins Wageningen, The Netherlands 121-127.
1416.	Sozinov AA 1985 Protein polymorphism and its importance in genetics, breeding and evolution. Molekulyarnye Mekhanizmy Geneticheskikh Protsessov. Molekulyarnaya Genetika, Evolyutsiya I Molekulyarno-Geneticheskie Osnovy Selektsii Institut Obshchei Genetiki, Moscow, USSR (Sozinov AA ed.): 219-238.
1417.	Srinivasan VK & Padmanabhan TS 1965 Inheritance of disease resistance and ear characters in tetraploid wheats. Indian Journal of Genetics 25: 91-99.
1418.	Stanford EH 1941 A new factor for resistance to bunt, *Tilletia tritici*, linked with the Martin and Turkey factors. Journal of the American Society of Agronomy 33: 559-568.
1419.	Starling TM, Roane CW & Camper HM 1984 Registration of Tyler wheat. Crop Science 24: 827.
1420.	Stebbins NB, Patterson FL & Gallun RL 1980 Interrelationships among wheat genes for resistance to Hessian fly. Crop Science 20: 177-180.
1421.	Stebbins NB, Patterson FL & Gallun RL 1982 Interrelationships among wheat genes *H3*, *H6*, *H9* and *H10* for Hessian fly resistance. Crop Science 22: 1029-1032.
1422.	Stebbins NB, Patterson FL & Gallun RL 1983 Inheritance of resistance of PI 94587 wheat to biotypes B and D of Hessian fly. Crop Science 23: 251-253.
1423.	Steinitz-Sears LM 1963 Cytogenetic studies bearing on the nature of the centromere. Proceedings of the XI International Congress of Genetics The Hague 1: 123.
1424.	Stelmakh AF 1987 Growth habit in common wheat (*Triticum aestivum* L. em Thell.). Euphytica 36: 513-519.

1425.	Stephenson P, Bryan GJ, Kirby J, Collins AJ, Devos KM, Busso CS & Gale MD 1998 Fifty new microsatellite loci for the wheat genetic map. Theoretical and Applied Genetics 97: 946-949.
1426.	Stewart G & Woodward RW 1930 Inheritance in a wheat cross between Hybrid 128 x White Odessa and Kanred. Journal of Agricultural Research 42: 507-520.
1427.	Stinissen HM, Peumans WJ, Law CN & Payne PI 1983 Control of lectins in *Triticum aestivum* and *Aegilops umbellulata* by homoeologous group 1 chromosomes. Theoretical and Applied Genetics 67: 53-58.
1428.	Streckeisen P & Fried PM 1985 (Analysis of the virulence of wheat powdery mildew in Switzerland in 1981 to 1983). Schweizerische Landwirtschaftliche Forschung 24: 261-269. *Cited* Plant Breeding Abstracts 56: 9432, p.1017.
1429.	Stubbs RW 1966 Recent aspects of the physiological specialisation of yellow rust in The Netherlands. Proceedings of the 3rd European Yellow Rust Conference, Cambridge, 1994: pp.47-54.
1430.	Stubbs RW 1985 Stripe rust. *In*, The Cereal Rusts II. Academic Press, Orlando. (Roelfs AP & Bushnell WR eds.): 61-101.
1431.	Stubbs RW, Fuchs E, Vecht H & Basset EJW 1974 The international survey of factors of virulence of *Puccinia striiformis* Westend. in 1969, 1970 and 1971. Nederlands Grain-Centrum Technisch Bericht NR. 21 Wageningen 88pp.
1432.	Stuckey J & Driscoll CJ Personal communication.
1433.	Sugiyama T, Ratalski A, Peterson D & Soll D 1985 A wheat HMW glutenin subunit gene reveals a highly repeated structure. Nucleic Acids Research 13: 8729-8737.
1434.	Sun GL, Fahima T, Korol AB, Turpeinen T, Grama A, Ronin YI & Nevo E 1997 Identification of molecular markers linked to the *Yr15* stripe rust resistance gene of wheat originated in wild emmer wheat, *Triticum dicoccoides*. Theoretical and Applied Genetics 95: 622-628.
1435.	Sun M & Dvorak J 1992 Chromosomal location of adenylate kinase, 6-phosphogluconate dehydrogenase, and glutamate-pyruvate transaminase structural loci in wheat, barley and *Lophopyrum elongatum*. Genome 35: 147-154.
1436.	Sunderman DW & Bruinsma B 1975 Registration of four wheat cultivars. Crop Science 15: 104-105.
1437.	Sunderman DW & Hatchett JH 1986 Relationship between resistance to Hessian fly and powdery mildew in soft white spring wheat PI 468960. Crop Science 26: 1071-1072.
1438.	Sunderman DW & Wise M 1973 Registration of Ranger wheat. Crop Science 13: 287.
1439.	Sunderman DW, O'Connell B & Hatchett JH 1986 Registration of PI 468960 Hessian fly resistant soft spring wheat germplasm. Crop Science 26: 1093.
1440.	Sunderwirth SD & Roelfs AP 1980 Greenhouse evaluation of the adult plant resistance of *Sr2* to wheat stem rust. Phytopathology 70: 634-637.
1441.	Suneson CA & Noble WB 1950 Further differentiation of genetic factors in wheat for resistance to the Hessian fly. United States Department of Agriculture Technical Bulletin 1004: 8pp.
1442.	Suseelan KN, Rao MVP, Bhatia CR & Rao IN 1982 Mapping of an alcohol dehydrogenase (*Adh-A1*) structural gene on chromosome 4A of *durum* wheat. Heredity 49: 353-357.
1443.	Suseelan KN, Rao PMV & Bhatia CR 1986 Transfer of a variant allele (*Adh-A1b*) of alcohol dehydrogenase isozyme gene from durum to *aestivum* wheat. Cereal Research Communications 14: 317-318.

1444.	Sutka J 1977 The association of genes for purple coleoptile with chromosomes of the wheat variety Mironovskaya 808. Euphytica 26: 475-479.
1445.	Sutka J & Kovacs G 1987 Chromosomal location of dwarfing gene *Rht12* in wheat. Euphytica 36: 521-523.
1446.	Sutka J & Snape JW 1989 Location of a gene for frost resistance on chromosome 5A of wheat. Euphytica 42: 41-44.
1447.	Swaminathan MS & Rao MVP 1961 Macro-mutations and sub-specific differentiation in *Triticum*. Wheat Information Service 13: 9-11.
1448.	Sybenga J 1983 Rye chromosome nomenclature and homoeology relationships. Zeitschrift fur Pflanzenzuchtung 90: 297-304.
1449.	Syme JR 1983 Flinders. Journal of the Australain Institute of Agricultural Science 49: 42.
1450.	Syme JR, Law DP, Martin DJ & Rees RG 1983 Bass. Journal of the Australian Institute of Agricultural Science 49: 46-47.
1451.	Syme JR, Martin DJ, Law DP & Rees RG 1983 King. Journal of the Australian Institute of Agricultural Science 49: 47-48.
1452.	Symes KJ 1965 The inheritance of grain hardness in wheat as measured by the particle size index. Australian Journal of Agricultural Research 16: 113-123.
1453.	Tahir ChM & Tsunewaki K 1969 Monosomic analysis of *Triticum spelta* var. *duhamelianum*, a fertility restorer for *T. timopheevi* cytoplasm. Japanese Journal of Genetics 44: 19.
1454.	Tai SE 1934 (Linkage inheritance of certain characters in wheat). Journal of the Agricultural Association of China 120: 10-55. *Cited* Plant Breeding Abstracts 8: 452, p.127.
1455.	Takahashi R & Yasuda S 1971 Genetics of earliness and growth habit in barley. *In*: Proceedings of the 2nd International Barley Genetics Symposium, (Nilan RA ed.) Washington State University Press, USA, pp388-408.
1456.	Talbert LE, Bruckner PL, Smith LY, Sears R & Martin TJ 1996 Development of PCR markers linked to resistance to wheat streak mosiac virus in wheat. Theoretical and Applied Genetics 93: 463-467.
1457.	Tang KS & Hart GE 1975 Use of isozymes as chromosome markers in wheat-rye addition lines and in triticale. Genetical Research, Cambridge 26: 187-201.
1458.	Tanner DG & Falk DE 1981 The interaction of genetically controlled crossability in wheat and rye. Canadian Journal of Genetics and Cytology 23: 27-32.
1459.	Taylor AJ, Smith GMB & Johnson R 1981 Race-specific genetic factors for resistance to *Puccinia striiformis* in wheat cultivars from the Plant Breeding Institute. Cereal Rusts Bulletin 9: 33-45.
1460.	The TT 1973 Chromosome location of genes conditioning stem rust resistance transferred from diploid to hexaploid wheat. Nature New Biology 241: 256.
1461.	The TT Personal communication.
1462.	The TT & McIntosh RA 1975 Cytogenetical studies in wheat. VIII. Telocentric mapping and linkage studies involving *Sr22* and other genes in chromosome 7AL. Australian Journal of Biological Sciences 28: 531-538.
1463.	The TT, Gupta RB, Dyck PL, Appels R, Hohmann U & McIntosh RA 1992 Characterization of stem rust resistant derivatives of wheat cultivar Amigo. Euphytica 58: 245-252.
1464.	The TT, McIntosh RA & Bennett FGA 1979 Cytogenetical studies in wheat. IX. Monosomic analyses, telocentric mapping and linkage relationships of genes *Sr21*, *Pm4*, and *Mle*. Australian Journal of Biological Sciences 32: 115-125.

1465.	Thiele V & Melz G 1992 Chromosomal location of genes controlling lactate dehydrogenase in rye, wheat and barley. Genome 35: 32-34.
1466.	Thiele V & Seidel A 1990 Chromosomal location of a catalase gene in wheat using rye-wheat-additions. Plant Breeding 105: 78-79.
1467.	Thomas JB & Conner RI 1986 Resistance to colonization by the wheat curl mite in *Aegilops squarrosa* and its inheritance after transfer to common wheat. Crop Science 26: 527-530.
1468.	Thomas JB & Whelan EDP 1991 Genetics of wheat curl mite resistance in wheat: recombination of *Cmc1* with the 6D centromere. Crop Science 31: 936-938.
1469.	Thomas JB, Kaltsikes PD & Anderson RG 1981 Relation between wheat-rye crossability and seed set of common wheat after pollination with other species in the Hordeae. Euphytica 30: 121-127.
1470.	Thompson RD, Bartels D & Harberd NP 1985 Nucleotide sequence of a gene from chromosome 1D of wheat encoding a HMW-glutenin subunit. Nucleic Acids Research 13: 6833-6846.
1471.	Thompson RD, Bartels D, Harberd NP & Flavell RB 1983 Characterisation of the multigene family coding for HMW glutenin subunits in wheat using cDNA clones. Theoretical and Applied Genetics 67: 87-96.
1472.	Tomar SMS & Singh B 1998 Hybrid chlorosis in wheat x rye crosses. Euphytica 99: 1-4.
1473.	Tomar SMS, Kochumadhavan M & Nambisan PNN 1987 Frequency and distribution of genes for necrosis and chlorosis in tetraploid species of *Triticum*. Indian Journal of Genetics 47: 71-75.
1474.	Tomar SMS, Kochumadhavan M & Nambisan PNN 1989 Hybrid weakness in *Triticum dicoccum* Schubl. Wheat Information Service 69: 21-23.
1475.	Tomar SMS, Kochumadhavan M, Nambisan PNN & Joshi BC 1988 Hybrid necrosis and chlorosis in wild emmer, *T. dicoccoides* Korn. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 165-168.
1476.	Torres JV & Garcia-Olmedo F 1974 Chromosomal location of a gene that controls sterol esterification in *Triticum aestivum* L. Plant Science Letters 3: 213-217.
1477.	Torrie JH 1936 Inheritance studies of several qualitative characters in spring wheat crosses between varieties relatively susceptible and resistant to drought. Canadian Journal of Research C 14: 368-385.
1478.	Tosa Y & Sakai K 1990 The genetics of resistance of hexaploid wheat to the wheatgrass powdery mildew fungus. Genome 33: 225-230.
1479.	Tosa Y & Tada S 1990 Operation of resistance genes in wheat to *Erysiphe graminis* f. sp. *tritici* against *E. graminis* f. sp. *agropyri*. Genome 33: 231-234.
1480.	Tosa Y & Tsujimoto H 1994 Telosomic mapping of wheat genes for resistance to inappropriate formae speciales of *Erysiphe graminis*. Wheat Information Service 79: 33-36.
1481.	Tosa Y, Tokunaga H & Ogura H 1988 Identification of a gene for resistance to wheatgrass powdery mildew fungus in common wheat cultivar Chinese Spring. Genome 30: 612-614.
1482.	Tosa Y, Tsujimoto H & Ogura H 1987 A gene involved in the resistance of wheat to wheatgrass powdery mildew fungus. Genome 29: 850-852.
1483.	Tsujimoto H 1986 Hybrid dysgenesis in wheat caused by gametocidal genes. PhD Thesis, Kyoto University, Japan.
1484.	Tsujimoto H 1994 Two new sources of gametocidal genes from *Aegilops longissima* and *Ae. sharonensis*. Wheat Information Service 79: 42-46.

1485.	Tsujimoto H 1995 Gametocidal genes in wheat and its relatives. IV. Functional relationships between six gametocidal genes. Genome 38: 283-289.
1486.	Tsujimoto H & Noda K 1988 Chromosome breakage in wheat induced by the gametocidal gene of *Aegilops triuncialis* L.: Its utilization for wheat genetics and breeding. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 455-460.
1487.	Tsujimoto H & Tsunewaki K 1984 Gametocidal genes in wheat and its relatives. I. Genetic analyses in common wheat of a gametocidal gene derived from *Aegilops speltoides*. Canadian Journal of Genetics and Cytology 26: 78-84.
1488.	Tsujimoto H & Tsunewaki K 1985 Gametocidal genes in wheat and its relatives. II. Suppressor of the chromosome 3C gametocidal gene of *Aegilops triuncialis*. Canadian Journal of Genetics and Cytology 27: 178-185.
1489.	Tsujimoto H & Tsunewaki K 1985 Hybrid dysgenesis in common wheat caused by gametocidal genes. Japanese Journal of Genetics 60: 565-578.
1490.	Tsujimoto H & Tsunewaki K 1988 Gametocidal genes in wheat and its relatives. III. Chromosome location and effects of two *Aegilops speltoides*-derived gametocidal genes in common wheat. Genome 30: 239-244.
1491.	Tsunewaki K 1960 Monosomic and conventional analysis in common wheat. III. Lethality. Japanese Journal of Genetics 35: 71-75.
1492.	Tsunewaki K 1964 Geographical distribution of necrosis genes in common wheat. I. Genetic basis of necrosis. Annual Report of the National Institute of Genetics, Japan 15.:
1493.	Tsunewaki K 1966 Comparative gene analysis of common wheat and its ancestral species. II. Waxiness, growth habit and awnedness. Japanese Journal of Botany 19: 175-254.
1494.	Tsunewaki K 1966 Comparative gene analysis of common wheat and its ancestral species. III. Glume hairiness. Genetics 53: 303-311.
1495.	Tsunewaki K 1966 Gene analysis on chlorosis of the hybrid, *Triticum aestivum* var. Chinese Spring x *T. macha* var. subletschumicum and its bearing on the genetic basis of necrosis and chlorosis. Japanese Journal of Genetics 41: 413-426.
1496.	Tsunewaki K 1969 Necrosis genes in *Triticum macha*, *T. spelta* and *T. vavilovii*. Wheat Information Service 28: 1-4.
1497.	Tsunewaki K 1971 Distribution of necrosis genes in wheat. V. *Triticum macha*, *T. spelta* and *T. vavilovii*. Japanese Journal of Genetics 46: 93-101.
1498.	Tsunewaki K 1992 Aneuploid analysis of hybrid necrosis and hybrid chlorosis in tetraploid wheats using the D genome chromosome substitution lines of durum wheat. Genome 35: 594-601.
1499.	Tsunewaki K 1998 Personal communication.
1500.	Tsunewaki K Personal communication.
1501.	Tsunewaki K & Hamada J 1968 A new type of hybrid chlorosis found in tetraploid wheats. Japanese Journal of Genetics 43: 279-288.
1502.	Tsunewaki K & Hori T 1967 Distribution of necrosis genes in wheat. IV. Common wheat from Australia, Tibet and Northern Europe. Japanese Journal of Genetics 42: 245-250.
1503.	Tsunewaki K & Hori T 1968 Necrosis genes in common wheat varieties from Australia, Tibet and Northern Europe. Wheat Information Service 26: 22-27.
1504.	Tsunewaki K & Kihara H 1961 F1 monosomic analysis of *Triticum macha*. Wheat Information Service 12: 1-2.

1505.	Tsunewaki K & Nakai Y 1964 Geographical distribution of necrosis genes in wheat. II. Distribution in Japanese local varieties. III. Distribution in Pakistan, Afganistan and Iran. Annual Report of the National Institute of Genetics, Japan 15.
1506.	Tsunewaki K & Nakai Y 1967 Distribution of necrosis genes in wheat I. Common wheat from Central Asia. Canadian Journal of Genetics and Cytology 9: 69-74.
1507.	Tsunewaki K & Nakai Y 1967 Distribution of necrosis genes in wheat II. Japanese local varieties of common wheat. Canadian Journal of Genetics and Cytology 9: 75-78.
1508.	Tsunewaki K & Nakai Y 1967 Distribution of necrosis genes in wheat III. U.S. common wheat. Canadian Journal of Genetics and Cytology 9: 385-393.
1509.	Tsunewaki K & Nakai Y 1967 Necrosis genes in US varieties of common wheat. Wheat Information Service 25: 9-18.
1510.	Tsunewaki K & Nakai Y 1972 Distribution of necrosis genes in wheat. VII. Common wheat from the Mediterranean. Japanese Journal of Genetics 47: 277-290.
1511.	Tsunewaki K & Nakai Y 1973 Considerations on the origin and speciation of four groups of wheat from the distribution of necrosis and chlorosis genes. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri (Sears ER & Sears LMS eds.): 123-129.
1512.	Tsunewaki K, Kasahara F & Fujita T 1971 Distribution of necrosis genes in wheat. VI. Chinese common wheat. Japanese Journal of Genetics 46: 103-107.
1513.	Tuleen NA, Yang Y-C & Hart GE 1992 Evidence that *Aco-B2* and *Aco-D2* of *Triticum aestivum* are located in chromosomes 4B and 4D. Theoretical and Applied Genetics 83: 1019-1021.
1514.	Tyler JM, Webster JA & Merkle OG 1987 Designations for genes in wheat germplasm conferring greenbug resistance. Crop Science 27: 526-527.
1515.	Tyler JM, Webster JA & Smith EL 1985 Biotype E greenbug resistance in WSMV resistant wheat germplasm lines. Crop Science 25: 686-688.
1516.	Uhlen AK & Ringland K 1987 Gene dosage effects on storage proteins in wheat (*Triticum aestivum*). Journal of Cereal Science 6: 219-223.
1517.	Unrau J 1950 The use of monosomes and nullisomes in cytogenetic studies in common wheat. Scientific Agriculture 30: 66-89.
1518.	Urbano M, Resta P, Benedettelli S & Bianco A 1989 A *Dasypyrum villosum* (L.) Candargy chromosome related to homoeologous group 3 of wheat. Proceedings of the 7th International Wheat Genetics Symposium IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 169-173.
1519.	Vacenko AA 1934 (Inheritance of glume pubescence and of the black colour of the ear in durum wheat.). C.R. Academy of Science, U.S.S.R. 4: 338-343. *Cited* Plant Breeding Abstracts 6: 133, p. 38.
1520.	Vacenko AA 1936 (Inheritance of grey-smokey colour in the ear of *Triticum vulgare* Vill.). Journal of Botany U.S.S.R. 21: 186-188. *Cited* Plant Breeding Abstracts 9: 175, p. 43.
1521.	Vahl U & Muller G 1991 Endopeptidase EP-1 as a marker for the eyespot resistance gene *Pch-1* from *Aegilops ventricosa* in wheat line 'H-93-70' Plant Breeding 107: 77-79.
1522.	Valkoun J, Kucerova D & Bartos P 1986 (Transfer of stem rust resistance from *Triticum monococcum* L. to *T. aestivum* L.). Sbornik UVTI Z. Genetika a Slechteni 22: 9-16. *Cited* Plant Breeding Abstracts 56: 4701, p. 504.
1523.	Vallega V 1986 High-molecular-weight glutenin subunit composition of Italian *Triticum durum* cultivars and spaghetti cooking quality. Cereal Research Communications 14: 251-257.

1524.	Vallega V 1988 Comparative analysis of high-molecular-weight glutenin subunit composition in various *Triticum* species. Plant Breeding 100: 241-246.
1525.	Vallega V 1988 High molecular weight glutenin subunit composition of 115 cultivars of *Triticum turgidum* var. *durum* from various origins. Genetica Agraria 42: 235-240.
1526.	Vallega V & Mello-Sampayo T 1987 Variation in high-molecular-weight glutenin subunits amongst cultivars of *Triticum turgidium* L. from Portugal. Euphytica 36: 755-762.
1527.	Vallega V & Waines JG 1987 High molecular weight glutenin subunit variation in *Triticum turgidum* var. *dicoccum*. Theoretical and Applied Genetics 74: 706-710.
1528.	Van Campenhout S & Volckaert G 1997 PCR-based isolation and chromosome assignment of members of the *Em* gene family of wheat. DNA Sequence: 289-300.
1529.	Van Deynze AE, Dubcovsky J, Gill KS, Nelson JC, Sorrells ME, Dvorak J, Gill BS, Lagudah ES, McCouch SR & Appels R 1995 Molecular-genetic maps for group 1 chromosomes of Triticeae species and their relation to chromosomes in rice and oat. Genome 38: 45-59.
1530.	Van Heemert C & Sybenga J 1972 Identification of the three chromosomes involved in the translocations which structurally differentiate the genome of *Secale cereale* L. from those of *Secale montanum* Guss. and *Secale vavilovii* Grossh. Genetica 43: 387-393.
1531.	Van Kints TMC 1986 Mildew of wheat. UK Cereal Pathogen Virulence Survey, Annual Report: 7-12.
1532.	Van Silfhout CH Personal communication.
1533.	Vapa L & Hart GE 1987 Genetic variation in enzyme phenotypes among Yugoslav wheat cultivars. Plant Breeding 98: 273-280.
1534.	Vaquero F, Rebordinos L, Vences FJ & Perez de la Vega M 1990 Genetic mapping of isozyme loci in *Secale cereale* L. Theoretical and Applied Genetics 80: 88-94.
1535.	Waines JG & Payne PI 1987 Electrophoretic analysis of the high-molecular-weight glutenin subunits of *Triticum monococcum*, *T. urartu*, and the A genome of bread wheat (*T. aestivum*). Theoretical and Applied Genetics 74: 71-76.
1536.	Walker-Simmons MK 1995 Personal communication.
1537.	Wall AM, Riley R & Gale MD 1971 The position of a locus on chromosome 5B of *Triticum aestivum* affecting homoeologous meiotic pairing. Genetical Research, Cambridge 18: 329-339.
1538.	Wang G, Snape JW, Hu H & Rogers WJ 1993 The high-molecular-weight glutenin subunit compositions of Chinese bread wheat varieties and their relationship with bread-making quality. Euphytica 68: 205-212.
1539.	Wang J, Xu P & Fincher GB 1992 (1-3)-beta-glucanase isozyme GIII from barley (*Hordeum vulgare*). European Journal of Biochemistry 209: 103-109.
1540.	Wang ML, Atkinson MD, Chinoy CN, Devos KM & Gale MD 1992 Comparative RFLP-based genetic maps of barley chromosome 5 (1H) and rye chromosome 1R. Theoretical and Applied Genetics 84: 339-344.
1541.	Wang ML, Atkinson MD, Chinoy CN, Devos KM, Harcourt RL, Liu CJ, Rogers WJ & Gale MD 1991 RFLP-based genetic map of rye (*Secale cereale* L.) chromosome 1R. Theoretical and Applied Genetics 82: 174-178.
1542.	Wang ML, Leitch A, Swarzacher T, Heslop-Hasrrison J & Moore G 1992 Construction of a chromosome enriched HpaII library from flow-sorted wheat chromosomes. Nucleic Acids Research 20: 1897-1901.

1543.	Wang RC, Barnes EE & Cook LL 1980 Transfer of wheat streak mosaic virus resistance from *Agropyron* to homoeologous chromosome of wheat. Cereal Research Communications 8: 2335-339.
1544.	Wang YC, Xue XZ, Tang GS & Wang QY 1982 (Monosomic analysis of height in the wheat variety Aibian 1). Acta Agronomica Sinica 8: 193-198. [In Chinese]. *Cited* Plant Breeding Abstracts 53: 4597, p.427.
1545.	Washington WJ & Sears ER 1970 Ethyl methanesulphonate-induced chlorophyll mutations in *Triticum aestivum*. Canadian Journal of Genetics and Cytology 12: 851-859.
1546.	Watanabe N 1994 Near-isogenic lines of durum wheat: their development and plant characteristics. Euphytica 72: 143-147.
1547.	Watanabe N, Yotani Y & Furuta Y 1996 The inheritance and chromosomal location of a gene for long glume in durum wheat. Euphytica 91: 235-239.
1548.	Waterhouse WL 1930 Australian rust studies. III. Initial results of breeding for rust resistance. Proceedings of the Linnean Society of New South Wales 55: 596-636.
1549.	Waterhouse WL 1933 On the production of fertile hybrids from crosses between vulgare and Khapli emmer wheats. Proceedings of the Linnean Society of New South Wales 58: 3.
1550.	Watkins AE 1927 Genetic and cytological studies in wheat. IV. Journal of Genetics 19: 81-96.
1551.	Watkins AE & Ellerton S 1940 Variation and genetics of the awn in *Triticum*. Journal of Genetics 40: 243-270.
1552.	Watson IA & Luig NH 1961 Leaf rust in Australia: A systematic scheme for the classification of strains. Proceedings of the Linnean Society of New South Wales 86: 241-250.
1553.	Watson IA & Luig NH 1963 The classification of *Puccinia graminis* var. *tritici* in relation to breeding resistant varieties. Proceedings of the Linnean Society of New South Wales 88: 235-258.
1554.	Watson IA & Luig NH 1966 *Sr15*-a new gene for use in the classification of *Puccinia graminis* var. *tritici*. Euphytica 15: 239-250.
1555.	Watson IA & Luig NH Personal communication.
1556.	Watson IA & Stewart DM 1956 A comparison of the rust reaction of wheat varieties Gabo, Timstein and Lee. Agronomy Journal 48: 514-516.
1557.	Watson IA & Waterhouse WL 1949 Australian rust studies VII. Some recent observations on wheat stem rust in Australia. Proceedings of the Linnean Society of New South Wales 74: 113-131.
1558.	Waud JL & Metzger RJ 1970 Inheritance of a new factor (*Bt8*) for resistance to common bunt of wheat. Crop Science 10: 703-704.
1559.	Wehling P 1991 Inheritance, linkage relationship and chromosomal localization of the glutamate oxaloacetate transaminase, acid phosphatase, and diaphorase isozyme genes in *Secale cereale* L. Theoretical and Applied Genetics 82: 569-576.
1560.	Wehling P & Schmidt-Stohn G 1984 Linkage relationships of esterase loci in rye (*Secale cereale* L.). Theoretical and Applied Genetics 67: 149-153.
1561.	Wehling P, Schmidt-Stohn G & Wricke G 1985 Chromosomal location of esterase, peroxidase, and phosphoglucomutase isozyme structural genes in cultivated rye (*Secale cereale* L.). Theoretical and Applied Genetics 70: 377-382.
1562.	Wellings CR 1986 Host: pathogen studies of wheat stripe rust in Australia. PhD Thesis, The University of Sydney, Australia.

1563.	Wellings CR, McIntosh RA & Hussain M 1988 A new source of resistance to *Puccinia striiformis* f. sp. *tritici* in spring wheats (*Triticum aestivum*). Plant Breeding 100: 88-96.
1564.	Wells DG & Swenson SP 1944 Inheritance and interaction of genes governing reaction to stem rust, leaf rust and powdery mildew in a spring wheat cross. Journal of the American Society of Agronomy 37: 127-133.
1565.	Wells DG, Bonnemann JJ, Gardiner WS, Finney KF, Giese HA & Stymiest CE 1983 Nell wheat. Crop Science 23: 804-805.
1566.	Welsh JR, Keim DL, Pirasteh B & Richards RD 1973 Genetic control of photoperiod response in wheat. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri, USA (Sears ER & Sears LMS eds.): 879-884.
1567.	Weng J, Wang Z-F & Nguyen HT 1991 A *Triticum aestivum* cDNA clone encoding a low-molecular-weight heat shock protein. Plant Molecular Biology 17: 273-275.
1568.	Weng J, Wang Z-F & Nguyen HT 1991 Nucleotide sequence of a *Triticum aestivum* cDNA clone which is homologous to the 26 kDa chloroplast-localized heat shock protein gene of maize. Plant Molecular Biology 17: 255-258.
1569.	Weng J, Wang Z-F & Nguyen HT 1993 Molecular cloning and sequence analysis of cDNA encoding cytoplasmic low molecular weight heat shock proteins in hexaploid wheat. Plant Science 92: 35-46.
1570.	Wenzel WG 1971 Monosomic analysis of the corroded characteristic in wheat. Canadian Journal of Genetics and Cytology 13: 227-230.
1571.	Werner JE, Endo TR & Gill BS 1992 Towards a cytogenetically based physical map of the wheat genome. Proceedings of the National Academy of Sciences, USA 89: 11307-11311.
1572.	Westhoff P 1988 Personal communication.
1573.	Whelan EDP 1988 Personal communication.
1574.	Whelan EDP 1988 Transmission of a chromosome from decaploid *Agropyron elongatum* that confers resistance to the wheat curl mite in common wheat. Genome 30: 293-298.
1575.	Whelan EDP & Hart GE 1988 A spontaneous translocation that confers wheat curl mite resistance from decaploid *Agropyron elongatum* to common wheat. Genome 30: 289-292.
1576.	Whelan EDP & Thomas JB 1989 Chromosomal location in common wheat of a gene (*Cmc1*) from *Aegilops squarrosa* that conditions resistance to colonisation by the leaf curl mite. Genome 32: 1033-1036.
1577.	Wiggin HC 1955 Monosomic analysis of stem rust reaction and awn expression in Kentana 52 wheat. Journal of Heredity 46: 239-242.
1578.	William MDHM, Pena RJ & Mujeeb-Kazi A 1993 Seed protein and isozyme variations in *Triticum tauschii* (*Aegilops squarrosa*). Theoretical and Applied Genetics 87: 257-263.
1579.	Williams KJ, Fisher JM & Langridge P 1994 Identification of RFLP markers linked to the cereal cyst nematode resistance gene (*Cre*) in wheat. Theoretical and Applied Genetics 89: 927-930.
1580.	Williams KJ, Fisher JM & Langridge P 1996 Development of a PCR-based allele-specific assay from an RFLP probe linked to resistance to cereal cyst nematode in wheat. Genome 39: 798-801.
1581.	Williams ND & Kaveh H 1976 Relationships of genes for reaction to stem rust from 'Marquis' and 'Reliance' wheat to other *Sr* genes. Crop Science 16: 561-564.
1582.	Williams ND & Maan SS 1973 Telosomic mapping of genes for resistance to stem rust of wheat. Proceedings of the 4th International Wheat Genetics Symposium Columbia, Missouri, USA (Sears ER & Sears LMS eds.): 765-770.

1583.	Williams ND, Joppa LR, Duysen ME & Freeman TP 1983 Monosomic analysis of an EMS-induced chlorina mutation in wheat. Proceedings of the 6th International Wheat Genetics Symposium, Kyoto, Japan (Sakamoto S. ed.): 303-306.
1584.	Williamson JD, Quatrano RS & Cumings AC 1985 Em polypeptide and its messenger RNA levels are modulated by ABA during embryogenesis in wheat. European Journal of Biochemistry 152: 501-507.
1585.	Williamson MS, Ford J & Kreis M 1988 Molecular cloning of two isoinhibitor forms of chymotrypsin inhibitor 1 (CI-1) from barley endosperm and their expression in normal and mutant barleys. Plant Molecular Biology 10: 521-535.
1586.	Wilson RE 1985 Inheritance of resistance to *Septoria tritici* in wheat. *In*: Septoria in Cereals, Proceedings of Workshop, Montana State University, Bozeman, Montana, USA, 1983, (Scharen AL ed.): 33-35.
1587.	Winzeler M, Winzeler H & Keller B 1995 Endopepidase polymorphism and linkage of the *Ep-D1c* null allele with the *Lr19* leaf-rust-resistance gene in hexaploid wheat. Plant Breeding 114: 24-28.
1588.	Wise RP, Rohde W & Salamini F 1990 Nucleotide sequence of the Bronze-1 homologous gene from *Hordeum*. Plant Molecular Biology 14: 277-279.
1589.	Wolf G & Rimpau J 1979 Structural and regulatory genes for phosphodiesterase in wheat. Proceedings of the 5th International Wheat Genetics Symposium, New Delhi, India (Ramanujam S ed.) l2: 705-712.
1590.	Wolf G, Rimpau J & Lelley T 1977 Localization of structural and regulatory genes for phosphodiesterase in wheat (*Triticum aestivum*). Genetics 86: 597-605.
1591.	Wolfe MS 1967 Physiologic specialization of *Erysiphe graminis* f. sp. *tritici* in the United Kingdom, 1964-5. Transactions of the British Mycological Society 50: 631-640.
1592.	Wolfe MS & Wright SE 1972 Annual Report, Plant Breeding Institute Cambridge, 1971: 142-143.
1593.	Woo SC & Konzak CF 1969 Genetic analysis of short culm mutants induced by ethyl methane sulphonate in *Triticum aestivum* L. *In*: Induced Mutations in Plants: Proceedings of the IAEA/FAO Symposium on the Nature, Induction and Utilization of Mutations in Plants, Pullman, Washington, USA, IAEA: 551-555.
1594.	Worland AJ 1995 Personal communication.
1595.	Worland AJ & Law CN 1980 The genetics of hybrid dwarfing in wheat. Zeitschrift fur Pflanzenzuchtung 85: 28-39.
1596.	Worland AJ & Law CN 1983 Cytoplasmic variation in wheat. 1982 Annual Report, Plant Breeding Institute Cambridge: 79-80.
1597.	Worland AJ & Law CN 1985 Aneuploidy in semidwarf wheat varieties. Euphytica 34: 317-327.
1598.	Worland AJ & Law CN 1986 Genetic analysis of chromosome 2D of wheat I. The location of genes affecting height, day-length insensitivity, hybrid dwarfism and yellow-rust resistance. Zeitschrift fur Pflanzenzuchtung 96: 331-345.
1599.	Worland AJ & Petrovic S 1988 The gibberellic acid insensitive dwarfing gene from the variety Saitama 27. Euphytica 38: 55-63.
1600.	Worland AJ & Sayers EJ 1995 *Rht1* (*B. dw*), an alternative allelic variant for breeding semi-dwarf wheat varieties. Plant Breeding 114: 397-400.
1601.	Worland AJ, Law CN & Parker BB 1984 Alternative semi-dwarfing genes. Annual Report, Plant Breeding Institute Cambridge, 1983: 59-61.

1602.	Worland AJ, Law CN & Shakoor A 1980 The genetical analysis of an induced height mutant in wheat. Heredity 45: 61-71.
1603.	Worland AJ, Law CN, Hollins TW, Koebner RMD & Guira A 1988 Location of a gene for resistance to eyespot (*Pseudocercosporella herpotrichoides*) on chromosome 7D of bread wheat. Plant Breeding 101: 43-51.
1604.	Worland AJ, Petrovic S & Law CN 1988 Genetic analysis of chromosome 2D of wheat II. The importance of this chromosome to Yugoslavian varieties. Plant Breeding 100: 247-259.
1605.	Worland AJ, Sayers EJ & Borner A 1994 The genetics and breeding potential of *Rht12*, a dominant dwarfing gene in wheat. Plant Breeding 113: 187-196.
1606.	Worland AJ 1986 Gibberellic acid insensitive dwarfing genes in southern European wheats. Euphytica 35: 857-866.
1607.	Wrigley CW & Shepherd KW 1973 Electrofocusing of grain proteins from wheat genotypes. Annals of the New York Academy of Science 209: 154-162.
1608.	Xia XC, Hsam SLK, Stephan U, Yang TM & Zeller FJ 1995 Identification of powdery-mildew-resistance genes in common wheat (*Triticum aestivum* L.). VI. Wheat cultivars grown in China. Plant Breeding 114: 175-175.
1609.	Xie DX, Devos KM, Moore G & Gale MD 1993 RFLP-based genetic maps of the homoeologous group 5 chromosomes of bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 87: 70-74.
1610.	Xin ZY, Johnson R, Law CN & Worland AJ 1984 A genetic analysis of genes for yellow rust resistance in the winter wheat variety Feng-Kang 13. Acta Agronomica Sinica 10: 217-222.
1611.	Xin ZY, Law CN & Worland AJ 1988 Studies of the effects of the vernalization responsive genes on the chromosomes of homoeologous group 5 of wheat. Proceedings of the 7th International Wheat Genetics Symposium, IPSR, Cambridge, UK (Miller TE & Koebner RMD eds.): 675-680.
1612.	Yamada T 1989 Identification of GA-insensitive *Rht* genes in Japanese modern varieties and landraces of wheat. Euphytica 43: 53-57.
1613.	Yamada T 1990 Classification of GA response, *Rht* genes and culm length in Japanese varieties and land races of wheat. Euphytica 50: 221-239.
1614.	Yamamori M 1994 An N-band marker for gene *Lr18* for resistance to leaf rust in wheat. Theoretical and Applied Genetics 89: 643-646.
1615.	Yamamori M & Endo TR 1996 Variation of starch granule proteins and chromosome mapping of their coding genes in common wheat. Theoretical and Applied Genetics 93: 275-281.
1616.	Yamamori M, Nakamura T & Nagamine T 1995 Polymorphism of two waxy proteins in the emmer group of tetraploid wheat, *Triticum dicoccoides*, *T. dicoccum*, and *T. durum*. Plant Breeding 114: 215-218.
1617.	Yamamori M, Nakamura T, Endo TR & Nagamine T 1994 Waxy protein deficiency and chromosomal location of coding genes in common wheat. Theoretical and Applied Genetics 89: 178-184.
1618.	Yang ZJ & Ren ZL 1996 Chromosome location of a new gene for resistance to powdery mildew in wheat (*Triticum aestivum* L.). Manuscript.
1619.	Yen F, Evans LE & Larter EN 1969 Monosomic analysis of fertility restoration in three restorer lines of wheat. Canadian Journal of Genetics and Cytology 11: 531-546.

1620.	Yu MQ, Jahier J & Person-Dedryver F 1992 Genetics of two mechanisms of resistance to *Meloidogyne naasi* (Franklin) in an *Aegilops variabilis* Eig accession. Euphytica 58: 267-273.
1621.	Yu MQ, Person-Dedrywer F & Jahier J 1990 Resistance to root knot nematode, *Meloidogyne naasi* (Franklin) transferred from *Aegilops variabilis* Eig to bread wheat. Agronomie 6: 451-456.
1622.	Zadoks JC 1961 Yellow rust on wheat. Studies on epidemiology and physiological specialization. Journal Pl. Ziekten 67: 69-256.
1623.	Zeller FJ 1973 1B/1R wheat-rye chromosome substitutions and translocations. Proceedings of the 4th International Wheat Genetics Symposium, Columbia, Missouri, USA (Sears ER & Sears LMS eds.): 209-221.
1624.	Zeller FJ & Fuchs E 1983 (Cytologie und Kronkheitsresistanz einer 1A/1R-und meherer 1B/1R-Weizen-Roggen-Translocationssorten). Zeitschrift fur Pflanzenzuchtung 90: 284-296.
1625.	Zeller FJ & Hsam SLK 1996 Chromosomal location of a gene suppressing powdery mildew resistance genes *Pm8* and *Pm17* in common wheat (*Triticum aestivum* L. em. Thell.). Theoretical and Applied Genetics 93: 38-40.
1626.	Zeller FJ & Oppitz K 1977 (The localization of the gene *SrEC* for stem rust resistance in the wheat Etoile de Choisy using monosomic analysis). Zeitschrift fur Pflanzenzuchtung 78: 79-82.
1627.	Zeller FJ & Sastrosumarjo S 1972 (The cytology of the wheat variety Weique (*T. aestivum* L.)). Zeitschrift fur Pflanzenzuchtung 68: 312-321.
1628.	Zeller FJ, Lutz J & Stephan U 1993 Chromosome location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L.).1. *Mlk* and other alleles at the *Pm3* locus. Euphytica 68: 223-229.
1629.	Zeller FJ, Lutz J, Reimlein EI, Limpert E & Koenig J 1993 Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L.) II. French cultivars. Agronomie 13: 201-207.
1630.	Zeven AC 1965 First supplementary list of genotypes of hybrid necrosis of wheat varieties. Euphytica 14: 239-243.
1631.	Zeven AC 1967 Second supplementary list of genotypes of hybrid necrosis of wheat varieties. Euphytica 16: 18-22.
1632.	Zeven AC 1968 Third supplementary list of wheat varieties classified according to their genotype for hybrid necrosis. Euphytica 17: 46-53.
1633.	Zeven AC 1969 Fourth supplementary list of wheat varieties classified according to their genotype for hybrid necrosis. Euphytica 18: 43-57.
1634.	Zeven AC 1969 Tom Pouce Blanc and Tom Pouce Barbu Rouge, two *Triticum aestivum* sources of very short straw. Wheat Information Service 29: 8-9.
1635.	Zeven AC 1971 Fifth supplementary list of wheat varieties classified according to their genotype for hybrid necrosis and geographical distribution of *Ne-genes*. Euphytica 20: 239-254.
1636.	Zeven AC 1972 Determination of the chromosome and its arm carrying the *Ne1*-locus of *Triticum aestivum* L., Chinese Spring and the *Ne1*-expressivity. Wheat Information Service 33-34: 4-6.
1637.	Zeven AC 1973 Sixth supplementary list of wheat varieties classified according to their genotype for hybrid necrosis and geographical distribution of *Ne*-genes. Euphytica 22: 618-632.

1638.	Zeven AC 1976 Seventh supplementary list of wheat varieties classified according to their genotype for hybrid necrosis and geographical distribution of *Ne*-genes. Euphytica 25: 255-276.
1639.	Zeven AC 1981 Eighth supplementary list of wheat varieties classified according to their genotype for hybrid necrosis. Euphytica 30: 521-539.
1640.	Zeven AC 1983 The character brown ear of wheat: A review. Euphytica 32: 299-310.
1641.	Zeven AC 1985 The genetics of auricle colour in wheat (*Triticum aestivum* L.): A review. Euphytica 34: 233-236.
1642.	Zeven AC 1987 Crossability percentages of some 1400 bread wheat varieties and lines with rye. Euphytica 36: 299-319.
1643.	Zeven AC 1991 Wheats with purple and blue grains a review. Euphytica 56: 243-258.
1644.	Zeven AC Personal communication.
1645.	Zeven AC & Knott DR Personal communication.
1646.	Zeven AC & van Heemert C 1970 Germination of pollen of weed rye (*Secale segetale* L.) on wheat (*Triticum aestivum* L.) stigmas and the growth of pollen tubes. Euphytica 19: 175-179.
1647.	Zhang HB & Dvorak J 1990 Characterization and distribution of an interspersed repeated nucleotide sequence from *Lophopyrum elongatum* and mapping of a segregation distortion factor with it. Genome 33: 927-936.
1648.	Zhang HT & Knott DR 1993 Inheritance of adult plant resistance to leaf rust in six durum wheat cultivars. Crop Science 33: 694-697.
1649.	Zhang YL, Luo MC, Yen C & Yang JL 1992 Chromosome location of a new crossability gene in common wheat. Wheat Information Service 75: 36-40.
1650.	Zhao XC, Batey IL, Sharp PJ, Crosbie G, Barclay I, Wilson R, Morell MK & Appels R 1998 A single genetic locus associated with starch granule properties and noodle quality in wheat. Journal of Cereal Science 27: 7-13.
1651.	Zhong GY & Qualset CO 1993 Allelic diversity of high-molecular-weight glutenin protein subunits in natural populations of *Dasypyrum villosum* (L.) Candargy. Theoretical and Applied Genetics 86: 851-858.
9901.	Dubcovsky J, Lukaszewski AJ, Echaide M, Antonelli EF & Porter DR 1998 Molecular characterization of two *Triticum speltoides* interstitial translocations carrying leaf rust and greenbug resistance genes. Crop Science 38: 1655-1660.
9902.	Kosner J & Pankova K 1998 The detection of allelic variation of the recessive *Vrn* loci of winter wheat. Euphytica 101: 9-16.
9903.	Kato K, Miura H, Akiyama M, Kuroshima M & Sawada S 1998 RFLP mapping of the three major genes, *Vrn1*, *Q*, and *B1*, on the long arm of chromosome 5A of wheat. Euphytica 101: 91-95.
9904.	Fahima T, Sun GL, Chaque V, Korol A, Grama A, Ronin Y & Nevo E 1997 Use of the near isogenic lines approach to identify molecular markers linked to the *Yr15* stripe rust resistance gene of wheat. Israel Journal of Plant Science 45: 262.
9905.	Liu JQ & Kolmer JA 1998 Genetics of stem rust resistance in wheat cultivars Pasqua and AC Taber. Phytopathology 88: 171-176.
9906.	Etremova TT, Maystrenko OI, Arbuzova VS & Laikova LI 1998 Genetic analysis of glume colour in common wheat cultivars from the former USSR. Euphytica 102: 211-218.
9907.	Klindworth DL, Williams ND & Joppa LR 1990 Chromosomal location of genes for supernumerary spikelet in tetraploid wheat. Genome 33: 515-520.

9908.	Peng ZS, Deng CL, Yen C & Yang JL 1998 Genetic control of supernumerary spikelet in common wheat line LYB. Wheat Information Service 86: 6-12.
9909.	Peng Z-S, Yen C & Yang J-L 1998 Genetic control of oligo-culms in common wheat. Wheat Information Service 86: 19-24.
9910.	Demeke T, Hucl P, Nair RB, Nakamura T & Chibbar R 1997 Evaluation of Canadian and other wheats for waxy proteins. Cereal Chemistry 74: 442-44.
9911.	Graybosh RA, Peterson CJ, Hansen LE, Rahman S, Hill A & Skerritt JH 1998 Identification and characterization of U. S. wheats carrying null alleles at the *Wx* loci. Cereal Chemistry 75: 162-165.
9912.	Miruta H, Tanii S, Nakamura T & Watanabe N 1994 Genetic control of amylose content in wheat endosperm starch and differential effects of three *Wx* genes. Theoretical and Applied Genetics 89: 276-280.
9913.	Rodriguez-Quijano M, Nieto-Taldriz MT & Carrillo JM 1998 Polymorphism of waxy proteins in Iberian hexaploid wheats. Plant Breeding 117: 341-344.
9914.	Urbano M, Colaprino G & Margiotta B 1996 Waxy protein variation in tetraploid and hexaploid wheats. In: C. W. Wrigley (ed), Gluten 1996, Proceedings of the 6th International gluten workshop, RAC1, North Melbourne, Australia pp64-67.
9915.	Yamamori M, Nakamura T & Kuroda A 1992 Variation in the content of starch-granule bound protein among several Japanese cultivars of common wheat (*Triticum aestivum* L.). Euphytica 64: 215-219.
9916.	Yamamori M, Nakamura T, Endo TR & Nagamine T 1994 Waxy protein deficiency and chromosomal location of coding genes in common wheat. Theoretical and Applied Genetics 89: 179-184.
9917.	Zeng M, Morris CT, Batey I & Wrigley CW 1997 Sources of variation for starch gelatinization, pasting and gelation properties in wheat. Cereal Chemistry 74: 63-71.
9918.	Marais GF, Horn M & Du Toit F 1994 Intergeneric transfer (rye to wheat) of a gene(s) for Russian wheat aphid resistance. Plant Breeding 113: 265-271.
9919.	Singh NK, Shepherd KW & McIntosh RA 1990 Linkage mapping of genes for resistance to leaf rust, stem rust and stripe rust and omega-secalins on the short arm of rye chromosome 1R. Theoretical and Applied Genetics 80: 609-616.
9920.	Blanco A, Bellomo MP, Lotti C, Maniglio T, Pasqualone A, Simeone R, Troccoli A & Di Fonzo N 1998 Genetic mapping of sedimentation values across environments using recombinant inbred lines of durum wheat. Plant Breeding 117: 413-417.
9921.	Sacco F, Suarez EY & Narango T 1998 Mapping of the leaf rust resistance gene *Lr3* of Sinvalocho MA wheat. Genome 41: 686-690.
9922.	Nieto-Taladriz MT, Rodriquez-Quijano M & Carrillo JM 1998 Biochemical and genetic characterization of a D glutenin subunit encoded at *Glu-B3* locus. Genome 41: 215-220.
9923.	Gold J, Harder D, Townley-Smith F, Aung T & Procunier J 1999 Development of a molecular marker for rust resistance genes *Sr39* and *Lr35* in wheat breeding lines. Electronic Journal of Biotechnology 'http://www.ejb.org'. 2(1).:
9924.	Faris JD, Anderson JA, Francl LJ & Jordahl JG 1997 RFLP mapping of resistance to chlorosis induction by *Pyrenophora tritici-repentis* in wheat. Theoretical and Applied Genetics 94: 98-103.
9925.	Waldron BL, Moreno-Sevilla B, Anderson JA, Stack RW & Frohberg RC 1999 RFLP mapping of QTL for *Fusarium* head blight resistance in wheat. Crop Science 39: 805-811.
9926.	Boyko EV, Gill KS, Mickelson-Young L, Nasuda S, Raupp WJ, Ziegle JN, Singh S, Hassawi DS, Fritz AK, Namuth D, Lapitan NLV & Gill BS 1999 A high-density genetic

	linkage map of *Aegilops tauschii*, the D-genome progenitor of bread wheat. Theoretical and Applied Genetics 99: 16-26.
9927.	Du C & Hart GE 1998 *Triticum turgidum* L. 6A and 6B recombinant substitution lines: extended linkage maps and characterization of residual background alien genetic variation. Theoretical and Applied Genetics 96: 645-653.
9928.	Boyko EV 1999 Personal communication.
9929.	Roder MS, Korzun V, Wendehake K, Plaschke J, Tixier M-H, Leroy P & Ganal MW 1998 A microsatellite map of wheat. Genetics 149: 2007-2023.
9930.	Koval SF & Goncharov NP 1998 Multiple allelism at the *Vrn1* locus of common wheat. Acta Agronomica Hungarica 46: 113-119.
9931.	Faris JD, Laddomada B & Gill BS 1998 Molecular mapping of segregation distortion loci in *Aegilops tauschii*. Genetics 149: 319-327.
9932.	Santa-Maria GE, Rubio F, Dubcovsky J & Rodriguez-Navarro A. 1997 The HAK1 gene of barley is a member of a large gene family and encodes a high-affinity potassium transporter. The Plant Cell 9: 2281-2289.
9933.	Kojima T & Ogihara Y 1998 High-resolution RFLP map of the long arm of chromosome 5A in wheat and its synteny among cereals. Genes and Genetic Systems 73: 51-58.
9934.	Kojima T, Tsujimoto H & Ogihara Y 1997 High-resolution RFLP mapping of the fertility restoration (*Rf3*) gene against *Triticum timopheevi* cytoplasm located on chromosome 1BS of common wheat. Genes and Genetic Systems 72: 353-359.
9935.	Kojima T, Nagaoka T, Noda K & Oghhara Y 1998 Genetic linkage map of ISSR and RAPD markers in Einkorn wheat in relation to that of RFLP markers. Theoretical and Applied Genetics 96: 37-45.
9936.	Parker GD, Chalmers KJ, Rathjen AJ & Langridge P 1998 Mapping loci associated with flour colour in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 97: 238-245.
9937.	Nagamine T, Yoshida H & Komae K 1997 Varietal differences and chromosome locations of multiple isoforms of starch branching enzyme in wheat endosperm. Phytochemistry 46: 23-26.
9938.	Seo YW, Johnson JW & Jarret RL 1997 A molecular marker associated with the *H21* Hessian fly resistance gene in wheat. Molecular Breeding 3: 177-181.
9956.	Nelson JC, Autrique JE, Fuentes-Davila G & Sorrells ME 1998 Chromosomal location of genes for resistance to Karnal bunt in wheat. Crop Science 38: 231-236.
9957.	Cadalen T, Sourdille P, Charmet G, Tixier MH, Gay G, Boeuf C, Bernard S, Leroy P & Bernard M 1998 Molecular markers linked to genes affecting plant height in wheat using a doubled-haploid population. Theoretical and Applied Genetics 96: 933-940.
9958.	Mingeot D & Jacquemin JM 1998 Mapping of RFLP probes characterized for their polymorphism on wheat. Theoretical and Applied Genetics 98: 1132-1137.
9959.	Blanco A, Bellomo MP, Cenci A, De Giovanni C, D'Ovidio R, Iacono E, Laddomada B, Pagnotta MA, Porceddu E, Sciancalepore A, Simeone R & Tanzarella OA 1998 A genetic linkage map of durum wheat. Theoretical and Applied Genetics 97: 721-728.
9960.	Flintham JE, Adlam R, Bassoi M, Holdsworth M & Gale MD 2002 Maping genes for resistance to sprouting damage in wheat. Euphytica 126: 39-45.
9961.	Bailey PC, McKibbin RS, Lenton JR, Holdsworth MJ, Flintham JE & Gale MD 1999 Genetic map locations for orthologous *Vp1* genes in wheat and rice. Theoretical and Applied Genetics 98: 281-284.
9962.	Worland AJ, Korzun V, Roder MS, Ganal MW & Law CN 1998 Genetic analysis of the dwarfing gene *Rht8* in wheat. Part II. The distribution and adaptive significance of allelic

	variants at the *Rht8* locus of wheat as revealed by microsatellite screening. Theoretical and Applied Genetics 96: 1110-1120.
9964.	Worland AJ, Korzun V & Petrovic S 1998 The presence of the dwarfing gene *Rht8* in wheat varieties of the former Yugoslavian republics as detected by a diagnostic molecular marker. Proc. 2nd Balkan Symposium on Field Crops. Pp. 51-55.
9965.	Qu L-J, Foote TN, Roberts MA, Money TA, Aragon-Alcaide L, Snape JW & Moore G 1998 A simple PCR-based method for scoring the *ph1b* deletion in wheat. Theoretical and Applied Genetics 96: 371-375.
9966.	Sourdille P, Charmet G, Trottet M, Tixier MH, Boeuf C, Negre S, Barloy D & Bernard M 1998 Linkage between RFLP molecular markers and the dwarfing genes *Rht-B1* and *Rht-D1* in wheat. Hereditas 128: 41-46.
9968.	Myburg AA, Cawood M, Wingfield BD & Botha A-M 1998 Development of RAPD and SCAR markers linked to the Russian wheat aphid resistance gene *Dn2* in wheat. Theoretical and Applied Genetics 96: 1162-1169.
9969.	Sarma RN, Gill GS, Sasaki T, Galiba G, Sutka J, Laurie D & Snape JW 1998 Comparative mapping of the wheat chromosome 5A *Vrn-A1* region with rice and its relationship to QTL for flowering time. Theoretical and Applied Genetics 97: 103-109.
9970.	Chen Q-F, Yen C & Yang J-L 1998 Chromosome location of the gene for brittle rachis in the Tibetan weedrace of common wheat. Genetic Resources and Crop Evolution 45: 407-410.
9972.	Riechers DE, Kleinhofs A, Irzyk GP & Jones SS 1998 Chromosomal location and expression of a herbicide safener-regulated glutathione S-transferase gene in *Triticum aestivum* and linkage relations in *Hordeum vulgare*. Genome 41: 368-372.
9973.	Riechers DE, Irzyk GP, Fuerst EP & Jones SS 1998 Nucleotide sequence of a cDNA encoding a safener-induced glutathione *S*-transferase (accession No. AF004358) from *Triticum tauschii* (PGR 97-110). Plant Physiology 114: 1568-1568.
9974.	Van Campenhout S, Aert R & Volckaert G 1998 Orthologous DNA sequence variation among 5S ribosomal RNA gene spacer sequences on homoeologous chromosomes 1B, 1D, and 1R of wheat and rye. Genome 41: 244-255.
9975.	Briney A, Wilson R, Potter RH, Barclay I, Crosbie G, Appels R & Jones MGK 1998 A PCR-based marker for selection of starch and potential noodle quality in wheat. Molecular Breeding 4: 427-433.
9976.	Van Campenhout S, Lagi L, Vander Stappen J & Volckaert G 1998 Characterisation of type-I thionin loci from the A, B, D and R genomes of wheat and rye. Theoretical and Applied Genetics 96: 80-86.
9981.	Metakovsky EV Personal communication.
9982.	Metakovsky EV, Branlard G, Chernakov VM, Upelniek VP, Redaelli R & Pogna NE 1997 Recombination mapping of some chromosome 1A-, 1B-, 1D- and 6B-controlled gliadins and low-molecular-weight glutenin subunits in common wheat. Theoretical and Applied Genetics 94: 788-795.
9983.	Metakovsky EV, Chernakov VM, Upelniek VP, Redaelli R, Dardevet M, Branlard G & Pogna NG 1996 Recombination mapping of minor omega-gliadin-coding loci on chromosome 1A of common wheat: A revision. Journal of Genetics and Breeding 50: 277-286.
9984.	Metakovsky EV, Davidov SD, Chernakov VM & Upelniek VP 1993 Gliadin allele identification in common wheat. III. Frequency of occurrence and appearance of

	spontaneous mutations at the gliadin-coding loci. Journal of Genetics and Breeding 47: 221-236.
9985.	Metakovsky EV, Gomez M, Vazquez JF & Carrillo JM 2000 High genetic diversity of Spanish common wheats as judged from gliadin alleles Plant Breeding 119: 37-42.
9986.	Metakovsky EV, Pogna NE, Biancardi AM & Redaelli R 1994 Gliadin allele composition of common wheat cultivars grown in Italy. Journal of Genetics and Breeding 48: 55-66.
9987.	Redaelli R, Metakovsky EV, Davidov SD & Pogna NE 1994 Two-dimensional mapping of gliadins using biotypes and null mutants of common wheat cultivar Saratovskaya 29. Hereditas 121: 131-137.
9988.	Vaccino P & Metakovsky EV 1995 RFLP patterns of gliadin alleles in *Triticum aestivum* L. : implications for analysis of the organization and evolution of complex loci. Theoretical and Applied Genetics 90: 173-181.
9989.	D'Ovidio R, Masci S, Porceddu E & Kasarda DD 1997 Duplication of the *Bx7* high-molecular-weight glutenin subunit gene in bread wheat (*Triticum aestivum* L.) cultivar 'Red River 68'. Plant Breeding 116: 525-531.
9990.	Watanabe N. 1999 Genetic control of the long glume phenotype in tetraploid wheat by homoeologous chromosomes. Euphytica 106: 39-43.
9991.	Romero D, Delibes A, Lopez Brana I, Mena M, Duce A & Andres MF 1994 Studies of the chromosome location of a gene conferring resistance to *Heterodera avenae* transferred from the wild grass *Aegilops ventricosa* to hexaploid wheat. Proc. 22nd International Nematology Symposium, Gent, Belgium (Abstr.).
0001.	Rong JK, Millet E, Manisterski J & Feldman M 2000 A new powdery mildew resistance gene: introgression from wild emmer into common wheat and RFLP-based mapping. Euphytica 115: 121-126.
0002.	Jarve K, Peusha HO, Tsymbalova J, Tamm S, Devos KM & Enno TM 2000 Chromosomal location of a *T. timopheevii*-derived powdery mildew resistance gene transferred to common wheat. Genome 43: 377-381.
0003.	Peng JH, Fahima T, Roder MS, Li YC, Dahan A, Grama A, Ronin YI, Korol AB & Nevo E 1999 Microsatellite tagging of the stripe rust resistance gene *YrH52* derived from wild emmer wheat, *Triticum dicoccoides*, and suggestive negative crossover interference on chromosome 1B. Theoretical and Applied Genetics 98: 862-872.
0004.	Labuschagne M & Maartens H 1999 The use of low molecular weight glutenin subunits to distinguish between wheat cultivars with and without resistance to the Russian wheat aphid, *Diuraphis noxia*. Plant Breeding 118: 91-92.
0005.	Bai GH, Kolb FL, Shaner G & Domier LL 1999 Amplified fragment length polymorphism markers linked to a major quantitative trait locus controlling scab resistance in wheat. Phytopathology 89: 343-348.
0006.	Mesterhazy A, Bartok T, Mirocha CG & Komoroczy R 1999 Nature of wheat resistance to Fusarium head blight and the role of deoxynivalenol for breeding. Plant Breeding 118: 97-110.
0007.	Anderson JA, Effertz RJ, Faris JD, Francl LJ, Meinhardt SW & Gill BS 1999 Genetic analysis of sensitivity to a *Pyrenophora tritici-repentis* necrosis-inducing toxin in durum and common wheat. Phytopathology 89: 293-297.
0008.	Graybosch RA, Lee JH, Peterson CJ, Porter DR & Chung OK 1999 Genetic, agronomic and quality comparisons of two IAL.IRS wheat-rye chromosomal translocations. Plant Breeding 118: 125-130.

0009.	Jahier J, Tanguy AM, Abelard P & Rivoal. R 1996 Utilization of deletions to localize a gene for resisistance to cereal cyst nematode, *Heterodera avenae*, on an *Aegilops ventricosa* chromosome. Plant Breeding 115: 282-284.
0010.	Boshoff WPH & Pretorius ZA 1999 A new pathotype of *Puccinia striiformis* f. sp. *tritici* on wheat in South Africa. Plant Disease 83: 591.
0011.	Hartl L, Mohler V, Zeller FJ, Hsam SLK & Schweizer G 1999 Identification of AFLP markers closely linked to the powdery mildew resistance genes *Pmlc* and *Pm4a* in common wheat (*Triticum aestivum* L.). Genome 42: 322-329.
12.	Paull JG, Chalmers KJ, Karakousis A, Kretschmer J, Manning S & Langridge P 1998 Genetic diversity in Australian wheat varieties and breeding material based on RFLP data. Theoretical and Applied Genetics 96: 435-446.
13.	Singh RP, Chen WQ & He ZH 1999 Leaf rust resistance of spring, facultative and winter wheat cultivars from China. Plant Disease 83: 644-651.
14.	Liu Z, Sun Q, Ni Z & Yang T 1999 Development of SCAR markers linked to the *Pm21* gene conferring resistance to powdery mildew in common wheat. Plant Breeding 118: 215-219.
0015.	Prasad M, Varshney RK, Kumar A, Balyan HS, Sharma PC, Edwards KJ, Singh H, Dhaliwal HS, Roy JK & Gupta PK 1999 A microsatellite marker associated with a QTL for grain protein content on chromosome 2DL of bread wheat. Theoretical and Applied Genetics 99: 341-345.
0016.	Chantret N, Pavoine MT & Doussinault G 1999 The race specific resistance gene to powdery mildew, *MIRE*, has a residual effect on adult plant resistance of winter wheat line RE714. Phytopathology 89: 533-539.
0017.	Liu DC, Yen C, Yang JL, Zhang YL & Lan XJ 1999 The chromosomal locations of high crossability genes in tetraploid wheat *Triticum turgidum* cv. Ailanmai native to Sichuan, China. Euphytica 108: 79-82.
0018.	Miura H, Araki E & Tarui S 1999 Amylose synthesis capacity of the three Wx genes of wheat cv. Chinese Spring. Euphytica 108: 91-95.
0019.	Peng JR, Richards DE, Hartley NM, Murphy GP, Devos KM, Flintham JE, Beales J, Fish LJ, Worland AJ, Pelica F, Duralalagaraja Sudhakar, Christou P, Snape JW, Gale MJ & Harberd NP. 1999 'Green revolution' genes encode mutant gibberellin response modulators. Nature 400: 256-261.
0020.	Fowler DB, Limin AE & Ritchie JT 1999 Low temperature tolerance in cereals: Model and genetic interpretation. Crop Science 39: 626-633.
0021.	Espitia-Rangel E, Baenziger PS, Graybosch RA, Shelton DR, Moreno-Sevilla B & Peterson CJ 1999 Agronomic performance and stability of 1A vs. 1AL.1RS genotypes derived from winter wheat 'Nekota'. Crop Science 39: 643-648.
0022.	Peusha H, Enno T & Pruliin O 2000 Chromosomal location of powdery mildew resistance genes and cytogenetic analysis of meiosis in common wheat cultivar Meri. Hereditas 132: 29-34.
0023.	Miura H, Nakagawa M & Worland AJ 1999 Control of ear emergence time by chromosome 3A of wheat. Plant Breeding 118: 85-87.
0024.	Worland AJ 1999 Personal communication.
0025.	Shah MM, Gill KS, Baenziger PS, Yen Y, Kaeppler SM & Ariyarathna HM 1999 Molecular mapping of loci for agronomic traits on chromosome 3A of bread wheat. Crop Science 39: 1728-1732.

0026.	Kato K, Miura H & Sawada S 1999 Detection of an earliness *per se* quantitative trait locus in the proximal region of wheat chromosome 5AL. Plant Breeding 118: 391-394.
0027.	Yamamori M & Quynh NT 2000 Differential effects of *Wx-A1*, *-B1* and *-D1* protein deficiencies on apparent amylose content and starch pasting properties in common wheat. Theoretical and Applied Genetics 100: 32-38.
0028.	Peusha H, Hsam SLK, Enno T & Zeller FJ 1996 Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em. Thell) VIII. Cultivars and advanced breeding lines grown in Finland. Heredity 124: 91-93.
0029.	McIntosh RA, Devos KM, Dubcovsky J & Rogers WJ 2000 Catalogue of gene symbols for wheat: 2000 Supplement. Wheat Information Service 91: 33-70.
0030.	Salina E, Borner A, Leonoval I, Korzun V, Laikova L, Maystrenko O & Roder MS 2000 Microsatellite mapping of the induced sphaerococcoid mutation genes in *Triticum aestivum*. Theoretical and Applied Genetics 100: 686-689.
0031.	Messmer MM, Keller M, Zanetti S & Keller B 1999 Genetic linkage map of a wheat x spelt cross. Theoretical and Applied Genetics 98: 1163-1170.
0032.	Roy JK, Prasad M, Varshney RK, Balyan HS, Blake TK, Dhaliwal HS, Singh H, Edwards KJ & Gupta PK 1999 Identification of a microsatellite on chromosomes 6B and a STS on 7D of bread wheat showing an association with preharvest sprouting tolerance. Theoretical and Applied Genetics 99: 336-340.
0033.	Borner A, Roder MS, Unger O & Meinel A 2000 The detection and molecular mapping of a major gene for non specific adult plant disease resistance against stripe rust (*Puccinia striiformis*) in wheat. Theoretical and Applied Genetics 100: 1095-1099.
0034.	Sarma RN, Fish LJ, Gill BS & Snape JW 2000 Physical characterisation of the homoeologous group 5 chromosomes of wheat in terms of rice linkage blocks, and physical mapping of some important genes. Genome 43: 191-198.
0035.	Korzun V, Roder MS, Wendehake K, Pasqualone A, Lotti C, Ganal MW & Blanco A 1999 Integration of dinucleotide microsatellites from hexaploid bread wheat into a genetic linkage map of durum wheat. Theoretical and Applied Genetics 98: 1202-1207.
0036.	Cenci A, D'Ovidio R, Tanzarella OA, Ceoloni C & Porceddu E 1999 Identification of molecular markers linked to Pm13, an *Aegilops longissima* gene conferring resistance to powdery mildew in wheat. Theoretical and Applied Genetics 98: 448-454.
0037.	Somers D 2000 Personal communication.
0038.	Blake TK, Kadyrzhanova D, Shepherd KW, Islam AKMR, Langridge PL, McDonald CL, Erpelding J, Larson S, Blake NK & Talkbert LE 1996 STS-PCR markers appropriate for wheat-barley introgression. Theoretical and Applied Genetics 93: 826-832.
0039.	Roder M 1999 Personal communication.
0040.	Effertz RJ, Anderson JA & Francl LJ 1998 QTLs associated with resistance to chlorosis induction by *Pyrenophora tritici-repentis* in adult wheat. Canadian Journal of Plant Pathology 20: 438-439.
0041.	Li Z, Rahman S, KosarHashemi B, Mouille G, Appels R & Morell MK 1999 Cloning and characterization of a gene encoding wheat starch synthase I. Theoretical and Applied Genetics 98: 1208-1216.
0042.	Li ZY, Chu XS, Mouille G, Yan LL, KosarHashemi B, Hey S, Napier J, Shewry P, Clarke B, Appels R, Morell MK & Rahman S 1999 The localization and expression of the class II starch synthases of wheat. Plant Physiology 120: 1147-1155.
0043.	Devos KM 2000 Personal communication.

0044.	Robert O, Abelard C & Dedryver F 1999 Identification of molecular markers for the detection of the yellow rust resistance gene *Yr17* in wheat. Molecular Breeding 5: 167-175.
0045.	Seyfarth R, Feuillet C, Schachermayr G, Winzeler M & Keller B 1999 Development of a molecular marker for the adult plant leaf rust resistance gene *Lr35* in wheat. Theoretical and Applied Genetics 99: 554-560.
0046.	Simonetti MC, Bellomo MP, Laghetti G, Perrino P, Simeone R & Blanco A 1999 Quantitative trait loci influencing free-threshing habit in tetraploid wheats. Genetic Resources and Crop Evolution 46: 267-271.
0047.	Araki E, Miura H & Sawada S 1999 Identification of genetic loci affecting amylose content and agronomic traits on chromosome 4A of wheat. Theoretical and Applied Genetics 98: 977-984.
0048.	Lagudah ES 2000 Personal communication.
0050.	Messmer MM, Seyfarth R, Keller M, Schachermayr G, Winzeler M, Zanetti S, Feuillet C & Keller B 2000 Genetic analysis of durable leaf resistance in winter wheat. Theoretical and Applied Genetics 100: 419-431.
0051.	Keller M, Keller B, Schachermayr G, Winzeler M, Schmid JE, Stamp P & Messmer MM 1999 Quantitative trait loci for resistance against powdery mildew in a segregating wheat x spelt population. Theoretical and Applied Genetics 98: 903-912.
0052.	Keller M, Karutz C, Schmid JE, Stamp P, Winzeler M, Keller B & Messmer MM 1999 Quantitative trait loci for lodging resistance in a segregating wheat x spelt population. Theoretical and Applied Genetics 98: 1171-1182.
0053.	Shimosaka E, Sasanuma T & Handa H 1999 A wheat cold-regulated cDNA encoding an early light-inducible protein (ELIP): Its structure, expression and chromosomal location. Plant Cell Physiology 40: 319-325.
0054.	GH, Wilen RW, Robertson AJ & Gusta LV 1999 Isolation, chromosomal localization, and differential expression of mitochondrial manganese superoxide dismutase and chloroplastic copper zinc superoxide dismutase genes in wheat. Plant Physiology 120: 513-520.
0055.	Biagetti M, Vitelozzi F & Ceoloni C 1999 Physical mapping of wheat - *Aegilops longissima* breakpoints in mildew-resistant recombinant lines using FISH with highly repeated and low copy DNA probes. Genome 42: 1013-1019.
0056.	Maystrenko OI, Laikova LI, Arbuzova VS & Melnik VM 1998 The chromosome location of the *S1*, *S2* and *S3* genes of induced sphaerococoid mutations in common wheat. EWAC Newsletter 127-130.
0057.	Law CN 1996 The genetic control of daylength response in wheat. *In* Manipulation of Flowering (Atheston JG ed.) Butterworth, London pp. 225-240.
0058.	Worland AJ 1996 The influence of flowering time genes on environmental adaptability in European wheats. Euphytica 89: 49-57.
0059.	Ma ZQ, Roder M & Sorrells ME 1996 Frequencies and sequence characteristics of di-, tri-, and tetra- nucleotide microsatellites in wheat. Genome 39: 123-130.
0060.	Anonymous 2000 GrainGenesdatabase (http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=graingenes).
0061.	Rebmann G, Mauch F & Dudler R 1991 Sequence of a wheat cDNA encoding a pathogen-induced thaumatin-like protein. Plant Molecular Biology 17: 282-285.
0062.	Worland AJ, Borner A, Korzun V, Li, WM, Petrovic S & Sayers EJ 1998 The influence of photoperiod genes on the adaptability of European winter wheats. Euphytica 100: 385-394.

0063.	Snape JW, Laurie DA & Worland AJ 1998 Understanding the genetics of abiotic stress responses in cereals and possible strategies for their amelioration. Aspects of Applied Biology 50: 9-14.
0064.	Ciaffi M, Dominici L, Tanzarella OA & Porceddu E 1999 Chromosomal assignment of gene sequences coding for protein disulphideisomerase (PDI) in wheat. Theoretical and Applied Genetics 98: 405-410.
0065.	Deal KR, Goyal S & Dvorak J 1999 Arm location of *Lophopyrum elongatum* genes affecting K^+/Na^+ selectivity under salt stress. Euphytica 108: 193-198.
0066.	Arbuzova VS, Maystrenko OI & Popovic OM 1998 Development of near isogenic lines of the common wheat cultivar 'Saratovskaya 29' Cereal Research Communications 26: 39-46.
0067.	Kato K, Miura H & Sawada S 1999 Comparative mapping of the wheat *Vrn-A1* region with the rice *Hd-6* region. Genome 42: 204-209.
0068.	Kato K, Miura H & Sawada S 1999 QTL mapping of genes controlling ear emergence time and plant height on chromosome 5A of wheat. Theoretical and Applied Genetics 98: 472-477.
0069.	Liu DJ, Liu JY, Toa WJ & Chen PD 1998 Molecular markers and breeding wheat for powdery mildew resistance. Proceedings 9th International Wheat Genetics Symposium, Volume 3 (Slinkard AE ed). University of Saskatchewan Extension Press pp. 128-131.
0070.	Sourdille P, Robe P, Tixier MH, Doussinault G, Pavoine MT & Bernard M 1999 Location of *Pm3g*, a powdery mildew resistance allele in wheat, by using a monosomic analysis and by identifying associated molecular markers. Euphytica 110: 193-198.
0071.	Mesfin A, Frohberg RC & Anderson JA 1999 RFLP markers associated with high grain protein from *Triticum turgidum* L. var. *dicoccoides* introgressed into hard red spring wheat. Crop Science 39: 508-513.
0072.	Mrva K & Mares DJ 1999 Regulation of high pI alpha-amylase synthesis in wheat aleurone by a gene(s) located on chromosome 6B. Euphytica 109: 17-23.
0073.	Murai J, Taira T & Ohta D 1999 Isolation and characterization of the three Waxy genes encoding the granule-bound starch synthase in hexaploid wheat. Gene 234: 71-79.
0074.	Udall JA, Souza E, Anderson J, Sorrells ME & Zemetra RS 1999 Quantitative trait loci for flour viscosity in winter wheat. Crop Science 39: 238-242.
0075.	Vrinten P, Nakamura T & Yamamori M 1999 Molecular characterization of waxy mutations in wheat. Molecular and General Genetics 261: 463-471.
0076.	Shan X, Blake TK & Talbert LE 1999 Conversion of AFLP markers to sequence-specific PCR markers in barley and wheat. Theoretical and Applied Genetics 98: 1072-1078.
0077.	Shariflou MR & Sharp PJ 1999 A polymorphic microsatellite in the 3' end of 'waxy' genes of wheat, *Triticum aestivum*. Plant Breeding 118: 275-277. SAME AS 0116
0078.	Waldron BL, Moreno-Sevilla B, Anderson JA, Stack RW & Frohberg RC 1999 RFLP mapping of QTL for fusarium head blight resistance in wheat. Crop Science 39: 805-811.
0079.	Kato K, Miura H, Akiyama M, Kuroshima M & Sawada S 1999 RFLP mapping of the three major genes, *Vrn1*, *Q* and *B1*, on the long arm of chromosome 5A of wheat. Euphytica 101: 91-95.
0080.	Dubcovsky J 2000 Personal communication.
0081.	Weng, Y, Tuleen NA & Hart G 2000 Extended physical maps and a consensus physical map of the homoeologous group-6 chromosomes of wheat (*Triticum aestivum* L. em Thell.) Theoretical and Applied Genetics 100: 519-527.

0082.	Lillemo M & Morris CF 2000 A leucine to proline mutation in puorindoline b is frequently present in hard wheats from Northern Europe. Theoretical and Applied Genetics 100: 1100-1107.
0083.	Tranquilli G, Lijavetzky D, Muzzi G & Dubcovsky J 1999 Genetic and physical characterization of grain texture-related loci in diploid wheat. Molecular and General Genetics 262: 846-850.
0084.	Lukaszewski AJ 2000 Manipulation of the 1RS. 1BL translocation in wheat by induced homoeologous recombination. Crop Science 40: 216-225.
0085.	Saini RG, Kaur M, Singh B, Sharma Shiwani, Nanda GS, Nayar SK, Gupta AK & Nagarajan S. 2002 Genes *Lr48* and *Lr49* for hypersensitive adult plant leaf rust resistance in wheat (*Triticum aestivum*) Euphytica 124: 365-370.
0086.	Bryan GJ, Stephenson P, Collins A, Kirby J, Smith JB & Gale MD 1999 Low levels of DNA sequence variation among adapted genotypes of hexaploid wheat. Theoretical and Applied Genetics 99: 192-198.
0087.	Adlam RE & Flintham JE 1999 Rapid identification of chromosome-specific sequence-tagged-sites in hexaploid wheat, using selective PCR from nullisomic-tetrasomic lines. Cereal Research Communications 27: 1-2.
0088.	Seyfarth S, Feuillet C & Keller B 1998 Development and characterization of molecular markers for the adult plant leaf rust resistance genes *Lr13* and *Lr35* in wheat. Proceedings 9th International Wheat Genetics Symposium (Slinkard AE ed). University of Saskatchewan, Extensien Press Vol 3: pp 154-155.
0089.	Khan IA 2000 Molecular and agronomic characterization of wheat-*Agropyron intermedium* recombinant chromosomes. Plant Breeding 119: 25-29.
0090.	Faris JD, Li WL, Liu DJ, Chen PD & Gill BS 1999 Candidate gene analysis of quantitative disease resistance in wheat. Theoretical and Applied Genetics 98: 219-225.
0091.	Li WL, Faris JD, Chittoor JM, Leach JE, Hulbert S, Liu DJ, Chen PD & Gill BS 1999 Genomic scanning of defence response genes in wheat. Theoretical and Applied Genetics 98: 226-233.
0092.	Collinge D 2000 Personal communication.
0093.	White F 2000 Personal communication.
0094.	Musket T 2000 Personal communication.
0095.	Hulbert S 2000 Personal communication.
0096.	Muthukrishnan S 2000 Personal communication.
0097.	Morris SW, Vernooij B, Titatam S, Starrett M, Thomas S, Wiltse CC, Frederiksen RA, Bhandhufalck A, Hulbert S & Uknes S 1998 Induced resistance responses in maize. Molecular Plant-Microbe Interactions 11: 643-658.
0098.	Christensen AB, Gregerson PL, Schroder J & Collinge DB 1998 A chalcone synthase with an unusual substrate preference is expressed in barley leaves in response to UV light and pathogen attack. Plant Molecular Biology 37: 849-857.
0099.	Christensen AB, Gregersen PL, Olsen CE & Collinge DB 1998 A flavonoid 7-O-methyltransferase is expressed in barley leaves in response to pathogen attack. Plant Molecular Biology 36: 219-227.
00100.	Gregersen PL, Thordal-Christensen H, Forster H & Collinge DB 1997 Differential gene transcript accumulation in barley leaf epidermis and mesophyll in response to attack by *Blumeria graminis* f. sp. *hordei* (syn. *Erysiphe graminis* f. sp. *hordei*). Molecular Plant Pathology 51: 85-97.

00101.	Brandt J, Thordal-Christensen H, Vad K, Gregersen PL & Collinge DB 1992 A pathogen-induced gene of barley encodes a protein showing high similarity to a protein kinase regulator. Plant Journal 2: 815-820.
00102.	Zhou F, Zhang Z, Gregersen PL, Mikkelsen JD, de Neergaard E, Collinge DB & Thordal-Christensen H 1998 Molecular characterization of the oxalate oxidase involved in the response of barley to the powdery mildew fungus. Plant Physiology 117: 33-41.
00103.	Wei Y, Zhang Z, Andersen CH, Schmelzer E, Gregersen PL, Collinge DB, Smedegaard-Petersen & Thordal-Christensen H 1998 An epidermis/papilla-specific oxalate oxidase-like protein in the defense response of barley attacked by the powdery mildew fungus. Plant Molecular Biology 36: 101-112.
00104.	Bryngelsson T, Sommer-Knudsen J, Gregersen PL, Collinge DB, Ek B & Thordal-Christensen H 1994 Purification, characterization, and molecular cloning of basic PR-1-type pathogenesis-related proteins from barley. Molecular Plant-Microbe Interactions 7: 267-275.
00105.	Allaby RG, Banerjee M & Brown TA 1999 Evolution of the high molecular weight glutenin loci of the A, B, D, and G genomes of wheat. Genome 42: 296-307.
00106.	Lee Y-K, Bekes F, Gupta R, Appels R & Morell MK 1999 The low-molecular-weight glutenin subunit proteins of primitive wheats. I. Variation in A-genome species. Theoretical and Applied Genetics 98: 119-125.
00107.	Lee Y-K, Ciaffi M, Appels R & Morell MK 1999 The low-molecular-weight glutenin subunit proteins of primitive wheats. II. The genes from A-genome species. Theoretical and Applied Genetics 98: 126-134.
00108.	Ciaffi M, Lee Y-K, Tamas L, Gupta R, Skerritt J & Appels R 1999 The low-molecular-weight glutenin subunit proteins of primitive wheats. III. The genes from D-genome species. Theoretical and Applied Genetics 98: 135-148.
00109.	Lee Y-K, Bekes F, Gras P, Ciaffi M, Morell MK & Appels R 1999 The low-molecular-weight glutenin subunit proteins of primitive wheats. IV. Functional properties of products from individual genes. Theoretical and Applied Genetics 98: 149-155.
00110.	Corbellini M, Empilli S, Vaccino P, Brandolini A, Borghi B, Heun M & Salamini F 1999 Einkorn characterization for bread and cookie production in relation to protein subunit composition. Cereal Chemistry 76: 727-733.
00111.	Igrejas G, Guedes-Pinto H, Carnide V & Branlard G 1999 The high and low molecular weight glutenin subunits and omega-gliadin composition of bread and durum wheats commonly grown in Portugal. Plant Breeding 118: 297-302.
00112.	Khelifi D, Branlard G & Bourgoin-Greneche M 1992 Diversity of some D zone omega gliadins of bread wheat as revealed by 2-step A-PAGE/SDS-PAGE technique. Journal of Genetics and Breeding 46: 351-358.
00113.	Jackson EA, Morel M-H, Sontag-Strohm T, Branlard G, Metakovsky EV & Redaelli R 1996 Proposal for combining the classification systems of alleles of *Gli-1* and *Glu-3* loci in bread wheat (*Triticum aestivum* L.). Journal of Genetics and Breeding 50: 321-336.
00114.	Nieto-Taladriz MT, Ruiz M, Martinez MC, Vazquez JF & Carrillo JM 1997 Variation and classification of B low-molecular-weight glutenin subunit alleles in durum wheat. Theoretical and Applied Genetics 95: 1155-1160.
00115.	Piergiovanni AR & Blanco A 1999 Variation of HMW glutenin and gamma-gliadin subunits in selected accessions of *Triticum dicoccon* (Schrank) and *T. spelta* (L.). Cereal Research Communications 27: 205-211.

00116.	Radic-Miehle H, Saam C, Huls R, Kling ChI & Hesemann CU 1998 Characterization of spelt (*Triticum spelta* L.) forms by gel-electrophoretic analyses of seed storage proteins. III. Comparative analyses of spelt and Central European winter wheat (*Triticum aestivum* L.) cultivars by SDS-PAGE and acid-PAGE. Theoretical and Applied Genetics 97: 1340-1346.
00117.	Radic H, Gunther T, Kling CI & Hesemann CU 1997 Characterisation of spelt (*Triticum spelta* L.) forms by gel electrophoretical analyses of seed storage proteins. II. The glutenins. Theoretical and Applied Genetics 94: 882-886.
00118.	Harsch S, Gunther T, Kling CI, Rozynek B & Hesemann CU 1997 Characterisation of spelt (*Triticum spelta* L.) forms by gel electrophoretical analyses of seed storage proteins. I. The gliadins. Theoretical and Applied Genetics 94: 52-60.
00119.	Metakovsky EV, Wrigley CW, Bekes F & Gupta RB 1990 Gluten polypeptides as useful genetic markers of dough quality in Australian wheats. Australian Journal of Agricultural Research 41: 289-306.
00120.	Dubcovsky J 2000 Personal communication.
0101.	Prins R & Marais GF 1998 An extended deletion map of the *Lr19* translocation and modified forms. Euphytica 103: 95-102.
0102.	Bartos P, Stuchlikova E & Hanusova R 1996 Adaptation of wheat rusts to the wheat cultivars in former Czeckoslovakia. Euphytica 92: 95-103.
0103.	Barloy D, Lemoine J, Dredryver F & Jahier J 2000 Molecular markers linked to the *Aegilops variabilis*- derived root knot nematode resistance gene *Rkn-mn1* in wheat. Plant Breeding 118: 169-172.
0104.	Delibes A 2000 Personal communication.
0105.	Romero MD, Montes MJ, Sin E, Lopez-Brana I, Duce I, Martin-Sanchez JA, Andres MF & Delibes A 1988 A cereal cyst nematode (*Heterodera avenae* Woll.) resistance gene transferred from *Aegilops triuncialis* to hexaploid wheat. Theoretical and Applied Genetics 96: 1135-1140.
0107.	Jahier J, Abelard P, Tonguy AM, Dedryver F, Rivoal R, Khatkar R & Bariana HS 2001 The *Aegilops ventricosa* segment on chromosome 2AS of the wheat cultivar 'VPM1' carries the cereal cyst nematode gene *Cre5*. Plant Breeding 120: 125-128.
0108.	Peng JH, Fahima T, Roder MS, LI YC, Grama A & Nevo E 2000 Microsatellite high-density mapping of the stripe rust resistance gene *YrH52* region on chromosome 1B and evaluation of its marker-assisted selection in the F2 generation in wild emmer wheat. New Phytologist 146: 141-154.
0109.	Koval SF 1997 The catolog of near-isogenic lines of Novosibirskaya-67 common wheat and principles of their use in experiments. Russian Journal of Genetics 33: 995-1000.
0110.	Chague V, Fahima T, Dahan A, Sun GL, Korol AB, Ronin YI, Grama A, Roder MS & Nevo E 1999 Isolation of microsatellite and RAPD markers flanking the *Yr15* gene of wheat using NILs and bulked segregant analysis. Genome 42: 1050-1056.
0111.	Nieto-Taladriz MT & Rodrigues-Quijano M 2000 Polymorphism of waxy proteins in Spanish durum wheats. Plant Breeding 119: 277-279.
0112.	Pukhal'skii VA & Bilinskaya EN 1997 Necrotic genotypes of modern spring varieties of common wheat *Triticum aestivum* L. in Russia, Ukraine, Belarus, and Kazakhstan. Russian Journal of Genetics 33: 1304-1308.
0113.	Pukhalskiy VA, Iordanskaya IV, Badaeva ED, Lapochkina & Bilinskaya EN 1999 Genetic analysis of spike waxlessness in a line of common wheat *Triticum aestivum* L. Russian Journal of Genetics 35: 1050-1054.

0114.	Sourdille P, Tixier MH, Charmet G, Gay G, Cadalen T, Bernard S & Bernard M 2000 Location of genes involved in ear compactness in wheat (*Triticum aestivum*) by means of molecular markers. Molecular Breeding 6: 247-255.
0115.	Camargo CE deO, Neto AT, Ferreira Filho AWP & Felicio JC 2000 Genetic control of aluminium tolerance in mutant lines of wheat cultivar Anahuac. Euphytica 114: 47-53.
0116.	Shariflou MR & Sharp PJ 1999 A polymorphic microsatellite on the 3' end of 'waxy' genes of wheat, *Triticum aestivum*. Plant Breeding 118: 275-277. SAME AS 0077
0117.	Shariflou MR, Hassani ME & Sharp PJ 2001 A PCR-based DNA marker for detection of mutant and normal alleles of the *Wx-D1* gene of wheat. Plant Breeding 120: 121-124.
0118.	Yasui T, Sasaki T & Matsuki J 1998 Waxy bread wheat mutants, K107Wx.1 and K107Wx2, have a new null allele on *Wx-D1* locus. Breeding Science 48: 405-407.
0119.	William M, Singh RP, Huerta-Espino J, Islas SO & Hoisington D 2003 Molecular marker mapping of leaf rust resistance gene *Lr46* and its association with stripe rust resistance gene *Yr29* in wheat. Phytopathology 93: 153-159.
0120.	Singh RP 2000 Personal communication.
0121.	Williams K 2000 Personal communication.
0122.	Thompson J 2000 Personal communication.
0123.	Clark JR, Robertson M, Ainsworth CC 1991 Nucleotide sequence of a wheat (*Triticum aestivum* L.) cDNA encoding the waxy protein. Plant Molecular Biology 16: 1099-1101.
0124.	Sanchez-Monge, Gomez L, Garcia- Olmedo F & Salcedo G. 1989 New dimeric inhibitor of heterologous alpha-amylases encoded by a duplicated gene in the short arm of chromosome 3B of wheat (*Triticum aestivum* L.) European Journal of Biochemistry 183: 37-40.
0125.	Singh J, Appels R, Sharp P & Skerritt J 2001 Albumin polymorphism and mapping of a dimeric alpha-amylase inhibitor in wheat. Australian Journal of Agricultural Research 52: 1173-1179.
0126.	Helguera M, Khan IA & Dubcovsky J 2000 Development of PCR markers for the wheat leaf rust gene *Lr47*. Theoretical and Applied Genetics 101: 625-631.
0127.	Kojima T, Habu Y, Iida S & Ogihara Y 2000 Direct isolation of differentially expressed genes from a specific chromosome region of common wheat: application of the amplified fragment length polymorphism-based in RNA fingerprinting (AMF) method in combination with a deletion line of wheat. Molecular and General Genetics 263: 635-641.
0128.	Laroche A, Demeke T, Gaudet DA, Puchalski B, Frick M & McKenzie R 2000 Development of a PCR marker for rapid identification of the *Bt10* gene for common bunt resistance in wheat. Genome 43: 217-223.
0129.	Zeller FJ, Kong L, Hartl L, Mohler V & Hsam SLK 2002 Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em Thell.) 7. Gene *Pm29* in line Pova. Euphytica 123: 187-194.
0130.	Watanabe N & Ikakata N 2000 The effects of homoeologous group 3 chromosomes on grain colour dependent seed dormancy and brittle rachis in tetraploid wheat. Euphytica 115: 215-220.
0131.	Khan AA, Bergstrom GC, Nelson JC & Sorrells ME 2000 Identification of RFLP markers for resistance to wheat spindle streak mosaic bymovirus (WSSMV) disease. Genome 43: 477-482.
0132.	Sourdille P, Snape JW, Cadalen T, Charmet G, Nakata N, Bernard S & Bernard M 2000 Detection of QTL's for heading time and photoperiod response in wheat using a doubled haploid population. Genome 43: 487-494.

0133.	Taylor C, Shepherd KW & Langridge P 1998 A molecular genetic map of the long arm of chromosome 6R of rye incorporating the cereal cyst nematode gene, *CreR*. Theoretical and Applied Genetics 97: 1000-1012.
0134.	Tixier MH, Sourdille P, Charmet G, Gay C, Cadalen T, Bernard S, Nicholas P & Bernard M 1998 Detection of QTL's for crossability in wheat using a doubled-haploid population. Theoretical and Applied Genetics 97: 1076-1082.
0135.	Spielmeyer W, Moullet O, Laroche A & Lagudah ES 2000 Highly recombinogenic regions at seed storage protein loci on chromosome 1DS of *Aegilops tauschii*, the D-genome donor of wheat. Genetics 155: 361-367.
0136.	Enns H & Konzak CF 1966 Genetically controlled seedcoat variegation in *Triticum aestivum*. Genetics 53: 1091-1099.
0137.	Yamamori M, Fujita S, Hayakawa K & Matsuki J 2000 Genetic elimination of a starch granule protein, SGP-1, of wheat generates an altered starch with apparent high amylose. Theoretical and Applied Genetics 101: 21-29.
0138.	Ogbonnaya FC, Seah S, Delibes A, Jahier J, Lopez-Brana I, Eastwood RF & Lagudah ES. 2001 Molecular-genetic characterization of a new nematode resistance gene in wheat. Theoretical and Applied Genetics 102: 623-629.
0139.	Tao W, Liu D, Liu J, Feng Y & Chen P 2000 Genetic mapping of the powdery mildew resistance gene *Pm6* in wheat by RFLP analysis. Theoretical and Applied Genetics 100: 564-568.
0140.	Luo MC, Yang ZL & Dvorak J 2000 The Q locus of Iranian and European spelt wheat. Theoretical and Applied Genetics 100: 602-606.
0141.	Perretant MR, Cadalen T, Charmet G, Sourdille P, Nicolas P, Boeuf C, Tixier MH, Branlard G, Bernard S & Bernard M 2000 QTL analysis of bread-making quality in wheat using a doubled haploid population. Theoretical and Applied Genetics 100: 1167-1175.
0142.	Chantret N, Sourdille P, Roder M, Tavaud M, Bernard M & Doussinault G 2000 Location and mapping of the powdery mildew resistance gene *MlRE* and detection of a resistance QTL by bulked segregant analysis (BSA) with microsatellites in wheat. Theoretical and Applied Genetics 100: 1217-1224.
0144.	Marcoz-Ragot C, Gateau I, Koenig J, Delaire V & Branlard G 2000 Allelic variants of granule-bound starch synthase proteins in European bread wheat varieties. Plant Breeding 119: 305-309.
0145.	Ahmad M 2000 Molecular marker-assisted selection of HMW glutenin alleles related to wheat bread quality by PCR-generated DNA markers. Theoretical and Applied Genetics 101: 892-896.
0146.	Chantret N, Sourdille P, Roder M, Tavaud M, Bernard M & Doussinault G 2000 Location and mapping of the powdery mildew resistance gene MlRE and detection of a resistance QTL by bulked segregant analysis (BSA) with microsatellites in wheat. Theoretical and Applied Genetics 100: 1217-1224.
0147.	De Bustos A, Rubio P & Jouve N 2000 Molecular characterisation of the inactive allele of the gene *Glu-A1* and the development of a set of AS-PCR markers for HMW glutenins of wheat. Theoretical and Applied Genetics 100: 1085-1094.
0148.	Faris JD, Haen KM & Gill BS 2000 Saturation mapping of a gene-rich recombination hot spot region in wheat. Genetics 154: 823-835.
0149.	Galili S, Avivi Y, Millet E & Feldman M 2000 RFLP-based analysis of three RbcS subfamilies in diploid and polyploid species of wheat. Molecular and General Genetics 263: 674-680.

0150.	Huang XQ, Hsam SLK, Zeller FJ, Wenzel G & Mohler V 2000 Molecular mapping of the wheat powdery mildew resistance gene *Pm24* and marker validation for molecular breeding. Theoretical and Applied Genetics 101: 407-414.
0151.	
0152.	Lotti C, Salvi S, Pasqualone A, Tuberosa R & Blanco A 2000 Integration of AFLP markers into an RFLP-based map of durum wheat. Plant Breeding 119: 393-401.
0153.	Prasad M, Varshney RK, Roy JK, Balyan HS & Gupta PK 2000 The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat. Theoretical and Applied Genetics 100: 584-592.
0154.	Dubcovsky J 2001 Personal communication.
0155.	Flore G 2001 Personal communication.
0156.	Rogers SG 2001 Personal communication.
0157.	Bernard M 2001 Personal communication.
0158.	Benoist P 2001 Personal communication.
0159.	Sharp P 2001 Personal communication.
0160.	Keller B 2001 Personal communication.
0161.	Devaux P 2001 Personal communication.
0162.	Wang RC 2001 Personal communication.
0163.	Liu ZY, Sun QX, Ni ZF, Nevo E & Yang TM 2002 Molecular characterization of a novel powdery mildew resistance gene *Pm30* in wheat originating from wild emmer. Euphytica 123: 21-29.
0164.	Tao W, Liu D, Liu J, Feng Y & Chen P 2000 Genetic mapping of the powdery mildew resistance gene Pm6 in wheat by RFLP analysis. Theoretical and Applied Genetics 100: 564-568.
0165.	Varshney RK, Prasad M, Roy JK, Harjit-Singh NK, Dhaliwal HS, Balyan HS & Gupta PK 2000 Identification of eight chromosomes and a microsatellite marker on 1AS associated with QTL for grain weight in bread wheat. Theoretical and Applied Genetics 100: 1290-1294.
0166.	Weibull P 2001 Personal communication.
0167.	Vrinten PL & Nakamura T 2000 Wheat granule-bound starch synthase I and II are encoded by separate genes that are expressed in different tissues. Plant Physiology 122: 255-263.
0168.	Yan LL, Bhave M, Fairclough R, Konik C, Rahman S & Appels R 2000 The genes encoding granule-bound starch synthases at the waxy loci of the A, B, and D progenitors of common wheat. Genome 43: 264-272.
0169.	Zanetti S, Winzeler M, Keller M, Keller B & Messmer M 2000 Genetic analysis of pre-harvest sprouting resistance in a wheat x spelt cross. Crop Science 40: 1406-1417.
0170.	Peng JH, Fahima T, Roder MS, Li YC, Grama A & Nevo E 2000 Microsatellite high-density mapping of the stripe rust resistance gene YrH52 region on chromosome 1B and evaluation of its marker-assisted selection in the F-2 generation in wild emmer wheat. New Phytologist 146: 141-154.
0171.	Peng J, Korol AB, Fahima T, Roder MS, Ronin YI, Li YC & Nevo E 2000 Molecular genetic maps in wild emmer wheat, *Triticum dicoccoides*: Genome-wide coverage, massive negative interference, and putative quasi-linkage. Genome Research 10: 1509-1531.
0172.	Venter E & Botha A-M 2000 Development of markers linked to *Diuraphis noxia* resistance in wheat using a novel PCR-RFLP approach. Theoretical and Applied Genetics 100: 965-970.

0173.	Pestsova E, Ganal MW & Roder MS 2000 Isolation and mapping of microsatellite markers specific for the D genome of bread wheat. Genome 43: 698-697.
0174.	Ban T & Suenaga K 2000 Genetic analysis of resistance to Fusarium head blight caused by *Fusarium graminearum* in Chinese wheat cultivar Sumai 3 and the Japanese cultivar Saikai 165. Euphytica 113: 87-99.
0175.	Anderson JA, Stack RW, Liu S, Waldron BL, Fjeld AD, Coyne C, Moreno-Sevilla B, Mitchell Fetch J, Song QJ, Cregan PB & Frohberg RC 2001 DNA markers for Fusarium head blight resistance QTLs in two wheat populations. Theoretical and Applied Genetics 102: 1164-1168.
0176.	Dubcovsky J, Tranquilli G, Khan IA, Pfluger LA, Suarez E, Rousset M & Dvorak J 2000 Comparisons of recombination frequencies in hybrids involving telocentric and bibrachial wheat chromosomes. Theoretical and Applied Genetics 100: 308-314.
0177.	Giroux MJ, Talbert L, Habernicht DK, Lanning S, Hemphill A & Martin JM 2000 Association of puroindoline sequence type and grain hardness in hard red spring wheat. Crop Science 40: 370-374.
0178.	Hammer K, Filatenko AA & Korzun V 2000 Microsatellite markers - a new tool for distinguishing diploid wheat species. Genetic Resources and Crop Evolution 47: 497-505.
0179.	Khan IA, Procunier JD, Humphreys DG, Tranquilli G, Schlatter AR, Marcucci-Poltri S, Frohberg R & Dubcovsky J 2000 Development of PCR-based markers for a high grain protein content gene from *Triticum turgidum* ssp *dicoccoides* transferred to bread wheat. Crop Science 40: 518-524.
0180.	Parker GD & Langridge P 2000 Development of a STS marker linked to a major locus controlling flour colour in wheat (*Triticum aestivum* L.). Molecular Breeding 6: 169-174.
0181.	Chalmers KJ, Rathjen AJ & Langridge P 1999 Mapping loci associated with milling yield in wheat (*Triticum aestivum* L.). Molecular Breeding 5: 561-568.
0182.	Zhang ZY, Xin ZY, Ma YZ, Chen X, Xu QF & Lin ZS 1999 Mapping of a BYV resistance gene from *Thinopyrum intermedium* in wheat background by molecular markers. Science In China Series C-Life Sciences 42: 663. Chinese Academy of Sciences.
0183.	Seah S, Spielmeyer W, Jahier J, Sivasithamparam K & Lagudah ES 2000 Resistance gene analogs within an introgressed chromosomal segment derived from *Triticum ventricosum* that confers resistance to nematode and rust pathogens in wheat. Molecular Plant-Microbe Interactions 13: 334-341.
0184.	Lotti C, Salvi S, Pasquallone A, Tuberosa R & Blanco A Integration of AFLP markers into an RFLP-based map of durum wheat. Plant Breeding 119: 393-401.
0185.	Blanco A, Bellomo MP, Cenci A, de Giovanni R, D'Ovidio R, Iocono E, Laddomada B, Pagnotta MA, Porceddu E, Sciencalepore A, Simeone R & Tanzarella OA 1998 A genetic linkage map of durum wheat. Theoretical and Applied Genetics 97: 721-728.
0186.	Arraiano LS, Worland, Ellerbrook C & Brown JKM 2001 Chromosomal location of a gene for resistance to septoria tritici blotch (*Mycosphaerella graminicola*) in a hexaploid wheat 'Synthetic 6X'. Theoretical and Applied Genetics 103: 758-764.
0187.	Brading PA, Verstaffen ECP, Kema GHJ & Brown JKM 2002 A gene-for-gene relationship between wheat and *Mycosphaerella graminicola*, the septoria tritici blotch pathogen. Phytopathology 92: 439-445.
0188.	McIntosh RA, Devos KM, Dubcovsky J & Rogers J 2001 Catalogue of gene symbols for wheat: 2001 Supplement Annual Wheat Newsletter 47: 333-354.
0189.	Endo TR 1996 Allocation of a gametocidal chromosome of *Aegilops cylindrica* to wheat homoeologous group 2. Genes and Genetic Systems 71: 243-246.

0190.	Endo TR 1990 Gametocidal chromosomes and their induction of chromosome mutations in wheat. Japanese Journal of Genetics 65: 135-162.
0191.	Endo TR & Gill BS 1996 The deletion stocks of common wheat. Journal of Heredity 87: 295-307.
0192.	Endo TR, Yamamoto M & Mukai Y 1994 Structural changes of rye chromosome 1R induced by a gametocidal chromosome. Japanese Journal of Genetics 69: 13-19.
0193.	Shi F & Endo TR 1997 Production of wheat and barley disomic addition lines possessing an *Aegilops cylindrica* gametocidal chromosome. Genes and Genetic Systems 72: 243-248.
0194.	Shi F & Endo TR 1999 Genetic induction of structural changes in barley chromosomes added to common wheat by a gametocidal chromosome derived from *Aegilops cylindrica*. Genes and Genetic Systems 74: 49-54.
0195.	Shi F & Endo TR 2000 Genetic induction of chromosomal rearrangements in barley chromosome 7H added to common wheat. Chromosoma 109: 358-363.
0196.	Ahmed TA, Tsujimoto H & Sasakuma T 2000 QTLs associated with plant height and related characters in hexaploid wheat. Breeding Science 50: 267-273.
0197.	Payne PI, Cornfield KG and Blackman JA 1979 Indentification of a high molecular weight subunit of glutenin whose presence correlates with breadmaking quality in wheat: Analysis of F5 progeny from Chinese Spring x Chinese Spring (Hope 1A). Journal of Cereal Science 6: 103-118.CORRECTED FROM MACGENE 2017
0198.	Payne PI, Nightingale MA, Krattiger AF & Holt LM 1987 The relationship between HMW glutenin subunit composition and the bread-making quality of British-grown wheat varieties. Journal of the Science of Food and Agriculture 40: 51-65.
0199.	Payne PI, Seekings JA, Worland AJ, Jarvis MG & Holt LM 1987 Allelic variation of gluten subunits and gliadins and its effect on bread making quality in wheat: Analysis of F_5 progeny from Chinese Spring x Chinese Spring (Hope 1A). Journal of Cereal Science 6: 103-118.
01100.	Obukhova LV, Maystrenko OI, Generalova GV, Ermakova MF & Popova RK 1997 Composition of high-molecular-weight glutenin subunits in common wheat substitution lines created from cultivars with contrasting bread-making qualities. Russian Journal of Genetics 33: 1005-1009.
01101.	Benmoussa M, Vezina LP, Page M, Yelle S & Laberge S 2000 Genetic polymorphism in low-molecular-weight glutenin genes from *Triticum aestivum*, variety Chinese Spring. Theoretical and Applied Genetics 100: 789-793.
01102.	Wei YM, Zheng YL, Liu DC, Zhou YH & Lan XJ 2000 Genetic diversity of *Gli-1*, *Gli-2* and *Glu-1* alleles in Sichuan wheat landraces. Acta Botanica Sinica 42: 496-501.
01103.	von Buren M, Luthy J & Hubner P 2000 A spelt-specific gamma-gliadin gene: discovery and detection. Theoretical and Applied Genetics 100: 271-279.
01104.	Scheets K, Rafalski JA, Hedgcoth C & Soll DG 1985 Heptapeptide repeat structure of a wheat gamma-gliadin. Plant Science Letters 37: 221-225.
01105.	DuPont FM, Vensel WH, Chan R & Kasarda DD 2000 Characterization of the 1B-type omega-gliadins from *Triticum aestivum* cultivar Butte. Cereal Chemistry 77: 607-614.
0201.	Ayala L, van Ginkel M, Khairallah M, Keller B & Henry M 2001 Expression of *Thinopyrum intermedium*- derived *barley yellow dwarf virus* resistance in elite bread wheat backgrounds. Phytopathology 91: 55-62.
0202.	Kosner J & Pankova K 1999 Impact of homoeologous group 5 chromosomes with different *vrn* loci on leaf size and tillering. Czech Journal of Genetics and Plant Breeding 35: 65-72.

0203.	Morris CF, King GE, Allan RE & Simeone MC 2001 Identification and characterization of near-isogenic hard and soft hexaploid wheats. Crop Science 41: 211-217.
0204.	Morris CF, Lillemo M, Simeone MC, Giroux MJ, Babb SL & Kidwell KK 2001 Prevalence of puroindoline grain hardness genotypes among historically significant North American spring and winter wheats. Crop Science 41: 218-228.
0205.	Lillemo M & Morris CF 2000 A leucine to proline mutation in puroindoline b is frequently present in hard wheats from Northern Europe. Theoretical and Applied Genetics 100: 1100-1107.
0206.	Martin JM, Frohberg RC, Morris CF, Talbert LE & Giroux MJ 2001 Milling and bread baking traits associated with puroindoline sequence type in hard red spring wheat. Crop Science 41: 228-234.
0207.	Krishnamurthy K & Giroux MJ 2001 Expression of wheat puroindolime genes in transgenic rice enhances grain softness Nature Biotechnology 19: 162-166.
0208.	Knox RE & Howes NK 1994 A monoclonal antibody chromosome marker analysis used to locate a loose smut resistance gene in wheat chromosome 6A. Theoretical and Applied Genetics 89: 787-793.
0209.	Quick JS, Ellis GE, Normann RM, Stramberger JA, Shanahan JF, Peairs FB, Rudolph JB & Lorenz K 1996 Registration of 'Halt' wheat. Crop Science 36: 210.
0210.	Toit F du 1989 Inheritance of resistance in two *Triticum aestivum* lines to Russian wheat aphid (Homoptera: Aphidae). Journal of Economic Entomology 82: 1251-1253.
0211.	Liu XM, Smith CM, Gill BS & Tolmay V 2001 Microsatellite markers linked to six Russian wheat aphid resistance genes in wheat. Theoretical and Applied Genetics 102: 504-510.
0212.	Cao W, Hughes GR, Ma H & Dong Z 2001 Identification of molecular markers for resistance to *Septoria nodorum* blotch in durum wheat. Theoretical and Applied Genetics 102: 551-554.
0213.	Seah S, Bariana H, Jahier J, Sivasithamparum K & Lagudah ES 2001 The introgressed segment carrying rust resistance genes *Yr17, Lr37* and *Sr38* in wheat can be assayed by a cloned disease resistance gene-like sequence. Theoretical and Applied Genetics 102: 600-605.
0214.	Gill KS & Gill BS 1996 A PCR-based screening assay of *Ph1*, the chromosome pairing regulator gene of wheat. Crop Science 36: 719-722.
0215.	Dudnikov AJ, Gorel FL & Berdnikov VA 2002 Chromosomal location of histone H1 genes in common wheat. Cereal Research Communications 30: 55-61.
0216.	Nasuda S, Liu Y, Sakamoto A, Nakayama T, Iwabuchi M & Tsunewaki K 1993 Chromosomal locations of the genes for histones and a histone-binding protein family HBP-1 in common wheat. Plant Molecular Biology 22: 603-614.
0217.	Segal G, Liu B, Vega JM, Abbo S, Rodova M & Feldman M 1997 Identification of a chromosome-specific probe that maps within the *Ph1* deletions in common and durum wheat. Theoretical and Applied Genetics 94: 968-970.
0218.	McKenzie RIH, Lamb RJ, Aung T, Wise IL, Barker P & Olfert OO. 2002 Inheritance of resistance to wheat midge, *Sitodiplosis mosellana*, in spring wheat. Plant Breeding 121: 383-388.
0219.	Roberts MA, Reader SM, Dalgliesh C, Miller TE, Foote TN, Fish LJ, Snape JW & Moore G 1999 Induction and characterization of *ph1* wheat mutants. Genetics 153: 1909-1918.

0220.	Williams KJ, Lewis JG, Bogacki P, Pallotta MA, Willsmore KL, Kuchel H & Wallwork H. 2003 Mapping of a QTL contributing to cereal cyst nematode tolerance and resistance in wheat. Australian Journal of Agricultural Research 54: 731-737.
0221.	Brown-Guerdira GL, Singh S & Fritz AK. 2003 Performance and mapping of leaf rust resistance to wheat from *Triticum timopheevii* subsp. *ameniacum*. Phytopathology 93: 784-789.
0222.	Malik R, Brown-Guerdira GL, Smith CM, Harvey TL & Gill BS. 2003 Genetic mapping of wheat curl mite resistance genes *Cmc3* and *Cmc4* in common wheat. Crop Science 43: 644-650.
0223.	Thomas J, Riedel E & Penner G 2002 An efficient method for assigning traits to chromosomes. Euphytica 119: 217-221.
0225.	Ayala L, Henry M, Gonzalez-de-Leon D, Van Ginkel M, Mujeeb-Kazi A, Keller B & Khairallah M 2001 A diagnostic molecular marker allowing the study of *Th. intermedium*-derived resistance to BYDV in bread wheat segregating populations. Theoretical and Applied Genetics 102: 942-949.
0226.	Kato K, Nakamura W, Tabiki T & Miura H 2001 Detection of loci controlling seed dormancy on group 4 chromosomes of wheat and comparative mapping with rice and barley genomes. Theoretical and Applied Genetics 291: 980-985.
0227.	Aghaee-Sarbarzeh M, Harjit-Singh & Dhaliwal HS 2001 A microsatellite marker linked to leaf rust resistance transferred from *Aegilops triuncalis* into hexaploid wheat. Plant Breeding 120: 259-261.
0228.	Kolmer JA 2001 Physiologic specialization of *Puccinia triticina* in Canada in 1998. Plant Disease 85: 155-158.
0229.	Park RF, Goyeau H, Felsenstein FG, Bartos P & Zeller FJ 2001 Regional phenotypic diversity of *Puccinia triticina* and wheat host resistance in western Europe, 1995. Euphytica 122: 113-127.
0230.	Yang TZ, Zhang XK, Liu HW & Wang ZH 1998 Chromosomal arm location of a dominant dwarfing gene *Rht21* in XN004 of common wheat. Proceedings of the 8th International Wheat Genetics Symposium, Beijing, 1993 (Li ZS & Xin Zy eds) 839-842.
0 231.	Borner A & Worland AJ 2002 Does the Chinese dwarf wheat variety 'XN004' carry *Rht21*? Cereal Research Communications 30: 25-29.
0232.	Marais GF, Marais AS & Groenewald JZ 2000 Evaluation and reduction of *Lr19*-149, a recombined form of the *Lr19* translocation of wheat. Euphytica 121: 289-295.
0233.	Seo YW, Jang CS & Johnson JW 2001 Development of AFLP and STS markers for identifying wheat-rye translocations possessing 2RL. Euphytica 121: 279-287.
0234.	Yanagasawa T, Kiribuchi-Otobe C & Yoshida H 2001 An alanine to threonine change in the *Wx-D1* protein reduces GBSS I activity in a waxy wheat mutant. Euphytica 121: 209-214.
0235.	Csocz M, Bartos P & Mesterhazy A 2001 Identification of stem rust resistance gene *Sr36* in the wheat cultivar GK Kincso and its derivatives. Cereal Research Communications 29: 267-273.
0236.	Ammiraju JSS, Dholakia BB, Santra DK, Singh H, Lagu MD, Tamhankar SA, Dhaliwal HS, Rao VS, Gupta VS & Ranjekar PK 2001 Identification of inter simple sequence repeat (ISSR) markers associated with seed size in wheat. Theoretical and Applied Genetics 102: 726-732.
0237.	Ammiraju JSS, Dholakia BB, Jawdekar G, Santra DK, Gupta VS, Roder MS, Singh H, Lagu MD, Dhaliwal HS, Rao VS & Ranjekar PK 2002 Inheritance and identification of

	DNA markers associated with yellow berry tolerance in wheat (*Triticum aestivum* L.). Euphytica 123: 229-233.
0238.	Harker N, Rampling LR, Shariflou MR, Hayden MJ, Holton TA, Morell MK, Sharp PJ, Henry RJ & Edwards KJ 2001 Microsatellites as markers for Australian wheat improvement. Australian Journal of Agricultural Research 52: 1121-1130.
0239.	Cregan P 2002 Personal communication.
0240.	Buerstmayr H, Lemmens M, Hartl L, Doldi L, Steiner B, Stierschneider M & Ruckenbauer P 2002 Molecular mapping of QTLs for Fusarium head blight resistance in spring wheat. I. Resistance to fungal spread (Type II resistance). Theoretical and Applied Genetics 104: 84-91.
0241.	Campbell KG, Finney PL, Bergman CJ, Gualberto DG, Anderson JA, Giroux MJ, Siritunga D, Zhu JQ, Gendre F, Roue C, Verel A & Sorrells ME 2001 Quantitative trait loci associated with milling and baking quality in a soft x hard wheat cross. Crop Science 41: 1275-1285.
0242.	Chalmers KJ, Campbell AW, Kretschmer J, Karakousis A, Henschke PH, Pierens S, Harker N, Pallotta M, Cornish GB, Shariflou MR, Rampling LR, McLauchlan A, Daggard G, Sharp PJ, Holton TA, Sutherland MW, Appels R & Langridge P 2001 Construction of three linkage maps in bread wheat, *Triticum aestivum*. Australian Journal of Agricultural Research 52: 1089-1119.
0243.	Chebotar SV, Korzun VN & Sivolap YM 2001 Allele distribution at locus WMS261 marking the dwarfing gene *Rht8* in common wheat cultivars of southern Ukraine. Russian Journal of Genetics 37: 894-898.
0244.	Chee PW, Elias EM, Anderson JA & Kianian SF 2001 Evaluation of a high grain protein QTL from *Triticum turgidum* L. var. *dicoccoides* in an adapted durum wheat background. Crop Science 41: 295-301.
0245.	Cloutier S, Rampitsch C, Penner GA & Lukow OM 2001 Cloning and expression of a LMW-i glutenin gene. Journal of Cereal Science 33: 143-154.
0246.	Galiba G, Kerepesi I, Vagujfalvi A, Kocsy G, Cattivelli L, Dubcovsky J, Snape JW & Sutka J 2001 Mapping of genes involved in glutathione, carbohydrate and COR14b cold induced protein accumulation during cold hardening in wheat. Euphytica 119: 173-177.
0247.	Gill KS & Sandhu D 2001 Candidate-gene cloning and targeted marker enrichment of wheat chromosomal regions using RNA fingerprinting - differential display. Genome 44: 633-639.
0248.	Rodriguez Milla MA & Gustafson JP 2001 Genetic and physical characterization of chromosome 4DL in wheat. Genome 44: 883-892.
0249.	Corona V, Gazza L, Boggini G & Pogna NE 2001 Variation in friabilin composition as determined by A-PAGE fractionation and PCR amplification, and its relationship to grain hardness in bread wheat. Journal of Cereal Science 34: 243-250.
0250.	Khlestkina EK, Pestsova EG, Roder MS & Borner A 2002 Molecular mapping, phenotypic expression and geographical distribution of genes determining anthocyanin pigmentation of coleoptiles in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 104: 632-737.
0251.	Rousset M, Brabant P, Kota RS, Dubcovsky J & Dvorak J 2001 Use of recombinant substitution lines for gene mapping and QTL analysis of bread making quality in wheat. Euphytica 119: 81-87.

0252.	Sandhu D, Champoux JA, Bondareva SN & Gill KS 2001 Identification and physical localization of useful genes and markers to a major gene-rich region on wheat group 1S chromosomes. Genetics 157: 1735-1747.
0253.	Torp AM, Hansen AL & Andersen SB 2001 Chromosomal regions associated with green plant regeneration in wheat (*Triticum aestivum* L.) anther culture. Euphytica 119: 377-387.
0254.	Wang H-J, Huang XQ, Roder MS & Borner A 2002 Genetic mapping of loci determining long glumes in the genus *Triticum*. Euphytica 123: 287-293.
0255.	Borner A, Schumann E, Furste A, Coster H, Leithold B, Roder MS & Weber WE 2001 Mapping of quantitative trait loci determining agronomic important characters in hexaploid wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 105: 921-936.
0256.	Martin-Sanchez JA, Gomez-Colmenarejo M, Del Morel J, Sin E, Montes MJ, Gonzalez-Belinchon C, Lopez-Brana I & Delibes A. 2003 A new Hessian fly resistance gene (H30) transferred from wild grass *Aegilops triuncialis* to hexaploid wheat. Theoretical and Applied Genetics 106: 1248-1255.
0257.	Hsam SLK, Huang XQ & Zeller 2001 Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em. Thell.) *6*. Alleles at the *Pm5* locus. Theoretical and Applied Genetics 102: 127-133.
0258.	Huang XQ, Wang LX, Xu MX & Roder MS. 2003 Microsatellite mapping of the wheat powdery mildew resistance gene *Pm5e* in common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 106: 858-865.
0259.	Huang XQ, Hsam SLK & Zeller FJ 2000 Chromosomal location of two novel genes for resistance to powdery mildew in Chinese landraces (*Triticum aestivum* L. em. Thell.). Journal of Genetics and Breeding 54: 311-317.
0260.	Singh D, Park RF & McIntosh RA 2001 Postulation of leaf (brown) rust resistance genes in 70 wheat cultivars grown in the United Kingdom. Euphytica 120: 205-215.
0261.	Frick MM, Hucl R, Nykiforuk CL, Conner RL, Kuzyk A & Laroche A 1998 Molecular characterisation of a wheat stripe rust resistance gene in Moro wheat. In: Proceedings 9th International Wheat Genetics Symposium, Saskatoon, Canada (Slinkard AE ed.) 3: 181-182.
0262.	Bariana HS, Brown GN, Ahmed NU, Khatkar S, Conner RL, Wellings CR, Haley S, Sharp PJ & Laroche A 2002 Characterisation of *Triticum vavilovii*-derived stripe rust resistance using genetic, cytogenetic and molecular analyses and its marker-assisted selection. Theoretical and Applied Genetics 104: 315-320.
0263.	Ciaffi M, Paolacci AR, Dominici L, Tanzarella OA & Porceddu E 2001 Molecular characterization of gene sequences coding for protein disulphide isomerase (PDI) in durum wheat (*Triticum turgidum* ssp *durum*). Gene 265: 147-156.
0264.	Effertz RJ, Anderson JA & Francl LJ 2001 Restriction fragment length polymorphism mapping of resistance to two races of *Pyrenophora tritici repentis* in adult and seedling wheat. Phytopathology 91: 572-578.
0265.	Faris J, Sirikhachornkit A, Haselkorn R, Gill BS & Gornicki 2001 Chromosome mapping and phylogenetic analysis of the cytosolic acetyl-CoA carboxylase loci in wheat. Molecular Biology & Evolution 18: 1720-1733.
0266.	Li WL, Faris JD, Muthukrishnan S, Liu DJ, Chen PD & Gill BS 2001 Isolation and characterization of novel cDNA clones of acidic chitinases and beta-1,3-glucanases from wheat spikes infected by *Fusarium graminearum*. Theoretical and Applied Genetics 102: 353-362.
0267.	Baenziger PS, Shelton DR, Shipman MJ & Graybosch RA 2001 Breeding for end-use quality: Reflections on the Nebraska experience. Euphytica 119: 95-100.

0268.	Kolmer JA & Liu JQ 2001 Simple inheritance of partial resistance to leaf rust in two wheat cultivars. Plant Pathology 50: 546-551.
0269.	Nachit MM, Elouafi I, Pagnotta MA, El Saleh A, Iacono E, Labhilili M, Asbati A, Azrak M, Hazzam H, Benscher D, Khairallah M, Ribaut JM, Tanzarella OA, Porceddu E & Sorrells ME 2001 Molecular linkage map for an intraspecific recombinant inbred population of durum wheat (*Triticum turgidum* L. var. *durum*). Theoretical and Applied Genetics 102: 177-186.
0270.	Peng JH, Fahima T, Roder MS, Huang QY, Dahan A, Li YC, Grama A & Nevo E 2000 High-density molecular map of chromosome region harboring stripe-rust resistance genes *YrH52* and *Yr15* derived from wild emmer wheat, *Triticum dicoccoides*. Genetica 109: 199-210.
0271.	Sasanuma T 2001 Characterization of the rbcS multigene family in wheat: subfamily classification, determination of chromosomal location and evolutionary analysis. Molecular Genetics & Genomics 265: 161-171.
0272.	Chantret N, Mingeot D, Sourdille P, Bernard M, Jacquemin JM & Doussinault G 2001 A major QTL for powdery mildew resistance is stable over time and at two development stages in winter wheat. Theoretical and Applied Genetics 103: 962-971.
0273.	Prins R, Groenewald JZ, Marais GF, Snape JW & Koebner RMD 2001 AFLP and STS tagging of *Lr19*, a gene conferring resistance to leaf rust in wheat. Theoretical and Applied Genetics 103: 618-624.
0274.	Sutka J 2001 Genes for frost resistance in wheat. Euphytica 119: 167-172.
0275.	Tsujimoto H, Yamada T, Hasegawa K, Usami N, Kojima T, Endo TR, Ogihara Y & Sasakuma T 2001 Large-scale selection of lines with deletions in chromosome 1B in wheat and applications for fine deletion mapping. Genome 44: 501-508.
0276.	Varshney RK, Prasad M, Roy JK, Roder MS, Balyan HS, Gupta PK 2001 Integrated physical maps of 2DL, 6BS and 7DL carrying loci for grain protein content and pre-harvest sprouting tolerance in bread wheat. Cereal Research Communications 29: 33-40.
0277.	Vasu K, Harjit-Singh, Singh S, Chhuneja P & Dhaliwal HS 2001 Microsatellite marker linked to a leaf rust resistance gene from *Triticum monococcum* L. transferred to bread wheat. Journal of Plant Biochemistry & Biotechnology 10: 127-132.
0278.	Yan L & Bhave M 2000 Sequences of the waxy loci of wheat: Utility in analysis of waxy proteins and developing molecular markers. Biochemical Genetics 38: 391-411.
0279.	Yan LL & Bhave M 2001 Characterization of waxy proteins and waxy genes of *Triticum timopheevii* and *T. zhukovskyi* and implications for evolution of wheat. Genome 44: 582-588.
0280.	Zanetti S, Winzeler M, Feuillet C, Keller B & Messmer M 2001 Genetic analysis of bread-making quality in wheat and spelt. Plant Breeding 120: 13-19.
0281.	Snape JW 2002 Personal communication.
0282.	Iwaki K, Nakagawa K & Kato K 2001 The possible candidate for *Vrn-B1* in wheat, as revealed by monosomic analysis of *Vrn* genes carried by Triple Dirk (B), the former *Vrn2*. Wheat Information Service 92: 9-11.
0283.	Kolb FL, Bai GH, Muehlbauer GJ, Anderson JA, Smith KP & Fedak G 2001 Host plant resistance genes for Fusarium head blight: mapping and manipulation with molecular markers. Crop Science 41: 611-619.
0284.	Liu SX, Griffey CA & Saghai-Maroof MA 2001 Identification of molecular markers associated with adult plant resistance to powdery mildew in common wheat cultivar Massey. Crop Science 41: 1268-1275.

0285.	Ma JX, Zhou RG, Dong YS, Wang LF, Wang XM & Jia JZ 2001 Molecular mapping and detection of the yellow rust resistance gene *Yr26* in wheat transferred from *Triticun turgidum* L. using microsatellite markers. Euphytica 120: 219-226.
0286.	Mohle V, Hsam SLK, Zeller FJ & Wenzel G 2001 An STS marker distinguishing the rye-derived powdery mildew resistance alleles at the *Pm8/Pm17* locus of common wheat. Plant Breeding 120: 448-450.
0287.	Boukhatem N, Baret PV, Mingeot D & Jacquemin JM 2002 Quantitative trait loci for resistance against yellow rust in two wheat-derived inbred wheat line populations. Theoretical and Applied Genetics 104: 111-115.
0288.	Singh D, Park RF & McIntosh RA 2001 Inheritance of seedling and adult plant resistance of selected Australian spring and English winter wheat varieties. Plant Breeding 120: 503-507.
0289.	Qi LL & Gill BS 2001 High-density physical maps reveal the dominant gene *Ms3* is located in a genomic region of low recombination in wheat and is not amenable to map-based cloning. Theoretical and Applied Genetics 103: 998-1006.
0290.	Klindworth DL, Williams ND & Maan SS 2002 Chromosomal location of genetic male sterility genes in four mutants of hexaploid wheat (*Triticum aestivum*). Crop Science 42: 1447-1450.
0291.	Snape JW, Semikhodskii A, Fish L, Sarma RN, Quarrie SA, Galiba G & Sutka J 1997 Mapping frost tolerance loci in wheat and comparative mapping with other cereals. Acta Agronomica Hungarica 45: 268-270.
0292.	Sutka J, Galiba G, Vagujfalvi A, Gill BS & Snape JW 1999 Physical mapping of the *Vrn-A1* and *Fr1* genes on chromosome 5A of wheat using deletion lines. Theoretical and Applied Genetics 99: 199-202.
0293.	Maan SS & Kianian SF 2001 Third dominant male sterility gene in common wheat. Wheat Information Service 93: 27-31.
0294.	Feuillet C, Penger A, Gellner K, Mast A & Keller B 2001 Molecular evolution of receptor-like kinase genes in hexaploid wheat. Independent evolution of orthologs after polyploidization and mechanisms of local rearrangements at paralogous loci. Plant Physiology 125: 1304-1313.
0295.	Morris CF 2002 Puroindolines: the molecular genetic basis of wheat grain hardness. Plant Molecular Biology 48: 633-647.
0296.	Feuillet C & Keller B 1999 High gene density is conserved at syntenic loci of small and large grass genomes. Proceedings of the National Academy of Sciences U.S.A. 96: 8265-8270.
0297.	Feuillet C, Reuzeau C, Kjellbom P & Keller B 1998 Molecular characterization of a new type of receptor-like kinase (wlrk) gene family in wheat. Plant Molecular Biology 37: 943-953.
0298.	Morris CF & Allan RE 2001 Registration of hard and soft near-isogenic lines of hexaploid wheat genetic stocks. Crop Science 41: 935-936.
0299.	Huang L & Gill BS 2001 An RGA-like marker detects all known *Lr21* leaf rust resistance gene family members in *Aegilops tauschii* and wheat. Theoretical and Applied Genetics 103: 1007-1013.
02100.	Raupp WJ, Sukhwinder-Singh, Brown-Guerdira GL & Gill BS 2001 Cytogenetic and molecular mapping of the leaf rust resistance gene *Lr39* in wheat. Theoretical and Applied Genetics 102: 347-352.

02101.	Watkins JE, Schimelfenikg J & Baenziger PS 2001 Virulence of *Puccinia triticina* on wheat in Nebraska during 1997 and 1998. Plant Disease 85: 159-164.
02102.	Singh RP, Huerta-Espino J, Rajaram S & Crossa J 2001 Grain yield and other traits of tall and dwarf isolines of modern bread and durum wheats. Euphytica 119: 241-244.
02103.	Worland AJ, Sayers EJ & Korzun V 2001 Allelic variation at the dwarfing gene *Rht8* locus and its significance in international breeding programs. Euphytica 119: 155-159.
02104.	Szunics L, Szunics Lu, Vida G, Bedo Z & Svec M 2001 Dynamics of changes in the races and virulences of wheat powdery mildew in Hungary between 1971 and 1999. Euphytica 119: 143-147.
02105.	Robert O, Dedryver F, Leconte M, Rolland B & de Vallavieille-Pope C 2000 Combination of resistance tests and molecular tests to postulate the yellow rust resistance gene *Yr17* in bread wheat lines. Plant Breeding 119: 467-472.
02106.	Juhasz A, Tamas L, Karsai I, Vida G, Lang L & Bedo Z 2001 Identification, cloning and characterisation of a HMW-glutenin gene from an old Hungarian wheat variety, Bankuti 1201. Euphytica 119: 75-79.
02107.	Buonocore F, Hickman DR, Caporale C, Porceddu E, Lafiandra D, Tatham AS & Shewry PR 1996 Characterisation of a novel high M_r glutenin subunit encoded by chromosome 1D of bread wheat. Journal of Cereal Science 23: 55-60.
02108.	Mackie AM, Lagudah ES, Sharp PJ & Lafiandra D 1996 Molecular and biochemical characterisation of HMW glutenin subunits from *Triticum tauschii* and the D genome of hexaploid wheat. Journal of Cereal Science 2: 213-225.
02109.	Gianibelli MC, Lagudah ES, Wrigley CW & MacRitchie F 2002 Biochemical and genetic characterization of a monomeric storage protein (T1) with an unusually high molecular weight in *Triticum tauschii*. Theoretical and Applied Genetics 104: 497-504.
02110.	Brites C & Carrillo JM 2000 Inheritance of gliadin and glutenin proteins in four durum wheat crosses. Cereal Research Communications 28: 239-246.
02111.	Sreeramulu G & Singh NK 1997 Genetic and biochemical characterization of novel low molecular weight glutenin subunits in wheat (*Triticum aestivum* L.). Genome 40: 41-48.
02112.	Gianibelli MC, Wrigley CW & MacRitchie F 2002 Polymorphism of low M_r glutenin subunits in *Triticum tauschii*. Journal of Cereal Science 35: 277-286.
02113.	Anderson OD, Hsia CC, Adalsteins AE, Lew EJ-L & Kasarda DD 2001 Identification of several new classes of low-molecular-weight wheat gliadin-related proteins and genes. Theoretical and Applied Genetics 103: 307-315.
02114.	Singh NK, Donovan GR & MacRitchie F 1990 Use of sonication and size-exclusion high performance liquid chromatography in the study of wheat flour proteins II. Relative quantity of glutenin as a measure of bread-making quality. Cereal Chemistry 67: 161-170.
02115.	Singh NK, Shepherd KW & Cornish GB 1991 A simplified SDS-PAGE procedure for separating LMW subunits of glutenin. Journal of Cereal Science 14: 203-208.
02116.	Sreeramulu G, Vishnuvardhan D & Singh NK 1994 Seed storage protein profiles of seven Indian wheat varieties (*Triticum aestivum* L.). Journal of Plant Biochemistry and Biotechnology 3: 47-51.
0301.	Xie CJ, Sun Q, Ni Z, Yang T, Nevo E & Fahima T 2003 Chromosomal location of a *Triticum dicoccoides*-derived powdery mildew resistance gene in common wheat by using microsatellite markers. Theoretical and Applied Genetics 106: 341-345.
0302.	Tabayashi N, Tosa Y, Oh HS & Mayama S 2002 A gene-for-gene relationship underlying the species-specific parasitism of *Avena/triticum* isolates of *Magnaporthe grisea* on wheat cultivars. Phytopathology 92: 1182-1188.

0303.	Morris CF & Allen RE 2001 Registration of hard and soft near-isogenic lines of hexaploid wheat genetic stocks. Crop Science 41: 935-936.
0304.	Moris CF & Konzak CF 2001 Registration of hard and soft homozygous waxy wheat germplasm. Crop Science 41: 934-935.
0305.	Iwaki K, Nishida J, Yanagisawa T & Yoshida H 2002 Genetic analysis of Vrn-B1 for vernalization requirement by using linked dCAPS markers in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 104: 571-576.
0306.	Dvorak J 1977 Transfer of leaf rust resistance from *Aegilops speltoides* to *Triticum aestivum*. Canadian Journal of Genetics and Cytology 19: 133-141.
0307.	Dvorak L & Knott DR 1980 Chromosome location of two leaf rust resistance genes transferred from *Triticum speltoides* to *T. aestivum*. Canadian Journal of Genetics and Cytology 22: 381-389.
0308.	Helguera M, Vanzetti L, Soria M, Khan IA, Kolmer J & Dubcovsky J 2005 PCR markers for *Triticum speltoides* leaf rust resistance gene *Lr51* and their use to develop isogenic hard red spring wheat lines. Crop Science 45: 728-734.
0309.	Sourdille P, Cadalen T, Gay G, Gill BS & Bernard M 2002 Molecular and physical mapping of genes affecting awning in wheat. Plant Breeding 121: 320-324.
0310.	McCartney CA, Brule-Babel AL & Lamari L 2002 Inheritance of race-specific resistance to *Mycosphaerella graminicola* in wheat. Phytopathology 92: 138-144.
0311.	McCartney CA, Brule-Babel AL, Lamari L & Somers DL. 2003 Chromosomal location of a race-specific resistance gene to *Mycosphaerella graminicola* in spring wheat ST6. Theoretical and Applied Genetics 107: 1181-1186.
0312.	Shindo C, Sasakuma T, Watanabe N & Noda K 2002 Two-gene systems of vernalization requirement and narrow-sense earliness in einkorn wheat. Genome 45: 563-569.
0313.	Bouget Y, Lemoine J, Pavoine MT, Barloy D & Doussinault G 2002 Identification of a microsatellite marker associated with *Pm3* resistance alleles to powdery mildew in wheat. Plant Breeding 121: 325-329.
0314.	Boshoff WHP, Pretorius ZA & Van Niekerk BD 2002 Establishment, distribution, and pathogenicity of *Puccinia striiformis* f. sp. *tritici* in South Africa. Plant Disease 86: 485-492.
0315.	Effertz RJ, Meinhardt SW, Anderson JA, Jordahl JD & Francl LJ 2002 Identification of a chlorosis-inducing toxin from *Pyrenophora tritici-repentis* and the chromosomal location of an insensitivity locus in wheat. Phytopathology 92: 527-533.
0316.	Taketa S, Chang CL, Ishii M & Takeda K 2002 Chromosome arm location of the gene controlling leaf pubescence of a Chinese local wheat cultivar 'Hong-mang-mai'. Euphytica 125: 141-147.
0317.	Lillemo M & Ringlund K 2002 Impact of puroindoline alleles on the genetic variation for hardness in soft x hard wheat crosses. Plant Breeding 121: 210-217.
0318.	Dundas IS, Frappell DE, Crack DM & Fisher JM 2001 Deletion mapping of a nematode resistance gene on rye chromosome 6R in wheat. Crop Science 41: 1771-1778.
0319.	Weng Y & Lazar MD 2002 Amplified fragment length polymorphism - and simple sequence repeat-based molecular tagging and mapping of greenbug resistance gene *Gb3* in wheat. Plant Breeding 121: 218-223.
320.	Khabaz-Saberi H, Graham RD, Pallotta MA, Rathjen AJ & Williams KJ 2002 Genetic markers for manganese efficiency in durum wheat. Plant Breeding 121: 224-227.

0321.	Wang LF, Ma JX, Zhou RH, Wang XM & Jia JZ 2002 Molecular tagging of the yellow rust resistance gene *Yr10* in common wheat, P.I. 178383 (*Triticum aestivum* L.). Euphytica 124: 71-73.
322.	Singrun CH, Hsam SLK, Hartl L, Zeller FJ & Mohler V 2002 Powdery mildew resistance gene *Pm22* in cultivar Virest is a member of the complex *Pm1* locus in common wheat (*Triticum aestivum* L. em Thell.). Theoretical and Applied Genetics 106: 1420-1424.
0323.	Neu C, Stein N & Keller B 2002 Genetic mapping of the *Lr20-Pm1* resistance locus reveals suppressed recombination on chromosome arm 7AL in hexaploid wheat. Genome 45: 737-744.
0324.	Faris JD & Gill BS 2002 Genomic targeting and high-resolution mapping of the domestication gene Q in wheat. Genome 45: 706-718.
0325.	Singh RP, William HM, Huerta-Espino J & Crosby M. 2003 Identification and mapping of gene *Yr31* for resistance to stripe rust in *Triticum aestivum* cultivar Pastor. Proceedings 10th International Wheat Genetics Symposium, Instituto Sperimentale per la Cerealcoltura, Roma, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.) 1: 411-413.
0326.	Adhikari TB, Anderson JM & Goodwin SB 2003 Identification and molecular mapping of a gene in wheat conferring resistance to *Mycosphaerella graminicola*. Phytopathology 93: 1158-1164.
0327.	Yang J, Sears RG, Gill BS & Paulson GM 2002 Quantitative and molecular characterization of heat tolerance in hexaploid wheat. Euphytica 126: 275-282.
0328.	Zhou WC, Kolb FL, Bai GH, Shaner G & Domier LL 2002 Genetic analysis of scab resistance QTL in wheat with microsatellite and AFLP markers. Genome 45: 719-727.
0329.	Bansal UK, Hayden MJ, Venkata BP, Khanna R, Saini RG & Bariana HS 2008 Genetic mapping of adult plant leaf rust resistance genes *Lr48* and *Lr49* in common wheat. Theoretical and Applied Genetics 117: 307-312.
0330.	Hovmoller MS 2007 Sources of seedling and adult plant resistance to *Puccinia striiformis* f.sp. *tritici* in European wheats. Plant Breeding 126: 225-233.
0331.	Taketa S, Choda M, Ohashi R, Ichii M & Takeda K 2002 Molecular and physical mapping of a barley gene on chromosome 1HL that causes sterility in hybrids with wheat. Genome 45: 617-625.
0332.	Williams CE, Collier CC, Sardesai N, Ohm HW & Cambron SE. 2003 Phenotypic assessment and mapped markers for *H31*, a new wheat gene conferring resistance to Hessian fly (Diptera: Cecidomyiidae). Theoretical and Applied Genetics 107: 1516-1523.
0333.	McIntosh RA, Devos KM, Dubcovsky J. Morris CF & Rogers WJ. 2003 Catalogue of gene symbols for wheat: 2003 Supplement. Annual Wheat Newsletter 49: 246-282.
0334.	Kolmer J 2002 Virulence phenotypes of *Puccinia triticina* in the south Atlantic states in 1999. Plant Disease 86: 288-291.
0335.	Murai K & Tsunewaki K 1995 Photoperiod-sensitive cytoplasmic male sterility induced in Japanese wheat cultivars by transferring *Aegilops crassa* cytoplasm. Breeding Science 45: 199-203.
0336.	Eliot C, Zhou FS, Spielmeyer W, Panstruga R & Schulze-Lefert P 2002 Functional conservation of wheat and rice *Mlo* orthologues in defense modulation to the powdery mildew fungus. Molecular Plant-Microbe Interactions 15: 1069-1077.
0337.	Barrett B, Bayram M & Kidwell K 2002 Identifying AFLP and microsatellite markers for vernalization response gene *Vrn-B1* in hexaploid wheat using reciprocal mapping populations. Plant Breeding 121: 400-406.

0338.	Long DL, Kolmer JA, Leonard KJ & Hughes ME 2002 Physiologic specialization of *Puccinia triticina* in the United States in 2000. Plant Disease 86: 981-986.
0339.	Huang XQ, Hsam SLK & Zeller FJ 2002 Chromosomal location of genes for resistance to powdery mildew in Chinese wheat lines Yieyan 94-1-1 and Siyan 94-2-1. Hereditas 136: 212-218.
0340.	Park RF, Bariana HS, Wellings CR & Wallwork H 2002 Detection and occurrence of a new pathotype of *Puccinia triticina* with virulence for *Lr24* in Australia. Australian Journal of Agricultural Research 53: 1068-1076.
0341.	Ahmad M & Sorrells ME 2002 Distribution of microsatellite alleles linked to *Rht8* dwarfing gene in wheat. Euphytica 123: 235-240.
0342.	Anderson JV & Morris CF 2001 An improved whole-seed assay for screening wheat germplasm for polyphenol oxidase activity. Crop Science 41: 1697-1705.
0343.	Blanco A, Pasqualone A, Troccoli A, Di Fonzo N & Simeone R 2002 Detection of grain protein content QTLs across environments in tetraploid wheats. Plant Molecular Biology 48: 615-623.
0344.	Demeke T, Morris CF, Campbell KG, King GE, Anderson JA & Chang HG 2001 Wheat polyphenol oxidase: Distribution and genetic mapping in three inbred line populations. Crop Science 41: 1750-1757.
0345.	Dong CM, Whitford R & Langridge P 2002 A DNA mismatch repair gene links to the *Ph2* locus in wheat. Genome 45: 116-124.
0347.	Groos C, Gay G, Perretant MR, Gervais L, Bernard M, Dedryver F & Charmet D 2002 Study of the relationship between pre-harvest sprouting and grain color by quantitative trait loci analysis in a white x red grain bread-wheat cross. Theoretical and Applied Genetics 104: 39-47.
0348.	Gupta PK, Balyan HS, Edwards KJ, Isaac P, Korzun V, Roder M, Gautier MF, Joudrier P, Schlatter AR, Dubcovsky J, De la Pena RC, Khairallah M, Penner G, Hayden MJ, Sharp P, Keller B, Wang RCC, Hardouin JP, Jack P & Leroy P 2002 Genetic mapping of 66 new microsatellite (SSR) loci in bread wheat. Theoretical and Applied Genetics 105: 413-422.
0349.	Guyomarc'h H, Sourdille P, Charmet G, Edwards KJ & Bernard M 2002 Characterisation of polymorphic microsatellite markers from *Aegilops tauschii* and transferability to the D-genome of bread wheat. Theoretical and Applied Genetics 104: 1164-1172.
0350.	Ikeda TM, Nagamine T, Fukuoka H & Yano H 2002 Identification of new low-molecular-weight glutenin subunit genes in wheat. Theoretical and Applied Genetics 104: 680-687.
0351.	Weng Y & Lazar MD 2002 Comparison of homoeologous group-6 short arm physical maps of wheat and barley reveals a similar distribution of recombinogenic and gene-rich regions. Theoretical and Applied Genetics 104: 1078-1085.
0352.	Liu XM, Smith CM & Gill BS 2002 Identification of microsatellite markers linked to Russian wheat aphid resistance genes *Dn4* and *Dn6*. Theoretical and Applied Genetics 104: 1042-1048.
0353.	Miller CA, Altinkut A & Lapitan NLV 2001 A Microsatellite marker for tagging *Dn2*, a wheat gene conferring resistance to the Russian wheat aphid. Crop Science 41: 1584-1589.
0354.	Mingeot D, Chantret N, Baret PV, Dekeyser A, Boukhatem N, Sourdille P, Doussinault G & Jacquemin JM 2002 Mapping QTL involved in adult plant resistance to powdery mildew in the winter wheat line RE714 in two susceptible genetic backgrounds. Plant Breeding 121: 133-140.
0356.	Pueyo A, Figueiras AM & Benito C 2002 Is the *Mnr* locus of Triticeae species the same as the *Ndh* and *Dia* loci? Theoretical and Applied Genetics 104: 513-517.

0357.	Smith PH, Koebner RMD & Boyd LA 2002 The development of a STS marker linked to a yellow rust resistance derived from the wheat cultivar Moro. Theoretical and Applied Genetics 104: 1278-1282.
0358.	Spielmeyer W, Sharp PJ & Lagudah ES 2003 Identification and validation of markers linked to broad-spectrum stem rust resistance gene *Sr2* in wheat (*Triticum aestivum* L.). Crop Science 43: 333-346.
0359.	Wang XW, Lai JR, Liu GT & Chen F 2002 Development of a scar marker for the *Ph1* locus in common wheat and its application. Crop Science 42: 1365-1368.
0360.	Spielmeyer W, Huang L, Bariana H, Laroche A, Gill BS & Lagudah E 2000 NBS-LRR sequence family is associated with leaf and stripe rust resistance on the end of homoeologous chromosome group 1S of wheat. Theoretical and Applied Genetics 101: 1139-1144.
0361.	Aoki N, Whitfield P, Hoeren F, Scofield G, Newell K, Patrick J, Offler C, Clarke B, Rahman S & Furbank RT 2002 Three sucrose transporter genes are expressed in the developing grain of hexaploid wheat. Plant Molecular Biology 50: 453-462.
0362.	Batey IL, Hayden MJ, Cai S, Sharp PJ, Cornish GB, Morell MK & Appels R 2002 Genetic mapping of commercially significant starch characteristics in wheat crosses. Australian Journal of Agricultural Research 52: 1287-1296.
0363.	Bougot Y, Lemoine J, Pavoine MT, Barloy D & Doussinault G 2002 Identification of a microsatellite marker associated with *Pm3* resistance alleles to powdery mildew in wheat. Plant Breeding 121: 325-329.
0364.	Bullrich L, Appendino ML, Tranquilli G, Lewis S & Dubcovsky J 2002 Mapping of a thermo-sensitive earliness per se gene on *Triticum monococcum* chromosome $1A^m$. Theoretical and Applied Genetics 105: 585-593.
0365.	Elouafi I, Nachit MM & Martin LM 2001 Identification of a microsatellite on chromosome 7B showing a strong linkage with yellow pigment in durum wheat (*Triticum turgidum* L. var. *durum*). Hereditas 135: 255-261.
0366.	Eujayl I, Sorrells ME, Baum M, Wolters P & Powell W 2002 Isolation of EST-derived microsatellite markers for genotyping the A and B genomes of wheat. Theoretical and Applied Genetics 104: 399-407.
0367.	Hessler TG, Thomson MJ, Benscher D, Nachit MM & Sorrells ME 2002 Association of a lipoxygenase locus, *Lpx-B1*, with variation in lipoxygenase activity in durum wheat seeds. Crop Science 42: 1695-1700.
0368.	Holton TA, Christopher JT, McClure L, Harker N & Henry RJ 2002 Identification and mapping of polymorphic SSR markers from expressed gene sequences of barley and wheat. Molecular Breeding 9: 63-71.
0369.	Kato K, Kidou S, Miura H & Sawada S 2002 Molecular cloning of the wheat CK2 alpha gene and detection of its linkage with *Vrn-A1* on chromosome 5A. Theoretical and Applied Genetics 104: 1071-1077.
0370.	Mohler V, Klahr A, Wenzel G & Schwarz G 2002 A resistance gene analog useful for targeting disease resistance genes against different pathogens on group 1S chromosomes of barley, wheat and rye. Theoretical and Applied Genetics 105: 364-368.
0371.	Nomura T, Ishihara A, Imaishi H, Endo TR, Ohkawa H & Iwamura H 2002 Molecular characterization and chromosomal localization of cytochrome P450 genes involved in the biosynthesis of cyclic hydroxamic acids in hexaploid wheat. Molecular Genetics and Genomics 267: 210-217.

0372.	Otto CD, Kianian SF, Elias EM, Stack RW & Joppa LR 2002 Genetic dissection of a major *Fusarium* head blight QTL in tetraploid wheat. Plant Molecular Biology 48: 625-632.
0373.	Sandhu D, Sidhu D & Gill KS 2002 Identification of expressed sequence markers for a major gene- rich region of wheat chromosome group 1 using RNA fingerprinting-differential display. Crop Science 42: 1285-1290.
0374.	Williams KJ, Taylor SP, Bogacki P, Pallotta M, Bariana HS & Wallwork H 2002 Mapping of the root lesion nematode (*Pratylenchus neglectus*) resistance gene *Rlnn1* in wheat. Theoretical and Applied Genetics 104: 874-879.
0375.	Spielmeyer W & Lagudah ES 2003 Homoeologous set of NBS-LRR genes located at leaf and stripe rust resistance loci on short arms of chromosome 1 of wheat. Functional and Integrative Genomics 3: 86-90.
0376.	Frick MM, Huel R, Nykiforuk CL, Conner RL Kusyk A & Laroche A 1998 Molecular characterisation of a wheat stripe rust resistance gene in Moro wheat. Proceedings 9th International Wheat Genetics Symposium (Slinkard AE ed) 3: 181-182.
0377.	Mago R, Spielmeyer W, Lawrence GJ, Lagudah ES, Ellis JG & Pryor A 2002 Identification and mapping of molecular markers linked to rust resistance genes located on chromosome 1RS of rye using wheat-rye translocation lines. Theoretical and Applied Genetics 104: 1317-1324.
0378.	Ellis MH, Spielmeyer W, Gale KR, Rebetzke GJ & Richards RA 2002 "Perfect" markers for the *Rht-B1b* and *Rht-D1b* dwarfing genes in wheat. Theoretical and Applied Genetics 105: 1038-1042.
0379.	Rebetzke GJ, Appels R, Morrison AD, Richards RA, McDonald G, Ellis MH, Spielmeyer W & Bonnett DG 2001 Quantitative trait loci on chromosome 4B for coleoptile length and early vigour in wheat (*Triticum aestivum* L.). Australian Journal of Agricultural Research 52: 1221-1234.
0380.	Muranty H, Jahier J, Tanguy A-M, Worland AJ & Law CN 2002 Inheritance of wheat to eyespot at the adult stage. Plant Breeding 121: 539-541.
0381.	Bettge AD, Morris CF & Greenblatt GA 1995 Assessing genotypic softness in single wheat kernels using starch granule-associated friabilin as a biochemical marker. Euphytica 86: 65-72.
0382.	Blochet JE, Chevalier C, Forest E, Pebay-Peyroula E, Gautier MF, Joudrier P, Pezolet M & Marion D 1993 Complete amino acid sequence of puroindoline, a new basic and cystine-rich protein with a unique tryptophan-rich domain, isolated from wheat by Triton X-114 phase partitioning. Federation of European Biochemical Societies Letters 329: 336-340.
0383.	Turner M, Mukai Y, Leroy B, Charef B, Appels R & Rahman S 1999 The *Ha* locus of wheat: Identification of a polymorphic region for tracing grain hardness in crosses. Genome 42: 1242-1248.
0384.	Rahman S, Jolly CJ Skerritt JH & Wallosheck A 1994 Cloning of a wheat 15-kDa grain softness protein (GSP). European Journal of Biochemistry 223: 917-925.
0385.	Cloutier S. 2003 Personal communication.
03101.	Urbano M, Margiotta B, Colaprico G & Lafiandra D 2002 Waxy proteins in diploid, tetraploid and hexaploid wheats. Plant Breeding 121: 465-468.
03102.	Sun Q, Wei Y, Ni C, Xie C & Yang T 2002 Microsatellite marker for yellow rust resistance gene *Yr5* introgressed from spelt wheat. Plant Breeding 121: 539-541.
03103.	Gautier, MF, Cosson P, Guirao A, Alary R & Joudrier P 2000 Puroindoline genes are highly conserved in diploid ancestor wheats and related species but absent in tetraploid *Triticum* species. Plant Science 153: 81-91.

03104.	Lillemo M, Simeone MC & Morris CF 2002 Analysis of puroindoline a and b sequences from *Triticum aestivum* cv. 'Penawawa' and related diploid taxa. Euphytica 126: 321-331.
03105.	Massa AN, Morris CF & BS Gill 2004 Sequence diversity of puroindoline-a, puroindoline-b and the grain softness protein genes in *Aegilops tauschii* Coss. Crop Science 44: 1808-1816.
03106.	Morris CF, DeMacon VL & Giroux MJ 1999 Wheat grain hardness among chromosome 5D homozygous recombinant substitution lines using different methods of measurement. Cereal Chemistry 76: 249-254.
03107.	Morris CF & King GE 2002 Registration of soft and hard red winter wheat near-isogenic sister lines of 'Weston'. Crop Science 42: 2218-2219.
03108.	Morris CF, Simeone MC, Gill BS, Mason-Gamer RJ & Lillemo M 2001 Comparison of puroindoline sequences from various diploid members of the triticeae and modern cultivated hexaploid wheats. Cereals 2000. Proceedings 11th ICC Cereal & Bread Congress and the 50th Australian Cereal Chemistry Conference. (M Wootton, IL Batey & CW Wrigley eds.) Royal Australian Chemical Institute, North Melbourne, Victoria, Australia 678-681.
03109.	Symes K J 1969 Influence of a gene causing hardness on the milling and baking quality of two wheats Australian Journal of Agricultural Research 20: 971-979.
03110.	Gautier MF, Aleman ME, Guirao A, Marion D & Joudier P 1994 *Triticum aestivum* puroindolines, two basic cystine-rich seed proteins: cDNA analysis and developmental gene expression. Plant Molecular Biology 25: 43-57.
03111.	Jolly CJ, Rahman S, Kortt AA & Higgins TJ 1990 Characterisation of grain-softness protein, a marker of endosperm texture in wheat. Royal Australian Chemical Institute 92-95.
03112.	Alvarez JB, Campos LAC, Martin A, Sillero JA, Martin LM 1999 Genetic analysis of prolamins synthesised by the H^{ch} genome and their effects on gluten strength in hexaploid tritordeum. Euphytica 107: 177-184.
03113.	Alvarez JB, Martin A, Martin LM 1999 Allelic variation of the D-prolamin subunits encoded at the H^{ch} genome in a collection of primary hexaploid tritordeums. Theoretical and Applied Genetics 99: 296-299.
03114.	Alvarez JB, Martin A & Martin LM 2001 Variation in the high-molecular-weight glutenin subunits coded at the Glu-Hch1 locus in *Hordeum chilense*. Theoretical and Applied Genetics 102: 134-137.
03115.	Amiour N, Bouguennec A, Marcoz C, Sourdille P, Bourgoin M, Khelifi D & Branlard G 2002 Diversity of seven glutenin and secalin loci within triticale cultivars grown in Europe. Euphytica 123: 295-305.
03116.	Amiour N, Dardevet A, Khelifi D, Bouguennec A & Branlard G 2002 Allelic variation of HMW and LMW glutenin subunits, HMW secalin subunits and 75K gamma-secalins of hexaploid triticale. Euphytica 123: 179-186.
03117.	Amiour N, Jahier J, Tanquy AM, Chiron H & Branlard G 2002 Effect of 1R(1A), 1R(1B) and 1R(1D) substitution on technological value of bread wheat. Journal of Cereal Science 35: 149-160.
03120.	Branlard G, Dardevet M, Amiour N & Igrejas G 2003 Allelic diversity of the HMW and LMW glutenin subunits and omega-gliadins in French bread wheat (*Triticum aestivum* L.). Genetic Resources and Crop Evolution 50: 669-679.
03121.	Brzezinski W & Lukaszewski AJ 1998 Allelic variation at the Glu-1, Sec-2 and Sec-3 in winter triticale. P. Juskiew (Ed.), Proc. 4th International Triticale Symposium, Alberta Vol. II: 6-12.

03122.	Caballero L, Martin LM & Alvarez JB 2001 Allelic variation of the HMW glutenin subunits in Spanish accessions of spelt wheat (*Triticum aestivum* ssp. *spelta* L. em. Thell.). Theoretical and Applied Genetics 103: 124-128.
03123.	Dubcovsky J, Bullrich L, Echaide M, Schlatter AR, Manifesto M, Tranquilli G, Pfluger L, Feingold S, Barneix AJ, Hopp EH & Suarez EY 1998 Determinantes geneticos de la calidad panadera de los trigos Argentinos. RIA 29: 1-30.
03124.	Gianibelli MC, Gupta RB, Lafiandra D, Margiotta B & MacRitchie F 2001 Polymorphism of high Mr glutenin subunits in *Triticum tauschii*: Characterization by chromatography and electrophoretic methods. Journal of Cereal Science 33: 39-52.
03125.	Gianibelli MC, Masci S, Larroque OR, Lafiandra D & MacRitchie F 2002 Biochemical characterisation of a novel polymeric protein subunit from bread wheat (*Triticum aestivum* L.). Journal of Cereal Science 35: 265-276.
03126.	Gianibelli MC & Solomon RG 2003 A novel y-type high Mr glutenin subunit (12.4t) present in *Triticum tauschii*. Journal of Cereal Science 37: 253-256.
03127.	Igrejas G, Guedes-Pinto H, Carnide V & Branlard G 1999 Seed storage protein diversity in triticale varieties commonly grown in Portugal. Plant Breeding 118: 303-306.
03129.	Islam N, Woo SH, Tsujimoto H, Kawasaki H & Hirano H 2002 Proteome approaches to characterize seed storage proteins related to ditelocentric chromosomes in common wheat (*Triticum aestivum* L.). Proteomics 2: 1146-1155.
03130.	Larroque O, Gianibelli MC & MacRitchie F 1999 Protein composition for pairs of wheat lines with contrasting dough extensibility. Journal of Cereal Science 29: 27-31.
03131.	Liu C-Y & Shepherd KW 1996 Variation of B subunits of glutenin in durum, wild and less widely cultivated tetraploid wheats. Plant Breeding 115: 172-178.
03132.	Luo C, Griffin WB, Branlard G & McNeil DL 2001 Comparison of low- and high molecular-weight wheat glutenin allele effects on flour quality. Theoretical and Applied Genetics 102: 1088-1098.
03133.	Margiotta B, Colaprico G, D'Ovidio R & Lafiandra D 1993 Characterization of high Mr subunits of glutenin by combined chromatographic (RP-HPLC) and electrophoretic separations and restriction fragment length polymorphism (RFLP) analyses of their coding genes. Journal of Cereal Science 17: 221-236.
03134.	Masci S, Rovelli L, Kasarda DD, Vensel WH & Lafiandra D 2002 Characterisation and chromosomal localisation of C-type low- molecular-weight glutenin subunits in the bread wheat cultivar Chinese Spring. Theoretical and Applied Genetics 104: 422-428.
03135.	Nagamine T, Kai Y, Takayama T, Yanagisawa T & Taya S 2000 Allelic variation at the *Glu-1* and *Glu-3* loci in Southern Japanese wheats, and its effects on gluten properties. Journal of Cereal Science 32: 129-135.
03136.	Payne PI, Jackson EA & Holt LM 1984 The association between gamma-gliadin 45 and gluten strength in durum wheat varieties: a direct causal effect or the result of genetic linkage? Journal of Cereal Science 2: 73-81.
03137.	Pfluger LA, Martin LM & Alvarez JB 2001 Variation in the HMW and LMW glutenin subunits from Spanish accessions of emmer wheat (*Triticum turgidum* ssp. *dicoccum* Schrank). Theoretical and Applied Genetics 102: 767-772.
03138.	Raciti CN, Doust MA, Lombardo GM, Boggini G & Pecetti L 2003 Characterization of durum wheat Mediterranean germplasm for high and low molecular weight glutenin subunits in relation with quality. European Journal of Agronomy 19: 373-382.

03139.	Rozinek B, Gunther T & Hesemann CU 1998 Gel electrophoretic investigations of prolamins in eu- and alloplasmatic octoploid primary triticale forms. Theoretical and Applied Genetics 96: 46-51.
03140.	Ruiz M & Carrillo JM 1995 Relationships between different prolamin proteins and some quality properties in durum wheat. Plant Breeding 114: 40-44.
03141.	Ruiz M, Rodriguez-Quijano M, Metakovsky EV, Francisco Vazquez J & Carrillo JM 2002 Polymorphism, variation and genetic identity of Spanish common wheat germplasm based on gliadin alleles. Field Crops Research 79: 185-196.
03142.	Tranquilli G, Cuniberti M, Gianibelli MC, Bullrich L, Larroque OR, MacRitchie F & Dubcovsky J 2002 Effect of *Triticum monococcum* glutenin loci on cookie making quality and on predictive tests for bread making quality. Journal of Cereal Science 36: 9-18.
03143.	Vaccino P, Redaelli R, Metakovsky EV, Borghi B, Corbellini M & Pogna NE 2002 Identification of novel low M-r glutenin subunits in the high quality bread wheat cv Salmone and their effects on gluten quality. Theoretical and Applied Genetics 105: 43-49.
10001.	Tsunewaki K and Ebona K 1999 Production of near-isogenic lines of common wheat for glaucousness and genetic basis of this trait clarified by their use. Genes and Genetic Systems 74: 33-41.
10002.	Kato K, Nakagawa K & Kuno H 1993 Chromosomal location of the genes for vernalization response *Vrn2* and *Vrn4* in common wheat, *Triticum aestivum* L. Wheat Information Service 76: 53.
10003.	Iwaki K, Haruna S, Niwa T & Kato K 2001 Adaptation and ecological differentiation in wheat habit and *Vrn* genotype. Plant Breeding 120: 107-114.
10004.	Kato K 2003 Genetic analysis of two genes for vernalization response, the former *Vrn2* and *Vrn4*, using PCR based molecular markers. Proceedings 10th International Wheat Genetics Symposium, Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.) 3: 971-973.
10005.	Kato K, Ikoma H & Hayashi K 1988 Geographical distribution of the genes for vernalization response and its implication for the adaptability of wheat. Proceedings of the 7th International Wheat Genetics Symposium, Cambridge, U.K. (Miller TE & Koebner RMD, eds.) 1: 533-539.
10006.	Iwaki K, Nishida J, Yanagasawa H, Yoshida X & Kato K 2002 Genetic analysis of *Vrn-B1* for vernalization requirement by using linked dCAPS markers in bread wheat *(Triticum aestivum* L). Theoretical and Applied Genetics 104: 571-576.
10007.	Leonova I, Pestova E, Salina E, Efremova T, Roder M & Borner A 2003 mapping of the *Vrn-B1* gene in *Triticum aestivum* using microsatellite markers. Plant Breeding 122: 209-212.
10008.	Liu ZH, Faris JD, Meinhardt S, Ali S, Rasmussen JB & Friesen TL 2004 Genetic and physical mapping of a gene conditioning sensitivity in wheat to a partially purified host-selective toxin produced by *Stagonospora nodorum*. Phytopathology 94: 1056-1060.
10009.	Liu ZH, Friesen TL, Meinhardt S, Ali S, Rasmussen JB & Faris JD 2003 Quantitative trait loci analysis and mapping of seedling resistance to *Stagonospora nodorum* leaf blotch in wheat. Phytopathlogy 94: 1061-1067.
10010.	Mundt CC, Cowger C & Garrett KA 2002 Relevance of integrated disease management to disease durability. Euphytica 124: 245-252.
10011.	Chartrain L, Berry ST & Brown JKM 2005 Resistance of wheat line Kavkaz-K4500 l.6.A.4 to Septoria tritici blotch controlled by isolate-specific resistance genes. Phytopathology 95: 664-671.

10012.	Chartrain L, Joaquim P, Berry ST, Arraiano F, Azanza F & Brown JKM. 2005 Genetics of resistance to septoria tritici blotch in the Portuguese breeding line TE 9111. Theoretical and Applied Genetics 110: 1138-1144.
10013.	De Majnik J, Ogbonnaya FC, Moullet O & Lagudah ES 2003 The *Cre1* and *Cre3* nematode resistance genes are located at homoeologous loci in the wheat genome. Molecular Plant-Microbe Interactions 16: 1129-1134.
10014.	Yan L, Loukoianov A, Tranquilli G, Helguera M, Fahima T & Dubcovsky J 2003 Positional cloning of the wheat vernalization gene *VRN1*. Proceedings of the National Academy of Sciences USA 100: 6263-6268.
10015.	Friesen TL & Faris JD. 2004 Molecular mapping of resistance to *Pyrenophora tritici-repentis* race 5 and sensitivity to Ptr ToxB in wheat. Theoretical and Applied Genetics 109: 464-471.
10016.	Eriksen L, Afshari F, Christiansen MJ, McIntosh RA, Jahoor A & Wellings CR 2004 *Yr32* for resistance to stripe (yellow) rust present in the wheat cultivar Carstens V. Theoretical and Applied Genetics 108: 567-575.
10017.	Calonnec A, Johnson R & de Vallavieille-Pope C 2002 Genetic analysis of resistance of the wheat differential cultivars Carstens V and Spaldings Prolific to two races of *Puccinia striiformis*. Plant Pathology 51: 777-786.
10018.	Gosal KS 2004 Aspects of Resistance to Wheat Stripe Rust in Australia. PhD Thesis, The University of Sydney.
10019.	Danyluk J, Kane NA, Breton G, Limin AE, Fowler DB & Sarhan F 2003 TaVRT-1, a putative transcription factor associated with vegetative to reproductive transition in cereals. Plant Physiology 132: 1849-1860.
10020.	Somers DJ, Fedak G & Savard M 2003 Molecular mapping of novel genes controlling *Fusarium* head blight resistance and deoxynivalenol accumulation in spring wheat. Genome 46: 555-564.
10021.	Bayles RA, Slater SE & Hopkins FG 2002 Yellow rust in wheat. UK Cereal pathogen Virulence Survey: 2001 Annual Report, pp28-35 The UK Cereal Pathogen Survey Committee, Cambridge UK.
10022.	Hovmoller MS 2001 Disease severity and pathotype dynamics of *Puccinia striiformis* f.sp. *tritici* in Denmark. Plant Pathology 50: 181-189.
10023.	Pathan A & Wellings CR 2003 Personal communication.
10024.	Buerstmayr H, Steiner B, Halzenbuhler E, Scholz U, Mesterhazy A, Lemmens M & Ruckenbauer P 2003 Resistance to *Fusarium* head blight in wheat. Vol 1: 447-450. Proceedings 10th International Wheat genetics Symposium Institue Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10025.	Hsam SLK, Lapochkina IF & Zeller FJ 2003 Chromosomal location of genes for powdery mildew resistance in common wheat (*Triticum aestivum* L. em Thell.). 8. Gene *Pm32* in a wheat-*Aegilops speltoides* translocation line. Euphytica 133: 367-370.
10026.	Bourdoncle W & Ohm HW 2003 Quantitative trait loci for resistance to Fusarium head blight in recombinant inbred lines from the cross Hualpei 57-2/Patterson. Euphytica 131: 131-136.
10027.	Chatrain L, Sourdille P, Bernard M & Brown JKM 2009 Identification and location of Stb9, a gene for resistance to septoria tritici blotch in wheat cultivars Courtot and Tonic. Plant Pathology 58: 547-555.
10028.	McIntosh RA, Yamazaki Y, Dubcovsky J, Rogers WJ & Appels R 2003 Catalogue of Gene Symbols for Wheat. Vol 4 & CD: Proceedings 10th International Wheat Genetics

	Symposium, Instiuto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10029.	Ahmadi Firouzabad A & Moore K 2003 Chromosomal location of powdery mildew resistance gene Td1055 in wild emmer wheat (*T. dicoccoides*) accessions TA1055 and TA1150. Vol 3: 1090-1092. Proceedings 10th International Wheat Genetics Symposium Instiuto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10030.	Friesen TL, Ali S, Kianian S, Francl LJ & Rasmussen JB 2003 Role of host sensitivity to Ptr ToxA in development of tan spot of wheat. Phytopathology 93: 397-401.
10031.	Leonova I, Borner A, Budashkina E, Kalinina N, Unger O, Roder M & Salina E 2004 Identification of microsatellite markers for a leaf rust resistance gene introgressed into common wheat from *Triticum timopheevii*. Plant Breeding 123: 93-95.
10032.	Nakamura T, Vrinten P, Saito M & Kondo M 2002 Rapid classification of partial waxy mutants using PCR-based markers. Genome 45: 1150-1156.
10033.	Feuillet C, Travella S, Stein N, Albar L, Nublat A & Keller B 2003 Map-based isolation of the leaf rust disease resistance gene *Lr10* from the hexaploid wheat (*Triticum aestivum* L.) genome. Proceedings of the National Academy of Sciences U.S.A. 100: 15253-15258.
10034.	Wallwork H, Butt M, Cheong J & Williams K 2003 Resistance to crown rot in wheat identified through an improved method for screening adult plants. Australasian Plant Pathology 33: 1-7.
10035.	Hiebert C, Thomas J & McCallum B 2005 Locating the broad-spectrum wheat leaf rust resistance gene *Lr52* by a new cytogenetic method. Theoretical and Applied Genetics 111: 1453-1457.
10036.	Ogihara Y & Tsunewaki K 2000 Chinese Spring wheat (*Triticum aestivum* L) chloroplast genome: complete sequence and contig clones. Kihara Memorial Foundation for the Advancement of Life Sciences, Yokohama, Japan.
10037.	Turnbull K-M, Turner M, Mukai Y, Yamamoto M, Morell MK, Appels R & Rahman H 2003 The organisation of genes tightly linked to the *Ha* locus in *Aegilops tauschii*, the D-genome donor to wheat. Genome 46: 330-338.
10038.	Hovmoller MS 2001 Disease severity and pathotype dynamics of *Puccinia striiformis* f. sp. *tritici* in Denmark. Plant Pathology 50: 181-189.
10039.	Zahravi M, Bariana HS, Shariflou MR, Balakrishna PV, Banks PM & Ghannadha MR 2003 Bulk segregant analysis of stripe rust resitance in wheat (*Triticum aestivum*) using microsatellite markers. Proceedings 10th International Wheat Genetics Symposium, Instituto Sperimentale per Cerealcoltura, Rome (Pogna NE, Romano M, Pogna EA & Galterio, eds): 861-863.
10040.	Bariana HS, Parry N, Barclay IR, Loughman R, McLean RJ, Shankar M, Wilson RE, Willey NJ & Francki M 2006 Identification and characterization of stripe rust resistance gene *Yr34* in common wheat. Theoretical and Applied Genetics 112: 1143-1148.
10041.	Akhunov ED, Goodyear AW, Geng S, Qi LL, Echalier B, Gill BS, Miftahudin MA, Gustafson JP, Lazo G, Chao SM, Anderson OD, Linkiewicz AM, Dubcovsky J, La Rota M, Sorrells ME, Zhang DS, Nguyen HT, Kalavacharla V, Hossain K, Kianian SF, Peng JH, Lapitan NLV, Gonzalez-Hernandeiz JL, Anderson JA, Choi DW, Close TJ, Dilbirligi M, Gill KS, Walker-Simmons MK, Steber C, McGuire PE, Qualset CO & Dvorak J 2003 The organization and rate of evolution of wheat genomes are correlated with recombination rates along chromosome arms. Genome Research 13: 753-763.

10042.	Akhunov ED, Akhunova AR, Linkiewicz AM, Dubcovsky J, Hummel D, Lazo G, Chao SM, Anderson OD, David J, Qi LL, Echalier B, Gill BS, Gustafson JP, La Rota M, Sorrells ME, Zhang DS, Nguyen HT, Kalavacharla V, Hossain K, Kianian SF, Peng JH, Lapitan NLV, Wennerlind EJ, Nduati V, Anderson JA, Sidhu D, Gill KS, McGuire PE, Qualset CO & Dvorak J 2003 Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. Proceedings of the National Academy Sciences USA 100: 10836-10841.
10043.	Sorrells ME, La Rota M, Bermudez-Kandianis CE, Greene RA, Kantety R, Munkvold JD, Miftahudin MA, Ma XF, Gustafson PJ, Qi LL, Echalier B, Gill BS, Matthews DE, Lazo GR, Chao SM, Anderson OD, Edwards H, Linkiewicz AM, Dubcovsky J, Akhunov ED, Dvorak J, Zhang DS, Nguyen HT, Peng JH, Lapitan NLV, Gonzalez-Hernandez JL, Anderson JA, Hossain K, Kalavacharla V, Kianian SF, Choi DW, Close TJ, Dilbirligi M, Gill KS, Steber C, Walker-Simmons MK, McGuire PE & Qualset CO 2003 Comparative DNA sequence analysis of wheat and rice genomes. Genome Research 13: 1818-1827.
10044.	Campbell BT, Baenziger PS, Gill KS, Eskridge KM, Budak H, Erayman M, Dweikat I & Yen Y 2003 Identification of QTLs and environmental interactions associated with agronomic traits on chromosome 3A of wheat. Crop Science 43: 1493-1505.
10045.	Czembor PC, Arseniuk E, Czaplicki A, Song QJ, Cregan PB & Ueng PP 2003 QTL mapping of partial resistance in winter wheat to Stagonospora nodorum blotch. Genome 46: 546-554.
10046.	Dudnikov AJ 2003 Allozymes and growth habit of *Aegilops tauschii*: genetic control and linkage patterns. Euphytica 129: 89-97.
10047.	Han FP, Fedak G, Ouellet T & Liu B 2003 Rapid genomic changes in interspecific and intergeneric hybrids and allopolyploids of Triticeae. Genome 46: 716-723.
10048.	Boeuf C, Prodanovic S, Gay G & Bernard M 2003 Structural organization of the group-1 chromosomes of two bread wheat sister lines. Theoretical and Applied Genetics 106: 938-946.
10049.	Forsstrom PO, Koebner R & Merker A 2003 The conversion of wheat RFLP probes into STS markers via the single-stranded conformation polymorphism technique. Genome 46: 19-27.
10050.	He P, Friebe BR, Gill BS & Zhou JM 2003 Allopolyploidy alters gene expression in the highly stable hexaploid wheat. Plant Molecular Biology 52: 401-414.
10051.	Igrejas G, Leroy P, Charmet G, Gaborit T, Marion D & Branlard G 2002 Mapping QTLs for grain hardness and puroindoline content in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 106: 19-27.
10052.	Maleki L, Faris JD, Bowden RL, Gill BS & Fellers JP 2003 Physical and genetic mapping of wheat kinase analogs and NBS-LRR resistance gene analogs. Crop Science 43: 660-670.
10053.	Devos KM, Sorrells ME, Anderson JA, Miller TE, Reader SM, Lukaszewski AJ, Dubcovsky J, Sharp PJ, Faris J & Gale MD 1999 Chromosome aberrations in wheat nullisomic-tetrasomic and ditelosomic lines. Cereal Research Communications 27: 231-239.
10054.	Nemoto Y, Kisaka M, Fuse T, Yano M & Ogihara Y 2003 Characterization and functional analysis of three wheat genes with homology to the CONSTANS flowering time gene in transgenic rice. Plant Journal 36: 82-93.
10055.	Prasad M, Kumar N, Kulwal PL, Roder MS, Balyan HS, Dhaliwal HS & Gupta PK 2003 QTL analysis for grain protein content using SSR markers and validation studies using NILs in bread wheat. Theoretical and Applied Genetics 106: 659-667.

10056.	Salina E, Dobrovolskaya O, Efremova T, Leonova I & Roder MS 2003 Microsatellite monitoring of recombination around the *Vrn-B1* locus of wheat during early backcross breeding. Plant Breeding 122: 116-119.
10057.	Shindo C, Tsujimoto H & Sasakuma T 2003 Segregation analysis of heading traits in hexaploid wheat utilizing recombinant inbred lines. Heredity 90: 56-63.
10058.	Danna CH, Sacco F, Ingala LR, Saione HA & Ugalde RA 2002 Cloning and mapping of genes involved in wheat-leaf rust interaction through gene-expression analysis using chromosome-deleted near-isogenic wheat lines. Theoretical and Applied Genetics 105: 972-979.
10059.	
10060.	Suenaga K, Singh RP, Huerta-Espino J & William HM 2003 Microsatellite markers for genes *Lr34/Yr18* and other quantitative trait loci for leaf rust and stripe rust resistance in bread wheat. Phytopathology 93: 881-890.
10061.	Watanabe N, Sugiyama K, Yamagishi Y & Sakata Y 2002 Comparative telosomic mapping of homoeologous genes for brittle rachis in tetraploid and hexaploid wheats. Hereditas 137: 180-185.
10062.	del Blanco IA, Frohberg RC, Stack RW, Berzonsky WA & Kianian SF 2003 Detection of QTL linked to Fusarium head blight resistance in Sumai 3-derived North Dakota bread wheat lines. Theoretical and Applied Genetics 106: 1027-1031.
10063.	Zhang W, Gianibelli MC, Ma W, Rampling L & Gale KR 2003 Identification of SNPs and development of allele-specific PCR markers for gamma-gliadin alleles in *Triticum aestivum*. Theoretical and Applied Genetics 107: 130-138.
10064.	Yahiaoui N, Srichumpa P, Dudler R & Keller B 2004 Genome analysis at different ploidy levels allows cloning of the powdery mildew resistance *Pm3b* from hexaploid wheat. Plant Journal 47: 85-98.
10065.	Schnurbusch T, Paillard S, Fossati D, Messmer M, Schachermayr G, Winzeler M & Keller B 2003 Detection of QTLs for Stagonospora glume blotch resistance in Swiss winter wheat. Theoretical and Applied Genetics 107: 1226-1234.
10066.	Schnurbusch T, Paillard S, Schori A, Messmer M, Schachermayr G, Winzeler M & Keller B 2004 Dissection of quantitative and durable leaf rust resistance in Swiss winter wheat reveals a major resistance QTL in the *Lr34* chromosomal region. Theoretical and Applied Genetics 108: 477-484.
10067.	Eriksen L, Borum F & Jahoor A 2003 Inheritance and localisation of resistance to *Mycosphaerella graminicola* causing septoria tritici blotch and plant height in the wheat (*Triticum aestivum* L.) genome with DNA markers. Theoretical and Applied Genetics 107: 515-527.
10068.	Friebe B, Zhang P, Nasuda S & Gill BS 2003 Characterisation of a knock-out mutation at the *Gc2* locus in wheat. Chromosoma 111: 509-517.
10069.	Gervais L, Dedryver F, Morlais JY, Bodusseau V, Negre S, Bilous M, Groos C & Trottet M 2003 Mapping of quantitative trait loci for field resistance to Fusarium head blight in an European winter wheat. Theoretical and Applied Genetics 106: 961-970.
10070.	Groenewald JZ, Marais AS & Marais GF 2003 Amplified fragment length polymorphism-derived microsatellite sequence linked to the *Pch1* and *Ep-D1* loci in common wheat. Plant Breeding 122: 83-85.
10071.	Groos C, Robert N, Bervas E & Charmet G 2003 Genetic analysis of grain protein-content, grain yield and thousand-kernel weight in bread wheat. Theoretical and Applied Genetics 106: 1032-1040.

10072.	Guo PG, Bai GH & Shaner GE 2003 AFLP and STS tagging of a major QTL for Fusarium head blight resistance in wheat. Theoretical and Applied Genetics 106: 1011-1017.
10073.	Helguera M, Khan IA, Kolmer J, Lijavetzky D, Zhong-qi L & Dubcovsky J 2003 PCR assays for the *Lr37-Yr17-Sr38* cluster of rust resistance genes and their use to develop isogenic hard red spring wheat lines. Crop Science 43: 1839-1847.
10074.	Mohler V, Hsam SLK, Zeller FJ & Wenzel G 2001 An STS marker distinguishing the rye-derived powdery mildew resistance alleles at the *Pm8/Pm17* locus of common wheat. Plant Breeding 120: 448-450.
10075.	Toth B, Galiba G, Feher E, Sutka J & Snape JW 2003 Mapping genes affecting flowering time and frost resistance on chromosome 5B of wheat. Theoretical and Applied Genetics 107: 509-514.
10076.	Buerstmayr H, Steiner B, Hartl L, Griesser M, Angerer N, Lengauer D, Miedaner T, Schneider B & Lemmens M 2003 Molecular mapping of QTLs for Fusarium head blight resistance in spring wheat. II. Resistance to fungal penetration and spread. Theoretical and Applied Genetics 107: 503-508.
10077.	Tranquilli G, Heaton J, Chicaiza O & Dubcovsky J 2002 Substitutions and deletions of genes related to grain hardness in wheat and their effect on grain texture. Crop Science 42: 1812-1817.
10078.	Meguro A, Takumi S, Ogihara Y & Murai K 2003 WAG, a wheat AGAMOUS homolog, is associated with development of pistil-like stamens in alloplasmic wheats. Sexual Plant Reproduction 15: 221-230.
10079.	Vagujfalvi A, Galiba G, Cattivelli L & Dubcovsky J 2003 The cold-regulated transcriptional activator Cbf3 is linked to the frost-tolerance locus *Fr-A2* on wheat chromosome 5A. Molecular Genetics and Genomics 269: 60-67.
10080.	Sourdille P, Cadalen T, Guyomarc'h H, Snape JW, Perretant MR, Charmet G, Boeuf C, Bernard S & Bernard M 2003 An update of the Courtot x Chinese Spring intervarietal molecular marker linkage map for the QTL detection of agronomic traits in wheat. Theoretical and Applied Genetics 106: 530-538.
10081.	Nagy ED, Eder C, Molnar-Lang M & Lelley T 2003 Genetic mapping of sequence-specific PCR-based markers on the short arm of the 1BL.1RS wheat-rye translocation. Euphytica 132: 243-250.
10082.	Peng JH, Ronin Y, Fahima T, Roder MS, Li YC, Nevo E & Korol A 2003 Domestication quantitative trait loci in *Triticum dicoccoides*, the progenitor of wheat. Proceedings of the National Academy of Sciences USA 100: 2489-2494.
10083.	Francia E, Rizza F, Cattivelli L, Stanca AM, Galiba G, Toth B, Hayes PM, Skinner JS & Pecchioni N 2004 Two loci on chromosome 5H determine low-temperature tolerance in a Nure (winter) X Tremois (spring) barley map. Theoretical and Applied Genetics 108: 670-680.
10084.	Qin GJ, Chen PD, Gu HY, Feng YG & Niu JS 2003 Isolation of resistance gene analogs from wheat based on conserved domains of resistance genes. Acta Botanica Sinica 45: 340-345.
10085.	Shen X, Zhou M, Lu W & Ohm H 2003 Detection of Fusarium head blight resistance QTL in a wheat population using bulked segregant analysis. Theoretical and Applied Genetics 106: 1041-1047.
10086.	Amiour N, Merlino M, Leroy P & Branlard G 2002 Proteomic analysis of amphiphilic proteins of hexaploid wheat kernels. Proteomics 2: 632-641.

10087.	Amiour N, Merlino M, Leroy P & Branlard G 2003 Chromosome mapping and identification of amphiphilic proteins of hexaploid wheat kernels. Theoretical and Applied Genetics 108: 62-72.
10088.	De Bustos A, Rubio P & Jouve N 2000 Molecular characterisation of the inactive allele of the gene *Glu-A1* and the development of a set of AS-PCR markers for HMW glutenins of wheat. Theoretical and Applied Genetics 100: 1085-1094.
10089.	Larroque OR, Gianibelli MC, Lafiandra D, Sharp P & Bekes F 2003 The molecular weight distribution of the glutenin polymer as affected by the number, type and expression levels of HMW-GS. Proceedings of the 10th International Wheat Genetics Symposium, Vol 1: 447-450 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10090.	Juhasz A, Gardonyi M, Tamas L & Bedo Z 2003 Characterisation of the promoter region of *Glu-1Bx7* gene from overexpressing lines of an old Hungarian wheat variety. Proceedings of the 10th International Wheat Genetics Symposium, Vol 3 : 1348-1350 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10091.	Wang Tao (personal communication).
10092.	Smith RL, Schweder ME & Barnett RD 1994 Identification of glutenin alleles in wheat and triticale using PCR-generated DNA markers. Crop Science 34: 1373-1378.
10093.	Radovanovic N & Cloutier S 2003 Gene-assisted selection for high molecular weight glutenin subunits in wheat doubled haploid breeding programs. Molecular Breeding 12: 51-59.
10094.	De Bustos A & Jouve N 2003 Characterisation and analysis of new HMW-glutenin alleles encoded by the *Glu-R1* locus of *Secale cereale*. Theoretical and Applied Genetics 107: 74-83.
10095.	Anderson OD, Larka L, Christoffers MJ, McCue KF & Gustafson JP 2002 Comparison of orthologous and paralogous DNA flanking the wheat high-molecular-weight glutenin genes: sequence conservation and divergence, transposon distribution, and matrix-attachment regions. Genome 45: 367-380.
10096.	Yan GP, Chen XM, Line RF & Wellings CR 2003 Resistance gene-analog polymorphism markers co-segregating with the *Yr5* gene for resistance to wheat stripe rust. Theoretical and Applied Genetics 106: 636-643.
10097.	Chen X, Soria MA, Yan G, Sun J & Dubcovsky J 2003 Development of user-friendly PCR markers for wheat stripe rust resistance gene *Yr5*. Crop Science 43: 2058-2064.
10098.	Yan L, Echenique V, Busso C, SanMiguel P, Ramakrishna W, Bennetzen JL, Harrington S & Dubcovsky J 2002 Cereal genes similar to SNF2 define a new subfamily that includes human and mouse genes. Molecular Genetics and Genomics 268: 488-499.
10099.	Pozniak CJ & Hucl PJ 2004 Genetic analysis of imidazolinone resistance in mutation-derived lines of common wheat. Crop Science 44: 23-30.
10100.	Newhouse K, Smith W, Starrett M, Schafer T & Singh BK 1992 Tolerance to imidazolinone herbicides in wheat. Plant Physiology 100: 882-886.
10101.	Pozniak CJ, Birk IT, O'Donoughue LS, Menard C, Hucl PJ & Singh BK 2004 Physiological and molecular characterization of mutation-derived Imidazolinone resistance in spring wheat. Crop Science 44: 1434-1443.
10102.	Pozniak CJ & Hucl PJ 2003 Characterization of imidazolinone resistance in *Triticum monococcum* L. Proceedings 10th International Wheat Genetics Symposium, Vol 2 : 902-

	904 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10103.	Nomura T, Ishihara A, Ohkawa H, Endo TR & Iwamura H 2003 Evolutionary diversity of the genes for the biosynthesis of benzoxinones in *Triticeae*. Proceedings 10th International Wheat Genetics Symposium, Vol 2 : 500-502 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10104.	Knox RE, Clarke JM, Houshmand S & Clarke FR 2003 Chromosomal location of the low grain cadmium concentration trait in durum wheat. Proceedings 10th International Wheat Genetics Symposium, Vol 3 : 977-979 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10105.	Adhikari TB, Wallwork H & Goodwin SB 2004 Microsatellite markers linked to the *Stb2* and *Stb3* genes for resistance to septoria tritici blotch in wheat. Crop Science 44: 1403-1411.
10106.	
10107.	Himi E & Noda K 2003 *R* gene for wheat grain colour might be a Myb-type transcription factor. Proceedings 10th International Wheat Genetics Symposium, Vol 3 : 958-960 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10108.	Goncharov NP 2003 Genetics of growth habit (spring vs winter) in common wheat: confirmation of the existence of dominant gene *Vrn4*. Theoretical and Applied Genetics 107: 768-772.
10109.	Huang XQ & Roder MS 2003 High-denstity genetic and physical mapping of the powdery mildew resistance gene *Pm24* on chromosome 1D of wheat. Proceedings 10th International Wheat Genetics Symposium, Vol 3 : 961-964 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10110.	Navabi A, Singh RP, Tewari JP & Briggs KG 2003 Genetic analysis of adult-plant resistance to leaf rust in five spring wheat genotypes. Plant Disease 87: 1522-1529.
10111.	Wamishe YA & Milus EA 2004 Seedling resistance genes to leaf rust in soft red winter wheat. Plant Disease 88: 136-146.
10112.	Zakari A, McIntosh RA, Hovmoller MS, Wellings CR, Shariflou MR, Hayden M & Bariana HS 2003 Recombination of *Yr15* and *Yr24* in chromosome 1BS. Proceedings 10th International Wheat Genetics Symposium, Vol 1 : 417-420 Instituto Sperimentale per la Cerealcoltura, Rome, Italy (Pogna NE, Romano N, Pogna EA & Galterio G eds.).
10113.	Liu SX & Anderson JA 2003 Marker assisted evaluation of Fusarium head blight resistant wheat germplasm. Crop Science 43: 760-766.
10114.	Shen XR, Ittu M & Ohm HW 2003 Quantitative loci conditioning resistance to Fusarium head blight in wheat line F201R. Crop Science 43: 850-857.
10115.	Bai GH, Guo PG & Kolb FL 2003 Genetic relationships among head blight resistant cultivars of wheat assessed on the basis of molecular markers. Crop Science 43: 498-507.
10116.	Lerner SE, Cogliatti M, Ponzio NR, Seghezzo ML, Molfese ER & Rogers WJ 2004 Genetic variation for grain protein components and industrial quality of durum wheat cultivars sown in Argentina. Journal of Cereal Science 40: 161-166.
10117.	Clarke BC, Phongkham T, Gianibelli MC, Beasley H & Bekes F 2003 The characterisation and mapping of a family of LMW-gliadin genes: effects on dough properties and bread volume. Theoretical and Applied Genetics 106: 629-635.

10118.	Gedye KR, Morris CF & Bettge AD 2004 Determination and evaluation of the sequence and textural effects of puroindoline a and puroindoline b genes in a population of synthetic hexaploid wheat. Theoretical and Applied Genetics 109: 1597-1603.
10119.	Pan, Z, Song W, Meng F, Xu L, Liu B & Zhu J 2004 Chracterization of genes encoding wheat grain hardness from Chinese cultivar GaoCheng 8901. Cereal Chemistry 81: 287-289.
10120.	Massa AN, Morris CF & Gill BS 2004 Personal communication.
10121.	Xia L, Chen F, He Z, Chen X & Morris CF 2005 Occurrence of puroindoline alleles in Chinese winter wheats. Cereal Chemistry 82: 38-43.
10122.	Chantret N, Cenci A, Sabot F, Anderson O & J Dubcovsky 2004 Sequencing of the *Triticum monococcum* hardness locus reveals good microcolinearity with rice. Molecular and General Genomics 271: 377-386.
10123.	Adhikari TB, Yang X, Cavallo JR, Hu X, Buechley G, Ohm HW, Shaner G & Goodwin SB 2004 Molecular mapping of the *Stb1*, a potentially durable gene for resistance to septoria tritici blotch in wheat. Theoretical and Applied Genetics 109: 944-953.
10124.	Song QJ, Shi JR, Singh S, Fickus EW, Costa JM, Lewis J, Gill BS, Ward R & Cregan PB. 2005 Development and mapping of microsatellite (SSR) markers in wheat Theoretical and Applied Genetics 110: 550-560.
10125.	Somers DJ, Isaac P & Edwards K 2004 A high-density wheat microsatellite consensus map for bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 109: 1105-1114.
10126.	Sourdille P, Singh S, Cadalen T, Brown-Guedira GL, Gay G, Qi L, Gill BS, Dufour P, Murigneux A & Bernard M 2004 Microsatellite-based deletion bin system for the establishment of genetic-physical map relationships in wheat (*Triticum aestivum* L.). Functional and Integrative Genomics 4: 12-25.
10127.	Mohler V, Zeller FJ, Wenzel G & Hsam SLK 2005 Chromosomal location of genes for powdery mildew resistance in common wheat (*Triticum aestivum* L.) 9. Gene *MlZec* from the *Triticum dicoccoides*-derived wheat line Zecoi-1. Euphytica 142: 161-167.
10128.	Arzani A, Peng JH & Lapitan NLV 2004 DNA and morphological markers for a Russian wheat aphid resistance gene. Euphytica 139: 167-172.
10129.	Mohler V, Lukman R, Ortiz-Islas S, William M, Worland AJ, Van Beem J & Wenzel G. 2004 Genetic and physical mapping of photoperiod insensitive gene *Ppd-B1* in common wheat. Euphytica 138: 33-40.
10130.	Watanabe N, Takeuchi A & Nakayama A. 2004 Inheritance and chromosome location of the homoeologous genes affecting phenol colour reaction of kernels in durum wheat. Euphytica 239: 87-93.
10131.	Wrigley CW & McIntosh RA. 1975 Genetic control of factors regulating the phenol reaction of wheat and rye grain. Wheat Information Service 40: 6-11.
10132.	Kanyuka K, Lovell DJ, Mitrofanova OP, Hammond-Kosack K & Adams MJ 2004 A controlled environment test for resistance to *Soil-borne cereal mosaic virus* (SBCMV) and its use to determine the mode of inheritance of resistance in wheat cv. Cadenza and for screening *Triticum monococcum* botypes for sources of SBCMV resistance. Plant Pathology 53: 154-160.
10133.	Watanabe N, Nakayama A & Ban T 2004 Cytological and microsatellite mapping of the genes determing liguleless phenotype in durum wheat. Euphytica 140: 163-170.
10134.	Li HJ, Arterburn M, Jones SS & Murray TD 2004 A new source or resistance to *Tapesia yallundae* associated with a homoeologous group 4 chromosome in *Thinopyrum ponticum*. Phytopathology 94: 932-937.

10135. Jamjod S, Niruntrayagul S & Rerkasem B 2004 Genetic control of boron efficiency in wheat (*Triticum aestivum*). Euphytica 135: 21-17.

10136. Castro AM, Vasicek A, Ellerbrook C, Gimenez DO, Tocho E, Tacaliti MS, Clua A & Snape JW 2002 Mapping quantitative trait loci in wheat for resistance against greenbug and Russian wheat aphid. Plant Breeding 123: 361-365.

10137. Sardesai N, Nemacheck JA, Subramanyam S & Williams CE 2005 Identification and mapping of *H32*, a new wheat gene conferring resistance to Hessian fly. Theoretical and Applied Genetics 111: 1167-1173.

10138. Chicaiza O, Khan IA, Zhang X, Brevis CJ, Jackson L, Chen X & Dubcovsky J 2005 Registration of five wheat isogenic lines for leaf rust and stripe rust resistance genes. Crop Science 46: 485-487.

10139. Marais GF, McCallum B, Snyman JE, Pretorius ZA & Marais AS 2005 Leaf rust and stripe rust resistance genes *Lr54* and *Yr37* transferred to wheat from *Aegilops kotschyi*. Plant Breeding 124: 538-541.

10140. Adhikari TB, Cavaletto JR, Dubcovsky J, Gieco JO, Schlatter AR & Goodwin SB 2004 Molecular mapping of the *Stb4* gene for resistance to septoria tritici blotch in wheat. Phytopathology 94: 1198-1206.

10141. Huang X.Q, & Roder MS 2004 Molecular mapping of powdery mildew resistance in wheat: a review Euphytica 137: 203-223.

10142. Hayden MJ, Kuchel H & Chalmers KJ 2004 Sequence tagged microsatellites for the *Xgwm533* locus provide new diagnostic markers to select for the presence of stem rust resistance gene *Sr2* in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 109: 1641-1647.

10143. Arseniuk E, Czembor PC, Czaplick A, Song QJ, Cregan PB, Hoffman DL & Ueng PP 2004 QTL controlling partial resistance to *Stagonospora nodorum* leaf blotch in winter wheat cultivar Alba. Euphytica 137: 225-231.

10144. Watanabe N 2004 *Triticum polonicum* IC12196: a possible alternative source of GA_3-insensitive semi-dwarfism. Cereal Research Communications 32: 429-434.

10145. Navabi Z, Shiran B & Assad MT 2004 Microsatellite mapping of a Russian wheat aphid resistance gene on chromosome 7B of an Iranian tetraploid wheat line: preliminary results. Cereal Research Communications 32: 451-457.

10146. Kolmer JA, Long DL & Hughes ME 2004 Physiologic specialization of *Puccinia triticina* in the United States in 2002. Plant Disease 88: 1079-1084.

10147. Prabhu KV, Gupta SK, Charpe A & Koul S 2004 SCAR marker tagged to the alien leaf rust resistance gene *Lr19* uniquely marking the *Agropyron elongatum* gene *Lr24* in wheat: a revision. Plant Breeding 123: 417-420.

10148. Lehmensiek A, Campbell AW, Williamson PM, Michalowitz M, Sutherland MW & Daggard GE 2004 QTLs for black-point resistance in wheat and identification of potential markers for use in breeding programmes. Plant Breeding 123: 410-416.

10149. Jimenez M & Dubocovsky J 1999 Chromosome location of genes affecting polyphenol oxidase activity in seeds of common and durum wheat. Plant Breeding 118: 395-398.

10150. Imtiaz M, Ahmad M, Cromey MG, Griffin WB & Hampton JG 2004 Detection of molecular markers linked to the durable adult plant stripe rust resistance gene *Yr18* in bread wheat (*Triticum aestivum*). Plant Breeding 123: 401-404.

10151. Simon MR, Ayala FM, Corda CA, Roder MS & Boerner A 2004 Molecular mapping of quantitative trait loci determining resistance to septoria tritici blotch caused by *Mycosphaerella graminicola*. Euphytica 138: 41-48.

10152.	Oelke LM & Kolmer JA 2004 Characterization of leaf rust resistance in hard red spring wheat cultivars. Plant Disease 88: 1127-1133.
10153.	Lamari L, McCallum GD & Depauw RM 2005 Forensic pathology of Canadian bread wheat: the case for tan spot. Phytopathology 95: 144-152.
10154.	
10155.	Singh PH & Hughes GR 2005 Genetic control of resistance to tan necrosis induced by *Pyrenophora tritici-repentis*. Phytopathology 95: 172-177.
10156.	Sharma HC, HW Ohm & KL Perry 1997 Registration of barley yellow dwarf virus resistant wheat germplasm line P29. Crop Science 37: 1032-1033.
10157.	Ohm HW, Anderson JM, Sharma HC, Ayala NL, Thompson N & Uphaus JJ 2005 Registration of yellow dwarf virus resistant wheat germplasm line P961341. Crop Science 45: 805-806.
10158.	Crasta OR, Francki MG, Bucholotz DB, Sharma HC, Zhang J, Wang R-C, Ohm HW & Anderson JM 2000 Identification and characterization of wheat-wheat grass translocation lines and localization of barley yellow dwarf virus resistance. Genome 43: 698-706.
10159.	Kong L, Anderson JM & Ohm HW 2009 Segregation distortion in common wheat of Thinopyrum intermedium chromosome 7B carrying Bdv3 and development of a Bdv3 marker. Plant Breeding 128: 591-597.
10160.	Singh RP & Huerta-Espino J 2001 Global monitoring of wheat rusts, and assessment of genetic diversity and vulnerability of popular cultivars. Research Highlights on the CIMMYT Wheat Program, 1999-2000. CIMMYT, Mexico, D.F. Pp38-40.
10161.	Gonzalez-Hernandez JL, Elias EM & Kianian SF 2004 Mapping genes for grain protein concentration and grain yield on chromosome 5B of *Triticum turgidum* (L.) var. *dicoccoides*. Euphytica 139: 217-225.
10162.	Marais GF 2001 An evaluation of three *Sr27* carrying wheat x rye translocations. South African Journal of Plant and Soil 18(3): 135-136.
10163.	Ogbonnaya FC, Subrahmanyam NC, Moullet O, De Majnik J, Eagles HA, Brown JS, Eastwood RF, Kollmorgen J, Appels R & Lagudah ES 2001 Diagnostic DNA markers for cereal cyst nematode resistance in bread wheat. Australian Journal of Agricultural Research 52: 1367-1374.
10164.	Kato K & Maeda H 1993 Gametophytic pollen sterility caused by three complementary genes in wheat, *Triticum aestivum* L. Proceedings of the 8th Internatinal Wheat Genetics Symposium, Beijing (Li ZS & Xin ZY, eds) 2: 871-875.
10165.	Kato K 2005 Personal communication.
10166.	Thomas JB, Conner RL & Graf RJ 2004 Comparison of different sources of vector resistance for controlling wheat streak mosaic in winter wheat. Crop Science 44: 125-130.
10167.	Mater Y, Baenziger S, Gill K, Graybosch R, Whitcher L, Baker C, Specht J & Dweikat I 2004 Linkage mapping of powdery mildew and greenbug resistance genes in recombinant 1RS from 'Amigo' and 'Kavkaz' wheat-rye translocations of chromosome 1RS.1AL. Genome 47: 292-298.
10168.	Gazza L, Nocente E, Ng PKW & Pogna NE 2005 Genetic and biochemical analysis of common wheat cultivars lacking puroindoline a. Theoretical and Applied Genetics 110: 470-478.
10169.	Weng Y, Li W, Devkota RN & Rudd JC 2005 Microsatellite markers associated with two *Aegilops tauschii*-derived greenbug resistance loci in wheat. Theoretical and Applied Genetics 110: 462-469.

10170.	McCartney CA, Somers DJ, McCallum BD, Thomas JG, Humphreys DG, Menzies JG & Brown PD 2005 Microsatellite tagging of the leaf rust resistance gene *Lr16* on wheat chromosome 2BSc. Molecular Breeding 15: 329-337.
10171.	Zhu LC, Smith CM, Fritz A, Boyko EV & Flynn MB 2004 Genetic analysis and molecular mapping of a wheat gene conferring tolerance to the greenbug (*Shizaphis graminum* Rondani). Theoretical and Applied Genetics 109: 289-293.
10172.	Paillard S, Schnurbusch T, Tiwari R, Messmer M, Winzeler M, Keller B & Schachermayr G 2004 QTL analysis of resistance to a Fusarium head blight in Swiss winter wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 109: 323-333.
10173.	McCartney CA, Somers DJ, Fedak G & Cao W 2004 Haplotype diversity at Fusarium head blight resistance QTLs in wheat. Theoretical and Applied Genetics 109: 261-271.
10174.	Steiner B, Lemmens M, Griesser M, Scholz U, Schondelmaier J & Buerstmayr H 2004 Molecular mapping of resistance to *Fusarium* head blight in the spring wheat cultivar Frontana. Theoretical and Applied Genetics 109: 215-224.
10175.	Singrun CH, Hsam SLK, Zeller FJ, Wenzel G & Mohler V 2004 Localization of a novel powdery mildew resistance gene from common wheat line RD30 in the terminal region of chromosome 7AL. Theoretical and Applied Genetics 109: 210-214.
10176.	Ma ZQ, Wei JB & Cheng SH 2004 PCR-based markers for the powdery mildew resistance gene *Pm-4a* in wheat. Theoretical and Applied Genetics 109: 140-145.
10177.	Zhang ZY, Xu JS, Xu XJ, Larkin P & Xin ZY 2004 Development of novel PCR markers linked to the BYDV resistance gene *Bdv2* useful in wheat for marker assisted selection. Theoretical and Applied Genetics 109: 433-439.
10178.	Kolmer JA 2001 Physiologic specialization of *Puccinia triticina* in Canada in 1998. Plant Disease 85: 155-158.
10179.	Kolmer JA & Liu JQ 2002 Inheritance of leaf rust resistance in the wheat cultivars AC Majestic, AC Splendor, and AC Karma. Canadian Journal of Plant Pathology 24: 327-331.
10180.	Brown-Guedira G 2005 Personal communication.
10181.	Knox R 2005 Personal communication.
10182.	Watanabe N, Kobal SF and Koval VS 2003 Wheat Near-Isogenic Lines. Sankeisha, Kita-ku, Nagoya 462-0056, Japan
10183.	
10184.	Ramburan VP, Pretorius ZA, Louw JH, Boyd LA, Smith PH, Boshoff WHP & Prins R 2004 A genetic analysis of adult plant resistance to stripe rust in the wheat cultivar Kariega. Theoretical and Applied Genetics 108: 1426-1433.
10185.	Zhang W, Gianibelli MC, Rampling LR & Gale KR 2004 Characterization and marker development for low molecular weight glutenin genes from *Glu-A3* alleles of bread wheat (*Triticum aestivum* L.) Theoretical and Applied Genetics 108: 1409-1419.
10186.	Xu SS, Khan K, Klindworth DL, Faris JD & Nygard G 2004 Chromosome location of genes from novel glutenin subunits and gliadins in wild emmer (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 108: 1221-1228.
10187.	Saito M, Konda M, Vrinten AP, Nakamura K & Nakamura T 2004 Molecular comparison of waxy null alleles in common wheat and identification of a unique null allele. Theoretical and Applied Genetics 108: 1205-1211.
10188.	Anderson GR, Papa D, Peng JH, Tahir M & Lapitan NLV 2003 Genetic mapping of *Dn7*, a rye gene conferring resistance to Russian wheat aphid in wheat. Theoretical and Applied Genetics 107: 1297-1303.

10189.	Sommers DJ, Isaac P & Edwards K 2004 A high density microsatellite consensus map for bread wheat. Theoretical and Applied Genetics 109: 1105-1114.
10190.	Lin F, Kong ZX, Zhu HL, Zue SL, JJZ, Tian DG, Wei JB, Zhang CQ & Ma ZQ 2004 Mapping QTL associated in with resistance to Fusarium head blight in the Nanda2419 X Wangshuibai population. I. Type II resistance. Theoretical and Applied Genetics 109: 1504-1511.
10191.	Ling HQ, Qiu JW, Singh RP & Keller B 2004 Identification and characterization of an *Aegilops tauschii* ortholog of the wheat leaf rust disease resistance gene *Lr1*. Theoretical and Applied Genetics 109: 1133-1138.
10192.	Boyko E, Starkey S & Smith M 2004 Molecular mapping of *Gby*, a new greenbug resistance gene in bread wheat. Theoretical and Applied Genetics 109: 1230-1236.
10193.	Spielmeyer W & Richards RA 2004 Comparative mapping of wheat chromosome 1AS which contains the tiller inhibition gene (*tin*) with rice chromosome 5S. Theoretical and Applied Genetics 109: 1303-1310.
10194.	Li H, Chen X, Xin ZY, Ma YZ, Xu HJ, Chen XY & Jia X 2005 Development and identification of wheat-*Haynaldia villosa* 6DL.6VS chromosome translocation lines conferring resistance to powdery mildew. Plant Breeding 124: 203-205.
10195.	Osa M, Kato K, Mori M, Shindo C, Torada A & Miura H 2003 Mapping QTLs for seed dormancy and the Vp1 homologue on chromosome 3A in wheat. Theoretical and Applied Genetics 106: 1491-1498.
10196.	Butow BJ, Gale KR, Ikea J, Juhasz A, Bedo Z, Tamas L & Gianibelli MC 2004 Dissemination of the highly expressed Bx7 glutenin subunit (*Glu-B1al* allele) in wheat as revealed by novel PCR markers and RP-HPLC. Theoretical and Applied Genetics 109: 1525-1535.
10197.	Juhasz A, Gardonyi M, Tamas L & Bedo Z 2003 Characterization of the promoter region of *Glu-1Bx7* gene from overexpressing lines of an old Hungarian wheat variety. Proceedings of the 10th International Wheat Genetics Symposium Vol 3 : 1348-1350 (Pogna NE, Romano N, Pogna EA & Galtterio G eds.). Instituto Sperimentale per la Cerealicoltura, Rome.
10198.	Yan L, Helguera M, Kato K, Fukuyama S, Sherman J & Dubcovsky J 2004 Variation at the VRN-1 promoter region in polyploidy wheat. Theoretical and Applied Genetics 109: 1677-1686.
10199.	Huang XQ, Hsam SLK, Mohler V, Roder MS & Zeller FJ 2004 Genetic mapping of three alleles at the *Pm3* locus conferring powdery mildew resistance in common wheat (*Triticum aestivum* L.). Genome 47: 1130-1136.
10200.	Zhou WC, Kolb FL, Yu JB, Bai GH, Boze LK & Domier IL 2004 Molecular characterization of *Fusarium* head blight resistance in Wangshuibai with simple sequence repeat and amplified fragment polymorphism markers. Genome 47: 1137-1143.
10201.	Wang ZL, Li LH, He ZH, Duan XY, Zhou YL, Chen XM, Lillemo M, Singh RP, Wang H & Xia ZC 2005 Seedling and adult plant resistance to powdery mildew in Chinese bread wheat cultivars and lines. Plant Disease 89: 457-463.
10202.	Fu D, Szucs P, Yan L, Helguera M, Skinner JS, Hayes P & Dubcovsky J 2005 Large deletions in the first intron of the VRN-1 vernalization gene are associated with spring growth habit in barley and polyploid wheat. Molecular and General Genomics 273: 54-65.
10203.	Marais GF, Pretorius ZA, Wellings CR, McCallum B & Marais AS 2005 Leaf and stripe rust resistance genes transferred to common wheat from *Triticum dicoccoides*. Euphytica 143: 115-123.

10204.	Marais GF, Pretorius ZA, Wellings CR & Marais AS 2003 Transfer of rust resistance genes from *Triticum* species to common wheat. South African Journal of Plant and Soil 20: 193-198.
10205.	Zhu ZD, Zhou RG, Kong XY, Dong YC & Jia JZ 2005 Microsatellite markers linked to 2 powdery mildew resistance genes introgressed from *Triticum carthlicum* accession PS5 into common wheat. Genome 48: 585-590.
10206.	Cook JP, Wichman DM, Martin JM, Bruckner PL & Talbert LE 2004 Identification of microsatellite markers associated with a stem solidness locus in wheat. Crop Science 44: 1397-1402.
10207.	Haen KM, Lu HJ, Friesen TL & Faris JD 2004 Genomic targeting and high-resolution mapping of the *Tsn1* gene in wheat. Crop Science 44: 951-962.
10208.	Chen F, He Z-H, Xia X-C, Xia L-Q, Zhang X-Y, Lillemo M & Morris CF 2006 Molecular and biochemical characterization of puroindoline a and b alleles in Chinese landraces and historical cultivars. Theoretical and Applied Genetics 112: 400-409.
10209.	Ram S, Jain N, Shoran J & Singh R 2005 New frame shift mutation in puroindoline b in Indian wheat cultivars Hyb65 and NI5439. Journal of Plant Biochemistry and Biotechnology 14: 45-48.
10210.	Feng J, Ma H & Hughes GR 2004 Genetics of resistance to Stagonospora nodorum blotch of hexaploid wheat. Crop Science 44: 2043-2048.
10211.	Xu XY, Bai GH, Carver BF, Shaner GE & Hunger RM 2005 Molecular characterization of slow leaf-rusting resistance in wheat. Crop Science 45: 758-765.
10212.	Zeller FJ & Hsam SLK 1998 Progress in breeding for resistance to powdery mildew in common wheat (*Triticum aestivum* L.) Proceedings 9th International Wheat Genetics Symposium, (Slinkard AE, ed.) University of Saskachewan Extension Press, Saskatoon, Canada 1: 178-180.
10213.	Yang ZP, Gilbert J, Fedak G & Somers DJ 2005 Genetic characterization of QTL associated with resistance to Fusarium head blight in a doubled-haploid spring wheat population. Genome 48: 187-196.
10214.	Cuthbert PA, Somers DJ, Thomas J, Cloutier S & Brule-Babel A 2006 Fine mapping *Fhb1*, a major gene controlling Fusarium head blight resistance in bread wheat (*Triticum aesitvum* L.). Theoretical and Applied Genetics 112: 1465-1472.
10215.	Martinez MC, Ruiz M & Carrillo JM 2004 New B low *Mr* glutenin subunit alleles at the *Glu-A3, Glu-B2* and *Glu-B3* loci and their relationship with gluten strength in durum wheat. Journal of Cereal Science 40: 101-107.
10216.	Castro AM, Vasicek A, Manifiesto M, Gimenez DO, Taculiti MS, Dobrovilskaya O, Roder MS, Snape JW & Borner A 2005 Mapping antixenosis genes on chromosome 6A to greenbug and to a new biotype of Russian wheat aphid. Plant Breeding 124: 229-233.
10217.	Chen XM, Luo YH, Xia XC, Xia LQ, Chen X, Ren ZL, He ZH & Jia JZ 2005 Chromosomal location of powdery mildew resistance gene *Pm16* in wheat using SSR marker analysis. Plant Breeding 124: 225-228.
10218.	Suanaga K, Khairallah M, William HM & Hoisington DA 2005 A new intervarietal linkage map and its application for quantitative trait locus analysis of "gigas" features in bread wheat. Genome 48: 65-75.
10219.	Park RP, Ash GJ & Rees RG 1992 Effects of temperature on the response of some Australian wheat cultivars to *Puccinia striiformis* f.sp. *tritici*. Mycological Research 96: 166-170.

10220.	Bariana HS, Hayden MJ, Ahmed NU, Bell JA, Sharp PJ & McIntosh RA 2001 Mapping of durable adult plant and seedling resistances to stripe rust and stem rust diseases in wheat. Australian Journal of Agricultural Research 52: 1247-1255.
10221.	Navabi A, Tewari JP, Singh RP, McCallum B, Laroche A & Briggs KG 2005 Inheritance and QTL analysis of durable resistance to stripe and leaf rusts in an Australian cultivar, *Triticum aestivum* 'Cook'. Genome 48: 97-107.
10222.	Zhou WC, Kolb FL, Domier LL & Wang SW 2005 SSR markers associated with fertility restoration genes against *Triticum timopheevii* cytoplasm in *Triticum aestivum*. Euphytica 141: 33-40.
10223.	Oelke LM & Kolmer JA 2005 Genetics of leaf rust resistance in spring wheat cultivars Olsen and Norm. Phytopathology 95: 773-778.
10224.	Marais GF, McCallum B & Marais AS 2006 Leaf rust and stripe rust resistance genes derived from *Triticum sharonense*. Euphytica 149: 373-380.
10225.	Cuthbert PA, Somers DJ & Brule-Babel A 2007 Mapping of *Fhb2* on chromosome 6BS: a gene controlling Fusarium head blight field resistance in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 114: 429-437.
10226.	Jones RAC, Coutts BA, Mackie AE & Dwyer GI 2005 Seed transmission of *Wheat streak mosaic virus* shown unequivocally in wheat. Plant Disease 89: 1049-1050.
10227.	Watanabe N, Takasada N, Shibata Y & Ban T 2005 Genetic mapping of the genes for glaucous leaf and tough rachis in *Aegilops tauschii*, the D-genome progenitor of wheat. Euphytica 144: 119-123.
10228.	Luo PG, Ren ZL, Zhang HQ & Zhang HY 2005 Identification, chromosome location, and diagnostic markers for a new gene (*YrCN19*) for resistance to wheat stripe rust. Phytopathology 95: 1266-1270.
10229.	Distelfeld A, Uauy C, Olmos S, Schlatter AR, Dubcovsky J & Fahima T 2004 Microcolinearity between a 2-cM region encompassing the grain protein content locus *Gpc-6B1* on wheat chromosome 6B and a 350-kb region on rice chromosome 2. Functional and Integrative Genomics 4: 59-66.
10230.	Pozniak CJ, Knox RE, Clarke FR & Clarke JM 2007 Identification of QTL and association of a phytoene synthase gene with endosperm colour in durum wheat. Theoretical and Applied Genetics 114: 525-537.
10231.	Kong L, Ohm HW, Cambron SE & Williams CE 2005 Molecular mapping determines that Hessian fly resistance gene *H9* is located on chromosome 1A of wheat. Plant Breeding 124: 525-531.
10232.	Collard BCY, Grams RA, Bovill WD, Percy CD, Jolley R, Lehmensiek A, Wildermuth G & Sutherland MW 2005 Development of molecular markers for crown rot resistance in wheat: mapping of QTLs for seedling resistance in a '2-49' x 'Janz' population. Plant Breeding 124: 532-537.
10233.	Mishra AN, Kaushal K, Shirsekar GS, Yadav SR, Brama RN & Pandey HN 2005 Genetic basis of seedling-resistance to leaf rust in bread wheat 'Thatcher'. Plant Breeding 124: 514-516.
10234.	Goncharov NP & Gaidalenok RF 2005 Localization of genes controlling sphaerical grain and compact ear in *Triticum antiquorum* Heer ex Udacz. Russian Journal of Genetics 41: 1262-1267.
10235.	Jan Y, Hsam SLK, Yu JZ, Jiang Y, Ohtsuka I & Zeller FJ 2003 HMW and LMW glutenin alleles among putative tetraploid and hexaploid European spelt wheat (*Triticum spelta* L.) progenitors. Theoretical and Applied Genetics 106: 1321-1330.

10236.	Cherukuri DP, Gupta PK, Charpe A, Koul S, Prabhu KV, Singh RB & Haq QMR 2005 Molecular mapping of *Aegilops speltoides* derived leaf rust resistance gene *Lr28* in wheat. Euphytica 143: 19-26.
10237.	Makandar R, Essig JS, Schapaugh MA, Trick HN & Shah J 2006 Genetically engineered resistance to Fusarium head blight in wheat by expression of *Arabidopsis* NPR1. Molecular Plant-Microbe Interactions 19: 123-129.
10238.	Santra DK, Watt C, Little L, Kidwell KK & Campbell KG 2006 Comparison of a modified assay method for the endopeptidase marker *Ep-D1b* with the Sequence Tag Site marker *XustSSR2001-7DL* for strawbreaker foot rot resistance in wheat. Plant Breeding 125: 13-18.
10239.	Chen J, Griffey CA, Saghai-Maroof MA, Stromberg EL, Bivashev RM, Zhoa W, Chappell MR, Pridgen TH, Dong Y & Zeng Z 2006 Validation of two major quantitative trait loci for Fusarium head blight resistance in Chinese wheat line W14. Plant Breeding 125: 99-101.
10240.	Griffiths S, Sharp R, Foote TN, Bertin I, Wanous M, Reader S, Colas I & Moore G 2006 Molecular characterization of *Ph1* as a major chromosome pairing locus in polyploid wheat. Nature 439: 749-752.
10241.	Miranda LM, Murphy JP, Leath S & Marshall DS 2006 *Pm34*: a new powdery mildew resistance gene transferred from *Aegilops tauschii* Coss. to common wheat. Theoretical and Applied Genetics 113: 1497-1504.
10242.	Watanabe N 2005 The occurrence and inheritance of a brittle rachis phenotype in Italian durum wheat cultivars. Euphytica 142: 247- 251.
10243.	Gilsinger J, Kong L, Shen X & Ohm H 2005 DNA markers associated with low Fusarium head blight incidence and narrow flower opening in wheat. Theoretical and Applied Genetics 110: 1218-1225.
10244.	Gupta SK, Charpe A, Koul S, Prabhu KV & Haq QMR 2005 Development and validation of molecular markers linked to an *Aegilops umbellulata*-derived leaf-rust-resistance gene, *Lr9*, for marker-assisted selection in bread wheat. Genome 48: 823-830.
10245.	Mori M, Uchino N, Chono M, Kato K & Miura H 2005 Mapping QTLs for grain dormancy on wheat chromosome 3A and the group 4 chromosomes, and their combined effect. Theoretical and Applied Genetics 110: 1315-1323.
10246.	Valarik M, Linkiewicz AM & Dubcovsky J 2006 A microcolinearity study at the earliness *per se* gene *Eps-*A^{m}1 region reveals an ancient duplication that preceded the wheat-rice divergence. Theoretical and Applied Genetics 112: 945-967.
10247.	Ma W, Appels R, Bekes F, Larroque O, Morell MK & Gale KR 2005 Genetic characterization of dough rheological properties in a wheat doubled haploid population: additive genetic effects and epistatic interactions. Theoretical and Applied Genetics 111: 410-422.
10248.	Faris JD & FriesenTL 2005 Identification of quantitative trait loci for race-nonspecific resistance to tan spot in wheat. Theoretical and Applied Genetics 111: 386-392.
10249.	Ellis MH, Rebetzke GJ, Azanza F, Richards RA & Spielmeyer W 2005 Molecular mapping of gibberellin-responsive dwarfing genes in bread wheat. Theoretical and Applied Genetics 111: 423-430.
10250.	Aguilar V, Stamp P, Winzeler M, Schachermayr, Keller B, Zanetti S & Messmer MM 2005 Inheritance of field resistance to *Stagonospora nodorum* leaf and glume blotch and correlations with other morphological traits in hexaploid wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 111: 325-336.

10251. Liu XM, Gill BS & Chen M-S 2005 Hessian fly resistance gene *H13* is mapped to a distal cluster of resistance genes in chromosome 6DS of wheat. Theoretical and Applied Genetics 111: 243-249.

10252. Liu XM, Fritz AK, Reese JC, Wilde GE, Gill BS & Chen M-S 2005 *H9, H10*, and *H22* compose a cluster of Hessian fly-resistance genes in the distal gene-rich region of wheat chromosome 1AS. Theoretical and Applied Genetics 111: 1473-1480.

10253. Obert DE, Fritz AK, Moran JL, Singh S, Rudd JC & Menz MA 2005 Identification and molecular tagging of a gene from PI 289824 conferring resistance to leaf rust (*Puccinia triticina*) in wheat. Theoretical and Applied Genetics 111: 1439-1444.

10254. Steed A, Chandler E, Thomsett M, Gosman N, Faure S & Nicholson P 2005 Identification of type 1 resistance to Fusarium head blight controlled by a major gene located on chromosome 4A of *Triticum macha*. Theoretical & Applied Genetics 111: 521-529.

10255. Zhang WJ, Lukaszewski AJ, Kolmer J, Soria A, Goyal S & Dubcovsky J 2005 Molecular characterization of durum and common wheat recombinant lines carrying leaf rust resistance (*Lr19*) and yellow pigment (*Y*) genes from *Lophopyrum ponticum*. Theoretical and Applied Genetics 111: 573-582.

10256. Liu ZH, Anderson JA, Hu J, Friesen TL, Rasmussen JB & Faris JD 2005 A wheat intervarietal genetic linkage map based on microsatellite and target region amplified polymorphism markers and its utility for detecting quantitative trait loci. Theoretical and Applied Genetics 111: 782-794.

10257. Mago R, Bariana HS, Dundas IS, Spielmeyer W, Lawence GJ, Pryor AJ & Ellis JG 2005 Development of PCR markers for the selection of wheat stem rust resistance genes *Sr24* and *Sr26* in diverse wheat germplasm. Theoretical and Applied Genetics 111: 496-504.

10258. Liu WH, Nie HA, Wang SB, Li X, He ZT, Han CG, Wang XL, Li LH & Yu JL 2005 Mapping a resistance gene in wheat cultivar Yanfu 9311 to yellow mosaic virus, using microsatellite markers. Theoretical and Applied Genetics 111: 651-657.

10259. Spielmeyer W, McIntosh RA, Kolmer J & Lagudah ES 2005 Powdery mildew resistance and *Lr34/Yr18* genes for durable resistance to leaf and stripe rust co-segregate at a locus on the short arm of chromosome 7D of wheat. Theoretical and Applied Genetics 111: 731-735.

10260. Schmolke M, Zimmerman G, Buerstmayer H, Schweizer G, Miedaner T, Korzun V, Ebmeyer E & Hartl L 2005 Molecular mapping of Fusarium head blight resistance in the winter wheat population Dream/Lynx. Theoretical and Applied Genetics 111: 747-756.

10261. Kulwal PL, Kumar N, Gaur A, Khurana P, Khurana JP, Tyagi AK, Balyan HS & Gupta PK 2005 Mapping a major QTL for pre-harvest sprouting tolerance on chromosome 3A in bread wheat. Theoretical and Applied Genetics 111: 1052-1059.

10262. Liu XM, Brown-Guedira GL, Hatchett JO & Chen M-S 2005 Genetic characterization and molecular mapping of a Hessian fly-resistance gene transferred from *T. turgidum* ssp. *dicoccum* to common wheat. Theoretical and Applied Genetics 111: 1308-1315.

10263. Khan RR, Bariana HS, Dholakia BB, Naik SV, Lagu MD, Rathjen AJ, Bhavani S & Gupta VS 2005 Molecular mapping of stem and leaf rust resistance in wheat. Theoretical and Applied Genetics 111: 846-850.

10264. Mardi M, Buerstmayr H, Ghareyazie B, Lemmens M, Mohammadi SA, Nolz R & Ruckenbauer P 2005 QTL analysis of resistance to Fusarium head blight in wheat using a 'Wangshuibai'-derived population. Plant Breeding 124: 329-333.

10265. Ma HX, Bai GH, Carver BF & Zhou LL 2005 Molecular mapping of a quantitative trait locus for aluminum tolerance in wheat cultivar Atlas 66. Theoretical and Applied Genetics 112: 51-57.

10266.	Sasaki T, Yamamoto Y, Ezaki B, Katsuhara M, Ahn SJ, Ryan PR, Delhaizie E & Matsumoto H 2004 A wheat gene encoding an aluminum-activated malate transporter. Plant Journal 37: 645-653.
10267.	Zhu LC, Smith CM, Fritz A, Boyko E, Voothuluru P & Gill BS 2005 Inheritance and molecular mapping of new greenbug resistance genes in wheat germplasms derived from *Aegilops tauschii*. Theoretical and Applied Genetics 111: 831-837.
10268.	Jia GF, Chen PD, Qin GJ, Bai GH, Wang XU, Wang SL, Zhou B, Zhang SZ & Liu DJ 2005 QTLs for Fusarium head blight response in a wheat DH population of Wangshuibai / Alondra 's'. Euphytica 146: 183-191.
10269.	Xu XY, Bai GH, Carver BF & Shaner GE 2005 A QTL for early heading in wheat cultivar Suwon 92. Euphytica 146: 233-237.
10270.	Jin Y & Singh RP 2006 Resistance in U.S. wheat to recent eastern African isolates of *Puccinia graminis* f. sp. *tritici* with virulence to resistance gene *Sr31*. Plant Disease 90: 476-480.
10271.	Zheng QP, Li QA, Wang XU, Wang HY, Lang SP, Wang YN, Wang SL, Chen PD & Liu DJ 2005 Development and characterization of a *Triticum aestivum- Haynaldia villosa* translocation line T4VS.4DL conferring resistance to wheat spindle streak mosaic virus. Euphytica 145: 317-320.
10272.	Uauy C, Brevis JC, Chen XM, Khan I, Jackson L, Chicaiza O, Distenfeld A, Fahima T & Dubcovsky J 2005 High-temperature adult-plant stripe rust resistance gene *Yr36* from *Triticum turgidum* ssp. *dicoccoides* is closely linked to the grain protein content locus *Gpc-B1*. Theoretical and Applied Genetics 112: 97-105.
10273.	Narasimhamoorthy B, Gill GS, Fritz AK, Nelson JC & Brown-Guerdira GL 2006 Advanced backcross QTL analysis of a hard winter wheat X synthetic wheat population. Theoretical and Applied Genetics 112: 787-796.
10274.	Srnic G, Murphy JP, Lyerly JH, Leath S & Marshall DS 2005 Inheritance and chromosomal assignment of powdery mildew resistance genes in two winter wheat germplasm lines. Crop Sci 45: 1578-1586.
10275.	Mares D, Mrva K, Cheong J, Williams K, Watson B, Storlie E, Sutherland M & Zou Y 2005 A QTL located on chromosome 4A associated with dormancy in white- and red-grained wheats of diverse origin. Theoretical and Applied Genetics 111: 1357-1364.
10276.	Yang J, Bai GH, & Shaner GE 2005 Novel quantitative trait loci (QTL) for Fusarium head blight resistance in wheat cultivar Chokwang. Theoretical and Applied Genetics 111: 1571-1579.
10277.	Tolmay VL, Du Toit F & Smith CM 2005 Registration of seven Russian wheat aphid resistant near isogenic lines developed in South Africa. Crop Science 46: 478-480.
10278.	Groenewald JZ, Fourie M, Marais AS & Marais GF 2005 Extension and use of physical map of the *Thinopyrum*-derived *Lr19* translocation. Theoretical and Applied Genetics 112: 131-138.
10279.	Mallard S, Gaudet D, Aldeia A, Abelard C, Bernard AL, Sourdille P & Dedryver F 2005 Genetic analysis of durable resistance to yellow rust in bread wheat. Theoretical and Applied Genetics 110: 1401-1409.
10280.	Nalam VJ, Vales MI, Watson CJW, Kianian SF & Riera-Lizarazu O 2006 Map-based analysis of genes affecting the brittle rachis character in tetraploid wheat (*Triticum turgidum* L.). Theoretical and Applied Genetics 112: 373-381.
10281.	Rosewarne GM, Singh RP, Huerta-Espino J, William HM, Bouchet S, Cloutier S, McFadden H & Lagudah ES 2006 Leaf tip necrosis, molecular markers and *beta*1-

	proteasome subunits associated with the slow rusting resistance genes *Lr46/Yr29*. Theoretical and Applied Genetics 112: 500-508.
10282.	Lin F, Xue SL, Zhang ZZ, Zhang CQ, Kong ZX, Yao GQ, Tian DG, Zhu HL, Li CJ, Cao Y, Wei JB, Luo QY & Ma ZQ 2006 Mapping QTL associated with resistance to *Fusarium* head blight in the Nanda2419 x Wangshuibai population. II: Type I resistance. Theoretical and Applied Genetics 112: 528-535.
10283.	Christiansen MJ, Feenstra B, Skovgaard IM & Andersen SB 2006 Genetic analysis of resistance to yellow rust in hexaploid wheat using a mixture model for multiple crosses. Theoretical and Applied Genetics 112: 581-591.
10284.	Liu DC, Zhang HY, Wang J, Sun JH, Guo XL & Zhang AM 2005 Allelic variation, sequence determination and microsatellite screening at the *Xgwm261* locus in Chinese hexaploid wheat (*Triticum aestivum*) varieties. Euphytica 145: 102-112.
10285.	Raman H, Zhang K, Cakir M, Appels R, Garvin DF, Maron LG, Kochian LV, Moroni JS, Raman R, Imtiaz M, Drake-Brochman F, Waters I, Martin P, Sasaki T, Yamamoto Y, Matsumoto H, Hebb DM, Delhaize E & Ryan PR 2005 Molecular characterization and mapping of ALMY1, the aluminium-tolerance gene of bread wheat (*Triticum aestivum* L.). Genome 48: 781-791.
10286.	Delhaize E, Ryan PR, Hebb DM, Yamamoto Y, Sasaki T & Matsumoto H 2004 Engineering high-level aluminum tolerance in barley with the ALMT1 gene. Proceedings of the National Academy of Sciences USA 101: 15249-15254.
10287.	McCartney CA, Somers DJ, Humphreys DG, Lukow O, Ames N, Noll J, Cloutier S & McCallum BD 2003 Mapping quantitative trait loci controlling agronomic traits in the spring wheat cross RL4452 x 'AC Domain'. Genome 48: 870-883.
10288.	Beales J, Laurie DA & Devos KM 2005 Allelic variation at the *AP1* and *PhyC* loci in hexaploid wheat is associated but not perfectly correlated with vernalization response. Theoretical and Applied Genetics 110: 1099-1107.
10289.	Devos KM, Beales J, Ogihara Y & Doust AN 2005 Comparative sequence analysis of the *Phytochrome C* gene and its upstream region in allohexaploid wheat reveals new data on the evolution of its three constituent genomes. Plant Molecular Biology 58: 625-641.
10290.	Sun DJ, He ZH, Xia XC, Zhang LP, Morris CF, Appels R, Ma WJ & Wang H 2005 A novel STS marker for polyphenol oxidase activity in bread wheat. Molecular Breeding 16: 209-218.
10291.	Thomas J, Fineberg N, Penner G, McCartney C, Aung T, Wise I & McCallum B 2005 Chromosome location and markers of *Sm*1: a gene of wheat that conditions antibiotic resistance to orange wheat blossom midge. Molecular Breeding 15: 183-192.
10292.	Srichumpa P, Brunner S, Keller B & Yahiaoui N 2005 Allelic series of four powdery mildew resistance genes at the *Pm3* locus in hexaploid bread wheat. Plant Physiology 139: 885-895.
10293.	ter Steege MW, den Ouden FM, Lambers H, Stam P, Peeters AJM 2005 Genetic and physiological architecture of early vigor in *Aegilops tauschii*, the D-genome donor of hexaploid wheat. A quantitative trait loci analysis. Plant Physiology 139: 1078-1094.
10294.	Kane NA, Danyluk J, Tardif G, Ouellet F, Laliberte' J-F, Limin AED, Fowler B & Sarhan F 2005 TaVRT-2, a member of the StMADS-11 clade of flowering repressors, is regulated by vernalization and photoperiod in wheat. Plant Physiology 138: 2354-2363.
10295.	Kubo A, Rahman S, Utsumi Y, Li ZY, Mukai Y, Yamamoto M, Ugaki M, Harada K, Satoh H, Konik-Rose C, Morell M & Nakamura Y 2005 Complementation of sugary-1 phenotype

	in rice endosperm with the wheat isoamylase 1 gene supports a direct role for isoamylase 1 amylopectin biosynthesis. Plant Physiology 137: 43-56.
10296.	Olmos S, Distelfeld A, Chicaiza O, Schlatter AR, Fahima T, Echenique V & Dubcovsky J 2003 Precise mapping of a locus affecting grain protein content in durum wheat. Theoretical and Applied Genetics 107: 1243-1251.
10297.	Distelfeld A, Uauy C, Fahima T & Dubcovsky J 2006 Physical map of the wheat high-grain protein content gene *Gpc-B1* and development of a high-throughput marker. New Phytologist 169: 753-763.
10298.	Uauy C, Brevis JC & Dubcovsky J 2006 The high grain protein content gene *Gpc-B1* accelerates senescence and has pleiotropic effects on protein content in wheat. Journal of Experimental Botany 57: 2785-2794.
10299.	Yan L, Loukoianov A, Blechl A, Tranquilli G, Ramakrishna W, SanMiguel P, Bennetzen JL, Echenique V & Dubcovsky J 2004 The wheat VRN2 gene is a flowering repressor down-regulated by vernalization. Science 303: 640-1644.
10300.	Loukoianov A, Yan L, Blechl A, Sanchez A & Dubcovsky J 2005 Regulation of VRN-1 vernalization genes in normal and transgenic polyploid wheat. Plant Physiology 138: 2364-2373.
10301.	Dubcovsky J, Loukoianov A, Fu D, Valarik M, Sanchez A & Yan L 2005 Effect of photoperiod on the regulation of wheat vernalization genes VRN1 and VRN2. Plant Molecular Biology 60: 469-480.
10302.	Miller AK, Galiba G & Dubcovsky J 2006 A cluster of eleven CBF transcription factors is located at the frost tolerance locus *Fr-A*^{m}2 in *Triticum monococcum*. Molecular and General Genomics 275: 193-203.
10303.	Carrera A, Echenique V, Zhang W, Helguera M, Manthey F, Picca A, Cervigni G & Dubcovsky J 2007 A deletion at the *Lpx-B1* locus is associated with low lipoxygenase activity and improved pasta color in durum wheat (*Triticum turgidum* ssp. *durum*). Journal of Cereal Science 45: 67-77.
10304.	Hua C, Takata K, Yang-Fen Z, Ikeda TM, Yanaka M, Nagamine T & Fujimaki H 2005 Novel high molecular weight glutenin subunits at the *Glu-D1* locus in wheat landraces from the Xinjiang District of China and relationship with winter habit. Breeding Science 55: 459-463.
10305.	Ikeda TM, Ohnishi N, Nagamine T, Oda S, Hisatomi T & Yano H 2005 Identification of new puroindoline genotypes and their relationship to flour texture among wheat cultivars. Journal of Cereal Science 41: 1-6.
10306.	Lu CM & Lu BR 2005 Molecular characterization of the HMW glutenin genes *D*^{t}x1.5 + *D*^{t}y10 from *Aegilops tauschii* and their PCR-mediated recombinants. Molecular Breeding 15: 247-255.
10307.	Nagy IJ, Takács I, Juhász A, Tamás L & Bedo Z 2005 Identification of a new class of recombinant prolamin genes in wheat. Genome 48: 840-847.
10308.	Mackie AM, Lagudah ES, Sharp PJ & Lafiandra D 1996 Molecular and biochemical characterisation of HMW glutenin subunits from *T. tauschii* and the D genome of hexaploid wheat. Journal of Cereal Science 23: 213-225.
10309.	Kirby J, Vinh HT, Reader SM & Dudnikov A Ju 2005 Genetic mapping of the *Acph1* locus in *Aegilops tauschii*. Plant Breeding 124: 523-524.
10310.	Heyns I, Groenewald E, Marais F, Du Toit F & Tolmay V 2006 Chromosomal location of the Russian wheat aphid resistance gene, *Dn5*. Crop Science 46: 630-636.

10311.	Huo HL, Luo J & He GY 2006 Cloning and sequence analysis of *Pina* mutations in *Aegilops*. GenBank entry, unpublished.
10312.	Law CN, Bhandari DG, Salmon SE, Greenwell PW, Foot IM, Cauvain SP, Sayers EJ & Worland AJ 2005 Novel genes on chromosome 3A influencing breadmaking quality in wheat, including a new gene for loaf volume, *Lvl 1*. Journal of Cereal Science 41: 317-326.
10313.	Chen F, He Z, Xia X, Lillemo M & Morris C 2005 A new puroindoline b mutation present in Chinese winter wheat cultivar Jingdong 11. Journal of Cereal Science 42: 267-269.
10314.	Chen M, Wilkinson M, Tosi P, He G & Shewry P 2005 Novel puroindoline and grain softness protein alleles in *Aegilops* species with the C, D, S, M and U genomes. Theoretical and Applied Genetics 111: 1159-1166.
10315.	Simeone M, Gedye KR, Mason-Gamer R, Gill BS & Morris CF 2006 Conserved regulator elements identified from a comparative puroindoline gene sequence survey of *Triticum* and *Aegilops* diploid taxa. Journal of Cereal Science 44: 21-33.
10316.	Chang C, Zhang H, Xu J, Li W, Li G, You M & Li B 2006 Identification of allelic variations of puroindoline genes controlling grain hardness in wheat using a modified denaturing PAGE. Euphytica 152: 225-234.
10317.	Ahmed N, Maekawa M, Utsugi S, Rikiishia K, Ahmad A & Noda K 2006 The wheat *Rc* gene for red coleoptile colour codes for a transcriptional activator of late anthocyanin biosynthesis genes. Journal of Cereal Science 44: 54-58.
10318.	Lei ZS, Gale KR, He ZH, Gianibelli C, Larroque O, Xia, XC, Butow BJ & Ma W 2006 Y-type gene specific markers for enhanced discrimination of high-molecular weight glutenin alleles at the *Glu-B1* locus in hexaploid wheat. Journal of Cereal Science 43: 94-101.
10319.	Hassani ME, Gianibelli MC, Shariflou MR & Sharp PJ 2004 Molecular structure of a novel y-type HMW glutenin subunit gene present in *Triticum tauschii*. Euphytica 141: 191-198.
10320.	Lu CM, Yang WY, Zhang WJ & Lu B-R 2005 Identification of SNPs and development of allelic specific PCR markers for high molecular weight glutenin subunit D^tx1.5 from *Aegilops tauschii* through sequence characterization. Journal of Cereal Science 41: 13-18.
10321.	Kan Y, Wan Y, Beaudoin F, Leader DJ, Edwards K, Poole R, Wang D, Mitchell RAC & Shewry PR 2006 Transcriptome analysis reveals differentially expressed storage protein transcripts in seeds of *Aegilops* and wheat. Journal of Cereal Science 44: 75-85.
10322.	Shailaja K, Rathore M, Puri N, Yadav D & Singh NK 2002 PCR amplification of the hypervariable region of wheat triticin genes. Journal of Cereal Science 35: 129-134.
10323.	Wang J-R, Yan Z-H, Wei Y-M, Nevo E, Baum B & Zheng Y-L 2006 Molecular characterization of dimeric *alpha*-amylase inhibitor genes in wheat and development of genome allele-specific primers for the genes located on chromosome 3BS and 3DS. Journal of Cereal Science 43: 360-368.
10324.	Wang J-R, Wei Y-M, Yan Z-H & Zheng Y-L 2005 Detection of single nucleotide polymorphisms in 24 kDa dimeric *alpha*-amylase inhibitors from cultivated wheat and its diploid putative progenitors. Biochemica et Biophysica Acta 1723: 309-320.
10325.	Gale KR, Blundell MJ & Hill AS 2004 Development of a simple, antibody-based test for granule-bound starch synthase *Wx-B1b* (Null-4A) wheat varieties. Journal of Cereal Science 40: 85-92.
10326.	Mateos-Hernandez M, Singh R, Hulbert SH, Bowden RL, Huerta-Espino J, Gill BS & Brown-Guedira G 2006 Targeted mapping of ESTs linked to the adult plant resistance gene *Lr46* in wheat using synteny with rice. Functional & Integrative Genomics 6: 122-131.

10327.	An X, Li Q, Yan Y, Xiao Y, Hsam SLK & Zeller FJ 2005 Genetic diversity of European spelt wheat (*Triticum aestivum* ssp. *spelta* L. em Thell.) revealed by glutenin subunit variations at the *Glu-1* and *Glu-3* loci. Euphytica 146: 193-201.
10328.	Kuraparthy V, Chunneja P, Dhaliwal HS, Kaur S, Bowden RL & Gill BS 2007 Charactertization and mapping of cryptic alien introgression from *Aegilops geniculata* with new leaf rust and stripe rust resistance genes *Lr57* and *Yr40* in wheat. Theoretical and Applied Genetics 114: 1379-1389.
10329.	Kuraparthy V, Sood S, Dhaliwal HS, Chhuneja P & Gill BS. 2007 Identification and mapping of a tiller inhibition gene (*tin3*) in wheat. Theoretical and Applied Genetics 114: 285-294.
10330.	Torada A, Koike M, Mochida K & Ogihara Y 2006 SSR-based linkage map with new markers using an intraspecific population of common wheat. Theoretical and Applied Genetics 112: 1042-1051.
10331.	Li ZF, Zheng TC, He ZH, Li GQ, Xu SC, Li XP, Yang GY, Singh RP & Xia XC 2006 Molecular tagging of stripe rust resistance gene *YrZh84* in Chinese wheat line Zhou 8425B. Theoretical and Applied Genetics 112: 1089-1103. DOI: 10.1007/s00122-006-0211-8.
10332.	Xing QH, Ru ZG, Zhou CJ, Xue X, Liang CY, Yang DE, Jin DM & Wang B 2003 Genetic analysis, molecular tagging and mapping of the thermo-sensitive gene (*wtms1*) in wheat. Theoretical and Applied Genetics 107: 1500-1504.
10333.	Guo RX, Sun DF, Tan ZB, Rong DF & Li CD 2006 Two recessive genes controlling thermophotoperiod-sensitive male sterility in wheat. Theoretical and Applied Genetics 112: 1271-1276.
10334.	Chu C-G, Faris JD, Friesen TL & Xu SS 2006 Molecular mapping of hybrid necrosis genes *Ne1* and *Ne2* in hexaploid wheat using microsatellite markers. Theoretical and Applied Genetics 112: 1374-1381.
10335.	Liang SS, Suenaga K, He ZH, Wang ZL, Liu HY, Wang DS, Singh RP, Sourdille P & Xia XC 2006 Quantitative trait loci mapping for adult-plant resistance to powdery mildew in bread wheat. Phytopathology 96: 784-789.
10336.	Bariana HS. 2003 Personal communication.
10337.	Lu HJ, Fellers JP, Friesen TL, Meinhardt SW & Faris JD 2004 Genomic analysis and marker development for the *Tsn1* locus in wheat using bin-mapped ESTs and flanking BAC contigs. Theoretical and Applied Genetics 112: 1132-1142.
10338.	Blanco A, Simeone R & Gadaleta A 2006 Detection of QTLs for grain protein content in durum wheat. Theoretical and Applied Genetics 112: 1195-1204.
10339.	Li GQ, Li ZF, Yang WY, Zhang Y, He ZH, Xu SC, Singh RP, Qu TT & Xia XC 2006 Molecular mapping of stripe rust resistance gene *YrCH42* in Chinese wheat cultivar Chuanmai 42 and its allelism with *Yr24* and *Yr26*. Theoretical and Applied Genetics 112: 1434-1440.
10340.	Xu X-Y, Bai G-H, Carver BF, Shaner GE & Hunger RM 2006 Molecular characterization of a powdery mildew resistance gene in wheat cultivar Suwon 92. Phytopathology 96: 496-500.
10341.	Arraiano LS, Chartrain L, Bossolini E, Slatter HN, Keller B & Brown JKM 2007 A gene in European wheat cultivars for resistance to an African isolate of *Mycosphaerella graminicola*. Plant Pathology 56: 73-78.
10342.	Miranda LM, Murphy JP, Marshall D, Cowger C & Leath S 2007 Chromosomal location of *Pm35*, a novel *Aegilops tauschii* derived powdery mildew resistance gene introgressed into common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 114: 1451-1456.

10343.	Williams KJ, Willsmore KL, Olson S, Matic M & Kuchel H 2006 Mapping of a novel QTL for resistance to cereal cyst nematode in wheat. Theoretical and Applied Genetics 112: 1480-1486.
10344.	Singh PK, Gonzalez-Hernandez JL, Mergoum M, Ali S, Adhikari TB, Kianian SF, Elias EM & Hughes GR 2006 Identification and molecular mapping of a gene conferring resistance to *Pyrenophora tritici-repentis* race 3 in tetraploid wheat. Phytopathology 96: 885-889.
10345.	Pathan AK & Park RF 2006 Evaluation of seedling and adult plant resistance to leaf rust in European wheat cultivars. Euphytica 149: 327-342.
10346.	Long DL, Leonard KJ & Roberts JJ 1998 Virulence and diversity of wheat leaf rust in the United States in 1993 to 1995. Plant Disease 82: 1391-1400.
10347.	Cowling SG, Brule-Babel AL, Somers DJ & Lamari L 2006 Identification and mapping of *Stb13*, an isolate-specific wheat resistance gene to isolate MG96-36 (group 1) of *Mycosphaerella graminicola*. Manuscript
10348.	Brule-Babel AL 2007 Personal communication.
10349.	Mardi M, Pazouki L, Delavar H, Kazemi MB, Ghareyazie B, Steiner B, Nolz R, Lemmens M & Buerstmeyr H 2006 QTL analysis of resistance to Fusarium head blight in wheat using a 'Frontana'-derived population. Plant Breeding 125: 313-317.
10350.	Tadesse W, Hsam SLK & Zeller FJ 2006 Evaluation of common wheat cultivars for tan spot resistance and chromosomal location of a resistance gene in cultivar 'Salamouni'. Plant Breeding 125: 318-322.
10351.	Houshmand S, Knox RE, Clarke FR & Clarke JM 2007 Microsatellite markers flanking a stem solidness gene on chromosome 3BL in durum wheat. Molecular Breeding 20: 261-270.
10352.	Guan HT, Guo YH, Wang YB, Liu TG, Lin RM & Xu SC 2005 Microsatellite marker of the resistance gen *YrSp* to wheat stripe rust. Sci Agric Sin 38: 1574-1577. (in Chinese).
10353.	Gosal KS 2000 Aspects of Resistance to Wheat Stripe Rust in Australia. PhD Thesis, The University of Sydney
10354.	Zhou KJ, Wang SH, Feng YQ, Liu ZX & Wang GX 2006 The 4E-*ms* system of producing hybrid wheat. Crop Science 46: 250-255.
10355.	Zhou KJ, Wang SH, Feng YQ, Ji WQ & Wang GX 2007 A new male sterile mutant in wheat (*Triticum aestivum*). Euphytica 159: 403-410.
10356.	Blanco A, Gadaleta A, Cenci A, Carluccio AV, Abdelbacki AMM & Simeone R 2008 Molecular mapping of the novel powdery mildew resistance gene *Pm36* introgressed from *Triticum turgidum* var. *dicoccoides* in durum wheat. Theoretical and Applied Genetics 117: 135-142.
10357.	He ZH, Xu ZH, Xia LQ, Xia XC, Yan J, Zhang Y & Chen XM 2006 Genetic variation for waxy proteins and starch properties in Chinese winter wheats. Cereal Research Communications 34: 1145-1151.
10358.	Bovill WD, Ma W, Ritter K, Collard BCY, Davis M, Wildermuth GB & Sutherland MW 2006 Identification of novel QTL for resistance to crown rot in the doubled haploid wheat population 'W21MMT70' / 'Mendos'. Plant Breeding 125: 538-543.
10359.	Das BK, Saini A, Bhagwat SG & Jawali N 2006 Development of SCAR markers for identification of stem rust resistance gene *Sr31* in the homozygous or heterozygous condition in bread wheat. Plant Breeding 125: 544-549.
10360.	Bougot Y, Lemoine J, Pavoine MT, Guyomar'ch H, Gautier V, Muranty H & Barloy D 2006 A major QTL effect controlling resistance to powdery mildew in winter wheat at the adult plant stage. Plant Breeding 125: 550-556.

10361.	McCartney CA, Somers DJ, Lukow O, Ames N, Noll J, Cloutier S, Humphries DG & McCallum BD 2006 QTL analysis of quality traits in the spring wheat cross RL4452 x 'AC Domain'. Plant Breeding 125: 565-575.
10362.	Watanabe N, Fujii Y, Takesada N & Martinek P 2006 Cytological and microsatellite mapping of the gene for brittle rachis in a *Triticum aestivum-Aegilops tauschii* introgression line. Euphytica 151: 63-68.
10363.	Kumar N, Kulwal PL, Gaur A, Tyagi AK, Khurana JP, Khurana P, Balyan HS & Gupta PK 2006 QTL analysis for grain weight in common wheat. Euphytica 151: 235-144.
10364.	Guo PG, Bai GH, Li RH, Shaner G & Baum M 2006 Resistance gene analogs associated with Fusarium head blight resistance in wheat. Euphytica 151: 251-261.
10365.	Weng DX, Xu SC, Lin RM, Wan AM, Li JP & Wu LR 2005 Microsatellite marker linked with stripe rust resistant gene*Yr9* in wheat. Acta Genetica Sinica 32: 937-941. (In Chinese with English summary).
10366.	Qiu YC, Sun XL, Zhou RH, Kong XY, Zhang SS & Jia JZ 2006 Identification of microsatellite markers linked to powdery mildew resistance gene *Pm2* in wheat. Cereal Research Communications 34: 1267-1273.
10367.	Zhu ZD, Zhou RH, Kong XY, Dong YC & Jia JZ 2006 Microsatellite marker identification of a *Triticum aestivum-Aegilops umbellulata* substitution line with powdery mildew resistance. Euphytica 150: 149-153.
10368.	Gupta SK, Charpe A, Koul S, Haque QMR & Prabhu KV 2006 Development and validation of SCAR markers co-segregating with an *Agropyron elongatum* derived leaf rust resistance gene *Lr24* in wheat. Euphytica 150: 233-240.
10369.	Li ZF, Xia XC, Zhou XC, Niu YC, He ZH, Zhang Y, 020, Wan AM, Wang DS, Chen XM, Lu QL & Singh RP 2006 Seedling and slow rusting resistance to stripe rust in Chinese common wheats. Plant Disease 90: 1302-1312.
10370.	Wang YB, Xu SC, Xu Z, Liu TG & Lin RM 2006 A microsatellite marker linked to the stripe rust resistance gene *YrV23* in the wheat variety Vilmorin 23. Hereditas (Beijing) 28: 306-310. (In Chinese with English summary).
10371.	Yao ZJ, Lin RM, Xu SC, Li ZF, Wan AM & Ma ZY 2006 The molecular tagging of the yellow rust resistance gene *Yr7* in wheat transferred from differential host Lee using microsatellite markers. Scientia Agricultura Sinica 39: 1146-1152. (In Chinese with English summary).
10372.	Perugini LD, Murphy JP, Marshall DS & Brown-Guedira G 2007 *Pm37*, a new broadly effective powdery mildew resistance gene from *Triticum timopheevii*. Theoretical and Applied Genetics 116: 417-425.
10373.	Spielmeyer W 2007 Personal communication.
10374.	Spielmeyer W, McIntosh RA, Kolmer J & Lagudah ES 2005 Powdery mildew reaction and *Lr34/Yr18* genes for adult plant resistance to leaf rust and stripe rust cosegregate at a locus on the short arm of chromosome 7D of wheat. Theoretical and Applied Genetics 111: 731-735.
10375.	Kuraparthy V, Sood S, Chhuneja P, Dhaliwal HS, Kaur S, Bowden RL & Gill BS 2007 A cryptic wheat-*Aegilops triuncialis* translocation with leaf rust resistance gene *Lr58*. Crop Science 47: 1995-2003.
10376.	Singh PK & Hughes GR 2006 Inheritance of resistance to the chlorosis component of tan spot of wheat caused by *Pyrenophora tritici-repentis*, races 1 and 3. Euphytica 152: 413-420.

10377.	Kottearachchi NS, Uchino N & Kato K 2007 Increased grain dormancy in white-grained wheat by introgression of preharvest grain dormancy QTLs. Euphytica 152: 421-428.
10378.	Khlestkina EK, Pshenichnikova TA, Roder MS, Salina EA, Arbuzova EA & Borner A 2006 Comparative mapping of genes for glume coloration and pubescence in hexaploid wheat (*Triticum aestivum*). Theoretical and Applied Genetics 113: 801-807.
10379.	Gupta SK, Charpe A, Prabhu KV & Haque QMR 2006 Identification and validation of molecular markers linked to the leaf rust resistance gene *Lr19* in wheat. Theoretical and Applied Genetics 113: 1027-1036.
10380.	Bossolini E, Krattinger SG & Keller B 2006 Development of simple sequence repeat markers specific for the *Lr34* resistance region of wheat using sequence information from rice and *Aegilops tauschii*. Theoretical and Applied Genetics 113: 1049-1062.
10381.	Zhao HX, Liu XM & Chen M-S 2006 *H22*, a major resistance gene to the Hessian fly (*Mayetiola destructor*), is mapped to the distal region of chromosome 1DS. Theoretical and Applied Genetics 113: 1491-1496.
10382.	Kuchel H, Hollamby G, Langridge P, Williams K & Jefferies SP 2006 Identification of genetic loci associated with ear-emergence in bread wheat. Theoretical and Applied Genetics 113: 1103-1112.
10383.	Khleskina EK, Roder MS, Unger O, Meinel A & Borner A 2007 More precise map position and origin of a durable non-specific adult plant disease resistance against stripe rust (*Puccinia striiformis*) in wheat. Euphytica 153: 1-10.
10384.	Ma LQ, Zhou EF, Huo NX, Zhou RH, Wang GY & Jia JZ 2007 Genetic analysis of salt tolerance in a recombinant inbred population of wheat (*Triticum aestivum* L.). Euphytica 153: 109-117.
10385.	Sun DJ, He ZH, Xia XC, Zhang LP, Morris CF, Appels, Ma WJ & Wang W 2005 A novel STS marker for polyphenol oxidase activity in bread wheat. Molecular Breeding 16: 209-218.
10386.	He XY, He ZH, Zhang LP, Sun DJ, Morris CF, Fuerst EP & Xia XC 2007 Allelic variation of polyphenol oxidase (PPO) genes located on chromosomes 2A and 2D and development of functional markers for the PPO genes in common wheat. Theoretical and Applied Genetics 115: 47-58.
10387.	Lagudah ES, McFadden H, Singh RP, Huerta-Espino, Bariana HS & Spielmeyer W 2006 Molecular genetic characterization of the *Lr34/Yr18* slow rusting resistance gene region in wheat. Theoretical and Applied Genetics 114: 21-30.
10388.	Wang T, Xu SS, Harris MO, Hu JG, Liu LW & Cai XW 2006 Genetic characterization and molecular mapping of Hessian fly resistance genes derived from *Aegilops tauschii* in synthetic wheat. Theoretical and Applied Genetics 113: 611-618.
10389.	Zhou RH, Zhu ZD, Kong XY, Huo NX, Tian QZ, Li P, Jin CY, Dong YC & Jia JZ 2006 Development of wheat near-isogenic lines for powdery mildew resistance. Theoretical and Applied Genetics 110: 640-648.
10390.	Janni M, Di Giovanni M, Roberti S, Capododicasa C & D'Ovidio R 2006 Characterization of expressed *Pgip* genes in rice and wheat reveals similar extent of sequence variation to dicot PGIPs and identifies an active PGIP lacking an entire LRR repeat. Theoretical and Applied Genetics 113: 1233-1245.
10391.	Li G, He Z, Lillemo M, Sun Q & Xia X 2008 Molecular characterization of allelic variations at *Pina* and *Pinb* loci in Shandong wheat landraces, historical and current cultivars. Journal of Cereal Science 47: 510-517.

10392.	Dobrovolskaya O, Arbuzova VS, Lohwasser U, Roder MS & Borner A 2006 Microsatellite mapping of complementary genes for purple grain colour in bread wheat (*Triticum aestivum* L.). Euphytica 150: 355-364.
10393.	Yao GQ, Zhang JL, Yang LL, Xu HX, Jiang YM, Xiong L, Zhang CQ, Zhang ZZ, Ma ZQ & Sorrells ME 2007 Genetic mapping of two powdery mildew resistance genes in einkorn (*Triticum monococcum* L.) accessions. Theoretical and Applied Genetics 114: 351-358.
10394.	Tadesse W, Hsam SLK, Wenzel G & Zeller FJ 2006 Identification and monosomic analysis of tan spot resistance genes in synthetic wheat lines (*Triticum turgidum* L. x *Aegilops tauschii* Coss.). Crop Science 46: 1212-1217.
10395.	Lanning SP, Fox P, Elser J, Martin JM, Blake NK & Talbert LE 2006 Microsatellite markers associated with a secondary stem solidness locus in wheat. Crop Science 46: 1701-1703.
10396.	Heyns I, Groenewald E, Marais F, du Toit F & Tolmay V 2006 Chromosomal location of the Russian wheat aphid resistance gene *Dn5*. Crop Science 46: 630-636.
10397.	Jyoti JL, Qureshi JA, Michaud JP & Martin TJ 2006 Virulence of two Russian wheat aphid biotypes to eight wheat cultivars at two temperatures. Crop Science 46: 774-780.
10398.	Berzonsky WA, Gebhard BL, Gamotin E, Leach GD & Ali S 2007 A reciprocal monosomic analysis of the scab resistant spring wheat (*Triticum aestivum* L.) cultivar 'Frontana'. Plant Breeding 126: 234-239.
10399.	Marais GF, McCallum B & Marais AS 2008 Wheat leaf rust resistance gene *Lr59* derived from Aegilops peregrina. Plant Breeding 127: 340-345.
10400.	Hiebert CW, Thomas JB, McCallum BD & Somers DJ 2008 Genetic mapping of the wheat leaf rust resistance gene Lr60 (LrW2). Crop Science 48: 1020-1026.
10401.	Kumar S, Stack RW, Friesen TL & Faris JD 2007 Identification of a novel Fusarium head blight resistance quantitative locus on chromosome 7A in tetraploid wheat. Phytopathology 97: 592-597.
10402.	Otto CD, Kianian SF, Elias E, Stack RW & Joppa LR 2002 Genetic dissection of a major QTL in tetraploid wheat. Plant Molecular Biology 48: 625-632.
10403.	Liu SX, Zhang XL, Pumphhrey O, Stack RW, Gill BS & Anderson JA 2006 Complex microcolinearity among wheat, rice, and barley revealed by fine mapping of the genomic region harboring a major QTL for resistance to Fusarium head blight in wheat. Functional and Integrative Genomics 6: 83-89.
10404.	Nalini E, Ghagwat SG & Jawali N 2005 Validation of allele specific primers for identification of *Rht* genes among Indian bread wheat varieties. Cereal Research Communications 33: 439-446.
10405.	Tommasini L, Yahiaoui N, Srichumpa P & Keller B 2006 Development of functional markers specific for seven *Pm3* resistance alleles and their validation in the bread wheat gene pool. Theoretical and Applied Genetics 114: 165-175.
10406.	Yahiaoui N, Brunner S & Keller B 2006 Rapid generation of new powdery mildew resistance genes after wheat domestication. The Plant Journal 47: 85-98.
10407.	Dudnikov AJu 2007 An acid phosphatase gene set (*Acph-2*) of common wheat orthologous to *Acph1* of *Aegilops tauschii*. Cereal Research Communications 35: 11-13.
10408.	Qiu JW, Schurch AC, Yahiaoui N, Dong LL, Fan HJ, Zhang ZJ, Keller B & Ling HQ 2007 Physical mapping and identification of a candidate for the leaf rust resistance gene *Lr1* of wheat. Theoretical and Applied Genetics 115: 159-168.
10409.	Johnson JC, Appels R & Bhave M 2006 The *PDI* genes of wheat and their syntenic relationship to the *esp2* locus of rice. Functional and Integrative Genomics 6: 104-121.

10410.	Raman R, Raman H, Johnstone K, Lisle C, Smith A, Martin P & Allen H 2005 Genetic and in silico comparative mapping of the polyphenol oxidase gene in bread wheat (*Triticum aestivum* L.). Functional and Integrative Genomics 5: 185-200.
10411.	Simeone R, Pasquapone A, Clodeveo ML & Blanco A 2002 Genetic mapping of polyphenol oxidase in tetraploid durum wheat. Cellular and Molecular Biology Letters 7: 763-769.
10412.	Watanabe N, Masum Akond ASMG & Nachit M 2006 Genetic mapping of the gene affecting polyphenol oxidase activity in tetraploid durum wheat. Journal of Applied Genetics 47: 201-205.
10413.	Lu HJ & Faris JD 2006 Macro- and microcolinearity between the genomic region of wheat chromosome 5B containing the *Tsn1* gene and the rice genome. Functional and Integrative Genomics 6: 90-103.
10414.	Baga M, Chodaparambil SV, Limin AE, Pecar M, Fowler DB & Chibbar 2007 Identification of quantitative trait loci and associated candidate genes for low-temperature tolerance in cold-hardy winter wheat. Functional and Integrative Genomics 7: 53-68.
10415.	Gill BS, Friebe B, Raupp WJ, Wilson DL, Cox TS, Sears RG, Brown-Guedira G & Fritz AK 2006 Wheat Genetics Resource Center: The first 25 years. Advances in Agronomy 89: 73-136.
10416.	Lin F & Chen XM 2007 Genetics and molecular mapping of genes for race- specific and all-stage resistance and non-specific high-temperature adult-plant resistance to stripe rust in spring wheat cultivar Alpowa. Theoretical and Applied Genetics 114: 1277-1287.
10417.	Nakamura S, Komatsuda T & Miura H 2007 Mapping diploid wheat homologues of *Arabidopsis* seed ABA signaling genes for seed dormancy. Theoretical and Applied Genetics 114: 1129-1139.
10418.	He XY, He ZH, Zhang LP, Sun DJ, Morris CF, Fuerst EP & Xia XC 2007 Allelic variation of polyphenol oxidase (PPO) genes located on chromosomes 2A and 2D and development of functional markers for the PPO genes in common wheat. Theoretical and Applied Genetics 115: 47-58.
10419.	Tadesse W, Schmolke M, Hsam SLK, Mohler V, Wenzel G & Zeller FJ 2007 Molecular mapping of resistance genes to tan spot [*Pyrenophora tritici-repentis*] in synthetic wheat lines. Theoretical and Applied Genetics 114: 855-862.
10420.	Huang L, Brooks SA, Li WL, Fellers JP, Trick HN & Gill BS 2003 Map-based cloning of leaf rust resistance gene *Lr21* from the large and polyploid genome of bread wheat. Genetics 164: 655-664.
10421.	Yan L, Fu D, Li C, Blechl A, Tranquilli G, Bonafede M, Sanchez A, Valarik M & Dubcovsky J 2006 The wheat and barley vernalization gene *VRN3* is an orthologue of *FT*. Proceedings National Academy of Sciences USA 103: 19581-19586.
10422.	Ciaffi M, Dominici L, Tanzarella OA & Porceddu E 1999 Chromosomal assignment of gene sequences coding for protein disulphide isomerase (PDI) in wheat. Theoretical and Applied Genetics 98: 405-410.
10423.	Ciaffi M, Paolacci AR, D'Aloisio E, Tanzarella OA & Porceddu E 2006 Cloning and characterization of wheat PDI (protein disulfide isomerase) homoeologous genes and promoter sequences. Gene 366: 209-218.
10424.	Johnson JC & Bhave M 2004 Molecular characterisation of the protein disulphide isomerase genes of wheat. Plant Science 167: 397-410.
10425.	Tohver M, Kann A, Täht R, Mihhalevski A & Hakman J 2005 Quality of triticale cultivars suitable for growing and bread-making in northern conditions. Food Chemistry 89: 125-132.

10426.	Zhang Y, Li Q, Yan Y, Zheng J, An X, Xiao Y, Wang A, Pei Y, Wang H, Hsam SLK & Zeller FJ 2006 Molecular characterization and phylogenetic analysis of a novel glutenin gene (Dy10.1^t) from *Aegilops tauschii*. Genome 49: 735-745.
10427.	Chen F, Yu Y, Xia X & He Z 2007 Prevalence of a novel puroindoline b allele in Yunnan endemic wheats (*Triticum aestivum* ssp. *yunnanense* King). Euphytica 156: 39-46.
10428.	Massa AN, Morris CF & Beecher B 2007 Personal communication.
10429.	Morris CF & GE King 2007 Registration of hard kernel puroindoline allele near-isogenic line hexaploid wheat genetic stocks. Journal of Plant Registrations 1: 67-68.
10430.	Pickering PA & Bhave M 2007 Comprehensive analysis of Australian hard wheat cultivars shows limited puroindoline allele diversity. Plant Science 172: 371-379.
10431.	Takeuchi et al. 2006 NCBI accession entry, unpublished.
10432.	Tanaka H, Morris CF, Haruna M & Tsujimoto H 2007 Prevalence of puroindoline alleles in wheat from eastern Asia including the discovery of a new SNP in puroindoline b. Plant Genetic Resources: Characterization and Utilization 6: 142-152.
10433.	Corona V, Gazza L, Zanier R & Pogna NE 2001 A tryptophan-to-arginine change in the tryptophan-rich domain of puroindoline b in five French bread wheat cultivars. Journal of Genetics and Breeding 55: 187-189.
10434.	Huang XQ, Cloutier S, Lycar L, Radovanovic N, Humphreys DG, Noll JS, Somers DJ & Brown PD 2006 Molecular detection of QTLs for agronomic and quality traits in a doubled haploid population derived from two Canadian wheats (*Triticum aestivum* L.). Theoretical and Applied Genetics 113: 753-766.
10435.	Smith PH, Hadfield J, Hart NJ, Koebner RMD & LA Boyd 2007 STS markers for the wheat yellow rust resistance gene *Yr5* suggest a NBS-LRR-type resistance gene cluster. Genome 50: 259-265.
10436.	Nelson JC, Andreescu C, Breseghello F, Finney PL, Gualberto D, Bergman CJ, Pena RJ, Perretant MR, Leroy P, Qualset CO & Sorrells ME 2006 Quantitative trait loci analysis of wheat quality traits. Euphytica 149: 145-159.
10437.	Monari AM, Simeone MC, Urbano M, Margiotta B & Lafiandra D 2005 Molecular characterization of new waxy mutants identified in bread and durum wheat. Theoretical and Applied Genetics 111: 1481-1489.
10438.	Uauy C, Distelfeld A, Fahima T, Blechl A, Dubcovsky J 2006 A NAC gene regulating senescence improves grain protein, zinc and iron content in wheat. Science 314: 1298-1300.
10439.	Wang JR, Yan ZH, Wei YM & Zheng YL 2004 A novel high-molecular-weight glutenin subunit gene *Ee1.5* from *Elytrigia elongate* (Host) Nevski. Journal of Cereal Science 40: 289-294.
10440.	Chantret N, Salse J, Sabot F. Rahman S, Bellec A, Bastien L, Dubois I, Dossat C, Sourdille P, Joudrier P, Gautier MF, Cattolico L, Beckert M, Aubourg S, Weissenbach J, Caboche M, Bernard M, Leroy P & Chalhoub B 2006 Molecular basis of evolutionary events that shaped the *hardness* locus in diploid and polyploid wheat species (*Triticum* and *Aegilops*). Plant Cell 17: 1033-1045.
10441.	Lane GB, Dunwell JM, Ray JA, Schmitt MR & Cuming AC 1993 Germin, a protein of early plant development, is an oxalate oxidase. Journal of Biological Chemistry 268: 12239-12242.
10442.	Feuillet C, Travella S, Stein N, Albar L, Nublat A & Keller B 2003 Map-based isolation of the leaf rust disease resistance gene *Lr10* from the hexaploid wheat (*Triticum aestivum* L.) genome. Proceedings of National Academy of Sciences USA 100: 15253-15258.

10443.	William HM, Singh RP, Huerta-Espino J, Palacios G & Suenaga K 2006 Characterization of genetic loci conferring adult plant resistance to leaf rust and stripe rust in spring wheat. Genome 49: 977-990.
10444.	Somers DJ 2007 Personal communication.
10445.	Somers DJ, Fedak G, Clarke J & Cao WG 2006 Mapping of FHB resistance QTLs in tetraploid wheat. Genome 49: 1586-1593.
10446.	Hiebert CW, Thomas JB, Somers DJ, McCallum BD & Fox SL 2007 Microsatellite mapping of adult-plant leaf rust resistance gene *Lr22a* in wheat. Theoretical and Applied Genetics (In press)
10447.	Ma HX, Zhang KM, Gao L, Bai GH, Chen HG, Cai ZX & Lu WZ 2006 Quantitative trait loci for resistance to fusarium head blight and deoxynivalenol accumulation in Wangshuibai wheat under field conditions. Plant Pathology 55: 739-745.
10448.	Chartrain L, Brading PA & Brown JKM 2005 Presence of the *Stb6* gene for resistance to septoria leaf blotch (*Mycosphaerella graminicola*) in cultivars used in wheat-breeding programmes worldwide. Plant Pathology 54: 134-143.
10449.	Yan ZH, Wei YM, Wang JR, Liu DC, Dai SF & Zheng YL 2006 Characterization of two HMW glutenin subunit genes from *T. aenitherum* Nevski. Genetica 127: 267-276.
10450.	Pahalawatta V & Chen XM. 2005 Genetic analysis and molecular mapping of wheat genes conferring resistance to the wheat stripe rust and barley stripe rust pathogens. Phytopathology 95: 427-432.
10451.	Singh K, Ghai M, Garg M, Chhuneja P, Kaur P, Schnurbusch, Keller B & Dhaliwal HS 2007 An integrated molecular linkage map of diploid wheat based on a *Triticum boeoticum* x *T. monococcum* RIL population. Theoretical and Applied Genetics 115: 301-312.
10452.	Lindsay MP, Lagudah ES, Hare RA & Munns R 2004 A locus for sodium exclusion (*Nax1*), a trait for salt tolerance, mapped in durum wheat. Functional Plant Biology 31: 1105-1114.
10453.	James RA, Davenport RJ & Munns R 2006 Physiologic characterization of two genes for Na^+ exclusion in durum wheat, *Nax1* & *Nax2*. Plant Physiology 142: 1437-1547.
10454.	Huang SB, Speilmeyer W, Lagudah ES, James RA, Platten JD, Dennis ES & Munns R 2006 A sodium transporter (HKT7) is a candidate for *Nax1*, a gene for salt tolerance in durum wheat. Plant Physiology 142: 1718-1727.
10455.	Byrt CS, Platten JD, Spielmeyer W, James RA, Lagudah ES, Dennis ES, Tester M & Munns R 2007 Plant Physiology 143: 1918-1928.
10456.	Liu S, Abate ZA, Lu H, Musket T, Davis GL & McKendry AL 2007 QTL associated with Fusarium head blight resistance in soft red winter wheat Ernie. Theoretical & Applied Genetics 115: 417-427.
10457.	Simons KJ, Fellers JP, Trick HN, Zhang ZC, Tai Y-S, Gill BS & Faris JD 2006 Molecular characterization of the major wheat domestication gene *Q*. Genetics 172: 547-555.
10458.	Liu Zh, Friesen TL, Ling H, Meinhardt SW, Oliver RP, Rasmussen JB & Faris JD 2006 The *Tsn1*-ToxA interaction in the wheat-*Stagonospora nodorum* pathosystem parallels that of the wheat-tan spot system. Genome 49: 1265-1273.
10459.	Friesen TL, Stukenbrock EH, Liu ZH, Meinhardt S, Ling H, Faris JD, Rasmussen JB, Solomon PS, McDonald BA & Oliver RP 2006 Emergence of a new disease as a result of interspecific virulence gene transfer. Nature Genetics 38: 953-956.
10460.	Schnurbusch T, Collins N, Eastwood RF, Sutton T, Jefferies SP & Langridge P 2007 Fine mapping and targeted SNP survey using rice-wheat colinearity in the region of the *Bo1* boron toxicity tolerance locus of bread wheat. Theoretical and Applied Genetics 115: 451-461.

10461.	Zhan SW, Mayama S & Tosa Y 2007 Identification of two genes for resistance to *Triticum* isolates of *Magnaporthe oryzae* in wheat. Genome 51: 216-221.
10462.	Hirata K, Tosa Y, Nakayashiki & Mayama S 2005 Significance of *PWT4-Rwt4* interaction in the species specificity of *Avena* isolates of *Magnaporthe oryzae* on wheat. Journal of General Plant Pathology 71: 340-344.
10463.	Seyfarth R, Feuillet, Schachermayr G, Messmer M, Winzeler M & Keller B 2000 Molecular mapping of the adult-plant rust resistance gene *Lr13* in wheat (*Triticum aestivum* L.). Journal of Genetics and Breeding 54: 193-198.
10464.	Draeger R, Gosman N, Steed A, Chandler E, Thomsett M, Srinivasachary, Schondelmaier J, Buerstmayr H, Lemmens M, Schmolke M, Mesterhazy A & Nicholson P 2007 Identification of QTLs for resistance to Fusarium head blight, DON accumulation and associated traits in the winter wheat variety Arina. Theoretical and Applied Genetics 115: 617-625.
10465.	Tommasini L, Schnurbusch T, Fossati D, Mascher F & Keller B 2007 Association mapping of *Stagonospora nodorum* blotch resistance in modern European winter wheat varieties. Theoretical and Applied Genetics 115: 697-708.
10466.	Beales J, Turner A, Griffiths S, Snape JW & Laurie DA 2007 A *Pseudo-Response Regulator* is misexpressed in the photoperiod insensitive *Ppd-D1a* mutant of wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 115: 721-733.
10467.	Hiebert CW, Thomas JB, Somers DJ, McCallum BD & Fox SL 2007 Microsatellite mapping of adult-plant resistance gene *Lr22a* in wheat. Theoretical and Applied Genetics 115: 877-884.
10468.	Yang Y, Zhao XL, Xia LQ, Chen XM, Xia XC, Yu Z, He ZH & Roder M 2007 Development and validation of a *Viviparous-1* STS marker for pre-harvest sprouting tolerance in Chinese wheats. Theoretical and Applied Genetics 115: 971-980.
10469.	Herrera-Foessel SA, Singh RP, Huerta-Espina, William M, Rosewarne G, Djurle A & Yuen J 2007 Identification and mapping of *Lr3* and a linked leaf rust resistance gene in durum wheat. Crop Science 47: 1459-1466.
10470.	Haberle J, Schmolke M, Schweizer G, Korzun V, Ebmeyer E, Zimmermann G & Hartl L 2007 Effects of two major Fusarium head blight resistance QTL verified in a winter wheat backcross population. Crop Science 47: 1823-1831.
10471.	Uphaus J, Walker E, Shankar M, Golzar H, Loughman R, Francki M & Ohm H 2007 Quantitative trait loci identified for resistance to Stagonospora glume blotch in wheat in the USA and Australia. Crop Science 47: 1813-1821.
10472.	Tsilo TJ, Jin Y & Anderson JA 2007 Microsatellite markers linked to stem rust resistance allele *Sr9a* in wheat. Crop Science 47: 2013-2020.
10473.	Klindworth DL, Miller JD, Jin Y & Xu SS 2007 Chromosomal locations of genes for stem rust resistance in monogenic lines derived from tetraploid wheat accession ST464. Crop Science 47: 1441-1450.
10474.	Lapitan NLV, Peng JH & Sharma V 2007 A high-density map and PCR markers for Russian wheat aphid resistance gene *Dn7* on chromosome 1RS/1BL. Crop Science 47: 811-820.
10475.	Gaudet DA, Lu ZX, Leggett F, Puchalski B & Laroche A 2007 Compatible and incompatible interactions in wheat involving the *Bt-10* gene for resistance to *Tilletia tritici*, the common bunt pathogen. Phytopathology 97: 1397-1405.

10476.	Niu JS, Wang BQ, Wang YH, Cao AZ, Qi ZJ & Shen TM 2008 Chromosome location and microsatellite markers linked to a powdery mildew resistance gene in wheat line 'Lankao 90(6)'. Plant Breeding 127: 346 -349.
10477.	Niu JS, Jia HY, Wang BQ, Chang Y & Ma ZQ 2007 Development of a *PmLK906* and *Pm4a* linked STS marker via gene chip hybridization. Manuscript.
10478.	Peng JH, Wang H, Haley SD, Peairs FB & Lapitan NLV 2007 Molecular mapping of the Russian wheat aphid resistance gene Dn2414 in wheat. Crop Science 47: 2418-2429.
10479.	Miranda LM, Perugini L, Srnic G, Brown-Guedira G, Marshall D, Leath S & Murphy JP 2007 Genetic mapping of a *Triticum monococcum*-derived powdery mildew resistance gene in common wheat. Crop Science 47: 2323-2329.
10480.	Lillemo M, Singh RP, Huerta-Espino J, Chen XM, He ZH & Brown JKM 2007 Leaf rust resistance gene *Lr34* is involved in powdery mildew resistance of CIMMYT bread wheat line Saar. Developments in Plant Breeding, Wheat Production in Stressed Environments. Springer, The Netherlands (Buck HT, Nisi JE, Salomon N eds) 12: 97-102.
10481.	Lillemo M, Asalf B, Singh RP, Huerta-Espino J, Chen XM, He ZH & Bjørnstad Å 2008 The adult plant rust resistance loci *Lr34/Yr18* and *Lr46/Yr29* are important determinants of partial resistance to powdery mildew in bread wheat line Saar. Theoretical and Applied Genetics 116: 1155-1166.
10482.	Chen XF, Faris JD, Hu JG, Stack RW, Adhikari T, Elias EM, Kianian SF & Cai XW 2007 Saturation and comparative mapping of a major Fusarium head blight resistance QTL in tetraploid wheat. Molecular Breeding 19: 113-124.
10483.	Zhou LL, Bai GH, Ma HX & Carver BF 2007 Quantitative trait loci for aluminium resistance in wheat. Molecular Breeding 19: 153-161.
10484.	Raman R, Raman H & Martin P 2007 Functional gene markers for polyphenol oxidase activity in bread wheat (*Triticum aestivum* L.). Molecular Breeding 19: 315-328.
10485.	Herrera-Foessel SA, Singh RP, Huerta-Espino J, William M, Djurle A & Yuen J 2008 Molecular mapping of a leaf rust resistance gene on the short arm of chromosome 6B of durum wheat. Plant Disease 92: 1650 -1654.
10486.	Barloy D, Lemoine J, Abelard P, Tanguy AM, Rivoal R & Jahier J 2007 Marker-assisted pyramiding of two cereal cyst nematode resistance genes from *Aegilops variabilis* in wheat. Molecular Breeding 20: 31-40.
10487.	Jahier J, Rivoal R, Yu MQ, Abelard P, Tanguy AM & Barloy D 2000 Transfer of genes for resistance to the cereal cyst nematode from *Aegilops variabilis* Eig to wheat. Journal of Genetics and Breeding 52: 253-257.
10488.	Kirigwi FM, van Ginkel M, Brown-Guedira G, Gill BS, Paulsen GM & Fritz AK 2007 Markers associated with a QTL for grain yield in wheat under drought. Molecular Breeding 20: 401-413.
10489.	Shen XR & Ohm HW 2007 Molecular mapping of *Thinopyrum*-derived Fusarium head blight resistance in common wheat. Molecular Breeding 20: 131-140.
10490.	Jiang GL, Shi JR & Ward RW 2007 QTL analysis of resistance to Fusarium head blight in the novel wheat germplasm CJ 9406. I. Resistance to fungal spread. Theoretical and Applied Genetics 116: 3-13.
10491.	Ayala-Navarrete L, Bariana HS, Singh RP, Gibson JM, Mecanicos AA & Larkin PJ 2007 Trigenomic chromosomes by recombination of *Thinopyrum intermedium* and *Th. ponticum* translocations in wheat. Theoretical and Applied Genetics 116: 63-75.
10492.	Tomar SMS, Vinod & Singh B 2007 Genetic analysis of apical lethality in *Triticum aestivum* L. Euphytica 156: 425-431.

10493.	Singh D, Park RF & McIntosh RA 2007 Characterisation of wheat leaf rust resistance gene *Lr34* in Australian wheats using components of resistance and the linked molecular marker csLV34. Australian Journal of Agricultural Research 58: 1106-1114.
10494.	Christopher MJ, Williamson PM, Michalowitz M, Jennings R, Lehmensiek A, Sheppard J & Banks P 2007 Simple sequence repeat markers associated with three quantitative trait loci for black point resistance can be used to enrich selection populations in bread wheat. Australian Journal of Agricultural Research 58: 867-873.
10495.	Arraiano LS, Kirby J & Brown JKM 2007 Cytogenetic analysis of the susceptibility of the wheat line Hobbit Sib (Dwarf A) to Septoria tritici blotch. Theoretical and Applied Genetics 116: 113-122.
10496.	Jiang GL, Dong YH, Shi JR & Ward RW 2007 QTL analysis of resistance to Fusarium head blight in the novel wheat germplasm CJ 9306. II. Resistance to deoxynivalenol accumulation and grain yield loss. Theoretical and Applied Genetics 115: 1043-1052.
10497.	Nalam VJ, Vales MI, Watson CJW, Johnson EB & Riera-Lizarazu O 2007 Map-based analysis of genetic loci on chromosome 2D that affect glume tenacity and threshability, components of the free-threshing habit in common wheat. Theoretical and Applied Genetics 116: 135-145.
10498.	Sukhwinder-Singh, Brown-Guedira GL, Grewal TS, Dhaliwal HS, Nelson JC, Singh H and Gill BS 2003 Mapping of a resistance gene effective against Karnal bunt pathogen of wheat. Theoretical and Applied Genetics 106: 287-292.
10499.	Sukhwinder-Singh, Sharma I, Sehgal SK, Bains NS, Guo ZG, Nelson JC & Bowden RL 2007 Molecular mapping of QTLs for Karnal bunt resistance in two recombinant inbred populations of bread wheat. Theoretical and Applied Genetics 116: 147-154.
10500.	Torada A, Koike M, Ikeguchi S & Tsutsui I 2008 Mapping a major locus controlling seed dormancy using backcrossed progenies in wheat. Genome 51: 426-432.
10501.	He XY, Zhang YL, He ZH, Wu YP, Xiao, Ma CX & Xia XC 2008 Characterization of phytoene synthase 1 gene (*Psy1*) located on common wheat chromosome 7A and development of a functional marker. Theoretical and Applied Genetics 116: 213-221.
10502.	Luo PG, Hu XY, Ren ZL, Ahang K, Shu K and Yang ZJ. 2008 Linkage relationships of stripe rust resistance genes located on wheat chromosome 2BS. Genome 51: 922-927.
10503.	Klahr A, Zimmermann G, Wenzel G & Mohler V 2007 Effects of environment, disease progress, plant height and heading date on the detection of QTLs for resistance to Fusarium head blight in an European winter wheat cross. Euphytica 154: 17-28.
10504.	Chang C, Zhang HP, Xu J, You MS, Li BY & Liu GT 2007 Variation in two PPO genes associated with polyphenol oxidase activity in seeds of common wheat. Euphytica 154: 181-193.
10505.	Tucker DM, Griffey CA, Liu S, Brown-Guedira G, Marshall DS & Saghai Maroof MA 2007 Confirmation of three quantitative trait loci conferring adult plant resistance to powdery mildew in two winter wheat populations. Euphytica 155: 1-13.
10506.	Singh PK, Mergoum M, Adhikari TB, Kianian SF & Elias EM 2007 Chromosomal location of genes for seedling resistance to tan spot and Stagonsopora nodorum blotch in tetraploid wheat. Euphytica 155: 27-34.
10507.	Friesen TL, Meinhardt SW & Faris JD 2007 The *Stagonospora nodorum*-wheat pathosystem involves multiple proteinaceous host-selective toxins and corresponding host sensitivity genes that interact in an inverse gene-for-gene manner. The Plant Journal 51: 682-693.

10508.	Cheong J, Wallwork H & Williams KJ 2007 Identification of a major QTL for yellow leaf spot resistance in the wheat varieties Brookton and Cranbrook. Australian Journal of Agricultural Research 55: 315-319.
10509.	Singh PK, Mergoum M, Gonzalez-Hernandez JL, Ali S, Adhikari TB, Kianian SF, Elias EM & Hughes GR 2008 Genetics and molecular mapping of resistance to necrosis inducing race 5 of *Pyrenophora tritici-repentis* in tetraploid wheat. Molecular Breeding 21: 293-304.
10510.	Liu Q, Ni ZF, Peng HR, Song W, Liu ZY & Sun QX 2007 Molecular mapping of a dominant non-glaucousness gene from synthetic hexaploid wheat (*Triticum aestivum* L.). Euphytica 155: 71-78.
10511.	Pathan AM & Park RF 2007 Evaluation of seedling and adult plant resistance to stem rust in European cultivars. Euphytica 155: 87-105.
10512.	Ellis MH, Bonnett DG & Rebetzke GJ 2007 A 102bp allele at the *Xgwm261* locus is not always associated with the *Rht8* dwarfing gene in wheat (*Triticum aestivum* L.). Euphytica 157: 209-214.
10513.	Leonard JM, Watson CJW, Carter AH, Hansen JL, Zemetra RS, Santra DK, Campbell KM & Riera-Lizarazu O 2008 Identification of a candidate gene for the wheat endopeptidase *Ep-D1* locus and two other STS markers kinked to the eyespot resistance gene *Pch1*. Theoretical and Applied Genetics 116: 261-270.
10514.	Toth B, Kaszonyi G, Bartok T, Varga J & Mesterhazy A 2008 Common resistance of wheat to members of the *Fusarium graminearum* species complex and *F. culmorum*. Plant Breeding 127: 1-8.
10515.	Zhou Y, Zhu HZ, Cai SB, He ZH, Zhang XK, Xia XC & Zhang GS 2007 Genetic improvement of grain yield and associated traits in the southern China winter wheat region: 1949 to 2000. Euphytica 157: 465-473.
10516.	Dobrovolskaya O, Pshenichnikova TA, Arbuzova VS, Lohwasser U, Roder MS & Borner A 2007 Molecular mapping of genes determining hairy leaf character in common wheat with respect to other species of the Triticeae. Euphytica 155: 285-293.
10517.	Song W, Xie H, Liu Q, Xie CJ, Ni ZY, Yang TM, Sun QX & Liu ZY Molecular identification of *Pm12*-carrying introgression lines in wheat using genomic and EST-SSR markers. Euphytica 158: 95-102.
10518.	Chhuneja P, Kaur S, Garg T, Ghai M, Kaur S, Prashar M, Bains NS, Goel RK, Keller B, Dhaliwal HS & Singh K 2008 Mapping of adult plant stripe rust resistance genes in diploid A genome wheat species and their transfer to bread wheat. Theoretical and Applied Genetics 116: 313-324.
10519.	Cao AQ, Wang XE, Chen YP, Zou ZW & Chen PD 2006 A sequence-specific PCR marker linked with *Pm21* distinguishes chromosomes 6AS, 6BS, 6DS of *triticum aestivum* and 6VS of *Haynaldia villosa*. Plant Breeding 125: 201-205.
10520.	Herrera-Foessel SA, Djurle A, Yuen J, Singh RP, William HM, Garcia V & Huerta-Espino J 2007 Identification and molecular characterization of leaf rust resistance gene *Lr14a* in durum wheat. Plant Disease 92: 469-473.
10521.	Narasimhamoorthy B, Gill BS, Fritz AK, Nelson JC & Brown-Guedira GL 2006 Advanced backcross QTL analysis of a hard winter wheat x synthetic wheat population. Theoretical and Applied Genetics 112: 787-796.
10522.	Bhave M & Morris CF 2008 Molecular genetics of puroindolines and related genes: allelic diversity in wheat and other grasses. Plant Molecular Biology 66: 205-219.

10523.	Bhave M & Morris CF 2008 Molecular genetics of puroindolines and related genes: regulation of expression, membrane binding properties and applications. Plant Molecular Biology 66: 221-231.
10524.	Morris CF & Bhave M 2008 Reconciliation of D-genome puroindoline allele designations with current DNA sequence data. Journal of Cereal Science 48: 277-287.
10525.	Bonafede M, Kong L, Tranquilli G, Ohm H & Dubcovsky J 2007 Reduction of a *Triticum monococcum* chromosome segment carrying the softness genes *Pina* and *Pinb* translocated to bread wheat. Crop Science 47: 821-828.
10526.	Bonafede M, Chicaiza O, Tranquilli G & Dubcovsky J 2008 Registration of a hexaploid wheat translocation line carrying a short segment of chromosome $5A^{m}$ including softness genes *Pina* and *Pinb* from *Triticum monococcum*. Journal of Plant Registrations 2: 1-2.
10527.	Sherman JD, Lanning D, Clark D & Talbert LE 2007 Registration of near-isogenic hard spring wheat lines differing in puroindoline alleles. Journal of Plant Registrations 1: 171-172.
10528.	Wang J & Wang D 2008 Personal communication.
10529.	Qi LL, Pumphrey MO, Friebe B, Chen PD & Gill BS 2008 Molecular cytogenetic characterization of alien introgressions with gene *Fhb3* for resistance to Fusarium head blight disease. Theoretical and Applied Genetics 117: 1155-1166.
10530.	Zhang W & Dubcovsky J 2008 Association between allelic variation at the *Phytoene synthase 1* gene and yellow pigment content in the wheat grain. Theoretical and Applied Genetics 116: 635-645.
10531.	Fu D, Dunbar M & Dubcovsky J 2007 Wheat VIN3-like PHD finger genes are up-regulated by vernalization. Molecular and General Genomics 277: 301-313.
10532.	Raman H, Ryan PR, Raman R, Stodart BJ, Zhank K, Martin P, Wood R, Sasaki T, Yamamoto Y, Mackay M, Hebb DM & Delhaize E 2008 Analysis of *TaALMT1* traces the transmission of aluminium resistance in cultivated common wheat (*Triticum aestivum*). Theoretical and Applied Genetics 116: 343-354.
10533.	Bonnin I, Rousset M, Madur D, Sourdille P, Dupuits C, Brunel D & Goldringer I 2008 FT genome A and D polymorphisms are associated with the variation of earliness components in hexaploid wheat. Theoretical and Applied Genetics 116: 383-394.
10534.	Regina A, Bird A, Topping D, Bowden S, Freeman J, Barsby T, Kosar-Hashemi B, Li ZY, Rahman S & Morell M 2006 High-amylose wheat generated by RNA interference improves indices of large-bowel health in rats. Proceedings of the National Academy of Sciences, USA 103: 3546-3551.
10535.	Gobaa S, Kleijer G & Stamp P 2007 $2^{\cdot\cdot}$, a new high molecular weight glutenin subunit coded by *Glu-A1*: its predicted structure and its impact on bread-making quality. Plant Breeding 126: 1-4.
10536.	Groos C, Bervas E, Chanliaud E & Charmet G 2007 Genetic analysis of bread-making quality scores in bread wheat using a recombinant inbred line population. Theoretical and Applied Genetics 115: 313-323.
10537.	Marais F, Marais A, McCallum B & Pretorius Z 2009 Transfer of leaf rust and stripe rust resistance genes *Lr62* and and *Yr42* from Aegilops neglecta Req. ex Bertol. to common wheat. Crop Science 49: 871-879.
10538.	Lagudah ES. 2007 Personal communication.
10539.	Luo PG, Luo HY, Chang ZJ, Zhang HY, Zhang M & Ren ZL 2009 Characterization and chromosomal location of *Pm40* in common wheat: a new gene for resistance to powdery

	mildew derived from *Elytrigia intermedium*. Theoretical and Applied Genetics 118: 1059-1064.
10540.	Oliver RP, Lord M, Rybak K, Faris JD & Solomon 2008 Emergence of tan spot disease caused by toxigenic *Pyrenophora tritici-repentis* in Australia is not associated with increased deployment of toxin-sensitive cultivars. Phytopathology 98: 488-491.
10541.	Kosuge K, Watanabe N, Kuboyama T, Melnik VM, Yanchenko VI, Rosova MA & Goncharov NP 2008 Cytological and microsatellite mapping of mutant genes for spherical grain and compact spikes in durum wheat. Euphytica 159: 289-296.
10542.	Nematollahi G, Mohler V, Wenzel G, Zeller FJ & Hsam SLK 2008 Microsatellite mapping of powdery mildew resistance allele Pm5d from common wheat line IGV1-455. Euphytica 159: 307-313.
10543.	Simmonds JR, Fish LJ, Leverington-Waite MA, Wang Y, Howell P & Snape JW 2008 Mapping of a gene (*Vir*) for a non-glaucous, viridescent phenotype in bread wheat derived from Triticum dicoccoides, and its association with yield variation. Euphytica 159: 333-341.
10544.	Wang CM, Zhang YP, Han DJ, Kang ZS, Li GP, Cao AH & Chen PD 2008 SSR and STS markers for wheat stripe rust resistance gene Yr26. Euphytica 159: 359-366.
10545.	Ji XL, Xie CJ, Ni ZF, Yang TM, Nevo E, Fahima T, Liu ZY & Sun QX 2008 Identification and genetic mapping of a powdery mildew resistance gene in wild emmer (*Triticum dicoccoides*) accession IW72 from Israel. Euphytica 159: 385-390.
10546.	Zhou KJ, Wang SH, Feng YQ, Ji WQ & Wang GX 2008 A new male sterile mutant LZ in wheat (*Triticum aestivum* L.). Euphytica 159: 403-410.
10547.	Hassani ME, Shariflou MR, Gianibelli MC & Sharp PJ 2006 *Gli -DtT1* and a novel gamma-gliadin gene in *Aegilops tauschii*. Plant Breeding 125: 27-31.
10548.	Ikeda TM, Araki E, Fujita Y & Yano H 2006 Characterization of low-molecular-weight glutenin subunit genes and their protein products in common wheats. Theoretical and Applied Genetics 112: 327–334.
10549.	Faris JD et al. 2008 Manuscript.
10550.	Kolmer J 2008 Personal communication (17 June).
10551.	Li G, Fang T, Zhang H, Xie C, Li H, Yang T, Nevo E, Fahima T, Sun Q & Liu Z 2009 Molecular identification of a new powdery mildew resistance gene *Pm41* on chromosome 3BL derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 119: 531-539.
10552.	Singh S, Bochus WW, Sharma I & Bowden RL 2008 A novel source of resistance to *Pyrenophora tritici-repentis* race 1. Plant Disease 92: 91-95.
10553.	Yi YJ, Liu HY, Huang XQ, An LZ, Wang F & Wang XL 2008 Development of molecular markers linked to the wheat powdery mildew resistance gene *Pm4b* and marker validation for molecular breeding. Plant Breeding 127: 116-120.
10554.	Hanzalova A, Dumalasova V, Sumikova T & Bartos P 2007 Rust resistance of the French wheat Renan. Czech Journal of Genetics and Plant Breeding 43(2): 53-60.
10555.	Taenxler B, Esposti RF, Vaccino P, Brandolini A, Effgen S, Heun M, Schafer-Pregl R, Borghi B & Salamini F 2002 Molecular linkage map of Einkorn wheat: mapping of storage -protein and soft-glume genes and bread-making quality QTLs. Genetic Research, Cambridge 80: 131-143.
10556.	Goodwin SB 2007 Back to basic and beyond: increasing the level of resistance to Septoria tritici blotch in wheat. Australasian Plant Pathology 36: 532-538.

10557.	Singh PK, Mergoum M, Ali S, Adhikari TB & Hughes GR 2008 Genetic analysis of resistance to *Pyrenophora tritici-repentis* races 1 and 5 in tetraploid and hexaploid wheat. Phytopathology 98: 702-708.
10558.	Appelbee M-J, Mekuria GT, Nagasandra V, Bonneau JP, Eagles HA, Eastwood RF & Mather DE 2009 Novel allelic variants encoded at the *Glu-D3* locus in bread wheat. Journal of Cereal Science 49: 254-261.
10559.	Wei H, Liu ZJ, Zhu J, Xie CJ, Yang TM, Zhou YL, Duan XY, Sun QX & Liu ZY 2009 Identification and genetic mapping of *pm42*, a new recessive wheat powdery mildew resistance gene derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 119: 223-230.
10560.	He RL, Chang ZJ, Yang ZJ, Yuan ZY, Liu JX, Zhan HX & Zhang XJ 2009 Inheritance and mapping of a powdery mildew resistance Pm43 introgressed from *Thinopyrum intermedium* into wheat. Theoretical and Applied Genetics 118: 1173-1180.
10561.	Cloutier S, McCallum BD, Loutre C, Banks TW, Wicker T, Feuillet C, Keller B & Jordan M 2007 Leaf rust resistance gene *Lr1*, isolated from bread wheat (*Triticum aestivum* L.) is a member of the large psr567 gene family. Plant Molecular Biology 65: 93-106.
10562.	Luo PG, Zhang HY, Shu K, Zhang HQ, Luo HY & Ren ZL 2007 Stripe rust (*Puccinia striiformis* f. sp. *tritici*) resistance in wheat with the wheat-rye 1BL/1RS chromosomal translocation. Canadian Journal of Plant Pathology 30: 1-6.
10563.	Zhang JX, Singh RP, Kolmer JA, Huerta-Espino J, Jin Y & Anderson JA 2008 Genetics of leaf rust resistance in Brambling wheat. Crop Science 92: 1111-1118.
10564.	Bansal UK, Hayden MJ, Keller B, Wellings CR, Park RF & Bariana HS 2009 Relationship between wheat rust resistance genes *Yr1* and *Srna48* and a microsatellite marker. Plant Pathology 58: 1039-1043.
10565.	Bansal UK, Bossolini E, Miah H, Keller B, Park RF, Bariana HS 2008 Genetic mapping of seedling and adult plant stem rust resistance in two European winter wheat cultivars. Euphytica 164: 821-828.
10566.	Lin F, Xue SL, Tian DG, Li CJ, Cao Y, Zhang ZZ, Zhang CQ & Ma ZQ 2008 Mapping chromosomal regions affecting flowering time in a spring wheat RIL population. Euphytica 164: 769-777.
10567.	Pankova K, Milec Z, Simmonds J, Leverington-Waite M, Fish L & Snape JW 2008 Genetic mapping of a new flowering time gene on chromosome 3B of wheat. Euphytica 164: 778-787.
10568.	Pfluger LA, D'Ovidio R, Margiotta B, Peña R, Mujeeb-Kazi A & Lafiandra D 2001 Characterisation of high- and low-molecular weight glutenin subunits associated to the D genome of *Aegilops tauschii* in a collection of synthetic hexaploid wheats. Theoretical and Applied Genetics 103: 1293-1301.
10569.	Datta D, Nayar SK, Bhardwaj SC, Prashar M & Kumar S 2008 Detection and inheritance of leaf rust resistance in common wheat lines Agra Local and IWP94. Euphytica 159: 343-351.
10570.	Wang LA, Li GY, Xia XC, He ZH & Mu PY 2008 Molecular characterization of *Pina* and *Pinb* allelic variations in Xinjiang land races of commercial wheat cultivars. Euphytica 164: 745-752.
10571.	Zhang JX, Singh RP, Kolmer JA, Huerta-Espino J, Jin Y & Anderson JA 2008 Inheritance of leaf rust resistance in the CIMMYT wheat Weebill 1. Crop Science 48: 1037-1047.
10572.	Bremenkamp-Barrett B, Faris JD & Fellers JP 2008 Molecular mapping of the leaf rust resistance gene *Lr17a* in wheat. Crop Science 48: 1124-1128.

10573. Nakamura H 2008 Possible transmission route for common wheat to the Far-East in Asia. Crop Science 48: 1117-1123.

10574. Voss H-H, Holzapfel J, Hartl L, Korzun V, Rabenstein F, Ebmeyer E, Coester H, Kempe H & Miedaner T 2008 Effect of the Rht-D1 dwarfing locus on Fusarium head blight rating in three segregating populations of winter wheat. Plant Breeding 127: 333-339.

10575. Gennaro A, Koebner RMB & Ceoloni C 2009 A candidate for *Lr19*, an exotic gene conditioning leaf rust resistance in wheat. Functional and Integrative Genomics 9: 325-334.

10576. Ji JH, Qin B, Wang HY, Cao AZ, Wang SL, Chen PD, Zhuang LF, Du Y, Liu DJ, Wang XE 2008 STS markers for powdery mildew resistance gene *Pm6* in wheat. Euphytica 163: 159-165.

10577. Li CJ, Zhu HL, Zhang CQ, Lin F, Xue SL, Cao Y, Zheng ZZ, Zhang LX & Ma ZQ 2008 Mapping QTLs associated with Fusarium-damaged kernels in the Nanda 2419 x Wangshuibai population. Euphytica 163: 185-191.

10578. Johnson EB, Nalam VJ, Zemetra RS & Riera-Lizarazu O 2008 Mapping the compactum locus in wheat (*Triticum aestivum* L.) and its relationship to other spike morphology genes of the Triticeae. Euphytica 163: 193-201.

10579. Pathan AK, Wellings CR, Bariana HS & Park RF 2008 Evaluation of seedling and adult plant resistance in European wheat cultivars to Australian isolates of *Puccinia striiformis* f. sp. *tritici*. Euphytica 163: 283-301.

10580. Chu C-G, Friesen TL, Xu SS & Faris JD 2008 Identification of novel tanspot resistance loci beyond the known host-selective toxin sensitivity genes in wheat. Theoretical and Applied Genetics 117: 873-880.

10581. Zhao XL, Zheng TC, Xia XC, He ZH, Liu DQ, Yang WX, Yin GH & Li ZF 2008 Molecular mapping of leaf rust resistance gene *LrZH84* in Chinese wheat line Zhou 8425B. Theoretical and Applied Genetics 117: 1069-1075.

10582. Guo Q, Zhang ZJ, Xu YB, Li GH, Feng J & Zhou Y 2008 Quantitative trait loci for high temperature adult-plant and slow-rusting resistance to *Puccinia striiformis* f. sp. *tritici* in wheat cultivars. Phytopathology 98: 803-809.

10583. Hao YF, Liu AF, Wang YH, Feng DS, Gao JR, Li XF, Liu SB & Wang HG 2008 *Pm23*: a new allele of *Pm4* located on chromosome 2AL in wheat. Theoretical and Applied Genetics 117: 1205-1212.

10584. Shankar M, Walker E, Golzar H, Loughman R, Wilson RE & Francki MG 2008 Quantitative trait loci for seedling and adult plant resistance to *Stagonospora nodorum* in wheat. Phytopathology 98: 886-893.

10585. Huerta-Espino J, Singh RP, Herrera-Foessel SA, Perez-Lopez JB & Figueroa-Lopez P 2009 First detection of virulence in *Puccinia triticina* to resistance genes *Lr27* + *Lr31* present in durum wheats in Mexico. Plant Disease 93: 110.

10586. Rosewarne GM, Singh RP, Huerta-Espino J & Rebetzke GJ 2008 Quantitative trait loci for slow-rusting resistance in wheat to leaf rust and stripe rust identified with multi-environment analysis. Theoretical and Applied Genetics 116: 1027-1034.

10587. Cabellero L, Bancel E, Debiton C & Branlard G 2008 Granule-bound starch synthase (GBSS) diversity of ancient wheat and related species. Plant Breeding 127: 548-553.

10588. Schmolke M, Zimmermann G, Schweizer G, Miedaner T, Korzun V, Ebmeyer E & Hartl L 2008 Molecular mapping of quantitative trait loci for field resistance to Fusarium head blight in a European winter wheat population. Plant Breeding 127: 459-464.

10589.	Melichar JPE, Berry S, Newell C, MacCormack R & Boyd LA 2008 QTL identification and microphenotype characterisation of the developmentally regulated yellow rust resistance in UK wheat cultivar Guardian. Theoretical and Applied Genetics 117: 391-399.
10590.	Tadesse W, Hsam SLK, Wenzell G & Zeller FJ 2008 Chromosome location of a gene conferring resistance to *Pyrenophora tritici-repentis* in Ethiopian wheat cultivars. Euphytica 162: 423-430.
10591.	Marais, GF, Bekker TA, Eksteen A, McCallum B, Fetch T & Marais AS 2009 Attempts to remove gametocidal genes co-transferred to wheat with rust resistance from *Aegilops speltoides*. Euphytica 171: 71-85.
10592.	Marais GF, Pretorius ZA, Marais AS & Wellings CR 2003 Transfer of rust resistance genes from Triticum species to common wheat. South African Journal of Plant and Soil 20: 193-198.
10593.	Buerstmayr H, Ban T & Anderson JA 2009 QTL mapping and marker-assisted selection for Fusarium head blight resistance in wheat: a review. Plant Breeding 128: 1-26.
10594.	Haberle J, Schweizer G, Schondelmaier J, Zimmermann G & Harl L 2009 Mapping of QTL for resistance against Fusarium head blight in the winter wheat population Pelican//Bussard/Ning8026. Plant Breeding 128: 27-35.
10595.	Kolmer JA, Long DL & Hughes ME 2009 Physiologic specialization of Puccinia triticina on wheat in the United States in 2007. Plant Disease 93: 538-544.
10596.	Yang ZJ, Li GR, Jia JQ, Zeng T, Lei MP, Zeng ZX, Tao Z & Ren ZL 2009 Molecular cytogenetic characterization of wheat-Secale africanum amphiploids and derived introgression lines with stripe rust resistance. Euphytica 167: 197-202.
10597.	Gonzalez-Hernandez JL, Singh PK, Mergoum M, Adhikari TB, Kianian SF, Simsek S & Elias EM 2009 A quantitative trait locus on chromosome 5B controls resistance of *Triticum turgidum* (L.) var. *dicoccoides* to Stagonospora nodorum blotch. Euphytica 166: 199-206.
10598.	Navakode S, Weidner A, Lohwasser U, Roder MS & Borner A 2009 Molecular mapping of quantitative trait loci (QTLs) controlling aluminium tolerance in bread wheat. Euphytica 166: 283-290.
10599.	Ogbonnaya FC, Imtiaz M, Ye G, Hearnden PR, Hernadez E, Eastwood RF, van Ginkel M, Shorter SC & Winchester JM 2008 Genetic and QTL analyses of seed dormancy and preharvest sprouting resistance in the wheat germplasm CN10955. Theoretical and Applied Genetics 116: 891-902.
10600.	Maccaferri M, Mantovani P, Tuberosa R, DeAmbrogio E, Giuliani S, Demontis A, Massi A & Sanguineti MC 2008 A major QTL for durable leaf rust resistance widely exploited in durum wheat breeding programs maps on the distal region of chromosome 7BL. Theoretical and Applied Genetics 117: 1225-1240.
10601.	Lin F & Chen XM 2008 Molecular mapping of genes for race-specific overall resistance to stripe rust in wheat cultivar Express. Theoretical and Applied Genetics 116: 797-806.
10602.	Santra DK, Chen XM, Santra M, Campbell KG & Kidwell K 2008 Identification and maping QTL for high-temperature adult-plant resistance to stripe rust in winter wheat (*Triticum aestivum* L.) cultivar 'Stephens'. Theoretical and Applied Genetics 117: 793-802.
10603.	Srinivasachary, Gosman N, Steed A, Simmonds J, Leverington-Waite M, Wang Y, Snape J & Nicholson P 2008 Susceptibility to Fusarium head blight is associated with the Rht-D1b semidwarfing allele in wheat. Theoretical and Applied Genetics 116: 1145-1153.
10604.	Xu HX, Yao GQ, Li XO, Yang LL, Jiang YM, Fu BS, Zhao WF, Zhang ZZ, Zhang CQ & Ma ZQ 2008 Identification and mapping of *pm2026*: a recessive powdery mildew resistance

	gene in einkorn (*Triticum monococcum* L.) accession. Theoretical and Applied Genetics 117: 471-477.
10605.	Cai SB, Bai GH & Zhang DD 2008 Quantitative trait loci for aluminium tolerance in Chinese landrace FSW. Theoretical and Applied Genetics 117: 49-56.
10606.	Li Y, Niu YC & Chen XM 2009 Mapping a stripe rust resistance gene *YrC591* in wheat variety C591 with SSR and AFLP markers. Theoretical and Applied Genetics 118: 339-346. DOI 10.1007/s00122-008-0903-3.
10607.	Bhavani S, Bansal UK, Hare RA & Bariana HS 2009 Genetic mapping of stem rust resistance in durum wheat cultivar 'Arrivato'. International Journal of Plant Breeding 2(1): 23 -26.
10608.	Di Giovanni M, Cenci A, Janni M & D'Ovidio 2008 ALTR copia retrotransposon and Mutator transposons interrupt *Pgip* genes in cultivated and wild wheats. Theoretical and Applied Genetics 116: 859-867.
10609.	Tsilo TJ, Jin Y & Anderson JA 2008 Diagnostic microsatellite markers for the detection of stem rust resistance gene *Sr36* in diverse genetic backgrounds of wheat. Crop Science 48: 253-261.
10610.	Janni M, Di Giovanni M, Roberti S, Capodicasa C & D'Ovidio 2006 Characterization of expressed *Pgip* genes in rice and wheat reveals similar extent of sequence variation to dicot PGIPs and identifies an active PGIP lacking an entire LRR repeat. Theoretical and Applied Genetics 113: 1233-1245.
10611.	Tanio M & Kato K 2009 Development of near-isogenic lines for photoperiod-insensitive genes *Ppd-B2* and *Ppd-D1* carried by Japanese wheat cultivars and their effect on apical development. Breeding Science 57: 65-72.
10612.	Wilhelm EP, Turner AS & Laurie DA 2009 Photoperid insensitive *Ppd-A1a* mutations in tetraploid wheat (*Triticum durum* Desf.). Theoretical and Applied Genetics 118: 285-294.
10613.	Garvin DF, Stack RW & Hanson JM 2009 Quantitative trait locus mapping of increased head blight susceptibility associated with a wild emmer wheat chromosome. Phytopathology 99: 447-452.
10614.	Bass C, Hendley R, Adams MJ, Hammond-Kosack KE & Kenyuka 2006 The *Sbm1* locus conferring resistance to soil-borne cereal mosaic virus maps to a gene-rich region on 5DL in wheat. Genome 49: 1140-1148.
10615.	Yang Y, Ma YZ, Xu ZS, Chen XM, He ZH, Yu Z, Wilkinson M, Jones HD, Shewry PR & Xia LQ 2007 Isolation and characterization of Vipiparous-1 genes in wheat cultivars with distinct ABA sensitivity and pre-harvest sprouting tolerance. Journal of Experimental Botany 58: 2863-2871.
10616.	Xia LQ, Ganal MW, Shewry PR, He ZH, Yang Y & Roder MS 2008 Exploiting the diversity of Viviparous-1 gene associated with pre-harvest sprouting tolerance in European wheat varieties. Euphytica 159: 411-417.
10617.	Zhang XK, Xiao YG, Zhang Y, Xia XC, Dubcovsky J & He ZH 2008 Allelic variation at the vernalization genes *Vrn-A1*, *Vrn-B1*, *Vrn-D1* and *Vrn-B3* in Chinese wheat cultivars and their association with growth habit. Crop Science 48: 458-470.
10618.	Fang TL, Cheng Y, Li GQ, Xu SC, Xie CJ, You MS, Yang ZM, Sun QX & Liu ZY 2008 Molecular characterization of a stripe rust resistance gene from wheat line S2199 and its allelism with *Yr5*. Acta Agronomica Sinica 34: 355-360. In Chinese
10619.	Hu TZ, Li HJ, Liu ZJ, Xie CJ, Zhou YL, Duan XY, Jia X, You MS, Yan ZM, Sun QX & Liu ZY 2008 Identification and molecular mapping of the powdery mildew resistance gene in wheat cultivar Yumai 66. Acta Agronomica Sinica 34: 545-550.

10620.	Li H, Brooks S, Li WL, Fellers J, Nelson JC & Gill B 2009 Evolution of new disease specificity at a simple resistance locus in a crop-weed complex: reconstitution of the Lr21 gene in wheat. Genetics 182: 595-602.
10621.	Yang Y, Chen XM, He ZH, Roder M & Xia LQ 2009 Distribution of Vp-1 alleles in Chinese white-grained landraces, historical and current wheat cultivars. Cereal Research Communications 37: 169-177.
10622.	Yang FP, Zhang XK, Xia XC, Laurie DA, Yang WX & He ZH 2009 Distribution of the photoperiod insensitive *Ppd1-D1a* allele in Chinese wheat cultivars. Euphytica 165: 445-452.
10623.	McCartney CA, Somers DJ, Fedak G, DePauw RM, Thomas J, Fox SL et al. 2007 The evaluation of FHB resistance QTLs introgressed into elite Canadian spring wheat germplasm. Molecular Breeding 20: 209-221.
10624.	Tamburic-Ilincic L, Somers DJ, Fedak G & Schaafsma A 2009 Different quantitative trait loci for Fusarium resistance in wheat seedlings and adult stage in the Wuhan/Nyubai wheat population. Euphytica 165: 453-458.
10625.	Zhang KP, Chen GF, Zhao L, Liu B, Xu XB & Tian JC 2009 Molecular genetic analysis of flour color using a doubled haploid population in bread wheat (*Triticum aestivum* L.). Euphytica 165: 471-484.
10626.	Fofana B, Humphreys DG, Rasul G, Cloutier S, Brule-Babel A, Woods S, Lukow OM & Somers DJ 2009 Mapping quantitative trait loci controlling pre-harvest sprouting resistance in a red x white seeded spring wheat cross. Euphytica 165: 509-521.
10627.	Pukhalsky VA, Udachin RA & Bilinskaya EN 2009 Hybrid necrosis genes in aboriginal wheats of Middle Asia in the light of the problem of the primary centers of biodiversity of the Triticum L. genus. Euphytica 165: 533-543.
10628.	Khlestkina EK, Giura A, Roder MS & Borner A 2009 A new gene controlling the flowering response to photoperiod in wheat. Euphytica 165: 578-585.
10629.	Yamamori M 2009 Amylose content and starch properties generated by five variant Wx alleles for granule-bound starch synthase in common wheat (*Triticum aestivum* L.). Euphytica 165: 607-614.
10630.	Pukhalsky VA, Bilinskaya EN, Martynov SP, Dobrotvorskaya TV & Obolenkova GA 2008 New data on the distribution of hybrid necrosis genes in winter bread wheat (*Triticum aestivum* L.) cultivars. Russian Journal of Genetics 44: 177-179.
10631.	Huynh B-L, Wallwork H, Stangoulis JCR, Graham RD, Willsmore KL, Olsen S & Mather DE 2008 Quantitative trait loci for grain fructan concentration in wheat (Triticum aestivum L.). Theoretical and Applied Genetics 117: 701-709.
10632.	Kaur J, Bansal UK, Khanna R, Saini RG & Bariana HS 2009 Molecular mapping of stem rust resistance in HD2009/WL711 recombinant inbred line population. International Journal of Plant Breeding 3: 29-33.
10633.	Ceoloni C, Forte P, Gennaro A, Micali S, Carozza R & Bitti A 2005 Recent developments in durum wheat chromosome engineering. Cytogenetic and Genome Research 109: 328-334.
10634.	Liu SB, Cai SB, Graybosch R, Chen CX & Bai GH 2008 Quantitative trait loci for resistance to pre-harvest sprouting in US hard white winter wheat Rio Blanco. Theoretical and Applied Genetics 117: 691-699.
10635.	Khlestkina EK, Salina EA, Pshenichnikova TA, Roder MS & Borner A 2009 Glume coloration in wheat: allelism, test, consensus mapping and its association with specific microasatellite allele. Cereal Research Communications 37: 37-43.

10636.	Peng ZS, Martinek P, Kosuge K, Kuboyama T & Watanabe N 2008 Genetic mapping of a mutant gene producing three pistils per floret in common wheat. Journal of Applied Genetics 49: 135-139.
10637.	Dolrovolskaya O, Martinek P, Voylokov V, Roder MS & Borner A 2009 Microsatellite mapping of mutant genes for altered inflorescence architecture in wheat (*T. aestivum*) and rye (*S. cereale*). Manuscript. (Jan 2009)
10638.	Khlestkina EK, Roder MS & Borner A 2009 Identification of glume coloration genes in synthetic hexaploid and common wheats. eWIS-2009-0006
10639.	Nga NTT, Hau VTB & Tosa Y 2009 Identification of genes for resistance to a Digitaria isolate of *Magnaporthe grisea* in common wheat cultivars. Genome 52: 801-809.
10640.	Li Y, Song Y, Zhou R, Branlard G & Jia J 2009 Detection of QTLs for bread-making quality in wheat using a recombinant inbred line population. Plant Breeding 128: 235-243.
10641.	Liu SX, Chao SM & Anderson JA 2008 New DNA markers for high molecular weight glutenin subunits in wheat. Theoretical and Applied Genetics 118: 177-183.
10642.	An XL, Li XH, Xiong XJ, Yan YM, Zhang YZ, Gao LY, Wang AL, Wang K, Zeller FJ & Hsam SLK 2009 Identification and isolation of a new x-type HMW glutenin subunit *1Dx1.6t* gene from Aegilops tauschii. Plant Breeding 128: 41-45.
10643.	Fang JY, Liu Y, Luo J, Wang YS, Shewry PR & He GY 2009 Allelic variation and genetic diversity of high molecular weight glutenin subunit in Chinese endemic wheats (*Triticum aestivum* L). Euphytica 166: 177-182.
10644.	Jauhar PP, Peterson TS & Xu SS 2009 Cytogenetic and molecular characterization of a durum alien disomic addition line with enhanced tolerance to Fusarium head blight. Genome 52: 467–483.
10645.	Hassani ME, Naghavi MR, Shariflou MR & Sharp PJ 2009 Identification of novel omega - gliadin gene in *Aegilops tauschii* using RFLP. Cereal Research Communications 37: 75-82.
10646.	Dyck PL & Bartos 1994 Attempted transfer of leaf rust resistance from *Triticum monococcum* and durum wheat to hexaploid wheat. Canadian Journal of Plant Science 74: 733-736.
10647.	Zhao JL, Chen MS, Ma YM, Li RJ, Ren YP, Sun QQ & Li SS 2009 QTL mapping for quality traits of Chinese dry noodle. Agriculture Sciences in China 8: 394-400.
10648.	Krattinger SG, Lagudah ES, Spielmeyer W, Singh RP, Huerta-Espino J, McFadden H, Bossolini E, Selter LL & Keller B 2009 A putative ABC transporter confers durable resistance to multiple fungal pathogens in wheat. Science 323: 1360-1363.
10649.	Fu D, Uauy C, Distelfeld A, Blechl A, Epstein, L, Chen X, Sela, H, Fahima T & Dubcovsky J 2009 A kinase-START gene confers temperature-dependent resistance to wheat stripe rust. Science 323: 1357-1360.
10650.	He XY, He ZH, Ma W, Appels R & Xia XC 2009 Allelic variants of phytoene synthase 1 (*Psy1*) genes in Chinese and CIMMYT wheat cultivars and development of functional markers for flour colour. Molecular Breeding 23: 553-563.
10651.	He XY, Wang JW, He ZH, Ammar K, Peña RJ & Xia XC 2009 Allelic variants at the *Psy-A1* and *Psy-B1* loci in durum wheat and their associations with grain yellowness. Crop Science 49: 2058-2064. DOI: 10.2135/cropsci2008.11.0651.
10652.	Wang JW, He XY, He ZH & Xia XC 2009 Cloning and phylogenetic analysis of *PSY1* genes in common wheat and related species. Hereditas 146: 208-256.
10653.	Singh A, Reimer S, Pozniak CJ, Clarke FR, Clarke JM, Knox RE & Singh AK. 2009 Allelic variation at *Psy-A1* and association with yellow pigment in durum wheat grain. Theoretical and Applied Genetics 118: 1539-1548.

10654.	Howitt CA, Cavanagh CR, Bowerman AF, Cazzonelli C, Rampling L, Mimica JL & Pogson BJ 2009 Alternative splicing, activation of cryptic exons and amino acid substitutions in carotenoid biosynthetic genes are associated with lutein accumulation in wheat endosperm. Functional & Integrative Genomics 9: 363 -376.
10655.	Wang JW 2009 Cloning of phytoene synthase 1 (*Psy1*) genes in common wheat and related species and development of functional markers. Doctoral Dissertation, Northwest Sci-Tech University of Agriculture and Forestry, Yangling, China
10656.	McIntosh et al. 2008 GeneCat
10657.	He XY, He ZH, Morris CF & Xia XC 2009 Cloning and phylogenetic analysis of polyphenol oxidase genes in common wheat and related species. Genetic Resources and Crop Evolution 56: 311-321.
10658.	Sun YW, He XY, He ZH & Xia XC 2009 GenBank registration
10659.	Elangovan M, Rai R, Dholakia BB, Lagu MD, Tiwari R, Gupta RK, Rao VS, Roder MS & Gupta VS 2008 Molecular genetic mapping of quantitative trait loci associated with loaf volume in hexaploid wheat (*Triticum aestivum*). Journal of Cereal Science 47: 587-598.
10660.	Feng DS, Chen FG, Zhao SY & Xia GM 2004 High-molecular-weight glutenin subunit genes in decaploid *Agropyron elongatum*. Acta Botanica Sinica 46: 489-496.
10661.	Feng DS, Chen FG, Zhao SY & Xia GM 2004 Study on a novel HMW glutenin subunit coding region from *Agropyron elongatum*. Acta Botanica Borealis Occidentalis Sinica 24: 237-242.
10662.	Liu S, Xin G & Xia G 2008 Characterizing HMW-GS alleles of decaploid *Agropyron elongatum* in relation to evolution and wheat breeding. Theoretical and Applied Genetics 116: 325-334.
10663.	Wang JR, Yan ZH, Wei YM & Zheng YL 2006 Characterization of high molecular weight glutenin subunit genes from *Elytrigia elongata*. Plant Breeding 125: 89-95.
10664.	Zhao XL, Ma W, Gale KR, Lei ZS, He ZH, Sun QX, & Xia XC 2007 Identification of SNPs and development of functional markers for LMW -GS genes at *Glu-D3* and *Glu-B3* loci in bread wheat (*Triticum aestivum* L.). Molecular Breeding 20: 223-231.
10665.	Zhao XL, Xia XC, He ZH, Lei ZS, Appels R, Yang Y, Sun QX & Ma W 2007 Novel DNA variations to characterize low molecular weight glutenin *Glu-D3* genes and develop STS markers in common wheat. Theoretical and Applied Genetics 114: 451-460.
10666.	Gadaleta A, Giancaspro A, Giove SL, Zacheo S, Mangini G, Someone R, Signorile A & Blanco A 2009 Genetic and physical mapping of new EST-derived SSRs on the A and B genome chromosomes of wheat. Theoretical and Applied Genetics 118: 1015-1025.
10667.	Wang LM, Zhang ZY, Liu HJ, He MZ, Liu HX, Veisz O & Xin ZY 2009 Identification, gene postulation and molecular tagging of a stripe rust resistance gene in synthetic wheat CI142. Cereal Research Communications 37: 209-215.
10668.	Singh PK, Mergoum M, Adhikari TB, Shah T, Ghavami F & Kianian SF 2010 Genetic and molecular analysis of wheat tan spot resistance effective against *Pyrenophora tritici-repentis* races 2 and 5. Molecular Breeding 25: 369-379.
10669.	Mares D, Rathjen J, Mrva K & Cheong J 2009 Genetic and environmental control of dormancy in white grained wheat (*Triticum aestivum* L.). Euphytica 168: 311-318.
10670.	Moher A, Kulwal P, Singh R, Kumar V, Rouf Mir R, Kumar J, Prasad M, Balyan HS & Gupta PK 2009 Genome-wide QTL analysis for pre-harvest sprouting tolerance in bread wheat. Euphytica 168: 319-329.

10671.	Rosul G, Humphreys DG, Brule-Babel A, McCartney CA, Knox RE, DePauw RM & Somers DJ 2009 Mapping QTLs for pre-harvest sprouting traits in the spring wheat cross 'RL4452/ACDomain'. Euphytica 168: 363-378.
10672.	Lin F & Chen XM 2009 Quantitative trait loci for non-race-specific, high temperature adult-plant resistance to stripe rust in wheat cultivar Express. Theoretical and Applied Genetics 118: 631-642.
10673.	Cheng P & Chen XM 2009 Molecular mapping of a gene for resistance to stripe rust in spring wheat cultivar IDO377s. Theoretical and Applied Genetics 121: 195-204.
10674.	Sui XX, Wang MN & Chen XM 2009 Molecular mapping of a stripe rust resistance gene in spring wheat cultivar Zak. Phytopathology 99: 1209-1215.
10675.	Hiebert CW, Thomas JB, McCallum BD, Humphries DG, DePauw RM, Hayden MJ, Mago R, Schnippenkoetter W & Spielmeyer W 2010 An introgression on wheat chromosome 4DL in RL6077 (Thatcher*6/PI 250413) confers adult plant resistance to stripe rust and leaf rust. Theoretical and Applied Genetics 121: 1083-1091.
10676.	Dyck PL, Kerber ER & Aung T 1994 An interchromosomal reciprocal translocation in wheat involving leaf rust resistance gene *Lr34*. Genome 37: 556-559.
10677.	Li Q, Chen XM, Wang MN & Jing JX 2011 *Yr45*, a new wheat gene for stripe rust resistance on the long arm of chromosome 3D. Theoretical and Applied Genetics 122: 189-197.
10678.	Herrera-Foessel SA, Lagudah ES, Huerta-Epino J, Hayden M, Bariana H, Singh D & Singh RP 2011 New slow-rusting leaf rust and stripe rust resistance genes *Lr67* and *Yr46* are pleiotropic or closely linked. Theoretical and Applied Genetics 122: 239-249.
10679.	Bansal UK, Forrest KL, Hayden MJ, Miah H, Singh D & Bariana HS 2011 Characterisation of a new stripe rust resistance gene *Yr47* and its genetic association with the leaf rust resistance gene *Lr52*. Theoretical and Applied Genetics 122: 1461-1466.
10680.	Lan CX, Liang SS, Wang ZL, Yan J, Zhang Y, Xia XC & He ZH 2009 Quantitative trait loci mapping for adult-plant resistance to powdery mildew in Chinese wheat cultivar Bainong 64. Phytopathology 99: 1121-1126.
10681.	Lillemo M, Skinnes H, Brown JKM 2010 Race-specific resistance to powdery mildew in Scandinavian wheat cultivars, breeding lines and introduced genotypes with partial resistance. Plant Breeding 129: 297-303.
10682.	Li ZF, Xia XC, He ZH, Zhang LJ, Wang HY, Meng QF, Yang WX, Li GQ & Liu DQ 2010 Seedling and slow rusting resistance to leaf rust in Chinese wheat cultivars. Plant Disease 94: 45-53.
10683.	Croley NA 2010 Personal communication.
10684.	Randhawa HS, Popovic Z, Menzies, Knox R & Fox S 2009 Genetics and identification of molecular markers linked to resistance to loose smut (*Ustilago tritici*) race T33 in durum wheat. Euphytica 169: 151-157.
10685.	Hall MD, Brown-Guedira G, Klatt A & Fritz AK 2009 Genetic analysis of resistance to soil-borne wheat mosaic virus derived from *Aegilops tauschii*. Euphytica 169: 169-176.
10686.	Ren TH, Yang ZJ, Yan BJ, Zhang HQ, Fu SL & Ren ZL 2009 Development and characterization of a new 1BL.1RS translocation line with resistance to stripe rust and powdery mildew of wheat. Euphytica 169: 207-313.
10687.	Singh D, Simmonds J, Park RF, Bariana HS & Snape JW 2009 Inheritance and QTL mapping of leaf rust resistance in the European winter wheat cultivar “Beaver”. Euphytica 169: 253-261.

10688.	Faris JD & Friesen TL 2009 Reevaluation of a tetraploid wheat population indicates that the Tsn1-ToxA interaction is the only factor governing *Stagonospora nodorum* blotch susceptibility. Phytopathology 99: 906-912.
10689.	Dedryver F, Paillard S, Mallard S, Robert O, Trottet M, Negre S, Verplancke G & Jahier J 2009 Characterization of genetic components involved in durable resistance to stripe rust in the bread wheat 'Renan'. Phytopathology 99: 969-973.
10690.	Singh PK, Singh RP, Duveiller E, Mergoum M, Adikhari TB & Elias EM 2010 Genetics of wheat-*Pyrenophora tritici-repentis* interactions. Euphytica 171: 1-13.
10691.	Marais GF, Badenhorst PE, Eksteen & Pretorius ZA 2010 Reduction of *Aegilops sharonensis* chromatin associated with resistance genes *Lr56* and *Yr38* in wheat. Euphytica 171: 15-22.
10692.	Khlestkina EK, Roder MS & Borner A 2010 Mapping genes controlling anthocayanin pigmentation on the glume and pericarp in tetraploid wheat (*Triticum durum* L.). Euphytica 171: 65-69.
10693.	Lan CX, Liang SS, Zhou XC, Zhou G, Lu QL, Xia XC & He ZH 2010 Identification of genomic regions controlling adult-plant stripe rust resistance in Chinese landrace Pingyuan 50 through bulked segregant analysis. Phytopathology 100: 313-318.
10694.	Tatineni S, Graybosch RA, Hein GL, Wegulo SN & French R 2010 Wheat cultivar-specific disease synergism and alteration of virus accumulation during co-infection with wheat streak mosaic virus and triticum mosaic virus. Phytopathology 100: 230-238.
10695.	Santra DK, Santra M, Allan RE, Campbell KG & Kidwell KK 2009 Genetic and molecular characterization of vernalization genes *Vrn-A1*, *Vrn-B1* and *Vrn-D1* in spring wheat germplasm from the Pacific Northwest region of the U.S.A. Plant Breeding 128: 576-584.
10696.	Pu ZJ, Chen GY, Wei YM, Han ZH & Zheng YL 2010 Identification and molecular tagging of a stripe rust resistance gene in wheat line P81. Plant Breeding 129: 53-57.
10697.	Singh D, Park RF, McIntosh RA & Bariana HS 2008 Characterisation of stem rust and stripe rust seedling resistance genes in selected wheat cultivars from the United Kingdom. Journal of Plant Pathology 90: 553-556.
10698.	Haberle J Holzapfel J, Schweizer G & Hartl L 2009 A major QTL for resistance against Fusarium head blight in European wheat. Theoretical and Applied Genetics 119: 325-332.
10699.	Anonymous 2008 Cereal Rust Bulletin No. 10. Cereal Disease Laboratory, USDA, University of Minnesota, St Paul, MN, USA
10700.	Khestkina EK, Pshenichnikova TA, Roder MS & Borner A 2010 Clustering of anthocyanin pigmentation genes in wheat group 7 chromosomes. Cereal Research Communications 37: 391-398.
10701.	Wang ZL, Lang L, Uhrin A, Veisz, Lu SD & Vida G 2010 Identification of the *Lr34/Yr18* rust resistance gene region in a Hungarian wheat breeding programme. Cereal Research Communications 37: 431-440.
10702.	Sun XC, Marza F, Ma HX, Carver BF & Bai GH 2010 Mapping quantitative trait loci for quality factors in an inter-cross of US and Chinese wheat. Theoretical and Applied Genetics 120: 1041-1051.
10703.	Ma J, Li HB, Zhang CY, Yang XM, Liu YX, Yan GJ & Liu CJ 2010 Identification and validation of a major QTL conferring crown rot resistance in hexaploid wheat. Theoretical and Applied Genetics 120: 1119-1128.
10704.	Bansal UK, Muhammad S, Forrest KL, Hayden MJ and Bariana HS. 2015 Mapping of a new stem rust resistance gene, *Sr49* in chromosome 5B of wheat. Theoretical and Applied Genetics 128: 2113-2119.

10705.	Lowe I, Jankuloski L, Chao SM, Chen XM, See D and Dubcovsky J 2011 Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat. Theoretical and Applied Genetics 123: 143-157.
10706.	Xu WG, Li CX, Hu L, Zhang L, Zhang JZ, Dong HB & Wang GS 2010 Molecular mapping of powdery mildew resistance gene PmHNK in winter wheat (*Triticum aestivum* L.) cultivar Zhoumai 22. Molecular Breeding 26: 31-38. DOI 10.1007/s11032-009-9374-8
10707.	Lan CX, Ni XW, Yan J, Zhang Y, Xia XC, Chen XM & He ZH 2010 Quantitative trait loci mapping of adult-plant resistance to powdery mildew in Chinese wheat cultivar Lumai 21. Molecular Breeding 25: 615-622.
10708.	Dhillon T, Pearce SP, Stockinger EJ, Distelfeld A, Li C, Knox AK, Vashegyi I, Vágújfalvi A, Galiba G, & Dubcovsky J 2010 Regulation of freezing tolerance and flowering regulation in cereals: the *VRN-1* connection. Plant Physiology 153: 1846-1858.
10709.	Iqbal M, Navabi A, Yang RC, Salmon DF & Spaner D 2007 Molecular characterization of vernalization response genes in Canadian spring wheat. Genome 50: 511-516.
10710.	Distelfeld A, Tranquilli G, Li C, Yan L & Dubcovsky J 2009 Genetic and molecular characterization of the *VRN2* loci in tetraploid wheat. Plant Physiology 149: 245-257.
10711.	Yoshida T, Nishida H, Zhu J, Nitcher R, Distelfeld A, Akashi Y, Kato K & Dubcovsky J 2010 *Vrn-D4* is a vernalization gene located on the centromeric region of chromosome 5D in hexaploid wheat. Theoretical and Applied Genetics 120: 543-552.
10712.	Zhang W, Olson E, Saintenac C, Rouse M, Abate Z, Jin Y, Akhunov ED, Pumphrey M & Dubcovsky J 2010 Genetic maps of stem rust resistance gene *Sr35* in diploid and hexaploid wheat. Crop Science 50: 2464-2474.
10713.	Lagudah ES, Krattinger SG, Herrera-Foessel S, Singh R, Huerta-Espino J, Spielmeyer W, Brown-Guedira, Selter LL & Keller B 2009 Gene-specific markers for the wheat gene *Lr34/Yr18/Pm38* which confer, resistance to multiple pathogens. Theoretical and Applied Genetics 119: 889-898.
10714.	Tsilo TJ, Chao SM, Jin Y & Anderson JA 2009 Identification and validation of SSR markers linked to the stem rust resistance gene *Sr6* on the short arm of chromosome 2D in wheat. Theoretical and Applied Genetics 118: 515-524.
10715.	El Bouhssini M, Chen M, Lhaloui S, Zharmukhamedova G & Rihawi F 2008 Virulence of Hessian fly (Diptera: Cecidomyiidae) in the Fertile Cresent. Journal of Applied Entomology 133: 381-385.
10716.	ZhangYL, Wu YP, Xiao YG, He ZH, Zhang Y, Yan J, Zhang Y, Xia XC & Ma CX 2009 QTL mapping for flour and noodle colour components and yellow pigment content in common wheat. Euphytica 165: 435-444.
10717.	Chu C-G, Friesen TL, Xu SS, Faris JD & Kolmer JA 2009 Identification of novel QTLs for seedling and adult plant leaf rust resistance in a wheat doubled haploid population. Theoretical and Applied Genetics 119: 263-269.
10718.	Srinivasachary, Gosman N, Steed A, Hollins TW, Bayles R, Jennings P & Nicholson P 2009 Semi-dwarfing *Rht-B1* and *Rht-D1* loci of wheat differ significantly in their influence on resistance to Fusarium head blight. Theoretical and Applied Genetics 11: 695-702.
10719.	Kumar U, Joshi AK, Kumar S, Chand R & Roder S 2009 Mapping of resistance to spot blotch caused by *Bipolaris sorokiniana* in spring wheat. Theoretical and Applied Genetics 118: 783-792.

10720.	Bansal UK, Hayden MJ & Bariana HS 2010 Chromosomal location of an uncharacterized stripe rust resistance gene in wheat. Euphytica 171: 121-127. DOI: 10.1007/s10681-009-0007-4.
10721.	Menzies JG, Knox RE, Popovic Z & Procunier JD 2006 Common bunt resistance gene *Bt10* located on chromosome 6D. Canadian Journal of Plant Science 86: 1409-1412.
10722.	Chen YH, Carver BF, Wang SW, Zhang FQ & Yan LL 2009 Genetic loci associated with stem elongation and winter dormancy release in wheat. Theoretical and Applied Genetics 118: 881-889.
10723.	Ma J, Li HB, Zhang CY, Yang XM, Liu YX, Yan GJ & Liu CJ 2010 dentification and validation of a major QTL conferring crown rot resistance in hexaploid wheat. Theoretical and Applied Genetics 120: 1119-1128.
10724.	Zhang Z, Friesen TL, Simons KJ, Xu SS & Faris JD 2009 Development, identification, and validation of markers for marker-assisted selection against the Stagonospora nodorum toxin sensitivity genes *Tsn1* and *Snn2* in wheat. Molecular Breeding 23: 35-49.
10725.	Abeysekara NS, Friesen TL, Keller B & Faris JD 2009 Identification and characterization of a novel-toxin interaction in the wheat-*Stagonospora nodorum* pathosystem. Theoretical and Applied Genetics 120: 117-126.
10726.	Friesen TL, Faris JD, Solomon PS & Oliver RP 2008 Host-specific toxins: effectors of necrotrophic pathogenicity. Cellular Microbiology 10: 1421-1428.
10727.	Reddy L, Friesen TL, Meinhardt SW, Chao SM & Faris JD 2008 Genomic analysis of the *Snn1* locus on wheat chromosome arm 1BS and the identification of candidate genes. The Plant Genome 1: 55-66.
10728.	Friesen TL, Zhang Z, Solomon PS, Oliver RP & Faris JD 2008 Characterization of the interaction of a novel *Stagonospora nodorum* host-selective toxin with wheat susceptibility gene. Plant Physiology 146: 682-693.
10729.	Wei B, Jing RL, Wang CS, Chen JB, Mao XG Chang XP & Jia JZ 2009 Dreb1 genes in wheat (*Triticum aestivum* L.): development of functional markers and gene mapping based on SNPs. Molecular Breeding 23: 13-22.
10730.	Xu SS, Chu CG, Chao S, Klindworth DL, Faris JD & Elias EM 2010 Marker-assisted characterization of durum wheat Langdon-Golden Ball disomic substitution lines. Theoretical and Applied Genetics 120: 1575-1585.
10731.	Sun XC, Bai GH & Carver BF 2009 Molecular markers for leaf rust resistance gene *Lr41*. Molecular Breeding 23: 311-321.
10732.	Saito M, Vrinten P, Ishikawa G, Graybosch R & Nakamura T 2009 A novel codominant marker for selection of the null *Wx-B1* allele in wheat breeding programs. Molecular Breeding 23: 209-217.
10733.	Hiebert CW, Fetch TG, Zegeye T, Thomas JB, Somers DJ, Humphreys DG, McCallum BD, Cloutier S, Singh D & Knott DR 2011 Genetics and mapping of seedling resistance to Ug99 stem rust in Canadian wheat cultivars 'Peace' and 'Cadillac'. Theoretical and Applied Genetics 122: 143-149.
10734.	Maccaferri M, Mantovani P, Tuberosa R, DeAmbrogio E, Giuliani S, Demontis A, Massi A & Sanguineti MC 2008 A major QTL for durable leaf rust resistance widely exploited in durum wheat breeding programs maps on the distal region of chromosome arm 7BL. Theoretical and Applied Genetics 117: 1225-1240.
10735.	Marone D, Del Olmo AI, Laido G, Sillera JC, Emeran AA, Russo MA, Ferragonio P, Giovanniello V, Mazzucotelli E, De Leonardis AM, De Vita P, Blanco A, Cattivelli L,

	Rubiales D & Mastrangelo AM 2009 Genetic analysis of durable resistance against leaf rust in durum wheat. Molecular Breeding 24: 25-39.
10736.	Maccaferri M, Sanguineti MC, Mantovani P, Demontis A, Massi A, Ammar K, Kolmer JA, Czembor JH, Ezrati S & Tuberosa R 2010 Association mapping of leaf rust response in durum wheat. Molecular Breeding 26: 189-228.
10737.	Bainotti C, Fraschina J, Salines JH, Nisi JE, Dubcovsky J, Lewis SM, Bullrich L, Vanzetti L, Cuniberti M, Campos P, Formica MB, Masiero B, Alberione E & Helguera M 2009 Registration of 'BIOINTA 2004' wheat. Journal of Plant Registrations 3(2): 165-169.
10738.	Samsampour D, Zanjani BM, Pallavi JK, Singh A, Charpe A, Gupta SK & Prabhu KV 2010 Identification of molecular markers linked to adult plant leaf rust resistance gene *Lr48* in wheat and detection of *Lr48* in the Thatcher near-isogenic line with gene *Lr25*. Euphytica 174: 337-342.
10739.	Wang Y, Peng H, Liu G, Xie C, Ni Z, Yang T, Liu Z & Sun Q 2010 Identification and molecular mapping of a leaf rust resistance gene in spelt wheat landrace Altgold. Euphytica 174: 371-375.
10740.	Singh R, Matus-Cadiz M, Baga M, Hucl P & Chibbar RN 2010 Identification of genomic regions associated with seed dormancy in white-grained wheat. Euphytica 174: 391-408.
10741.	Mago R, Zhang P, Bariana H, Verlin DC, Bansal UK, Ellis JG & Dundas IS 2009 Development of wheat lines carrying stem rust resistance gene *Sr39* with reduced *Aegilops speltoides* chromatin and simple PCR markers for marker-assisted selection. Theoretical and Applied Genetics 119: 1441-1450.
10742.	Kolmer JA 2010 Genetics of leaf rust resistance in the soft red winter wheat cultivars Coker 9663 and Pioneer 26R61. Plant Disease 94: 628-632.
10743.	Li T & Bai GH 2009 Lesion mimic associates with adult plant resistance to leaf rust infection in wheat. Theoretical and Applied Genetics 119: 13-21.
10744.	Schmolke M, Mohler V, Hartl L, Zeller FJ & Hsam SLK 2012 A new powdery mildew resistance allele at the *Pm4* wheat locus transferred from einkorn (*Triticum monococcum*). Molecular Breeding 29: 449-456. DOI: 10.1007/s110342-011-9561-2
10745.	Anugrahwati DR, Shepherd KW, Verlin DC, Zhang P, Mirzaghaderi G, Alker E, Francki MG & Dundas IS 2008 Isolation of wheat-rye 1RS recombinants that break the linkage between the stem rust resistance gene *SrR* and secalin. Genome 51: 341-349.
10746.	Spielmeyer W, et al. 2010 Personal communication.
10747.	Singh B, Bansal UK, Forrest KL, Hayden MJ, Hare RA & Bariana HS 2010 Inheritance and chromosome location of leaf rust resistance in durum wheat cultivar Wollaroi. Euphytica 175: 351-355.
10748.	Tikhenko N, Tsvetkova N, Voylokov A, Dobrovolskaya O, Zaynali K, Nezhad KZ, Röder MS & Börner A 2010 Embryo lethality in wheat x rye hybrids – mode of inheritance and the identification of a complementary gene in wheat. Euphytica 176: 191-198.
10749.	Singh K, Chhuneja P, Singh I, Sharma SK, Garg T, Garg M, Keller B & Dhaliwal HS 2010 Molecular mapping of cereal cyst nematode resistance in *Triticum monococcum* L. and its transfer to the genetic background of cultivated wheat. Euphytica 176: 213-222.
10750.	Nishio Z, Kojima H, Hayata A, Iriki N, Tabiki T, Ito M, Yamauchi H & Murray TD 2010 Mapping a gene conferring resistance to wheat yellow mosaic virus in European winter wheat cultivar 'Ibis' (Triticum aestivum L.). Euphytica 176: 223-229.
10751.	Bariana HS, Bansal UK, Schmidt A, Lehmensiek A, Kaur J, Miah H, Howes N & McIntyre CL 2010 Molecular mapping of adult plant stripe rust resistance in wheat and identification of pyramided QTL genotypes. Euphytica 176: 251-260.

10752.	Leonova IN, Budashkina EB, Flath K, Weidner A, Börner A & Röder MS 2010 Microsatellite mapping of a leaf rust resistance gene transferred to common wheat from *Triticum timopheevii*. Cereal Research Communication 38: 211-219.
10753.	Sun XC, Bockus W & Bai GH 2010 Quantitative trait loci for resistance to *Pyrenophora tritici-repentis* race 1 in a Chinese wheat. Phytopathology 100: 468-473.
10754.	Sharp PJ 2010 Personal communication.
10755.	Cane K, Sharp PJ, Eagles HA, Eastwood RF, Hollamby GJ, Kuchel H, Lu M & Martin PJ 2008 The effects on grain quality traits of a grain serpin protein and the VPM1 segment in southern Australian wheat breeding. Australian Journal of Agricultural Research 59: 883-890.
10756.	Faris JD, Zhang Z, Lu H, Lu S, Reddy L, Cloutier S, Fellers JP, Meinhardt SW, Rasmussen JB, Xu SS, Oliver RP, Simons KJ & Friesen TL 2010 A unique wheat disease resistance-like gene governs effector-triggered susceptibility to necrotrophic pathogens. Proceedings of the National Academy of Sciences of USA 107: 13544-13549.
10757.	Chu CG, Friesen TL, Xu SS, Faris JD & Kolmer JA 2009 Identification of novel QTLs for seedling and adult plant leaf rust resistance in a wheat doubled haploid population. Theoretical and Applied Genetics 119: 263-269.
10758.	Cowger C, Parks R & Marshall D 2009 Appearance of powdery mildew of wheat caused by *Blumeria graminis* f. sp. *tritici* on *Pm17*-bearing cultivars in North Carolina. Plant Disease 93: 1219.
10759.	Zhang P, McIntosh RA, Hoxha S, Dong CM 2009 Wheat stripe rust resistance genes *Yr5* and Yr7 are allelic. Theoretical and Applied Genetics 120: 25-29.
10760.	Loutre C, Wicker T, Travella S, Galli P, Scofield S, Fahima T, Feuillet C, Keller B 2009 Two different CC-NBS-LRR genes are required for Lr10-mediated leaf rust resistance in tetraploid and hexaploid wheat. The Plant Journal 60: 1043-1054.
10761.	Okubara PA, Steber CM, DeMacon VL, Walter NL, Paulitz TC, & Kidwell KK 2009 Scarlet-Rz1, an EMS-generated hexaploid wheat with tolerance to the soilborne necrotrophic pathogens Rhizoctonia solani AG-8 and R. oryzae. Theoretical and Applied Genetics 119: 293-303.
10762.	Marais GF, Kotze L & Ekstein A 2010 Allosyndetic recombinants of the *Aegilops peregrina*-derived *Lr59* translocation in common wheat. Plant Breeding 129: 356-361.
10763.	Vanzetti LS, Pfluger L, Bainotti CT, Jensen C & Helguera M 2010 Identification of a null allele at the *Wx-A1* locus in durum wheat (*Triticum turgidum* L. ssp. *durum* Desf.). Plant Breeding 129: 718-720.
10764.	Lu H, Rudd JC, Burd JD & Weng Y 2011 Molecular mapping of greenbug resistance genes *Gb2* and *Gb6* in 1AL.1RS wheat-rye translocations. Plant Breeding 129: 472-476.
10765.	Tadesse W, Reents HJ, Hsam SLK & Zeller FJ 2010 Monosomic analysis of tanspot resistance gene in the winter cultivar 'Arina'. Plant Breeding 129: 477-479.
10766.	Fu YB, Peterson GW, McCallum BD & Huang L 2010 Population-based resequencing analysis of improved wheat germplasm in wheat leaf rust resistance locus *Lr21*. Theoretical and Applied Genetics 121: 271-281.
10767.	Watanabe N 2008 Genetic collection and development of near-isogenic lines in durum wheat. Vestnik VOGiS 12: 636-643.
10768.	Haberle J, Holzapfel J, Schweizer G & Hartl L 2009 A major QTL for resistance against Fusarium head blight in European winter wheat. Theoretical and Applied Genetics 119: 325-332.

10769.	Sood S, Kuraparthy V, Bai GH & Bill BS 2009 The major threshability genes soft glume (*sog*) and tenacious glume (*Tg*), of diploid and polyploid wheat, trace their origin to independent mutations at non-orthologous loci. Theoretical and Applied Genetics 119: 341-351.
10770.	Kuraparthy V, Sood S, See DR & Gill BS 2009 Development of a PCR assay and marker-assisted transfer of leaf rust and stripe rust rersistance genes *Lr57* and *Yr40* into hard red winter wheats. Crop Science 49: 120-126.
10771.	Burt C, Hollins TW & Nicholson 2011 Identification of a QTL conferring seedling and adult plant resistance to eyespot on chromosome 5A of Cappelle Desprez. Theoretical and Applied Genetics 122: 119-128.
10772.	Periyannan SK, Bansal UK, Bariana HS, Pumphrey M & Lagudah ES 2011 A robust molecular marker for the detection of shortened introgressed segment carrying the stem rust resistance gene *Sr22* in common wheat. Theoretical and Applied Genetics 122: 1-7.
10773.	Olsen E, Brown-Guedira G, Marshall D, Stack E, Bowden RL, Jin Y, Rouse M & Pumphrey MO 2010 Development of wheat lines having a small introgressed segment carrying stem rust resistance gene *Sr22*. Crop Science 50: 1823-1830.
10774.	Qi LL, Pumphrey MO, Friebe B, Zhang P, Qian C, Bowden RL, Rouse MN, Jin Y and Gill BS 2011 A novel Robertsonian event leads to transfer of a stem rust resistance gene (*Sr52*) effective against race Ug99 from *Dasypyrum villosum* into wheat. Theoretical and Apllied Genetics 123: 159-167.
10775.	Liu W, Seifers DL, Qi LL, Pumphrey MO, Friebe B & Gill BS 2011 A compensating wheat-*Thinoprum intermedium* Robertsonian translocation conferring resistance to wheat streak mosaic virus and Triticum mosaic virus. Crop Science 61: 2382-2390.
10776.	Uphaus J, Walker M, Shankar H, Golzar H, Loughman R, Francki M & Ohm H 2009 Quantitative trait loci identified for resistance to Stagonospora glume blotch in wheat in the USA and Australia. Crop Science 47: 1813-1822.
10777.	Simons K, Abate Z, Chao SM, Zhang WJ, Rouse M, Jin Y, Elias E & Dubcovsky J 2011 Genetic mapping of stem rust resistance gene *Sr13* in tetraploid wheat (*Triticum turgidum* ssp. *durum* L.). Theoretical and Applied Genetics 122: 649-658.
10778.	Admassu B, Perovic D, Friedt W & Ordan F 2011 Genetic mapping of the stem rust (*Puccinia graminis* f. sp. *tritici* Eriks. & E. Henn) resistance gene *Sr13* in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 122: 6430-648.
10779.	Dubcovsky J, Ordan F, Perovic D, Admassu B, Friedt W, Abate Z, Zhang W & Chao S 2011 Conflicting mapping results for stem rust resistance gene *Sr13*. Theoretical and Applied Genetics 122: 659.
10780.	Dadkhodaie NA, Karaoglou H, Wellings CR & Park RF 2011 Mapping genes *Lr53and Yr35* on the short arm of chromosome 6B of common wheat with microsatellite markers and studies of their association with *Lr36*. Theoretical and Applied Genetics 122: 479-487.
10781.	Su ZQ, Hao CY, Wang LF, Dong YC & Zhang ZY 2011 Identification and development of a functional marker of *TaGW2* associated with grain weight in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 122: 211-223.
10782.	Li HB, Yan W, Liu GR, Wen SM & Liu CJ 2011 Identification and validation of quantitative trait loci conferring tan spot resistance in the bread wheat variety Ernie. Theoretical and Applied Genetics 122: 395-403.
10783.	Wang SW, Knox RE, DePauw RM, Clarke FR, Clarke JM & Thomas JB 2009 Markers to a common bunt resistance gene derived from 'Blizzard' wheat (*Triticum aestivum* L.) and mapped to chromosome arm 1BS. Theoretical and Applied Genetics 119: 541-553.

10784.	Deng SM, Wu XR, Wu YY, Zhou RH, Wang HG, Jia JZ & Liu SB 2011 Characterization and precise mapping of a QTL increasing spike number with pleiotropic effects in wheat. Theoretical and Applied Genetics 122: 281-289.
10785.	Jagger LJ, Newell C, Berry ST, MacCormack R & Boyd LA 2011 The genetic characterization of stripe rust resistance in the German wheat cultivar Alcedo. Theoretical and Applied Genetics 122: 723-733.
10786.	Mago R, Brown-Guedira G, Dreisigacker S, Breen J, Jin Y, Singh R, Appels R, Lagudah ES, Ellis J & Spielmeyer W 2011 An accurate DNA marker assay for stem rust resistance gene *Sr2* in wheat. Theoretical and Applied Genetics 122: 635-744.
10787.	Kolmer JA 2009 Genetics of leaf rust resistance in the soft red winter wheat 'Caldwell'. Crop Science 49: 1187-1192.
10788.	Friebe B, Qi LL, Wilson DL, Chang ZJ, Seifers DL, Martin TJ, Fritz AK & Gill BS 2009 Wheat-*Thinopyrum intermedium* recombinants resistant to wheat streak mosaic virus and Triticum mosaic virus. Crop Science 49: 1221-1226.
10789.	Liu WX, Jin Y, Rouse M, Friebe B, Gill B & Pumphrey MO 2011 Discovery and molecular mapping of a new gene conferring resistance to stem rust, *Sr53*, derived from *Aegilops geniculata* and characterization of spontaneous translocation stocks with reduced alien chromatin. Chromosome Research 19: 669-682.
10790.	Chen Y, Zhang ZY, Li HJ, Liu ZY, Veisz O, Vida G 2011 *Pm44*, a new gene for powdery mildew resistance on the short arm of wheat chromosome 3A. Draft manuscript. **CURATOR'S NOTE:** Publication of this work could not be located.
10791.	Ma HQ, Kong Z, Fu B, Li N, Zhang L, Jia H & Ma Z 2011 Identification and mapping of a new powdery mildew resistance gene on chromosome 6D of common wheat. Theoretical and Applied Genetics 123: 1099-1106.
10792.	Goyeau H & Lannou C 2011 Specific resistance to leaf rust expressed at the seedling stage in cultivars grown in France from 1983 to 2007. Euphytica 178: 45-62.
10793.	Holzapfel J, Voss H-H, Miedaner T, Korzun V, Haberle J, Schweizer G, Mohler V & Zimmerman G 2008 Inheritance of resistance to Fusarium head blight in three European winter wheat populations. Theoretical and Applied Genetics 117: 1119-1128.
10794.	Hysing S-C, Singh RP, Huerta-Espino J, Merker A, Liljeroth E & Diaz O 2006 Leaf rust (*Puccinia triticina*) resistance in wheat (*Triticum aestivum*) cultivars grown in Northern Europe 1992-2002. Hereditas 143: 1-14.
10795.	Rafiei Boroujeni F, Arzani A, Afshari F & Tobari M 2011 Identification and inheritance of leaf rust resistance genes in the wheat cultivar 'Marvdasht'. Cereal Research Communications 39: 67-76.
10796.	Jia JQ, Li GR, Liu C, Lei MP & Yang ZJ 2011 Characterization of wheat yellow rust resistance gene *Yr17* using EST-SSR and rice syntenic region. Cereal Research Communications 39: 88-99.
10797.	Feng J, Zuo LL, Zhang ZY, Lin RM, Cao YY & Xu SC 2011 Quantitative trait loci for temperature-sensitive resistance to *Puccinia striiformis* f. sp. *tritici* in wheat cultivar Flinor. Euphytica 178: 321-329.
10798.	Jayatilake DV, Bai GH & Dong YH 2011 A novel quantitative trait locus for Fusarium head blight resistance in chromosome 7A of wheat. Theoretical and Applied Genetics 122: 1189-1198.
10799.	Kaloshian I, Waines JG, Roberts P & Thomason IJ 1991 Chromosomal location of root-knot-resistance gene in the D genome of wheat. Journal of Heredity 82: 254-256.

10800.	Coriton O, Barloy D, Huteau V, Lemoine J, Tanguy AM & Jahier J 2009 Assignment of *Aegilops variabilis* Eig chromosomes and translocations carrying resistance to nematodes in wheat. Genome 52: 338-346.
10801.	Williamson VM, Thomas V, Ferris H and Dubcovsky J 2013 An *Aegilops ventricosa* translocation confers resistance against root-knot nematodes to common wheat. Crop Science 53: 14120-14128.
10802.	Lu HJ, Kottke R, Devkota R, St Amand P, Bernado A, Bai GH, Martin J, Haley S & Rudd J 2011 Molecular mapping of *Wsm2* for wheat streak virus resistance in winter wheat line CO960293-2. Plant & Animal Genome Conf., San Diego, CA.
10803.	Liu WX, Jin Y, Rouse M, Friebe B, Gill B, Pumphrey MO 2011 Development and characterization of wheat-*Ae. searsii* Robertsonian translocations and a recombinant chromosome conferring resistance to stem rust. Theoretical and Applied Genetics 122: 1537-1545.
10804.	Liu L, Ikeda TM, Branlard G, Peña RJ, Rogers WJ, Lerner SE, Kolman MA, Xia X, Wang L, Ma W, Appels R, Yoshida H, Wang A, Yan Y & He Z 2010 Comparison of low molecular weight glutenin subunits identified by SDS-PAGE, 2-DE, MALDI-TOF-MS and PCR in common wheat. BMC Plant Biology 2010 10: 124.
10805.	Alvarez JB, Moral A & Martín LM 2006 Polymorphism and genetic diversity for the seed storage proteins in Spanish cultivated einkorn wheat (*Triticum monococcum* L. ssp. *monococcum*). Genetic Resources and Crop Evolution 53: 1061-1067.
10806.	Caballero L, Martín MA & Alvarez JB 2008 Allelic variation for the high- and low-molecular-weight glutenin subunits in wild diploid wheat (*Triticum urartu*) and its comparison with durum wheats. Australian Journal of Agricultural Research 59: 906-910.
10807.	Gao X, Appelbee MJ, Mekuria GT, Chalmers KJ & Mather DE Two different x-type glutenin subunits encoded by a novel allele at the *Glu-B1* locus of wheat (submitted).
10808.	Liu L, Wang A, Appels R, Ma J, Xia X, Lan P, He Z, Bekes F, Yan Y & Ma W 2009 A MALDI-TOF based analysis of high molecular weight glutenin subunits for wheat breeding. Journal of Cereal Science 50: 295-301.
10809.	Carmona S, Alvarez JB & Caballero L 2010 Genetic diversity for morphological traits and seed storage proteins in Spanish rivet wheat. Biologia Plantarum 54: 69-75.
10810.	Caballero L, Peña RJ, Martín LM & Alvarez JB 2010 Characterization of Mexican Creole wheat landraces in relation to morphological characteristics and HMW glutenin subunit composition. Genetic Resources and Crop Evolution 57: 657-665.
10811.	Martín MA, Martín LM & Alvarez JB 2008 Polymorphisms at the Gli-A^{u}1 and Gli-A^{u}2 loci in wild diploid wheat (*Triticum urartu*). Euphytica 163: 303-307.
10812.	Ma DY, Yan J, He ZH, Wu L & Xia XC 2012 Characterization of a cell wall invertase gene TaCwi-A1 on common wheat chromosome 2A and development of functional markers. Molecular Breeding 29: 43-52.
10813.	Appelbee MJ 2011 Personal communication.
10814.	Xi YJ, Ma XF, Zhong H, Liu SD, Wang ZL, Song YY & Zhao CH 2011 Characterization of a male sterile mutant from progeny of a transgenic plant containing a leaf senescence-inhibition gene in wheat. Euphytica 177: 241-251.
10815.	Yoshiya K, Watanabe N & Kuboyama T 2011 Genetic mapping of the genes for non-glaucous phenotypes in tetraploid wheat. Euphytica 177: 293-297.
10816.	Ghazvini H, Hiebert CW, Thomas JB and Fetch T 2013 Development of a multiple bulked segregant analysis (MBSA) method used to locate a new stem rust resistance gene (*Sr54*) in the winter wheat cultivar Norin 40. Theoretical and Applied Genetics 126: 443-449.

10817.	Herrera-Foessel SA, Singh RP, Huerta-Espino J, Rosewarne GM, Periyannan SK, Viccars L, Calvo-Salazar V, Lan C and Lagudah ES 2011 *Lr68*: A new gene conferring slow rusting resistance to leaf rust in wheat. Theoretical and Applied Genetics 124: 1475-1486.
10818.	Haque MA, Martinek P, Watanabe N & Kuboyama T 2011 Genetic mapping of gibberellic acid-insensitive genes for semi-dwarfism in durum wheat. Cereal Research Communications 39: 171-178.
10819.	Kuraparthy V, Sood S, Brown-Guedira & Gill BS 2011 Development of a PCR assay and marker-assisted transfer of leaf rust resistance gene *Lr58* into adapted winter wheats. Euphytica 180: 227-234.
10820.	Kosuge K, Watanabe N & Kuboyama T 2011 Comparative genetic mapping of homoeologous genes for the *chlorina* phenotype in the genus *Triticum*. Euphytica 179: 257-263.
10821.	Morgounov A, Ablova I, Babayants O, Babayants L, Bespalova L, Khudokormov ZL, Litvinenko N, Shamanin V & Syukov V 2011 Genetic protection of wheat from rusts and development of resistant varieties in Russia and Ukraine. Euphytica 179: 297-311.
10822.	Huang L, Zhang LQ, Liu BL, Yan ZH, Zhang B, Zhang YL & Liu DC 2011 Molecular tagging of a stripe rust resistance gene in *Aegilops tauschii*. Euphytica 179: 313-318.
10823.	Khleskina EK, Salina EA, Matties, Leonova IN, Borner A & Roder MS 2011 Comparative molecular marker-based genetic mapping of flavones 3-hydoxylase genes in wheat, rye and barley. Euphytica 179: 333-341.
10824.	Tsilo TJ, Jin Y & Anderson JA 2008 Diagnostic microsatellite markers for the detection of stem rust resistance gene *Sr36* in diverse genetic backgrounds of wheat. Crop Science 48: 253-261.
10825.	Wu SG, Pumphrey M & Bai GH 2009 Molecular mapping of stem-rust-resistance gene *Sr40* in wheat. Crop Science 49: 1681-1686.
10826.	Murphy LR, Santra D, Kidwell K, Yan GP, Chen XM & Garland Campbell K 2009 Linkage maps of wheat stripe rust resistance genes *Yr5* and *Yr15* for use in marker-assisted selection. Crop Science 49: 1786-1790.
10827.	Ghaffary SMT, Robert O, Laurent V, Lonnet P, Margale E, van der Lee TAJ, Visser RGF & Kema GHJ 2011 Genetic analysis of resistance to Septoria tritici blotch in the French winter wheat cultivars Balance and Apache. Theoretical and Applied Genetics 123: 741-754.
10828.	McIntosh RA, Zhang P, Cowger C, Parks R, Lagudah ES & Hoxha S 2011 Rye-derived powdery mildew resistance gene *Pm8* in wheat is suppressed by the *Pm3* locus. Theoretical and Applied Genetics 123: 359-367.
10829.	Zhou XL, Wang WL, Wang LL, Hou DY, Jing JX, Wang Y, Xu ZQ, Yao Q, Yin JL & Ma DF 2011 Genetics and molecular mapping of genes for high-temperature resistance to stripe rust in wheat cultivar Xiaogan 54. Theoretical and Applied Genetics 123: 431-438.
10830.	Kolmer JA, Long DL & Hughes ME 2011 Physiologic specialization of *Puccinia triticina* on wheat in the United States in 2009. Plant Disease 95: 935-940.
10831.	Abate ZA, Liu S & McKendry AL 2008 Quantitative trait loci associated with deoxynivalenol content and kernel quality in the soft red winter wheat 'Ernie'. Crop Science 48: 1408-1418.
10832.	Jefferies SP, Pallotta MA, Paull JG, Karakousis A, Kretschmer JM, Manning S, Islam AKMR, Langridge P & Chalmers KJ 2000 Mapping and validation of chromosome regions conferring boron toxicity tolerance in wheat (*Triticum aestivum*). Theoretical and Applied Genetics 101: 767-777.

10833.	Schnurbusch T, Collins NC, Eastwood RF, Sutton T, Jefferies SP & Langridge P 2007 Fine mapping and targeted SNP survey using rice-wheat gene collinearity in the region of the *Bo1* boron toxicity locus of bread wheat. Theoretical and Applied Genetics 115: 451-461.
10834.	Schnurbusch T, Langridge P & Sutton T 2008 The Bo1-specific PCR marker AWW5L7 is predictive of boron tolerance status in a range of exotic durum and bread wheats. Genome 51: 963-971.
10835.	Schnurbusch T, Hayes J & Sutton T 2010 Boron toxicity in wheat and barley: Australian perspectives. Breeding Science 60: 297-304.
10836.	Quincke MC, Peterson CJ, Zemetra RS, Hansen JL, Chen JL, Riera-Lizarazu & Mundt CC 2011 Quantitative trait loci for resistance to Cephalosporium stripe, a vascular wilt disease of wheat. Theoretical and Applied Genetics 122: 1339-1349.
10837.	Li T, Bai GH, Wu SY & Gu SL 2011 Quantitative trait loci for resistance to Fusarium head blight in a Chinese wheat landrace Haiyanzhong. Theoretical and Applied Genetics 122: 1497-1502.
10838.	Himi E, Maekawa M, Miura H & Noda K 2011 Development of PCR markers for *Tamyb10* related to *R-1*, red grain color in wheat. Theoretical and Applied Genetics 122: 1561-1576.
10839.	Sherman JD, Souza E, See D & Talbert LE 2011 Microsatellite markers for grain color in wheat. Crop Science 48: 1419-1424.
10840.	Sun XC, Bai GH, Carver BF & Bowden R 2010 Molecular mapping of wheat leaf rust resistance gene *Lr42*. Crop Science 50: 59-66.
10841.	Blake NK, Stougaard RN, Weaver DK, Sherman JD, Lanning SP, Naruoka Y, Xue Q, Martin JM & Talbert LE 2011 Identification of a quantitative trait locus for resistance to *Sitodiplosis mosellana* Gehn, the orange blossom midge, in spring wheat. Plant Breeding 130: 25-50.
10842.	Singh A, Pallavi JK, Gupta P & Prabhu KV 2011 Identification of microsatellite markers linked to leaf rust adult plant resistance (APR) gene *Lr48* in wheat. Plant Breeding 130: 31-34.
10843.	Mohler V, Baur A, Baur C, Flath K, Schweizer G & Hartl L 2011 Genetic analysis of powdery mildew resistance in German winter wheat cultivar Cortez. Plant Breeding 130: 35-40.
10844.	Miranda LM, Bland DE, Cambron SE, Lyerly JH, Johnson J, Buntin GD & Murphy JP 2010 Genetic mapping of an *Aegilops tauschii*-derived Hessian fly resistance gene in common wheat. Crop Science 50: 612-616.
10845.	Olsen EL, Brown-Guedira G, Marshall DS, Jin Y, Mergoum M, Lowe I & Dubcovsky J 2010 Genotyping of U.S. wheat germplasm for presence of stem rust resistance genes *Sr24*, *Sr26* and *Sr1RSAmigo*. Crop Science 59: 668-675.
10846.	Yu GT, Williams CE, Harris MO, Cai XW, Mergoum M & Xu SS 2010 Development and validation of molecular markers closely linked to *H32* for resistance to Hessian fly in wheat. Crop Science 50: 1325-1332.
10847.	Herrera-Foessel SA, Singh RP, Lillemo M, Huerta-Espino J, Bhavani S, Singh S, Lan C, Calvo-Salazar V & Lagudah ES 2014 *Lr67/Yr46* confers adult plant resistance to stem rust and powdery mildew in wheat. Theoretical and Applied Genetics 127: 781-789. DOI: 10.1007/s00122-013-2256-9.
10848.	Mohler V, Singh D, Singrun C & Park RF 2012 Characterization and mapping of *Lr65* in spelt wheat 'Altgold Rotkorn'. Plant Breeding 131: 252-257.

10849.	Liu J, Chang ZJ, Zhang XJ, Yang ZJ, Li X, Jia JQ, Zhan HX, Guo HJ and Wang JM 2013 Putative *Thinopyrum intermedium*-derived stripe rust resistance gene *Yr50* maps on wheat chromosome 4BL. Theoretical and Applied Genetics 126: 265-274.
10850.	Randhawa M, Bansal U, Valarik M, Klocova B, Dolezel J and Bariana H. 2014 Molecular mapping of stripe rust resistance gene *Yr51* in chromosome 4AL of wheat. Theoretical and Applied Genetics 127: 317-324.
10851.	Bansal U, Bariana H, Wong D, Randhawa M, Wicker T, Hayden M and Keller B. 2014 Molecular mapping of an adult plant stem rust resistance gene *Sr56* in winter wheat cultivar Arina. Theoretical and Applied Genetics 127: 1441-1448. DOI 10.1007/s00122-014-2311-1
10852.	Ren RS, Wang MN, Chen XM & Zhang ZJ 2012 Characterization and molecular mapping of *Yr52* for high-temperature adult-plant resistance to stripe rust in spring wheat germplasm PI 183527. Theoretical and Applied Genetics 125: 847-857. DOI: 10.1007/s00122-012-1877-8.
10853.	Wang MN, Chen XM, Xu LS, Cheng P & Bockelman HE 2012 Registration of 70 common spring wheat germplasm lines resistant to stripe rust. Journal of Plant Registrations 6: 104-110. DOI: 10.3198/jpr2011.05.0261crg
10854.	Xu LS, Wang MN, Cheng P, Kang ZS, Hulbert SH & Chen XM 2013 Molecular mapping of *Yr53*, a new gene for stripe rust resistance in durum wheat accession PI 480148 and its transfer to common wheat. Theoretical and Applied Genetics 126: 523-533.
10855.	Joshi AK, Chand R, Kumar S & Singh RP 2004 Leaf tip necrosis: A phenotypic marker associated with resistance to spot blotch disease in wheat. Crop Science 44: 792-796.
10856.	Lillemo M, Joshi AK, Prasad R, Chand R and Singh RP 2013 QTL for spot blotch in bread wheat line Saar co-locate to the biotrophic disease resistance loci *Lr34* and *Lr46*. Theoretical and Applied Genetics 126: 711-719.
10857.	Peng ZS, Li X, Yang ZJ & Liao ML 2011 A new reduced height gene found in the tetraploid semi-dwarf wheat landrace Aiganfanmai. Genetics and Molecular Research 10: 2349-2357.
10858.	Hiebert CW, Fetch TG & Zegeye T 2010 Genetics and mapping of stem rust resistance to UG99 in the wheat cultivar Webster. Theoretical and Applied Genetics 121: 65-69.
10859.	Cao AZ, Xing LP, Wang XY, Yang XM, Wang W, Sun YL, Qian C, Ni YL, Chen YP, Liu DJ, Wang XE & Chen PD 2011 Serine/threonine kinase gene *Stpk-V*, a key member of powdery mildew resistance gene *Pm21*, confers powdery mildew resistance in wheat. Proceedings of the National Academy of Sciences USA 108: 7727-7732.
10860.	Chu CG, Niu ZX, Zhong SB, Chao SM, Friesen TL, Halley S, Elias EM, Dong YH, Faris JD & Xu SS 2011 Identification and molecular mapping of two QTLs with major effects for resistance to Fusarium head blight in wheat. Theoretical and Applied Genetics 123: 1107-1119.
10861.	Singh RP, Herrera-Foessel SA, Huerta-Espino J, Bariana HS, Bansal U, McCallum BD, Hiebert CW, Bhavani S, Singh S, Lan C and Lagudah ES 2012 *Lr34/Yr18/Sr57/Pm38/Bdv1/Ltn1* confers slow rusting, adult plant resistance to *Puccinia graminis tritici*. In: 13th Cereal Rusts and Powdery Mildews Conference, August 28–September 1, 2012. Beijing p173.
10862.	Krattinger SG, Lagudah ES, Spielmeyer W, Singh RP, Huerta-Espino J, McFadden M, Bossolini E, Selter LL & Keller B. 2009 A putative ABC transporter confers durable resistance to multiple fungal pathogens in wheat. Science 323: 1360-63. DUPLICATE OF 10648 – CHANGES MADE IN THE DISEASE SECTION

10863.	Bhavani S, Singh RP, Argillier O, Huerta-Espino J, Singh S, Njau P, Brun S, Lacam S & Desmouceaux N 2011 Mapping durable adult plant stem rust resistance to the race Ug99 group in six CIMMYT wheats. In: McIntosh R (ed.) Proceedings of the Borlaug Global Rust Initiative 2011 Technical Workshop, June 13-16, Saint Paul, Minnesota, U.S.A. Borlaug Global Rust Initiative, www.globalrust.org, ISBN: 978-0-615-54519-6 43-53.
10864.	Kolmer JA, Garvin DF & Jin Y 2011 Expression of a Thatcher wheat adult plant stem rust resistance QTL on chromosome arm 2BL is enhanced by *Lr34*. Crop Science 51: 526-533.
10865.	Kerber ER & Green GJ 1980 Suppression of stem rust resistance in the hexaploid wheat cv. Canthatch by chromosome 7DL. Canadian Journal of Botany 58: 1347-1350.
10866.	Kerber ER & Aung T 1999 Leaf rust resistance gene *Lr34* associated with nonsuppression of stem rust resistance in the wheat cultivar Canthatch. Phytopathology 89: 518-521.
10867.	Abeysekara NS, Faris JD, Chao AM, McClean PE & Friesen TL 2012 Whole-genome QTL analysis of Stagonospora nodorum blotch resistance and validation of the *SnTox40-Snn4* interaction. Phytopathology 102: 94-104.
10868.	Guedira M, Brown-Guedira G, Van Sanford D, Sneller C, Souza E & Marshall D 2010 Distribution of *Rht* genes in modern and historic winter wheat cultivar from eastern and cental USA. Crop Science 50: 1811-1822.
10869.	Olson EL, Brown-Guedira G, Marshall D, Stack E, Bowden RL, Jin Y, Rouse M & Pumphrey M 2010 Development of wheat lines having a small introgressed segment carrying stem rust resistance gene *Sr22*. Crop Science 50: 1823-1830.
10870.	Tsilo TJ, Jin Y & Anderson JA 2010 Identification of flanking markers for the stem rust resistance gene *Sr6* in wheat. Crop Science 50: 1967-1970.
10871.	Abeysekara NS, Friesen TL, Liu ZH, McClean PE, Faris JD 2010 Marker development and saturation mapping of the tan spot Ptr ToxB sensitivity locus *Tsc2* in hexaploid wheat. The Plant Genome 3: 179-189.
10872.	Klindworth DL, Niu ZX, Chao SM, Friesen TL, Jin Y, Faris JD, Cai XW & Xu SS 2012 Introgression and characterization of a goatgrass gene for a high level of resistance to Ug99 stem rust in tetraploid wheat. Genes, Genomes & Genetics 2: 665-673.
10873.	Maxwell JJ, Lyerly JH, Srnic G, Parks R, Cowger C, Marshall D, Brown-Guedira G & Murphy JP 2010 MlAB10: A *Triticum turgidum* subsp. *dicoccoides* derived powdery mildew resistance gene identified in common wheat. Crop Science 50: 2261-2267.
10874.	Thomas J, Nilmalgoda S, Hiebert C, McCallum B, Humphries G & DePauw R 2010 Genetic markers and leaf rust resistance of the wheat gene *Lr32*. Crop Science 50: 2310-2317.
10875.	Kolmer JA, Anderson JA & Flor JM 2010 Chromosome location, linkage with simple sequence repeat markers, and leaf rust resistance conditioned by gene *Lr63* in wheat. Crop Science 50: 2392-2395.
10876.	Zhang WJ, Olson E, Saintenac C, Rouse M, Abate Z, Jin Y, Akhunov E, Pumphrey M & Dubcovsky J 2010 Genetic maps of stem rust resistance gene *Sr35* in diploid and hexaploid wheat. Crop Science 50: 2464-2474.
10877.	Liu XL, Yang XF, Wang CY, Wang YJ, Zhang H & Ji WQ 2012 Molecular mapping of resistance to English grain aphid (*Sitobion avenae* F.) in *Triticum durum* wheat line C273. Theoretical and Applied Genetics 124: 287-293.
10878.	Simons KJ, Gehlhar SB, Maan SS & Kianian SF 2003 Detailed mapping of the species cytoplasm-specific (*scs*) gene in durum wheat. Genetics 165: 2129-2136.

10879.	Ghaffary SMT, Faris JD, Friesen TL, Visser RGF, van der Lee TAG, Robert O & Kema GHJ 2012 New broad-spectrum resistance to Septoria tritici blotch derived from synthetic hexaploid wheat. Theoretical and Applied Genetics 124: 125-142.
10880.	Chu C-G, Tan CT, Yu GT, Xu SS & Lan L 2011 A novel retrotransposon inserted in the dominant *Vrn-B1* allele confers spring growth habit in tetraploid wheat (*Triticum turgidum* L.). Genes, Genomes & Genetics 1: 637-645.
10881.	Diaz A, Zikhali M, Turner AS, Isaac P, Laurie DA 2012 Copy number variation affecting the photoperiod-B1 and vernalization-A1 genes is associated with altered flowering time in wheat (*Triticum aestivum*). PloS One 7(3): 233-234.
10882.	Ayala-Navarrete L, Thompson N, Ohm H & Anderson J 2010 Molecular markers show a complex mosaic pattern of wheat-*Thinoyrum intermedium* translocations carrying resistance to YDV. Theoretical and Applied Genetics 121: 961-970.
10883.	Bovillo WD, Horne M, Herde D, Davis M, Wildermuth GB & Sutherland MW 2010 Pyramiding QTL increases seedling resistance to crown rot (*Fusarium pseudograminearum*) of wheat (*Triticum aestivum*). Theoretical and Applied Genetics 121: 127-136.
10884.	Xue SL, Li GQ, Jia HY, Xu F, Lin F, Tang MZ, Wang Y, An X, Xu HB, Zhang LX, Kong ZX & Ma ZQ 2010 Fine mapping *Fhb4*, a major QTL conditioning resistance to Fusarium infection in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 121: 147-156.
10885.	Xue SL, Li GQ, Jia HY, Lin F, Cao Y, Xu F, Tang MZ, Wang Y, Wu XY, Zhang ZZ, Kong ZX & Ma ZQ 2009 Marker-assisted development and evaluation of near-isogenic lines for scab resistance QTLs of wheat. Molecular Breeding 25: 397-405.
10886.	Ben-David R, Xie WL, Peleg Z, Saranga Y, Dinoor A & Fahima T 2010 Identification and mapping of *PmG16*, a powdery mildew resistance gene derived from wild emmer wheat. Theoretical and Applied Genetics 121: 499-510.
10887.	Dakouri A, McCallum BD, Walichnowski AZ & Cloutier S 2010 Fine-mapping of the leaf rust *Lr34* locus in *Triticum aestivum* (L.) and characterization of large germplasm collections support the ABC transporter as essential for gene function. Theoretical and Applied Genetics 121: 373-384.
10888.	Cao SH, Carver BF, Zhu XK, Tang TL, Chen YH, Hunger RM & Yan LL 2010 A single-nucleotide polymorphism that accounts for allelic variation in the *Lr34* gene and leaf rust reaction in hard wheat. Theoretical and Applied Genetics 121: 385-392.
10889.	McCallum BD, Humphries DG, Somers DJ, Dakouri A & Cloutier S 2012 Allelic variation for the rust resistance gene *Lr34/Yr18* in Canadian wheat cultivars. Euphytica 183: 261-274.
10890.	Vazquez MD, Peterson CJ, Riera-Lizarazu, Chen XM, Heesacker A, Ammar K, Crossa J & Mundt CC 2012 Genetic analysis of adult plant, quantitative resistance to stripe rust in wheat cultivar 'Stephens' in multi-environment trials. Theoretical and Applied Genetics 124: 1-11.
10891.	Ma J, Yan GJ & Liu CJ 2012 Development of near-isogenic lines for a major QTL on 3BL conferring Fusarium crown rot resistance in hexaploid wheat. Euphytica 183: 147-152.
10892.	Zhang HT, Huan HY, Li JT, Zhu J, Xie CJ, Zhou YL, Duan XY, Yang TM, Sun QX & Liu ZY 2010 Genetic and comparative genomics mapping reveals that a powdery mildew resistance gene *Ml3D232* originating from wild emmer co-segregates with an NBS-LRR analog in common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 121: 1613-1621.

10893.	Liu SB & Bai GH 2010 Dissection and fine mapping of a major QTL for preharvest sprouting resistance in white wheat Rio Blanco. Theoretical and Applied Genetics 121: 1395-1404.
10894.	Knox RE, Pozniak CJ, Clarke FR, Clarke JM, Housgmand S & Singh AK 2009 Chromosomal location of the cadmium uptake gene (*Cdu1*) in durum wheat. Genome 52: 741-747.
10895.	Wiebe K, Harris NS, Faris JD, Clarke JM, Knox RE, Taylor GJ & Pozniak CJ 2010 Targeted mapping of Cdu1, a major locus regulating grain cadmium concentration in durum wheat (*Triticum turgidum* L. var *durum*). Theoretical and Applied Genetics 121: 1047-1058.
10896.	Xue SL, Xu F, Tang MZ, Zhou Y, Li GQ, An X, Lin F, Xu HB, Jia HY, Zhang LX, Kong ZX & Ma ZQ 2011 Precise mapping of *Fhb5*, a major QTL conditioning resistance to Fusarium infection in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 123: 1055-1063.
10897.	Xu WG, Li CX, Hu L, Wang HW, Dong HB, Zhang JZ & Zan XC 2011 Identification and molecular mapping of *PmHNK54*: a novel powdery mildew resistance gene in common wheat. Plant Breeding 130: 603-607.
10898.	Lu HJ, Price J, Devkota R, Rush C & Rudd K 2011 A dominant gene for resistance to Wheat Streak Mosaic Virus in winter wheat line CO960293-2. Crop Science 51: 5-12.
10899.	Morris CF, Simeone MN, King GE & Lafiandra D 2011 Transfer of soft kernel texture from *Triticum aestivum* to durum wheat, *Triticum turgidum* ssp. *durum*. Crop Science 51: 114-122.
10900.	Yabalo DN, Mergoum M & BerzonskyWA 2011 Further characterization of the scab resistance of 'Frontana' spring wheat and the relationship between resistance mechanisms. Plant Breeding 130: 521-525.
10901.	Risser P, Ebmeyer E, Korzun V, Hartl L & Miedaner T 2011 Quantitative trait loci for adult-plant resistance to *Mycosphaerella graminicola* in two winter wheat populations. Phytopathology 101: 1209-1216.
10902.	Kolmer JA, Garvin DF & Jin Y 2011 Expression of Thatcher wheat adult plant stem rust resistance QTL on chromosome arm 2BL is enhanced by *Lr34*. Crop Science 51: 526-533.
10903.	Barcellos Rosa S et al. 2012 Personal communication
10904.	Hiebert CW, McCallum BD and Thomas JB. 2014 *Lr70*, a new gene for leaf rust resistance mapped in common wheat accession KU3198. Theoretical and Applied Genetics 127: 2005-2009.
10905.	Cenci A, Somma S, Chantret N, Dubcovsky J & Blanco A 2004 PCR identification of durum wheat BAC clones containing genes coding for carotenoid biosynthesis enzymes and their chromosome localization. Genome 47: 911-917.
10906.	Zhang CY, Dong CH, He XY, Zhang LP, Xia XC & He ZH 2011 Allelic variants at the *Tzds-D1* locus on wheat chromosome 2DL and their association with yellow pigment content. Crop Science 51: 1580-1590.
10907.	Azhaguvel P, Rudd JC, Ma YQ, Luo MC & Weng YQ 2012 Fine mapping of greenbug aphid-resistance gene *Gb3* in *Aegilops tauschii*. Theoretical and Applied Genetics 124: 555-564.
10908.	Eagles HA, Cane K, Appelbee M, Kuchel H, Eastwood RF & Martin PJ 2012 The storage protein activator gene *Spa-B1* and grain quality traits in southern Australian wheat breeding programs. Crop & Pasture Science 63: 311-318.

10909.	Guillaumie S, Charmet G, Linossier L, Torney V, Robert N & Ravel C 2004 Co-location between a gene encoding the bZIP factor SPA and an eQTL for a high-molecular-weight glutenin subunit in wheat (*Triticum aestivum*). Genome 47: 705-713.
10910.	Mohler V, Singh D, Singrun C and Park RF 2012 Characterization and mapping of *Lr65* in spelt wheat 'Altgold Rotkorn'. Plant Breeding 131: 252-257.
10911.	Singh D, Mohler V and ParK RF 2013 Discovery, characterization and mapping of wheat leaf rust resistance gene *Lr71*. Euphytica 190: 131-136.
10912.	Xiao MG, Song FJ, Jiao JF, Wang XM, Xu HX & Li HJ 2013 Identification of the gene *Pm47* on chromosome 7BS conferring resistance to powdery mildew in the Chinese wheat landrace Hongtanglazi. Theoretical and Applied Genetics 126: 1397-1403.
10913.	Dubcovsky JD 2012 Personal communication
10914.	Hao YF, Chen ZB, Wang YY, Bland D, Buck J, Brown-Guedira G & Johnson J 2011 Characterization of a major QTL for adult plant resistance to stripe rust in US soft red winter wheat. Theoretical and Applied Genetics 123: 1301-1411.
10915.	Bentley, AR, Turner AS, Gosman N, Leigh FJ, Maccaferri M, Dreisgacher S, Greenland A & Laurie DA 2011 Frequency of photoperiod insensitive *Ppd-A1a* alleles in tetraploid, hexaploid and synthetic hexaploid wheat germplasm. Plant Breeding 130: 10-15.
10916.	Eagles HA, Cane K & Trevaskis B 2011 Veery wheat carry an allele of *Vrn-A1* that has implications for freezing tolerance in winter wheats. Plant Breeding 130: 412-418.
10917.	Genc Y, Oldach K, Verbyla AP, Lott G, Hassan M, Tester M, Wallwork H & McDonald G 2010 Sodium exclusion QTL associated with improved seedling growth in bread wheat under salinity stress. Theoretical and Applied Genetics 121: 877-894.
10918.	Xie WL, Ben-David R, Zeng B, Dinoor A, Xie CJ, Sun QX, Roder MS, Fahoum A & Fahima T 2012 Suppressed recombination rate in 6VS/6AL translocation region carrying the *Pm21* locus introgressed from *Haynaldia villosa* into hexaploid wheat. Molecular Breeding 29: 399-412.
10919.	Chang C, Zhang HP, Zhao QX, Feng JM, Si HQ, Lu J & Ma CX 2011 Rich allelic variations of Viviparous-1A and their associations with seed dormancy/pre-harvest sprouting of common wheat. Euphytica 179: 343-353.
10920.	Crawford AC, Stefanova K, Lambe W, McLean R, Wilson R, Barclay I & Francki MG 2011 Functional relationships of phytoene synthase I alleles on chromosome 7A controlling flour variation in selected Australian wheat genotypes. Theoretical and Applied Genetics 123: 95-108.
10921.	Liu ZJ, Zhu J, Cui Y, Liang Y, Wu HB, Song W, Liu Q, Yang TM, Sun QX and Liu ZY 2012 Identification and comparative mapping of a powdery mildew resistance gene derived from wild emmer (*Triticum turgidum* var. *dicoccoides*) on chromosome 2BS. Theoretical and Applied Genetics 124: 1041-1049.
10922.	Bertin I, Fish L, Foote TN, Knight E, Snape J and Moore G 2009 Development of consistently crossable wheat genotypes for alien wheat gene transfer through fine mapping of the *Kr1* locus. Theoretical and Applied Genetics 119: 1371-1381.
10923.	Pearce S, Saville R, Vaughan SP, Chandler PM, Wilhelm EP, Sparks CA, Al-Kaff N, Korolev A, Boulton MI, Phillips AL, Heddon P, Nicholson P and Thomas SG 2011 Molecular characterization of Rht-1 dwarfing genes in hexaploid wheat. Plant Physiology 157: 1820-1831.
10924.	Divashuk MG, Vasilyev AV, Bespalova LA and Karlov GI 2012 Identity of the *Rht-11* and *Rht-B1e* reduced plant height genes. Russian Journal of Genetics 48: 897-900.

10925.	Friesen TL, Chu CG, Xu SS and Faris JD 2012 SnTox5-Snn5: a novel *Stagonospora nodorum* effector-wheat gene interaction and its relationship with the SnToxA-Tsn1 and SnTox3-Snn3-B interactions. Molecular Plant Pathology 13: 1101-1109.
10926.	Wang CY, Ji WQ, Zhang GS, Wang QY, Cai DM and Xue Z 2007 SSR markers and preliminary chromosomal location of a powdery mildew resistance gene in common wheat germplasm NJ134. Acta Agronomica Sinica 33: 163-166.
10927.	Xue F, Ji WQ, Wang CY, Zhang H and Yang BJ 2012 High-density mapping and marker development for the powdery mildew resistance gene *PmAS846* derived from emmer wheat (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 124: 1549-1560.
10928.	Rosewarne GM, Singh RP, Huerta-Espino H, Herrera-Foessel SA, Forrest KL, Hayden MJ and Rebetzke GJ 2012 Analysis of leaf and stripe rust severities reveals pathotype changes and multiple minor QTLs associated with resistance in a Avocet × Pastor wheat population. Theoretical and Applied Genetics 124: 1283-1294.
10929.	Ingala L, Lopez M, Darino M, Pergolesi MF, Dieguez MJ and Sacco F 2012 Genetic analysis of leaf rust resistance genes and associated markers in the durable resistant wheat cultivar Sinvalocho MA. Theoretical and Applied Genetics 124: 1305-1314.
10930.	Beecher B and Skinner DZ 2011 Molecular cloning and expression analysis of multiple polyphenol oxidase genes in developing wheat (*Triticum aestivum*) kernels. Journal of Cereal Science 53: 371-378.
10931.	Beecher BS, Carter AH and See DR 2012 Genetic mapping of new seed-expressed polyphenol oxidase genes in wheat (*Triticum aestivum*). Theoretical and Applied Genetics 124: 1463-1473.
10932.	Poole GJ, Smiley RW, Paulitz TC, Walker CA, Carter AH, See DR and Garland-Campbell K 2012 Identification of quantitative trait loci (QTL) for resistance to Fusarium crown rot (*Fusarium pseudograminearum*) in multiple assay environments in the Pacific Northwestern US. Theoretical and Applied Genetics 125: 91-107.
10933.	Agenbag GM, Pretorius ZA, Boyd LA, Bender CM and Prins R 2012 Identification of adult plant resistance to stripe rust in the wheat cultivar Cappelle-Desprez. Theoretical and Applied Genetics 125: 109-120.
10934.	Lu QX, Bjornstad A, Ren Y, Asad MA, Xia XC, Chen XM, Ji F, Shi JR and Lillemo M 2012 Partial resistance to powdery mildew in German spring wheat 'Naxos' is based on multiple genes with stable effects in diverse environments. Theoretical and Applied Genetics 125: 297-309.
10935.	Gao HD, Zhu FF, Jiang YG, Wu JH, Yan W, Zhang QF, Jacobi A and Cai SB 2012 Genetic analysis and molecular mapping of a new powdery mildew resistant gene *Pm46* in common wheat. Theoretical and Applied Genetics 125: 967-973. Note: Although the title of this paper as published refers to *Pm46*, it is listed here as *Pm48*.
10936.	Olsen EL, Rouse MN, Pumphrey MO, Bowden RL, Gill BG and Poland J 2013 Introgression of stem rust resistance genes *SrTa10187* and *SrTA10171* from *Aegilops tauschii* to wheat. Theoretical and Applied Genetics 126: 2477-2484.
10937.	Piarulli L, Gadaleta A, Mangini G, Signorile MA, Pasquini M, Blanco A and Simeone R 2012 Molecular identification of a powdery mildew resistance gene on chromosome 2BS from *Triticum turgidum* ssp. *dicoccum*. Plant Science 196: 101-106. Personal communication
10938.	Simeone R 2012 Personal communication

10939.	Inoue Y, Mori R, Takahashi Y, Kiguchi S, Enomoto T, Chuma I and Tosa Y 2012 Identification and molecular mapping of a wheat gene for resistance to an unadapted isolate of *Colletotrichum cereale*. Phytopathology 103: 575-582.
10940.	Kassa MT, Menzies J and McCartney 2012 Genetics and mapping of resistance to *Ustilago tritici* in the hexaploid wheat (*Triticum aestivum*) variety 'AC Foremost'. Unpublished abstr
10941.	Pretorius ZA, Jin Y, Bender CM, Herselman L and Prins R 2012 Seedling resistance to stem rust race Ug99 and marker analysis for *Sr2*, *Sr24* and *Sr31* in South African wheat cultivars and lines. Euphytica 186: 15-23.
10942.	Mohler V, Bauer C, Schweizer G, Kempf H and Hartl L 2013 *Pm50*: a new powdery mildew resistance gene in common wheat derived from cultivated emmer. Journal of Applied Genetics 54: 259–263. DOI: 10.1007/s13353-013-0158-9.
10943.	Basnet BR, Singh RP, Herrera-Foessel SA, Ibrahim AMH, Huerta-Espino J, Calvo-Salazar V and Rudd JC 2012 Genetic analysis of adult plant resistance to yellow rust and leaf rust in common spring wheat 'Quaiu 3'. Plant Disease 97: 728-736. DOI: 10.1094/PDIS-02-12-0141-RE.
10944.	Basnet BR, Singh RP, Ibrahim AMH, Herrera-Foessel SA, Huerta-Espino J, Lan C and Rudd JC 2014 Characterization of *Yr54* and other genes associated with adult plant resistance to yellow rust and leaf rust in common wheat Quaiu 3. Molecular Breeding 33: 385-399. DOI: 10.1007/s11032-013-9957-2.
10945.	Agenbag GM, Pretorius ZA, Boyd LA, Bender CM and Prins R 2012 Identification of adult plant resistance to stripe rust in the wheat cultivar Cappelle-Desprez. Theoretical and Applied Genetics 125: 109-120.
10946.	Tereschenko OY, Pshenichnikova TA, Salina EA and Khlestkina EK 2012 Development and molecular characterization of a novel wheat genotype having purple grain colour. Cereal Research Communications 40: 210-214.
10947.	Herrera-Foessel SA, Huerta-Espino J, Calvo-Salazar V, Lan C and Singh RP 2014 *Lr72* confers resistance to leaf rust in durum wheat cultivar Atil C2000. Plant Disease 98: 580-703. DOI: 10.1094/PDIS-07-13-0741-RE
10948.	Vy TTP, Hyon G-S, Nga NTT, Inoue Y, Chuma I and Tosa Y 2013 Genetic analysis of host-pathogen incompatibility between Lolium isolates of *Pyricularia oryzae* and wheat. Journal of General Plant Pathology 80: 59-65.
10949.	Cumagun CJR, Ahn VL, Vy TTP, Inoue Y, Asano H, Hyon G-S, Chuma I and Tosa Y 2012 Identification of a hidden gene in tetraploid wheat using laboratory strains of *Pyricularia oryzae* produced by backcrossing. Phytopathology 104: 634-640.
10950.	Zhang XH, Pan HY and Bai GH 2012 Quantitative trait loci responsible for Fusarium head blight resistance in Chinese landrace Baishanyuehuang. Theoretical and Applied Genetics 125: 495-502.
10951.	Singh S and Bowden RL 2011 Molecular mapping of adult-plant race-specific leaf rust resistance gene in bread wheat. Molecular Breeding 28: 137-142.
10952.	Ghazvini H, Hiebert CW, Zegeye T, Liu SX, Dilawari M, Tsilo T, Anderson JA, Rouse MN, Jin Y and Fetch T 2012 Inheritance of resistance to Ug99 stem rust in wheat cultivar Norin 40 and genetic mapping of *Sr42*. Theoretical and Applied Genetics 125: 817-824.
10953.	Bariana HS 2013 Personal communication
10954.	Williams C 2013 Personal communication
10955.	Bansal UK, Kazi AG, Singh B, Hare RA and Bariana HS 2014 Mapping of durable stripe rust resistance in a durum wheat cultivar Wollaroi. Molecular Breeding 33, 51-59. DOI:

10956.	Nui ZX, Puri KD, Chao SM, Jin Y, Steffenson BJ, Maan SS, Xu SS and Zhong SB 2013 Genetic and molecular mapping of crown rust resistance in common wheat. Manuscript
10957.	Huang XQ and Roder MS 2011 High-density genetic and physical bin mapping of wheat chromosome 1D reveals that the powdery mildew resistance gene *Pm24* is located in a highly recombinogenic region. Genetica 139: 1179-1187.
10958.	Takumi S, Koyama K, Fujiwara K and Kobayashi F 2011 Identification of a large deletion in the first intron of the *Vrn-D1* locus, associated with the loss of vernalization requirement in wild wheat progenitor *Aegilops tauschii* Coss. Genes and Genetic Systems 86: 183-196.
10959.	Kulwal P, Ishikawa, Benscher D, Feng ZY, Yu LX, Jadhav A, Mehetre S and Sorrells ME 2012 Association mapping for pre-harvest sprouting resistance in white winter wheat. Theoretical and Applied Genetics 125: 793-805.
10960.	Crook AD, Friesen TL, Liu ZH, Ojiambo and Cowger C 2012 Novel necrotrophic effectors from *Stagonospora nodorum* and corresponding host severities in winter wheat germplasm in the southeastern United States. Phytopathology 102: 498-505.
10961.	Hu TZ, Ki HJ, Xie CJ, You MS, Yang ZM, Sun QX and Liu ZY 2008 Molecular mapping and chromosomal location of powdery mildew resistance gene in wheat cultivar Tangmai 4. Acta Agronomica Sinica 34: 1193-1198.
10962.	Powell NM, Lewis CM, Berry ST, MacCormack R and Boyd LA 2013 Stripe rust resistance genes in the UK winter wheat cultivar Claire. Theoretical and Applied Genetics 126: 1599-1612.
10963.	Randhawa MS, Bariana HS, Mago R and Bansal UK. 2015 Mapping of a new stripe rust resistance locus *Yr57* on chromosome 3BS of wheat. Molecular Breeding 35: 65. DOI 10.1007/s11032-0150-0270-0
10964.	Chhetri M, Bariana H, Kandiah P and Bansal U 2016 *Yr58*: A new stripe rust resistance gene and its interaction with *Yr46* for enhanced resistance. Phytopathology 106: 1530-1534. DOI: 10.1094/PHYTO-04-16-0182-R.
10965.	Singh RP, Herrera-Foessel SA, Huerta-Espino J, Lan CX, B. Basnet R, Bhavani S & Lagudah ES 2013 Pleiotropic gene *Lr46/Yr29/Pm39/Ltn2* confers slow rusting, adult plant resistance to wheat stem rust. Manuscript under preparation
10966.	Zhou XL, Wang MN, Chen XM, Lu Y, Kang ZS and Jing JX 2013 Identification of *Yr59* conferring high-temperature adult-plant resistance to stripe rust in wheat germplasm PI 178759. Theoretical and Applied Genetics 127: 935-945. DOI: 10.1007/s00122-014-2269-z.
10967.	Wang MN, Chen XM, Xu LS, Cheng P and Bockelman HE 2012 Registration of 70 common spring wheat germplasm lines resistant to stripe rust. Journal of Plant Registrations 6: 104-110.
10968.	Herrera-Foessel SA, Singh RP, Lan CX, Huerta-Espino J, Calvo-Salazar V, Bansal Bariana HS and Lagudah ES. 2015 *Yr60*: A gene conferring moderate resistance to stripe rust in wheat. Plant Disease 99: 508-511.
10969.	Park RF, Mohler V, Nazari K and Singh D 2014 Characterization and mapping of gene *Lr73* conferring seedling resistance to *Pucciniia triticina* in common wheat. Theoretical and Applied Genetics 127: 2041-2049. DOI: 10.1007/s00122-014-2359-y.
10970.	Zhou XL, Han DJ, Chen XM, Gou HL, Guo SJ, Rong L, Wang QL, Huang LL and Kang ZS 2014 Characterization and molecular mapping of stripe rust resistance gene *Yr61* in winter wheat cultivar Pindong 34. Theoretical and Applied Genetics 127: 2349-2358. DOI: 10.1007/s00122-014-2381-0.

10971.	Fahim M, Mechanicos A, Ayala-Navarrete, Haber S and Larkin PJ 2012 Resistance to Wheat Streak Mosaic Virus – a survey of resources and development of molecular markers. Plant Pathology 61: 425-440.
10972.	Lu QX, Szabo-Hever A, Bjornstad A, Lillimo M, Semagn K, Mesterhazy A, Ji F, Shi JR and Skinnes H 2011 Two major quantitative trait loci are required to counteract the increased susceptibility to Fusarium head blight of the *Rht-D1b* dwarfing gene in wheat. Crop Science 51: 2430-2438.
10973.	Fang TL, Campbell GG, Liu ZY, Chen XM, Wan AN, Li S, Liu ZJ, Cao SG, Chen YH, Bowden RL, Carver BF and Yan LL 2011 Stripe rust resistance in wheat cultivar Jagger is due to *Yr17* and a novel resistance gene. Crop Science 51: 2455-2465.
10974.	Millet E, Rong J-K, Qualset CO, McGuire PE, Bernard M, Sourdille P and Feldman M 2013 Production of chromosome-arm substitution lines of wild emmer in common wheat. Euphytica 190: 1-17.
10975.	Njau P, Bhavani S, Huerta-Espino, Keller B and Singh RP 2013 Identification of QTL associated with durable adult plant resistance to stem rust race Ug99 in wheat cultivar 'Pavon 76'. Euphytica 190: 33-34.
10976.	Liu YY, Zhang LL, Thompson IA, Goodwin SB and Ohm HW 2013 Molecular mapping re-locates the *Stb2* gene for resistance to Septoria tritici blotch derived from cultivar Veranopolis on wheat chromosome 1BS. Euphytica 190: 145-156.
10977.	Shcherban AB, Effremova TT and Salina EA 2012 Identification of a new *Vrn-B1* allele using two near-isogenic wheat lines with difference in heading time. Molecular Breeding 29: 675-685.
10978.	Milec Z, Tomkova L, Sumikova T and Pankova K 2012 A new multiplex PCR test for the determination of *Vrn-B1* alleles in bread wheat (*Triticum aestivum* L.). Molecular Breeding 30: 317-323.
10979.	Li Q, Huang J, Hou L, Liu P, Jing JX, Wang BT and Lang ZS 2012 Genetic and molecular mapping of stripe rust resistance gene in wheat-*Psathyrostachys huashanica* translocation line H9020-1-6-8-3. Plant Disease 96: 1482-1487.
10980.	German SE and Kolmer JA 2012 Leaf rust resistance in selected Uruguayan common wheat cultivars with early maturity. Crop Science 52: 601-608.
10981.	Valdez VA, Byrne PF, Lapitan NLV, Peairs FB, Bernardo A, Bai GH and Haley SD 2012 Inheritance and genetic mapping of Russian wheat aphid resistance in Iranian wheat landrace accession PI 626580. Crop Science 52: 676-682.
10982.	Lu HJ, Kottke R, Devkota R, St. Amand P, Bernardo A, Bai GH, Byrne P, Martin TJ, Haley SD and Rudd JC 2012 Consensus mapping and identification of markers for marker-assisted selection of *Wsm2* in wheat. Crop Science 52: 720-728.
10983.	Yu GT, Wang T, Anderson KM, Harris MO, Cai XW and Xu SS 2012 Evaluation and haplotype analysis of elite synthetic hexaploid wheat lines for resistance to Hessain fly. Crop Science 52: 752-763.
10984.	Kosellek C, Pillen K, Nelso JC, Weber WE and Saal B 2013 Inheritance of field resistance to Septoria tritici blotch in the wheat doubled haploid population Solitar × Mazurka. Euphytica 194: 161-176.
10985.	Vikas VK, Tomar SMS, Sivasamy M, Kumar J, Jayaprakash, Kumar A, Peter J, Nisha R and Punniakotti E 2013 Hybrid necrosis in wheat: evolutionary significance or potential barrier for gene flow? Euphytica 194: 261-275.

10986.	Singh SK, Singh AM, Jain N, Singh GP, Ahlawat AK & Ravi I 2013 Molecular characterization of vernalization and photoperiod genes in wheat varieties from different agro-climatic zones in India. Cereal Research Communications 41: 376-387.
10987.	Periyannan S, Moore J, Ayliffe M, Bansel U, Wang XJ, Huang L, Deal K, Luo MC, Kong XY, Bariana H, Mago R, McIntosh R, Dodds P, Dvorak J and Lagudah E 2013 The gene *Sr33*, an ortholog of barley *Mla* genes, encodes resistance to wheat stem rust race Ug99. Science 341: 786-788.
10988.	Saontenac C, Zhany WJ, Salcedo A, Rouse MN, Trick HN, Akhunov E and Dubcovsky J 2013 Identification of wheat gene *Sr35* that confers resistance to UG99 stem rust race group. Science 341: 783-786.
10989.	Yamamori M and Yamamoto K 2011 Effects of two novel Wx-A1 alleles of common wheat (*Triticum aestivum* L.) on amylase and starch properties. Journal of Cereal Science 54: 229-235.
10990.	Yamamori M and Guzman C 2013 SNPs and an insertion in five *Wx-A1* alleles as factors for variant Wx-A1 protein in wheat. Euphytica 192: 325-338.
10991.	Milec Z, Sumikova T, Tomkova L and Pankova K 2013 Distribution of different *Vrn-B1* alleles in hexaploid spring wheat germplasm. Euphytica 192: 371-378.
10992.	Mergoum M, Harilal VE, Singh PK, Adhikari TB, Kumar A, Ghavami F, Elias E, Alamri MS and Kianian SF 2013 Genetic analysis and mapping of seedling resistance to Septoria tritici blotch in 'Steele-ND'/'ND 736' bread wheat population. Cereal Research Communications 41: 199-210.
10993.	Buerstmayr M, Huber K, Heckmann J, Steiner B, Nelson JC and Buerstmayr H 2012 Mapping of QTL for Fusarium head blight resistance and morphological and developmental traits in three backcross populations derived from *Triticum dicoccum* × *Triticum durum*. Theoretical and Applied Genetics 125: 1751-1765.
10994.	Xue F, Wang CY, Li C, Duan XY, Zhou YL, Zhao NJ, Wang YJ and Ji WQ. 2012 Molecular mapping of a powdery mildew resistance gene in common wheat landrace Baihulu and its allelism with *Pm24*. Theoretical and Applied Genetics 125: 1425-1432.
10995.	Hagenblad J, Asplund L, Balfourier F, Ravel C and Leino MW 2012 Strong presence of the high grain protein content allele of *Nam-B1* in Fennscandian wheat. Theoretical and Applied Genetics 125: 1677-1686.
10996.	Zhang J, Wang YY, Wu SW, Yang JP, Liu HW and Zhou Y 2012 A single nucleotide polymorphism at the *Vrn-D1* promoter region in common wheat is associated with vernalization response. Theoretical and Applied Genetics 125: 1697-1704.
10997.	Goates BJ 2012 Identification of new pathogenic races of common bunt and dwarf bunt fungi and evaluation of known races using an expanded set of differential wheat lines. Plant Disease 96: 361-369.
10998.	Chang C, Zhang HP, Feng JM, Yin B, Si HQ and Ma SX 2010 Identifying alleles of Viviparous-1B associated with pre-harvest sprouting in micro-core collections of Chinese wheat germplasm. Molecular Breeding 25: 481-490.
10999.	Chang C, Feng JM, Si HQ, Yin B, Zhang HP and Ma CX 2010 Validating a novel allele of viviparous-1 (*Vp-1Bf*) associated with high seed dormancy of Chinese wheat landrace Wanxianbaimaizi. Molecular Breeding 25: 517-523.
11000.	
11001.	Basnet BJ, Glover KD, Ibrahim AMH, Yen Y and Chao SM 2012 A QTL on chromosome 2DS of 'Sumai 3' increases susceptibility to Fusarium head blight in wheat. Euphytica 186: 91-101.

11002. Ansari MJ, Kumar R, Singh K and Dhaliwal HS 2012 Characterization and molecular mapping of EMS-induced brittle culm mutants of diploid wheat (*Triticum monococcum* L.). Euphytica 186: 165-176.

11003. Dumalasova V, Simmonds J, Bartos P and Snape J 2012 Location of genes for common bunt resistance in the European winter wheat cv. Trintella. Euphytica 186: 257-264.

11004. Maxwell JJ, Lyerly JH, Srnic G, Murphy JP, Cowger C, Parks R, Marshall D, Brown-Guerdira G and Miranda L 2012 MlNCD1: A novel *Aegilops tauschii*-derived powdery mildew resistance gene identified in common wheat. Crop Science 52: 1162-1170.

11005. Zhang XH, Bai Gh, Bochus W, Ji XJ and Pan HY 2012 Quantitative trait loci for Fusarium head blight resistance in U.S. hard winter wheat cultivar Heyne. Crop Science 52: 1187-1194.

11006. Seifers DL, Martin TJ and Haber S 2013 Temperature-sensitive resistance to wheat streak mosaic virus in CO960333 and KS06HW79 wheat. Plant Disease 97: 983-987.

11007. Nazari K 2013 First report of resistance of wheat line Avocet 'S' to stripe rust caused by *Puccinia stritiformis* f. sp. *tritici* (*Pst*) in Syria. Plant Disease 97: 996.

11008. Hao YF, Cambron SE, Chen SB, Wang YY, Bland DE, Buntin GD and Johnson JW 2013 Characterization of new loci for Hessian fly resistance in common wheat. Theoretical and Applied Genetics 126: 1067-1076.

11009. Fu BS, Chen Y, Li N, Ma HQ, Kong ZX, Zhang LX, Jia HY and Ma ZQ 2013 *pmx*: a recessive powdery mildew resistance gene at the *Pm4* locus identified in wheat landrace Xiaohongpi. Theoretical and Applied Genetics 126: 913-921.

11010. Rouse MN, Nirmala J, Jin Y, Chao S, Fetch TG, Pretorius ZA and Hiebert CW 2014 Characterization of *Sr9h*, a wheat stem rust resistance allele effective to Ug99. Theoretical and Applied Genetics 127: 1681-1688.

11011. Liu WX, Danilova TV, Rouse MN, Bowden RL, Friebe B, Gill BS and Pumphrey MO 2013 Development and characterization of a compensating wheat-*Thinopyrum intermedium* Robertsonian translocation with *Sr44* resistance to stem rust (Ug99). Theoretical and Applied Genetics 126: 1167-1177.

11012. Olsen EL, Rouse MN, Pumphrey MO, Bowden RL, Gill BS and Poland JA 2013 Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (UG99) from *Aegilops tauschii* to wheat. Theoretical and Applied Genetics 126: 1179-1188.

11013. Ning SZ, Wang N, Sakuma S, Pourkheirandish M, Wu JH, Matsumoto, Koba T and Komatsuda T 2013 Structure, transcription and post-transcriptional regulation of the bread wheat orthologs of the barley cleistogamy gene *Cly1*. Theoretical and Applied Genetics 126: 1273-1282.

11014. Li WL, Zhu HL, Challa GS and Zhang ZZ 2013 A non-additive interaction in a single locus causes a very short root phenotype in wheat. Theoretical and Applied Genetics 126: 1189-1200.

11015. Terracciano I, Maccaferri M, Bassi F, Mantovani P, Sanguineti MC, Salvi S, Simkova H, Dolezel J, Massi A, Ammar K, Kolmer J and Tuberosa R 2013 Development of COS-SNP and HRM markers for high-throughput and reliable haplotype-based detection of *Lr14a* in durum wheat (*Triticum durum* Desf.). Theoretical and Applied Genetics 126: 1077-1101.

11016. Li Y, Xiao J, Duan J, Liu Y, Ye X, Zhang S, Gu Y, Zhang L, Jia J and Kong X 2012 A tandom segmental duplication (TSD) in green revolution gene *Rht-D1b* region underlies plant height variation. New Phytologist 196: 282-291.

11017.	Wilhelm EP, Howells RH, Al-Kaff N, Jia JZ, Baker C, Leverington-Waite MA, Griffiths S, Greeland AJ, Boulton MI and Powell W 2013 Genetic characterization and mapping of the *Rht-1* homeologs and flanking markers in wheat. Theoretical and Applied Genetics 126: 1321-1336.
11018.	Li CL, Chen MS, Chao SM, Yu JM and Bai GH 2013 Identification of a novel gene, *H34*, in wheat using recombinant inbred lines and single nucleotide polymorphism markers. Theoretical and Applied Genetics 126: 2065-2071.
11019.	Singh S, Singh RP, Bhavani S, Huert-Espino J and Lopez-Vera EE 2013 QTL mapping of slow-rusting, adult plant resistance to race Ug99 of the stem rust fungus in PBW343/Muu RIL population. Theoretical and Applied Genetics 126: 1367-1375.
6.	Yang EN, Rosewarne GM, Herrera-Foessel SA, Huerta-Espino J, Tang ZX, Sun CF, Ren ZL and Singh RP 2013 QTL analysis of the spring wheat ‘Chapio’ identifies stable stripe rust resistance despite inter-continental genotype × environment interactions. Theoretical and Applied Genetics 126: 1721-1732.
11021.	Kolmer JA, Lin M and Bai G 2012 Genetics of leaf rust resistance in the winter wheat CI 13227. Crop Science 52: 2166-2172.
11022.	Liu SY, Christopher MD, Griffey CA, Hall MD, Gundrum PG and Brooks WS 2012 Molecular characterization of resistance to Fusarium head blight in U.S. soft red winter wheat breeding line VA00W-38. Crop Science 52: 2283-2292.
11023.	Lu Y, Wang MN, See D, Chen XM, Chao SM and Jing JX 2014 Mapping of *Yr62* and small-effect QTL for high-temperature adult-plant resistance to stripe rust in spring wheat PI 192252. Theoretical and Applied Genetics 127: 1449-1459.
11024.	Wang MN, Chen XM, Xu LS, Cheng P and Bockelman HE 2012 Registration of 70 common spring wheat germplasm lines resistant to stripe rust. Journal of Plant Registrations 6: 104-110.
11025.	Hao YF, Chen ZB, Wang YY, Bland D, Parks R, Cowger C and Johnson J 2012 Identification of *Pm8* suppressor at the *Pm3* locus in soft red winter wheat. Crop Science 52: 2438-2445.
11026.	Zhan HX, Li GR, Zhang XJ, Li X, Guo HJ, Gong WP, Jia JQ, Qiao LY, Ren YK, Yang ZJ and Chang ZJ 2014 Chromosomal location and comparative genomics analysis of powdery mildew resistance gene *Pm51* in a putative wheat-*Thinopyrum ponticum* introgression line. PLoS One 9(11): e113455.
11027.	Bansal U and Bariana HS 2013 Personal communication
11028.	Zhao ZH, Sun HG, Song W, Lu M, Huang LF, Wang ZM and Li HJ 2013 Genetic analysis and detection of the gene *MlLX99* on chromosome 2BL conferring resistance to powdery mildew in the wheat cultivar Liangxing 99. Theoretical and Applied Genetics 126: 3081-3089.
11029.	Song W, Sun HG, Zhang D, Sun YL, Wang XM and Li HJ 2014 Genetic analysis and detection of the gene *PmLX99* on chromosome 2BL conferring resistance to powdery mildew in the wheat cultivar Liangxing 99. Unpublished supplement to Reference 11028.
11030.	Cheng P, Xu LS, Wang MN, See D and Chen XM 2014 Molecular mapping of genes *Yr64* and *Yr65* for stripe rust resistance in hexaploid derivatives of durum wheat accessions PI 331260 and PI 480016. Theoretical and Applied Genetics 127: 2267-2277. DOI: 10.1007/s00122-014-2378-8.
11031.	Temesgen B, Chhetri M et al. 2015 Personal communication

11032.	Bariana H, Kant L, Qureshi N, Forrest K, Miah, H and Bansal U. 2022 Identification and characterisation of stripe rust resistance genes *z* and *Yr67* in wheat cultivar VL Gehun 892. Agronomy 2022, 12, 318. Doi: 10.3390/agronomy12020318.
11033.	Li Y, Niu YC and Chen XM 2009 Mapping a stripe rust resistance gene *YrC591* in wheat variety C591 with SSR and AFLP markers. Theoretical and Applied Genetics 118: 339-346.
11034.	Li ZF, Singh RP, Singh S, Lopez-Vera EE and Huerta-Espino J 2013 Genetics of resistance to yellow rust in PBW343 × Kenya Kudu recombinant inbred line population and mapping of a new resistance gene *YrKK*. Theoretical and Applied Genetics 32: 821-829.
11035.	Lopez-Vera EE, Nelson S, Singh RP, Basnet BR, Haley SD, Bhavani S, Huert-Espino J, Xoconostle-Cazares BG, Medrano RR, Rouse MN and Singh S 2014 Resistance to stem rust UG99 in six bread wheat cultivars maps to chromosome 6DS. Theoretical and Applied Genetics 127: 231-239.
11036.	Tang XQ, Shi D, Xu J, Li YL, Li WJ, Ren ZL and Fu TH 2014 Molecular cytogenetic characteristics of a translocation line between common wheat and *Thinopyrum intermedium* with resistance to powdery mildew. Euphytica 197: 201-210.
11037.	Niu ZX, Klindworth DL, Friesen TL, Chao SM, Jin Y, Cai XW and Xu SS 2011 Targeted introgression of a wheat stem rust resistance gene by DNA marker-assisted chromosome engineering. Genetics 187: 1011-1021.
11038.	Xing LF, Wang CF, Xia XC, He ZH, Chen WQ, Liu TG, Li ZF and Liu DQ 2014 Molecular mapping of leaf rust resistance gen *LrFun* in Romanian wheat line Fundulea 900. Molecular Breeding 33: 931-937.
11039.	Kamran A, Iqbal M, Navabi A, Randahawa H, Pozniak C and Spaner D 2013 Earliness per se QTLs and their interaction with photoperiod insensitive allele *Ppd-D1a* in the Cutler × AC Barrie spring wheat population. Theoretical and Applied Genetics 126: 1965-1976.
11040.	Singh A, Knox RE, DePauw RM, Singh AK, Cuthbert RD, Campbell HL, Singh D, Bhavani S, Fetch T and Clarke F 2013 Identification and mapping in spring wheat of genetic factors controlling stem rust resistance and the study of their epistatic interactions across multiple environments. Theoretical and Applied Genetics 126: 1951-1964.
11041.	Xue SL, Xu F, Li GQ, Zhou Y, Lin MS, Gao ZX, Su XH, Xu XW, Jiang G, Zhang SA, Jia HY, Kong ZX, Zhang LX and Ma ZQ 2013 Fine mapping *TaFLW1*, a major QTL controlling flag leaf width in bread wheat (*Triticum aestivum* L.) Theoretical and Applied Genetics 126: 1941-1049.
11042.	Zhang H, Xia XC, He ZH, Li X, Li ZF and Liu DG 2011 Molecular mapping of leaf rust resistance gene *LrBi16* in Chinese wheat cultivar Bimai 16. Molecular Breeding 28: 527-534.
11043.	Zhou HX, Xia XC, He YH, Li X, Wang CF, Li ZF and Liu DQ 2013 Molecular mapping of leaf rust resistance gene *LrNJ97* in Chinese wheat line Neijiang 977671. Theoretical and Applied Genetics 126: 2141-2147.
11044.	Randahawa H, Asif M, Pozniak C, Clarke JM, Graf RF, Fox SL, Humphreys G, Knox RE, DePauw RM, Singh AK, Cuthbert RD, Hucl P and Spaner D 2013 Application of molecular markers to wheat breeding in Canada. Plant Breeding 132: 458-471.
11045.	Peterson S, Lyerly JH, Worthington ML, Parks R, Cowger C, Marshall DS, Brown-Guedira G and Murphy JP 2014 Mapping of novel powdery mildew resistance gene, *PmNC-S16* introgressed from *Aegilops speltoides* into soft red winter wheat. Draft manuscript
11046.	Tagle AG, Chuma I and Tosa Y 2015 *Rmg7*, a new gene for resistance to Triticum isolates of *Pyricularia oryzae* identified in tetraploid wheat. Phytopathology 105: 495-499. Manuscript

11047.	Sun YW, Jones HD, Yang Y, Dreisigacker S, Li SM, Chen XM, Shewry PR and Xia LQ 2012 Haplotype analysis of Viviparous-1 gene in CIMMYT elite bread wheat germplasm. Euphytica 186: 25-43.
11048.	Cainong JC, Bockus WW, Feng YG, Chen PD, Qi LL, Sehgal SK, Danilova TV, Koo D-H, Friebe B and Gill BS 2015 Chromosome engineering, mapping, and transferring of resistance to Fusarium head blight disease from *Elymus tsukushiensis* into wheat. Theoretical and Applied Genetics 128: 1019-1027.
11049.	Ma PT, Xu HX, Xu YF, Li LH, Qie YM, Luo QL, Zhang XT, Li XQ, Zhou YL and An DG 2015 Molecular mapping of a new powdery mildew resistance gene *Pm2b* in Chinese breeding line KM2939. Theoretical and Applied Genetics 128: 613-622.
11050.	Hao YF, Parks R, Cowger C, Chen ZB, Wang YY, Bland D, Murphy, Guedira M, Brown-Guedira and Johnson J 2015 Molecular characterization of a new powdery mildew resistance gene *Pm54* in soft red winter wheat. Theoretical and Applied Genetics 128: 465-476.
11051.	Spielmeyer W 2014 Personal communication
11052.	Hou LY, Jia JQ, Zhang XJ, Li X, Yang ZJ, Ma JA, Guo HJ, Zhan HX, Qiao LY, and Chang ZJ 2016 Molecular mapping of stripe rust resistance gene *Yr69* on wheat chromosome 2AS. Plant Disease 100: 1521-1799. DOI: 10.1094/PDIS-07-13-0741-RE.
11053.	Singla J, Luthi L, Wicker T, Bansal U, Krattinger SG and Keller B 2017 Characterization of *Lr75*: a partial, broad-spectrum leaf rust resistance gene in wheat. Theoretical and Applied Genetics 130: 1-12. DOI 10.1007/s00122-016-2784-1
11054.	Kolmer J 2014 Personal communication
11055.	Bansal M, Kaur S, Dhaliwal HS, Baines NS, Bariana HS, Chhuneja P and Bansal UK 2017 Mapping of *Aegilops umbellulata* – derived leaf rust and stripe rust loci in wheat. Plant Pathology 66: 38-44. DOI: 10.1111/ppa.12549
11056.	Bariana H, Forrest K, Qureshi N, Miah H, Hayden M and Bansal U 2016 Adult plant stripe rust resistance gene *Yr71* maps close to *Lr24* in chromosome 3D of common wheat. Molecular Breeding 36, 98. DOI: 10.1007/s11032-016-0528-1.
11057.	Singh RP, Hodson DP, Jin Y, Lagudah ES, Ayliffe MA, Bhavani S, Rouse MN, Pretorius ZA, Szabo L, Huerta-Espino J, Basnet BJ, Lan CX and Hovmoller MS 2015 Emergence and spread of new races of wheat stem rust fungus: Continued threat to food security and prospects for genetic control. Phytopathology 105: 872-884.
11058.	Kong LR, Cambron SE and Ohm HW 2008 Hessian fly resistance genes *H16* and *H17* are mapped to a resistance gene cluster in the distal region of chromosome 1AS in wheat. Molecular Breeding 21: 183-194.
11059.	Chhetri M, Miah H, Wong D, Hayden M, Bansal U and Bariana H 2023 Mapping of a stripe rust resistance gene *Yr72* in the common wheat landraces AUS27506 and AUS27894 from the Watkins Collection. Genes 2023, 14, 1993. DOI: 10.3390/genes14111993.
11060.	Guo J, Zhang ZL, Hou YL, Cai JN, Shen XR, Zhou TT, Xu HH, Ohm HW, Wang HW, Li AF, Han FP, Wang HG and Kong LR 2015 High-density mapping of the major FHB resistance gene *Fhb7* derived from *Thinopyrum ponticum* and its pyramiding with *Fhb1* by marker-assisted selection. Theoretical and Applied Genetics 128: 2301-2316. DOI: 10.1007/s00122-015-2586-x.
11061.	Xu HX, Yi YJ, Ma PT, Qie YM, Fu XY, Xu YG, Zhang XT and An DG 2015 Molecular tagging of a new broad-spectrum powdery mildew resistance allele *Pm2* in Chinese wheat landrace Niaomai. Theoretical and Applied Genetics 128: 2077-2084.

11062. Dracatos PM, Zhang P, Park RF, McIntosh RA and Wellings CW 2016 Complementary resistance genes in wheat selection ‘Avocet R’ confer resistance to stripe rust. Theoretical and Applied Genetics 129: 65-76.

11063. Wellings CR, McIntosh RA, Hussain M 1988 A new source of resistance to *Puccinia striiformis* f. sp. *tritici* in spring wheats. Plant Breeding 100: 88-96.

11064. Bariana HS 1991 Genetic studies on stripe rust resistance in wheat. PhD Thesis, University of Sydney.

11065. Bansal U 2015 Personal communication.

11066. Rahmatov M, Rouse MN, Nirmala J, Danilova T, Friebe B, Steffenson BJ and Johannson E 2016 A new 2DS.2RL Robertsonian translocation transfers stem rust resistance gene *Sr59* into wheat. Theoretical and Applied Genetics 129: 1383-1392. DOI: 10.1007/s00122-016-2710-6.

11067. Xiang C, Feng JY, Wang MN, Chen XM, See D, Wan AM and Wang T 2016 Molecular mapping of *Yr76* for resistance to stripe rust in winter club wheat cultivar Tyee. Phytopathology 106: 1186-1193. DOI: 10.1094/PHYTO-01-16-0045-F1.

11068. Zhang P, Hiebert CW, McIntosh RA, McCallum BD, Thomas JB, Hoxha S, Singh D and Bansal U 2016 The relationship of leaf rust resistance gene *Lr13* and hybrid necrosis gene *Ne2m* on wheat chromosome 2BS. Theoretical and Applied Genetics 129: 485-493.

11069. Sohail Y, Bansal U, Bariana H, Chhuneja P, Mumtaz A, Atiq R and Trethowan R 2014 Identification of a co-dominant eSTS marker linked with leaf rust resistance gene *Lr28* in wheat (*Triticum aestivum* L.). Australian Journal of Crop Science 8: 1210-1215.

11070. Moore JW, Herrera-Foessel S, Lan CX, Schnippenkoetter W, Ayliffe M, Guerta-Espino J, Lillemo M, Viccars L, Milne R, Periyannan S, Kong XY, Spielmeyer W, Talbot M, Bariana H, Patrick JW, Dodds P, Singh R and Lagudah E 2015 A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. Nature Genetics 47: 1494-1498.

11071. Li X, Shin SH, Heinen S, Dill-Macky R, Berthiller F, Nersesian N, Clemente T, McCormack S and Muehlbauer G 2015 Transgenic wheat expressing a barley UDP-glucosyltransferase detoxifies deoxynivalenol and provides high levels of resistance to *Fusarium graminareaum*. Molecular Plant-Microbe Interactions 28: 1237-1246.

11072. Guo XR, Wang YY, Meng LZ, Liu HW, Yang L, Zhou Y and Zhang HJ 2015 Distribution of the *Vrn-D1b* allele associated with facultative growth habit in Chinese wheat accessions. Euphytica 206: 1-10.

11073. Zhu XB, Wang HY, Guo J, Wu ZZ, Cao AH, Bie TD, Nie MJ, You FM, Cheng ZB, Xiao J, Liu YY, Cheng SH, Chen PD and Wang XE 2012 Mapping and validation of quantitative trait loci associated with wheat yellow mosaic bymovirus resistance in bread wheat. Theoretical and Applied Genetics 124: 177-188.

11074. Darino MA, Dieguez MJ, Singh D, Ingala LR, Pergolesi MF, Park RF, McIntosh RA and Sacco F 2015 Detection and location of *Lr11* and other leaf rust resistance genes in the durably resistant wheat cultivar Buck Poncho. Euphytica 206: 135-147.

11075. Lu YQ, Wu XY, Yao MM, Zhang JP, Liu WH, Yang XM, Li XQ, Du JA, Gao An and Li LH 2015 Genetic mapping of a putative *Agropyron cristatum*-derived powdery mildew resistance gene by a combination of bulked segregant analysis and single nucleotide polymorphism array. Molecular Breeding 35: 96, 13pp.

11076. Niu Z, Klindworth DL, Yu G, Friessen TL, Chao S, Jin Y, Cai X, Ohm J-B, Rasmussen JB and Xu SS 2014 Development and characterization of wheat lines carrying stem rust

	resistance gene *Sr43* derived from *Thinopryrum ponticum*. Theoretical and Applied Genetics 127: 969-980.
11077.	Chen SL, Gao RH, Wang HY, Wen MX, Xiao J, Bian NF, Zhang RQ, Hu WH, Cheng SH, Die TD and Wang XE 2015 Characterization of a novel reduced height gene (*Rht23*) regulating panicle morphology and plant architecture in bread wheat. Euphytica 203: 583-594.
11078.	Fazel-Najafabadi M, Peng JH, Peairs FB, Simkova H, Kilian A and Lapitan NLV 2015 Genetic mapping of resistance to *Diuaphis noxia* (Kurdjomov) biotype 2 in wheat (*Triticum aestivum* L.) accession CI2401. Euphytica 303: 607-614.
11079.	Salina EA, Adonina IG, Badaeva ED, Kroupin PU, Stasyuk AI, Leonova IN, Shishkina AA, Divashuk MG, Starikova EV, Khuat TM, Syukov VV and Karlov GI 2015 A *Thinopyrun intermedium* chromosome in bread wheat cultivars as a source of genes conferring resistance to fungal diseases. Euphytica 204: 91-101.
11080.	Li WL and Gill BS 2006 Multiple genetic pathways for seed shattering in the grasses. Functional and Integrative Genomics 6: 300-309.
11081.	Jayatilake DV, Tucker EJ, Brueggemann J, Lewis J, Garcia M, Dreisigacker S, Hayden MJ, Chalmers K and Mather DE 2015 Genetic mapping of the *Cre8* locus for resistance against cereal cyst nematode (*Heterodera avenae* Woll.) in wheat. Molecular Breeding 35: 66, 12pp.
11082.	Zhang PP, Zhou HX, Lan CX, Li ZF and Liu DQ 2015 An AFLP marker linked to the leaf rust resistance gene *LrBi16* and test of allelism with *Lr14* on chromosome arm 7BL. The Crop Journal 3: 152-156.
11083.	Ahn VL, Anh NT, Tagle AG, Vy TTP, Inoue Y, Takumi S, Chuma I and Tosa Y 2015 *Rmg8*, a new gene for resistance to *Triticum* isolates of *Pyricularia oryzae* in hexaploid wheat. Phytopathology 105: 1568-1572.
11084.	Wang YJ, Wang CY, Qual W, Jia XJ, Fu Y, Zhang H, Liu XL and Chen CH 2016 Identification and mapping of *PmSE5785*, a new recessive powdery mildew resistance locus in synthetic hexaploid wheat. Euphytica 207: 619-626.
11085.	Feng J, Xu JJ, Lin RM, He YQ and Xu SC 2013 Genetic analysis and location of a gene for resistance to stripe rust in wheat international differential host Strubes Dickkopf. Journal of Genetics 92: 267-192.
11086.	Kolmer JA 2015 First report of a wheat leaf rust (*Puccinia triticina*) phenotype with high virulence to durum wheat in the Great Plains region of the United States. Plant Disease 99: 156-157.
11087.	Gao LL, Kielsmeier-Cook J, Bagjain P, Zhang XF, Chao SM, Rouse MN and Anderson JA 2015 Development of genotyping by sequencing (GBS)- and array-derived SNP markers for stem rust resistance gene *Sr42*. Molecular Breeding 35: 207, 14pp.
11088.	Buerstmeyer M, Alimari A, Steiner B and Buerstmeyer H 2013 Genetic mapping of QTL for resistance to Fusarium head blight (type 2 resistance) in a *Triticum dicoccoides* × *Triticum durum* backcross derivative. Theoretical and Applied Genetics 126: 2825-2834.
11089.	Roswarne GM, Herrera-Foessel SA, Singh RP, Huerta-Espino J, Lan CX and He ZH 2013 Quantitative trait loci of stripe rust resistance in wheat. Theoretical and Applied Genetics 126: 2427-2449.
11090.	Adamski NM, Bush MS, Simmonds J, Turner AS, Mugford SG, Jones A, Findlay K, Pedentchouk N, von Wettstein-Knowles and Uauy C 2013 The inhibitor of wax 1 locus (*Iw1*) prevents formation of b- and OH-b-diketones in wheat cuticular waxes and maps to a sub-cm interval on chromosome arm 2BS. The Plant Journal 74: 989-1002.

11091.	Feng JY, Wang MN, Chen XM, Dee DR, Zheng YL, Chao SM and Wan AM 2015 Molecular mapping of *YrSp* and its relationship with other genes for stripe rust resistance in wheat chromosome 2BL. Phytopathology 105: 1206-1213.
11092.	Basnet BR, Singh S, Lopez-Vera E, Huerta-Espino J, Bhavani S, Jin Y, Rouse MN and Singh RP 2015 Molecular mapping and validation of *SrND643* A new wheat gene for resistance to the stem rust pathogen Ug99 race group. Phytopathology 105: 470-476.
11093.	Kolmer JA and Hughes ME 2015 Physiologic specialization of *Puccinia triticina* on wheat in the United States in 2013. Plant Disease 99: 1261-1267.
11094.	Wu HB, Qin JX, Han J, Zhao XJ, Ouyang SH, Liang Y, Zhang D, Wang ZZ, Wu QH, Xie JZ, Cui Y, Peng SH, Sun QX and Liu ZY 2013 Comparative high resolution mapping if the wax inhibitors *Iw1* and *Iw2* in hexaploid wheat. PLoS One 8(12): e84691.
11095.	Ouyang SH, Zhang D, Han J, Zhao XJ, Cui Y, Song W, Huo NX, Liang Y, Xie JZ, Wang ZZ, Wu QH, Chen YX, Lu P, Zhang DY, Wang LL, Yang TM, Keeble-Gagnere G, Appels R, Dolezel R, Ling HQ, Luo MC, Gu YQ, Sun QX and Liu ZY 2014 Fine physical and genetic mapping of powdery mildew resistance gene *MlIW172* originating from wild emmer (*Triticum dicoccoides*). PLOS One 9(6): e100160.
11096.	Yang ZY, Zheng JC, Liu CY, Wang YS, Condon AG, Chen YF and Hu YG 2015 Effects of the GA-responsive dwarfing gene *Rht18* from tetraploid wheat on agronomic traits of common wheat. Field Crops Research 18: 92-101.
11097.	Ayala-Navarrete LI, Mechanicos AA, Gibson JM, Singh D, Bariana HS, Fletcher J, Shorter S and Larkin PJ 2013 The *Pontin* series of recombinant alien translocations in bread wheat: single translocations integrating combinations of *Bdv2, Lr19* and *Sr25* disease-resistance genes from *Thinopyrum intermedium* and *Th. ponticum*. Theoretical and Applied Genetics 126: 2467-2475.
11098.	Li QA, Ma DF, Fan Y, Shen XX, Jing JX, Wang BT and Kang ZS 2016 Genetic analysis and molecular mapping of a stripe rust resistance gene in Chinese wheat differential Guinong 22. Journal of Phytopathology 164: 476-484. DOI: 10.111/jph.12473.
11099.	Xu HX, Zhang J, Zhang P, Qie YM, Niu YC, Li HJ, Ma PT, Xu YF and An DG 2014 Development and validation of molecular markers closely linked to the wheat stripe rust resistance gene *YrC591* for marker-assisted selection. Euphytica 198: 317-323. DOI: 1007/s10681-014-1108-2
11100.	Ma DF, Zhou XL, Hou L, Bai YB, Li Qiang, Wang HG, Yang MS and Jing JX 2013 Genetic analysis and molecular mapping of a stripe rust resistance gene derived from *Psathynrostachys huashanica* Keng in wheat line H9014-121-5-5-9. Molecular Breeding 32: 365-372.
11101.	Wu L, Xia XC, Rosewarne GM, Zhu HH, Li SZ and Zhang ZY 2015 Stripe rust resistance gene *Yr18* and its suppressor gene in Chinese wheat landraces. Plant Breeding 134: 634-640.
11102.	Wu Lf, Cui L, Li HL, Sun L, Gao X, Qiu D, Sun YL, Wang XM, Murray TD and Li HJ 2015 Characterization of resistance to cereal cyst nematode in the soft white winter wheat ‘Madsen’. Plant Disease 100: 679-685.
11103.	Rouse MN, Talbert LE, Singh D, Sherman JD 2014 Complementary epistasis involving *Sr12* explains adult plant resistance to stem rust in Thatcher wheat *Triticum aestivum* L.). Theoretical and Applied Genetics 127: 1549-1559.
11104.	Hiebert CW, Kolmer JA, McCartney CA, Briggs J, Fetch T, Bariana H, Choulet F, Rouse MN, Spielmeyer W 2016 Major gene for field stem rust resistance co-locates with resistance gene *Sr12* in ‘Thatcher’ wheat. PLoS One 11(6): e0157029.

11105.	McIntosh RA, Park RF and Wellings CR 1995 Wheat Rusts: An Atlas of Resistance Genes CSIRO Publications, East Melbourne, Australia.
11106.	Igrejas G, Branlard G, Carnide V, Gateau I and Guedes-Pinto H 1997 Storage protein diversity within the old Portuguese bread wheat Barbela population. Journal of Genetics and Breeding 51: 167-173.
11107.	Ribeiro M, Bancel E, Faye A, Dardevet M, Ravel C, Branlard G and Igrejas G 2013 Proteogenomic characterization of novel x-type high molecular weight glutenin subunit 1Ax1.1. International Journal of Molecular Sciences 14: 5650-5667.
11108.	Zhang RQ, Sun BX, Chen J, Cao AZ, Xing LP, Feng YG, Lan CX and Chen PD 2016 *Pm55*, a developmental-stage and tissue-specific powdery mildew resistance gene introgressed from *Dasypyrum villosum* into common wheat. Theoretical and Applied Genetics 129: 1975-1984. DOI: 10.1007/s00122-016-2753-8.
11109.	Zhang RQ, Cao YP, Wang XE, Feng YG and Chen PD 2010 Development and characterization of a 11164*Triticum aestivum–D. villosum* T5VS.5DL translocation line with soft grain texture. Journal of Cereal Science 51: 220-225.
11110.	Chen SS, Rouse MN, Zhang WJ, Jin Y, Akhenov E, Wei YM and Dubcovsky J 2015 Fine mapping and characterization of *Sr21*, a temperature sensitive diploid wheat resistance gene effective against the *Puccinia graminis* f. sp. *tritici* race group. Theoretical and Applied Genetics 128: 645-656.
11111.	Briggs J, Chen SS, Zheng WJ, Nelson S, Dubcovsky J and Rouse MN 2015 Mapping of *SrTm4*, a recessive stem rust resistance gene from diploid wheat effective to UG99. Phytopathology 105: 1347-1354.
11112.	Nsabiyera V, Qureshi N, Bariana HS, Wong D, Forrest KL, Hayden MJ and Bansal UK 2016 Molecular markers for adult plant leaf rust resistance gene *Lr48* in wheat. Molecular Breeding 36: 65, 9pp.
11113.	
11114.	Amagai Y, Kubayama T and Watanabe N 2016 Microsatellite mapping of the gene conferring compact spike in Japanese "Gumbai" landraces of common wheat (*Triticum aestivum* L.) Euphytica 209: 709-714. DOI 10.1007/s10681-016-1661-y
11115.	Dong LL, Wang FM, Liu T, Dong ZY, Li AL, Jing RL, Mao L, Li YW, Liu X, Zhang KP and Wang DW 2014 Natural variation of *TaGASR7-A1* affects grain length in common wheat under multiple cultivation conditions. Molecular Breeding 34: 937-947. DOI 10.1007/s11032-014-0087-2
11116.	Zhang YJ, Liu JD, Xia XC and Zhonghu He 2014 *TaGS-D1*, an ortholog of rice *OsGS3*, is associated with grain weight and grain length in common wheat. Molecular Breeding 34: 1097. DOI 10.1007/s1132-014-0102-7
11117.	Chang JZ, Zhang JN, Mao XG, Li A, Jia JZ and Jing RL 2013 Polymorphism of *TaSAP1-A1* and its association with agronomic traits in wheat. Planta 237: 1495-1508.
11118.	Zhang XL, Shen XR, Hao YF, Cai JJ, Ohm HW and Kong LR. 2011 A genetic map of *Lophopyrum ponticum* chromosome 7E, harbouring resistance genes to Fusarium head blight and leaf rust. Theoretical and Applied Genetics 122: 263-270.
11119.	Zhang YJ, Miao XL, Xia XC and He ZH. 2014 Cloning of seed dormancy genes (*TaSdr*) associated with tolerance to pre-harvest sprouting in common wheat and development of a functional marker. Theoretical and Applied Genetics. 127: 855-866.
11120.	Alvarez MA, Tranquilli G, Lewis S, Kippes N and Dubcovsky J. 2016 Genetic and physical mapping of the earliness per se locus *Eps-Am1* in *Triticum monococcum* identifies

	EARLY FLOWERING 3 (ELF3) as a candidate gene. Functional and Integrative Genomics 16: 365-382.
11121.	Simmonds J, Scott P, Leverington-Waite M, Turner AS, Brinton J, Korzun V, Snape J and Uauy C. 2014 Identification and independent validation of a stable yield and thousand grain weight QTL on chromosome 6A of hexaploid wheat (*Triticum aestivum* L.). BMC Plant Biology 14: 191.
11122.	Simmonds J, Scott P, Brinton J, Mestre TC, Bush M, Del Blanco A and Dubcovsky J, and Uauy C. 2016 A splice acceptor site mutation in *TaGW2-A1* increases thousand grain weight in tetraploid and hexaploid wheat through wider and longer grains. Theoretical and Applied Genetics 129: 1099-1112.
11123.	Kippes N, Debernardi JM, Vasquez-Gross H, Akpinar A, Budak H, Kato K, Chao S, Akhunov E and Dubcovsky J. 2015 Identification of the VERNALIZATION 4 gene reveals the origin of spring growth habit in ancient wheats from South Asia. Proceedings of the National Academy of Sciences of the United States of America 112: E5401-E5410. PMC4593092
11124.	Kippes N, Chen A, Zhang X, Lukaszewski AJ and Dubcovsky J. 2016 Development and characterization of a spring hexaploid wheat line with no functional *VRN2* genes. Theor Appl Genet 129: 1417-1428.
11125.	Hazard B, Zhang X, Naemeh M and Dubcovsky J. 2014 Registration of durum wheat germplasm lines with combined mutations in *SBEIIa* and *SBEIIb* genes conferring increased amylose and resistant starch. Journal of Crop Registrations 8: 334-338. PMC4840879
11126.	Schönhofen A, Hazard B, Zhang X and Dubcovsky J. 2016 Registration of common wheat germplasm with mutations in *SBEII* genes conferring increased grain amylose and resistant starch content. Journal of Crop Registrations 10: 200-205.
11127.	Cruz CD, Peterson GL, Bockus WW, Kankanala P, Dubcovsky J, Jordan KW, Akhunov E, Chumley F, Baldelomar DF and Valent B. 2016 The 2NS translocation from *Aegilops ventricosa* confers resistance to the Triticum pathotype of *Magnaporthe oryzae*. Crop Science 56: 990-1000.
11128.	Guo J-Y, Li K, Wu K, Wang X, Lin H, Cantu D, Uauy C, Dobon-Alonso A, Midorikawa T, Inoue K, Sánchez J, Fu D, Blechl A, Wallington E, Fahima T, Meeta M, Epstein L and Dubcovsky J. 2015 Wheat stripe rust resistance protein WKS1 reduces the ability of the thylakoid-associated ascorbate peroxidase to detoxify reactive oxygen species. The Plant Cell 27: 1755-1770.
11129.	Bonafede MD, Tranquilli G, Pflüger LA, Peña RJ and Dubcovsky J. 2015 Effect of allelic variation at the *Glu-3/Gli-1* loci on breadmaking quality parameters in hexaploid wheat (*T. aestivum* L.). Journal of Cereal Science 62: 143-150.
11130.	Chhuneja P, Kumar K, Stirnweis D, Hurni S, Keller B, Dhaliwal HS and Singh K. 2012 Identification and mapping of two powdery mildew resistance genes in *Triticum aestivum* L.). Theoretical and Applied Genetics 124: 1051-1058.
11131.	Bennett D, Izaanloo A, Edwards J, Kuchel H, Chalmers K, Tester M, Reynolds M, Schnurbusch T and Langridge P. 2012 Identification of novel quantitative trait loci for days to ear emergence and flag leaf glaucousness in a bread wheat (*Triticum aestivum* L.) population adapted to southern Australian conditions. Theoretical and Applied Genetics 124: 697-711.
11132.	Lopez-Vera EE, Nelson S, Singh RP, Basnet BR, Haley SD, Bhavani S, Huerta-Espino J, Xoconostle-Cazares BG, Ruiz-Medrano R and Rouse MN. 2014 Resistance to stem rust

	UG99 in six bread wheat cultivars maps to chromosome 6DS. Theoretical and Applied Genetics 127: 231-239.
11133.	Cockram J, Scuderi A, Barber T, Furuki E, Gardiner KA, Gosman N, Kowalczyk R, Phan HP, Rose GA, Tan K-C and Oliver RP. 2016 Fine-mapping of the wheat *Snn1* locus conferring sensitivity to the *Parastagonospora nodorum* necrotrophic effector SnTox1 using an Eight Founder Multiparent Advanced Generation Inter-Cross Population. G3: XXXXX DOI: 10.1534/g3.115.021584
11134.	Periyannan S, Bansal U, Bariana H, Deal K, Luo M-C, Dvorak J and Lagudah E. 2014 Identification of a robust molecular marker for the detection of the stem rust resistance gene *Sr45* in common wheat. Theoretical and Applied Genetics 127: 947-955.
11135.	Spanic V, Rouse MN, Kolmer JA and Anderson JA. 2015 Leaf and stem seedling rust resistance in wheat cultivars grown in Croatia. Euphytica 203: 437-448.
11136.	Gordeeva EI, Shoeva OY and Khletkina EK. 2015 Marker-assisted development of wheat near-isogenic lines carrying various combinations of purple pericarp genes. Euphytica 203: 469-476.
11137.	Kassa MT, Haas S, Schliephake E, Lewis C, You FM, Pozniak CJ, Kramer I, Perovic D, Sharpe AG et al. 2016 A saturated linkage map for the orange blossom midge resistance gene *Sm1*. Theoretical and Applied Genetics 129: 1507-1517.
11138.	Perovic D, Forster J, Davaux P, Hariri D, Guilleroux M, Kanyuka K, Lyons R, Weyen J et al. 2009 Mapping and diagnostic marker development for Soil-borne cereal mosaic virus resistance in bread wheat. Molecular Breeding 23: 641-653.
11139.	Lu YM, Lan CX, Liang SS, Zhou XC, Liu D, Zhou G, Lu QL, Jing JX et al. 2009 QTL mapping for adult-plant resistance to stripe rust in Italian common wheat cultivars Libellula and Strampelli. Theoretical and Applied Genetics 119: 1349-1359.
11140.	Saintenac C, Zhang WJ, Salcdo A, Rouse MN, Trick HN, Akhunov E and Dubcovsky J. 2013 Identification of wheat gene *Sr35* that confers resistance to Ug99 stem rust race group. Science 341: 783-786.
11141.	Dundas I, Zhang P, Verlin D, Graner A and Shepherd K. 2015 Chromosome engineering and physical mapping of the *Thinopyrum ponticum* translocation in wheat carrying the rust resistance gene *Sr26*. Crop Science 55: 648-657.
11142.	Christopher MD, Liu SY, Hall MD, Marshall DS, Fountain MD, Johnson JW, Milus EA, Garland-Campbell KA, Chen XM and Griffey CA. 2013 Identification and mapping of adult-plant stripe rust resistance in soft red winter wheat cultivar 'USG 3555'. Plant Breeding 132: 563-60.
11143.	Dong PH, Hu YG, Guo GG, He BR, Wang LM and Yuan JG. 2012 Inheritance and chromosome location of photoperiod-thermo sensitive male sterility in wheat line Xinong 291S. Plant Breeding 131: 695-699.
11144.	Sorensen CK, Hovmoller MS, Leconte M, Dedryver F and de Vallavieille-Pope C. 2014 New races of *Puccinia striiformis* found in Europe reveal race specificity of long-term effective adult plant resistance in wheat. Phytopathology 104: 1042-1051.
11145.	Liu W, Frick M, Huel R, Nykiforuk CL, Wang XM, Gaudet DA, Eudes F, Conner RL, Kuzyk A, Chen Q, Kang ZS and Laroche A 2014 The stripe rust resistance gene *Yr10* encodes an evolutionary-conserved and unique CC-NBS-LRR sequence in wheat. Molecular Plant 7: 1740-1755.
11146.	Periyannan SK, Qamar ZU, Bansal UK and Bariana H. 2014 Development and validation of molecular markers linked with stem rust resistance gene *Sr13* in durum wheat. Crop & Pasture Science 65: 74-70.

11147.	Babilker EM, Gordon TC, Bonman JM, Chao S, Rouse MN, Brown-Guedira G, Williamson S and Pretorius ZA. 2016 Rapid identification of resistance loci effective against *Puccinia graminis* f. sp. *tritici* race TTKSK in 33 spring wheat landraces. Plant Disease 100: 331-336.
11148.	Rouse MN, Nava IC, Chao SM, Anderson JA and Jin Y. 2012 Identification of markers linked to the race Ug99 effective stem rust resistance gene *Sr28* in wheat (*Triticum aestivum* L. Theoretical and Applied Genetics 125: 877-885.
11149.	Bansal UK, Zwart R, Bhavani S, Wanyera R, Gupta V and Bariana HS. 2013 Microsatellite mapping identifies TTKSK-effective stem rust resistance gene in wheat cultivars VL404 and Janz. Molecular Breeding 30: 1757-1765.
11150.	Zhou XL, Han DJ, Gou HL, Wang QL, Zeng QD, Yuan FP, Zhan GM, Huang LL and Kang ZS. 2014 Molecular mapping of a stripe rust resistance gene in wheat cultivar Wuhan 2. Euphytica 196: 251-259.
11151.	Song XY, Qian HH and Zhong LL. 2014 Cytogenetic analysis of cytoplasmic male sterility in wheat line KTP116A and molecular mapping of two thermo-sensitive restoration lines. Euphytica 196: 129-136.
144.	Newcomb M, Olovera PD, Rouse MN, Szabo LJ, Johnson J, Gale S, Luster DG, Wanyera R, Macheria G, Bhavani S, Hodson D, Patpour M, Hovmoller MS, Fetch TG Jr and Jin Y. 2016 Kenyan isolates of *Puccinia graminis* f. sp. *tritici* from 2008 to 2014: Virulence to *SrTmp* in the Ug99 race group and implications for breeding programs. Phytopathology 106: 729-736.
11153.	McGrann GRD, Smith PH, Burt C, Rodriguez Mateos G, Chama TN, MacCormack R, Wessels E, Agenbag G and Boyd LA. 2014 Genomic and genetic analysis of the wheat race-specific yellow rust resistance gene *Yr5*. Plant Science & Molecular Breeding XXXX. DOI: 10.7243/2050-2389-3-2.
11154.	Abrouk M, Balcarkova B, Simkova H, Kominkova E, Martis MM, Jakobson I, Timofejeva L, Rey E, Vrana J, Kilian A, Jarve K, Dolezel J and Valarik M. 2016 The in silico identification of a bread wheat/*Triticum militinae* introgression line. Plant Biotechnolgy Journal XX: 1-8. DOI: 10.1111/pbi.12610
11155.	Hao M, Liu M, Luo JT, Fan CL, Yi YJ, Zhang LQ, Yuan ZW, Ning SZ, Zheng YL and Liu DC 2018 Introgression of powdery mildew resistance gene *Pm56* on rye chromosome arm 6RS to wheat. Frontiers in Plant Science 9, 1040. DOI: 10.3389/fpls.2018.01040.
11156.	Lan CX, Singh RP, Calvo-Salazar V, Herrera-Foessel SA, and Huerta-Espino J. 2014 Genetic analysis of resistance to leaf rust and stripe rust in wheat cultivar Francolin#1. Plant Disease 98: 1227-1234.
11157.	Ru ZG, Zhang LP, Hy TZ, Liu HY, Yang QK, Weng ML, Wang B and Zhao CP. 2015 Genetic analysis and chromosome mapping of a thermo-sensitive genic male sterile gene in wheat. Euphytica 201: 321-327.
11158.	Mizuno M, Hosogi N, Park P and Takumi S. 2010 Hypersensitive response-like reaction is associated with hybrid necrosis in interspecific crosses between tetraploid wheat and *Aegilops tauschii* Coss. PLoS ONE 5(6): e11326.
11159.	Liu WX, Koo DH, Xia Q, Li CX, Bai FQ, Song YL, Friebe B and Gill BS. 2017 Homoeologous recombination-based transfer and molecular cytogenetic mapping of powdery mildew-resistance gene *Pm57* from *Aegilops searsii* into wheat. Theoretical and Applied Genetics 130: 8410848. DOI: 10.1007/s00122-017-2855-y.

11160.	Wang YQ, Hou XJ, Zhang B, Chen WJ, Liu DC, Liu BL and Zhang HG. 2016 Identification of a candidate gene for *Rc-D1*, a locus controlling red coleoptile colour in wheat. Cereal Research Communications 44: 35-46.
11161.	Kokhmetova A, Madenova A, Kampitova G, Urazaliev R, Yessimbekova M, Morgounov A and Purnhauser L. 2016 Identification of leaf rust resistance genes in wheat cultivars produced in Kazakhstan. Cereal Research Communications 44: 240-250.
11162.	Sun YL, Zou JW, Sun HG, Wang XM and Li HJ. 2015 *PmLX66* and *PmW14*: new alleles of *Pm2* for resistance to powdery mildew in the Chinese winter wheat cultivars Lingxing 66 and Wennong 14. Plant Disease 99: 1118-1124.
11163.	Tan CT and Yan LL. 2016 Duplicated, deleted and translocated *VRN2* genes in hexaploid wheat. Euphytica 208: 277-284.
11164.	Kolmer JA, Su ZQ, Bernardo A, Bai GH and Chao SM 2018 Mapping and characterization of the new adult plant leaf rust resistance gene *Lr77* derived from Santa Fe winter wheat. Theoretical and Applied Genetics 131: 1553-1560. DOI: 10.1007/s00122-018-3097-3.
11165.	Zhu ZW, Bonnett D, Ellis M, He XY, Heslot N, Dreisigacker S and Gao CH. 2016 Characterization of Fusarium head blight resistance in a CIMMYT synthetic-derived bread wheat line. Euphytica 208: 367-375.
11166.	Ma PT, Xu HX, Han GH, Luo QL, Xu YF, Zhang XT and An DG. 2016 Characterization of a segregation distortion locus with powdery mildew resistance in a wheat-*Thinopyrum intermedium* introgression line WE99. Plant Disease 100: 1541-1547.
11167.	Brar GS and Kutcher HR. 2016 Race characterization of *Puccinia striiformis* f. sp. *tritici*, the cause of wheat stripe rust, in Saskatchewan and southern Alberta, Canada and virulence comparison with races from the United States. Plant Disease 100: 1744-1753.
11168.	Knox RE, Campbell HL, Clarke FR, Menzies JG, Popovic Z, Procunier JD, Clarke JM, DePauw RD, Cuthbert RD and Somers DJ. 2014 Quantitative trait loci for resistance in wheat (*Triticum aestivum*) to *Ustilago tritici*. Canadian Journal of Plant Pathology 36: 187-201.
11169.	Kassa MT, Menzies and McCartney CA. 2014 Mapping of the loose smut resistance gene *Ut6* in wheat (*Triticum aestivum* L.). Molecular Breeding 33: 569-576.
11170.	Zhang XF, Rouse MN, Nava IC, Jin Y and Anderson JA. 2016 Development and verification of wheat germplasm containing both *Sr2* and *Fhb1*. Molecular Breeding 36: 85. DOI 10.1007/s11032-016-0502-y
11171.	Wiersma AT, Pulman JA, Brown LK, Cowger C and Olson EL. 2017 Identification of *PmTA1662* from *Aegilops tauschii*. Draft manuscript CANNOT LOCATE THE PAPER
11172.	Nsabiyera V, Qureshi N, Bariana HS, Wong D, Forrest KL, Hayden MJ and Bansal UK. 2016 Molecular markers for adult plant leaf rust resistance gene *Lr48* in wheat. Molecular Breeding 36: 65. DOI 10.1007/s11032-016-0488-5
11173.	Yaniv E, Raats D, Ronin Y, Korol AB, Grama A, Bariana H, Dubcovsky H, Schulman AH and Fahima T. 2015 Evaluation of marker-assisted selection for the stripe rust resistance gene *Yr15*, introgressed from wild emmer wheat. Molecular Breeding 35: 43. DOI 10.1007/s11032-015-0238-0.
11174.	Dong ZZ, Hegarty J, Zhang JL, Zhang WJ, Chao SM, Chen XM, Zhou YH and Dubcovsky J 2017 Validation and characterization of a QTL for adult plant resistance to stripe rust on wheat chromosome arm 6BS (*Yr78*). Theoretical and Applied Genetics 130: 2127-2137. DOI: 10.1007/s00122-017-2946-9.

11175.	Subramanian NK, Mason RE, Milus EA, Moon DE and Brown-Guedira. 2016 Characterization of two adult-plant stripe rust resistance genes on chromosomes 3BS and 4BL in soft red winter wheat. Crop Science 56: 143-153.
11176.	Komaromi J, Jankovics T, Fabian A, Puslas K, Zhang ZY, Zhang M, Li HJ, Jager K, Lang L and Vida G. 2016 Powdery mildew resistance in wheat cultivar Mv Hombar is conferred by a new gene, *PmHo*. Phytopathology 106: 1326-1334.
11177.	Nirmala J, Chao SM, Olivera P, Babiker EM, Abeyo B, Tadesse Z, Imtiaz M, Talbert L, Blake N, Akhunov E, Pumphrey MO, Jin Y and Rouse MN. 2016 Markers linked to wheat stem rust resistance gene *Sr11* effective to *Puccinia graminis* f. sp. t*ritici* race TKTTF. Phytopathology 106: 1352-1358.
11178.	Loladze A, Kthiri D, Pozniak C and Ammar K. 2016 Genetic analysis of leaf rust resistance in six durum wheat genotypes. Phytopathology 104: 1322-1328.
11179.	Tatineni S, Wasula EN, Bartels M, Hein GL and Graybosch RA. 2016 Temperature-dependent *Wsm1* and *Wsm2* gene-specific blockage of viral long-distance transport provides resistance to wheat streak mosaic virus and Triticum mosaic virus in wheat. Molecular Plant-Microbe Interactions 29: 724-738.
11180.	Campbell BW, Liu Y, Wise K, Jin Y and Ohm HW. 2016 Inheritance and mapping of stem rust resistance of wheat line PI 410966. Cereal Research Communications 44: 414-423.
11181.	Wiersma AT, Brown LK, Brisco EI, Liu TL, Childs KL, Poland JA, Sehgal SK and Olsen EL. 2016 Fine mapping of the stem rust resistance gene *SrTA101287*. Theoretical and Applied Genetics 129: 2369-2378. DOI 10. 1007/s00122-016-2776-1
11182.	Chen JL, Guttieri MJ, Zhang JL, Hole D, Souza E and Goates B. 2016 A novel QTL associated with dwarf bunt resistance in Idaho 444 winter wheat. Theoretical and Applied Genetics 129: 2369-2378. DOI 10. 1007/s00122-016-2783-2
11183.	Griffiths S, Simmonds J, Leverington M, Wang Y, Fish L, Sayers L, Alibert L, Orford S, Wingen L and Snape J. 2012 Meta-QTL analysis of the genetic control of crop height in elite European winter wheat germplasm. Molecular Breeding 29: 159-171.
11184.	Li XM, Xia XC, Xiao YG, He Zhong Hu, Wang DS, Trethowan R, Wang HJ and Chen XM. 2015 QTL mapping for plant height and yield components in common wheat under water-limited and full irrigation environments. Crop and Pasture Science 66: 660-670.
11185.	Tian XL, Wen W, Xie L, Fu LP, Xu DA, Fu C, Wang DS, Chen XM, Xia XC, Qu YY, He ZH and Cao SH. 2016 Molecular mapping of reduced plant height gene *Rht24* in bread wheat. Frontiers in Plant Science 8, 1379. DOI: 10.3389/fpls.2017.01379.
11186.	Xiao J, Chen XL, Xu ZT, Guo J, Wu ZZ, Wang HY, Zhu XB, Nie MJ, Be TD, Cheng SH, Zhu TT, Luo MC, You FM and Wang XE. 2016 Validation and diagnostic marker development for a genetic region associated with wheat yellow mosaic virus resistance. Euphytica 211: 91-101.
11187.	Ma J, Wingen LU, Orford S, Fenwick P, Wang JK and Griffiths S. 2015 Using the UK reference population Avalon x Cadenza as a platform to compare breeding strategies in elite Western European bread wheat. Molecular Breeding 35: 70. DOI: 10.1007/s11032-015-0268-7.
11188.	Gardiner L-J, Bansept-Basler P, Olohan L, Joynson R, Brenchley R, Hall N, O'Sullivan DM and Hall A. 2016 Mapping-by-sequencing in complex polyploidy genomes using genic sequence capture: a case study to map yellow rust resistance in hexaploid wheat. The Plant Journal 87: 403-409. DOI: 10.1111/tpj.13204

11189. Ahmad FT, Mather DE, Law H-Y, Li M, Yousif SA-J, Chalmers KJ, Asenstorfer RE and Mares DJ. 2016 Genetic control of lutein esterification in wheat (*Triticum aestivum* L.). Journal of Cereal Science 64: 109-115. DOI 10.1016/j.jcs.2015.05.007

11190. Liang JC, Fu BS, Tang WB, Khan NU, and Ma ZQ. 2016 Fine mapping of two wheat powdery mildew resistance genes located at the *Pm1* cluster. The Plant Genome 9: 9. DOI: 10.3835/plantgenome2015.09.0084.

11191. Goodwin SB, Cavaletto JR, Hale IL, Thompson I, Xu SS, Adhikari TB and Dubcovsky J. 2015 A new map location of gene *Stb3* for resistance to Septoria tritici blotch in wheat. Crop Science 55: 1-9. PMC5089079

11192. Debernardi JM, Lin HQ, Chuck G, Faris JD and Dubcovsky J 2017 MicroRNA172 plays a crucial role in wheat spike morphogenesis and grain threshability. Development 144: 1966-1975. DOI: 10.1242/DEV.146399.

11193. Zikhali M, Wingen LU and Griffiths S. 2016 Delimitation of the earliness per se D1 (*Eps-D1*) flowering gene to a subtelomeric chromosomal deletion in bread wheat (*Triticum aestivum*). Journal of Experimental Botany 67: 287-299. DOI:

11194. Wang JP, Wen WE, Hanif M, Xia XC, Wang HG, Liu SB, Liu JD, Yang L, Cao SH and He ZH 2016 *TaELF3-1DL*, a homolog of *ELF3*, is associated with heading date in bread wheat. Molecular Breeding 36: 161. DOI: 10.1093/jxb/erv458.

11195. Chen C, He ZH, Lu JL, Li J, Ren Y, Ma CX and Xia XC. 2016 Molecular mapping of stripe rust resistance gene *YrJ22* in Chinese wheat cultivar Jimai 22. Molecular Breeding 36: 118.

11196. Hanif M, Gao FM, Liu JD, Wen WE, Zhang YJ, Rasheed A, Xia XC, He ZH and Cao SH. *TaTGW6-A1*, an ortholog of rice *TGW6*, is associated with grain weight and yield in bread wheat. Molecular Breeding 36: 1. DOI 10.1007/s11032-015-0425-z.

11197. Hu MJ, Zhang HP, Liu K, Cao JJ, Wang SX, Jiang H, Wu ZY, Lu J, Zhu XF, Xia XC, Sun GL, Ma CX and Chang C. 2016 Cloning and characterization of *TaTGW-7A* gene associated with grain weight in wheat via SLAF-seq-BSA. Frontiers in Plant Science 7: 1902. DOi: 10.3389/fpls.2016.0-1902.

11198. Zhu XF, Zhang HP, Hu MJ, Wu ZY, Jiang H, Cao JJ, Xia XC, Ma CX and Chang C. 2016 Cloning and characterization of *Tabas1-B1* gene associated with flag leaf chlorophyll content and thousand-grain weight and development of a gene-specific marker in wheat. Molecular Breeding 36: 142. DOI10.1007/s11032-016-0563-y

11199. Zhang YJ, Xia XC and He ZH. 2017 The seed dormancy allele *TaSdr-A1a* associated with pre-harvest sprouting tolerance is mainly present in Chinese wheat landraces. Theoretical and Applied Genetics 130: 81-89. DOI 10.1007/s00122-016-2793-0

11200. Qureshi N, Bariana H, Forrest K, Hayden M, Keller B, Wicker T, Faris J, Salina E, and Bansal U. 2017 Fine mapping of the chromosome 5B region carrying closely linked rust resistance genes *Yr47* and *Lr52* in wheat. Theoretical and Applied Genetics DOI 10.1007/s00122-016-2829-5.

11201. Emebiri LC, Tan M-K, El-Bouhssini M, Wildman O, Jighly A, Tadesse W and Ogbonnaya FC 2017 QTL mapping identifies a major locus for resistance in wheat to Sunn pest (*Eurygaster Integriceps*) feeding at the vegetative growth stage. Theoretical and Applied Genetics 130: 309-318. DOI: 10/1007s00122-016-2812-1.

11202. Yu L, Barbier H, Rouse MN, Singh S, Singh RP, Bhavani S, Huerta-Espino J and Sorrells M 2014 A consensus map for UG99 stem rust resistance loci in wheat. Theoretical and Applied Genetics 127: 1561-1581. DOI 10.1007/s00122-014-2326-7.

11203.	Friesen TL, Chu CG, Xu SS and Faris JD 2012. Tox5-Snn5: a novel *Stagonospora nodorum* effector-wheat gene interaction and its relationship with *SnToxA-Tsn1* and *SnTox3-Snn3-B1* interactions. Molecular Plant Pathology 13: 1101-1109. DOI: 10.1111/J.1364-3703.2012.00819.X.
11204.	Virdi S, Liu ZH, Overlander ME, Zhang ZC, Xu SS, Friesen TL and Faris JD 2016 New insights into the roles of host gene-necrotrophic effector interactions in governing susceptibility of durum wheat to tan spot and Septoria nodorum blotch. Genes, Genomes, Genetics (G3) 6: 4139-4150. DOI: 10.1534/g3.116.036525/-/DC1.
11205.	Rawat N, Pumphrey MO, Liu SX, Zhang XF, Tiwari VK, Ando K, Trick HN, Bockus WW, Akhunov E, Anderson JA and Gill BS 2017 Wheat *Fhb1* encodes a chimeric lectin with agglutinin domains and a pore-forming toxin-like domain conferring resistance to Fusarium head blight. Nature Genetics 48: 1576-1580. DOI: 10.1038/ng.3706.
11206.	Gao Y, Faris JD, Liu Z, Kim YM, Syme RA, Oliver RP, Xu SS and Friesen TL 2015 Identification and characterization of the *SnTox6-Snn6* interaction in the *Parastagonospora nodorum*-wheat pathosystem. Molecular Plant Microbe Interactions 28: 615-625. DOI: 10.1094/MPMI-12-14-0396-R.
11207.	Saluja M, Kaur S, Bansal U, Bhardwaj SC and Chhuneja P 2017 Molecular mapping of linked leaf rust resistance and non-glaucousness gene introgressed from *Aegilops tauschii* Coss. in hexaploid wheat *Triticum aestivum* L. Plant Genetic Resources 1-7. DOI: 10.1017/S1479262116000240.
11208.	Chen SS, Guo Y, Briggs J, Dubach F, Chao SM, Zhang WJ, Rouse MN and Dubcovsky J 2018 Mapping and characterization of wheat stem rust resistance genes *SrTm5* and *Sr60* from *Triticum monococcum*. Theoretical and Applied Genetics 131: 625-635. DOI: 10.1007/s00122-017-3024-z.
11209.	Thind AK, Wick WE, Sinkova H, Fossati D, Moullet O, Brabent C, Vrana J, Dolezel J and Krattinger SG 2017 Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range assembly. Nature Biotechnology DOI: 10.1038/nbt/3877.
11210.	Zhang ZF, Rouse MN, Nava IC, Jin Y and Anderson JA 2016 Development and verification of wheat germplasm containing both *Sr2* and *Fhb1*. Molecular Breeding 36: 85. DOI: 10.1007/s11032-016-0502-Y.
11211.	Li GQ, Xu XY, Carver BF, Guo PG and Puterka 2018 Dn10, a new gene conferring resistance to Russian wheat aphid biotype 2 in Iranian wheat landrace PI 682675. Crop Science 58: 1219-1225. DOI: 10.2135/cropsci2017.10.0649.
11212.	Kolmer JA, Bernardo A, Bai G, Hayden MJ and Kolmer 2018 Adult plant leaf rust resistance derived from Toropi wheat is conditioned by *Lr78* and three minor QTL. Phytopathology 108: 246-253. DOI: 10.1094/PHYO-07-17-0254-R.
11213.	Steuernagel B, Periyannan S, Hernandez-Pinzon I, Witek K, Rouse MN, Yu GT, Hatta A, Ayliffe M, Bariana H, Jones JDG, Ladudah ES and Wulff BH 2016 Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. Nature Biotechnology 34: 652-655. DOI: 10.1038/nbt.3543.
11214.	Tan CC, Li CQ, Cowger C, Carver BF, and Xu XY 2018 Characterization of Pm59, a novel powdery mildew resistance gene in Afghanistan wheat landrace PI 181356. Theoretical and Applied Genetics 131: 1145-1152. DOI: 10.1007/s00122-018-3067-9.
11215.	Fu BH, Chen Y, Li N, Ma HQ, Kong ZX, Zhang LX, Jia HY and Ma ZQ 2013 pmX: a recessive powdery mildew resistance gene at the *Pm4* locus identified in wheat landrace Xiaohongpi. Theoretical and Applied Genetics 126: 913-921. DOI 10.1007/s00122-012-2025-1.

11216.	Worthington M, Lyerly J, Petersen S, Brown-Guidera G, Marshall D, Cowger C, Parks R and Murphy JP (2015) *MlUM15*: an *Aegilops neglecta*-derived powdery mildew resistance gene in common wheat. Crop Sci 54:1397-1406. DOI 102125/cropsci2013.09.0634.
11217.	Zhang WJ, Chen SS, Abate Z, Nirmala J, Rouse MN and Dubcovsky 2017 Identification and characterization of Sr13, a tetraploid wheat gene that confers resistance to the Ug99 stem rust race group. Proceedings of the National Academy of the United States of America, Early Edition. DOI: 10.1073/pnas.1706277114.
11218.	Lan CX, Singh RP, Huerta-Espino J, Calvo-Salazar V and Herrera-Foessel SA 2014 Genetic analysis of resistance to leaf rust and stripe rust in wheat cultivar Francolin#1. Plant Disease 98: 1227-1234. DOI: 10.1094/PDIS-07-13-1717-RE
11219.	Lan CX, Rosewarne GM, Singh RP, Herrera-Foessel SA, Huerta-Espino J, Basnet BR, Zhang YL and Yang EN 2019 QTL characterization of resistance to leaf rust and stripe rust in the spring wheat Francolin#1. Molecular Breeding 34: 789-803. DOI 10.1007/s11032-014-0075-6.
11220.	Amagai Y, Kuboyama T and Watanabe N 2017 Genetic mapping of diagnostic markers for the *Lg2* locus conferring ligules in *Triticum aestivum* L. and derived from *Aegilops tauschii* Coss. Euphytica 213, 59. DOI: 10.1007/s10681-o17-1852-1.
11221.	Sthapit J, Gbur EE, Brown-Guidira G, Marshall DS and Milus EA 2012 Characterization of resistance to stripe rust in contemporary cultivars and lines of winter wheat from the Eastern United States. Plant Disease 96: 737-745. DOI: 10.1094/PDIS-07-11-0612.
11222.	Feng JY, Wang MN, See DR, Chao SM, Zheng YL, Chen XM Characterization of novel gene *Yr79* and four additional QTL for all-stage and high-temperature adult-plant resistance to stripe rust in spring wheat PI 182103. Phytopathology 108: 731-747. DOI: 10.1094/PHYTO-11-17-0375-R.
11223.	Qureshi N, Bariana H, Kolmer JA, Miah H and Bansal U 2017 Genetic and molecular characterization of leaf rust resistance in two durum wheat landraces. Phytopathology 107: 1381-1387. DOI: 10.1094/PHYTO-01-17-0005-R.
11224.	Qureshi N, Bariana H, Kumran VV, Muruga S, Forrest KL, Hayden M and Bansal U 2017 A new leaf rust resistance gene *Lr79* mapped in chromosome 3BL from the durum wheat landrace Aus26582. Theoretical and Applied Genetics 131: 1091-1098. DOI: 10.1007/s00122-018-3060-3.
11225.	Liu XM, Smith CM, Friebe BR and Gill BS 2005 Molecular mapping and allelic relationships of Russian wheat aphid–resistance genes. Crop Science 45:2273–2280. DOI: 10.2135/cropsci2004.0704.
11226.	Tonk FA, Istipliler D, V Tosun, Ilbi H and Cakir M 2016 Genetic mapping and inheritance of Russian wheat aphid resistance gene in accession IG 100695. Plant Breeding 135: 21-25. DOI: 10.1111/pbr.12339.
11227.	Valdez VA, Byrne PF, Lapitan NLV, Peairs FB, Bernardo A, Bai GH and Haley SD 2012 Inheritance and genetic mapping of Russian wheat aphid resistance in Iranian wheat landrace accession PI 626580. Crop Science 52: 676–682. DOI: 10.2135/cropsci2011.06.0331.
11228.	Yang ZJ, Chen ZY, Peng ZS, Yu Y, Liao ML and Wei SH 2017 Development of a high-density linkage map and mapping of the three-pistil gene (*Pis1*) in wheat using GBS markers. BMC Genomics 18, 567. DOI 10.1186/s12864-017-3960-7.
11229.	Ma DF, Fang ZW, Yin JL, Chao KX, Jing JX, Li Q and Wang BT (2016) Molecular mapping of stripe rust resistance gene *YrHu* derived from *Psathyrostachys huashanica*. Molecular Breeding 36, 64. DOI: 10.1007/s11032-016-0487-6.

11230. Cook JP, Blake NK, Heo H-Y, Martin JM, Waver DK and Talbert LE (2017) Phenotypic and haplotype diversity among tetraploid and hexaploid wheat accessions with potentially novel insect resistance genes for wheat stem sawfly. Plant Genome 10: DOI: 10.3835/plantgenome2016.03.0026.

11231. Getie B, Singh D, Bansal U, Simmonds J, Uauy C and Park RF 2015 Identification and mapping of resistance to stem rust in the European winter wheat cultivars Spark and Rialto. Molecular Breeding 36, 114. DOI: 10.1007/s11032-016-0537-0.

11232. Prins R, Pretorius ZA, Bender CM and Lehmensiek A 2011 QTL mapping of stripe, leaf and stem rust resistance genes in a Kariega × Avocet S doubled haploid wheat population. Molecular Breeding 27: 259-270. DOI10.1007s11032-010-9428-y.

11233. Wei JX, Geng HW, Zhang Y, Liu JD, Wen WI, Zhang Y, Xia XC, Chen XM and He ZH 2015 Mapping quantitative trait loci for peroxidase activity and developing gene-specific markers for *TaPod-A1* on wheat chromosome 3AL. Theoretical and Applied Genetics 128: 2067-2076. DOI: 10.1007/s00122-015-2567-0

11234. Dholakia BB, Rajwade AV, Hosmani P, Khan RR, Chavan S, Reddy DMR, Lagu MD, Bansal UK, Saini RG and Gupta VS. 2013 Molecular mapping of leaf rust resistance gene *Lr15* in hexaploid wheat. Molecular Breeding 341: 743-747. DOI: 10.1007/s11032-012-9813-9.

11235. Hou L, Chen XM, Wang M, See DR, Chao SM, Bulli P and Jing JX 2015 Mapping a large number of QTL for durable resistance to stripe rust in winter wheat Druchamp using SSR and SNP markers. PLoS One 10e0126794. DOI: 10.1371/journal.pone.0126794.

11236. Klindworth DL, Saini J, Long YM, Rouse MN, Faris JD, Jin Y & Xu SS 2017 Physical mapping of DNA markers linked to stem rust resistance gene *Sr47* in durum wheat. Theoretical and Applied Genetics 130: 1135-1154. DOI: 10.1007/s00122-017-2875-7.

11237. Bokore FE, Knox RE, DePauw RM, Clarke F, Cuthbert RD, Campbell HL, Brule-Babel AL, Gilbert J and Ruan Y 2017 Validation of molecular markers for use with adapted sources of Fusarium blight resistance in wheat. Plant Disease 101: 1292-1299. DOI: 10.1094/PDIS-10-16-1421-RE.

11238. Zhang LL, Liu C, An XY, Wu HY, Feng Y, Wang H & Sun DJ 2017 Identification and genetic mapping of a novel incompletely dominant yellow leaf color gene, *Y1718*, on chromosome 2BS in wheat. Euphytica 213, 141. DOI: 10.1007/s10681-017-1894-4.

11239. Varella AC, Weaver DK, Cook JP, Blake NK, Holland ML, Lamb PF and Talbert LE 2017 Characterization of resistance to the wheat stem sawfly in spring wheat landrace accessions from targeted geographic regions of the world. Euphytica 213, 153. DOI10.1007/s10681-017-1945-x.

11240. Ramirez-Gonzalez RH, Segovia V, Bird N, Fenwick P, Holdgate S, Berry S, Jack P, Caccamo M and Uauy C 2015 RNA-Seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. Plant Biotechnology Journal 13: 613-624. DOI: 10.1111/pbi.12281.

11241. Li HY, Wang QL, Xu LS, Mu JM, Wu JH, Zeng QD, Yu SZ, Huang LL and Kang ZS 2017 Rapid identification of a major effect QRL conferring adult plant resistance to stripe rust in wheat cultivar Yaco'S'. Euphytica 213, 124. DOI 10.1007/s10681-017-1912-6.

11242. Soto-Cerda BJ, Inostroza-Blancheteau C, Mathias M, Penaloza E, Zuniga J, Munoz G, Rengel Z and Salvo-Garrido H 2015 Marker-assisted breeding for *TaALMT1*, a major gene conferring aluminium tolerance to wheat. Biologia Plantarum 50: 83-91. DOI 10.1007/s.

11243.	Zheng Z, Kilian A, Yan G and Liu C (2014) QTL conferring Fusarium crown rot resistance in the elite bread wheat variety EGA Wylie. PLoS One 9: e96011. DOI: 10.1371/journal.pone.0096011.
11244.	Zheng Z, Ma J, Stiller J, Zhao QA, Fen Q, Choulet C, Feullet C, Zhang YL, Wei YM, Han B, Manners JM & Liu CL 2015 Fine mapping of a large-effect QTL conferring Fusarium crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. BMC Genomics 16, 850. DOI: 10.1186/s12864-015-2105-0.
11245.	Xu ZC, Yuan CL, Wang JR, Fu DL and WU JJ 2015 Mapping the glaucousness suppressor *Iw1* from wild emmer wheat "PI 481521". The Crop Journal 3: 37-45. DOI:1016/j.cj.2014.09.004.
11246.	Liu YJ, Liu YX, Zhou Y, Wight C, Pu ZE, Qi PF, Jiang QT, Deng M, Wang ZX, Wei YM, Cao WG, Liu DC, Zheng YL, Liu CJ, Fregeau-Reid J and Wang JR 2017 Conferring resistance to pre-harvest sprouting in durum wheat by a QTL identified in *Triticum spelta*. Euphytica 213,19. DOI: 10.1007/s10681-016-1796-x.
11247.	Lu P, Qin JX, Wang GX, Wang LL, Wang ZZ, Wu QH, Xie JH, Liang Y, Wang Y, Zhang DY, Sun QX and Liu ZY 2015 Comparative fine mapping of the waxy (*W1*) locus in hexaploid wheat. Theoretical and Applied Genetics 128: 1595-1603. DOI: 10.1007/s00122-015-2534-9.
11248.	Ren Y, Singh RP, Basnet BR, Lan CX, Huerta-Espino J, Lagudah ES and Ponce-Molina LJ 2017 Identification and mapping of adult plant resistance loci to leaf rust and stripe rust in common wheat cultivar Kundan. Plant Disease 101: 456-463. DOI: 10.1094/PDIS-06-0890-RE.
11249.	Babiker EM, Gordon TC, Bonman JM, Chao S, Rouse MN, Jin Y, Newcomb M, Wanyera R and Bhavani S 2017 Genetic loci conditioning adult plant resistance to the Ug99 race group and seedling resistance to races TRTTF and TTTTF of the stem rust pathogen in wheat landrace CItr 15026. Plant Disease 101: 496-501. DOI: 10.1094/PDIS-10-16-1447-RE.
11250.	Zou SH, Wang HA, Li YW, Kong ZS and Tang DZ 2017 The NB-LRR gene *PmR2* confers powdery mildew resistance in diploid wheat. New Phytologist 218: 298-309. DOI: 10.111/nph.14964.
11251.	Qiu YC, Zhou RH, Kong XY, Zhang SS and Jia JZ 2005 Microsatellite mapping of a *Triticum urartu* Tum. derived powdery mildew resistance gene transferred to common wheat (*Triticum aestivum* L). Theoretical and Applied Genetics 111: 1524-1531. DOI: 10.1007/s00122-005-0081-5.
11252.	Yao Q, He MM, Hou L, Han JH, Guo, Jing JX and Kang ZS 2017 Genetic analysis and molecular mapping of stripe rust resistance genes in Chinese native wheat (*Triticum aestivum*) Lankao 5. Australasian Plant Pathology 46: 213-221. DOI: 10.1007/s13313-017-0478-z.
11253.	McCallum, BD, Hiebert CW, Cloutier S, Bakkeren G, Rosa SB, Humphreys DG, Marais GF, McCartney CA, Panwar V, Rampitsch C, Saville BJ and Wang XB 20126 A review of wheat leaf rust research and the development of resistant cultivars in Canada. Canadian Journal of Plant Pathology 38: 1-18. DOI: 10.1080/07060661.2016.1145508.
11254.	Zhang SG, Li YF, Lu L, Liu ZH, Zhang CH, Ao DH, Li LR, Zhang CY, Liu R, Luo CP, Wu Y and Zhang L 2017 Evaluating the contribution of genes to stripe rust resistance breeding through marker-assisted detection in wheat. Euphytica 213, 50. DOI 10: 1007/s10681-016-1826-6.

11255.	Kumar S, Roder MS, Bhushan S, Tripathi SB, Kumar S, Chand R, Joshi AK and Kumar U 2015 Mendelization and fine mapping of a bread wheat spot blotch resistance QTL. Molecular Breeding 35, 218. DOI: 10.1007/s11032-015-0411-5.
11256.	Lu P, Liang Y, Li DL, Wang ZZ, Li WB, Wang GX, Wang Y, Zhou SH, Wu QH, Xie JZ, Zhang DY, Chen YX, Li MM, Zhang Y, Sun QX and Liu ZY 20126 Fine genetic mapping of spot blotch resistance gene *Sb3* in wheat (*Triticum aestivum*). Theoretical and Applied Genetics 128: 577-589. DOI: 10.1007/s00122-015-2649-z.
11257.	Wang ZZ, Li HW, Zhang DY, Guo L, Chen JJ, Chen YX, Wu QH, Xie JZ, Zhang Y, Sun QX, Dvorak J, Luo M-C & Liu ZY 2015 Genetic and physical mapping of powdery mildew resistance gene *MlHLT* in Chinese wheat landrace Hulutou. Theoretical and Applied Genetics 128: 365-373. DOI: 10.1007/s00122-014-2436-2.
11258.	Liu DC, Zhang LQ, Hao M, Ning SZ, Yuan ZW, Dai SF, Huang L, Wu BH, Yan ZH, Lan XJ and Zheng YL 2018 Wheat breeding in the hometown of Chinese Spring. The Crop Journal 6: 82-90. DOI: 10.1016/j/cj.2017.08.009.
11259.	Huerta-Espino J and Singh RP 2017 First detection of virulence in *Puccinia striiformis* f. sp. *tritici* to wheat resistance genes *Yr10* and *Yr24* (=*Yr26*) in Mexico. Plant Disease 101: 1676. DOI :10.1094/PDIS-04-17-0532-PDN.
11260.	Patpour M, Hovmoller MS and Hodson D 2017 First report of virulence to *Sr25* in race TKTTF of *Puccinia graminis* f. sp. *tritici* causing stem rust on wheat. Plant Disease 101: 1678. DOI: 10.10904.PDIS-11-16-1666-PDN.
11261.	Nsabiyera V, Bariana HS, Qureshi N, Wong D, Hayden MJ and Bansal UK 2018 Characterization and mapping of adult plant stripe rust resistance in wheat accession Aus27284. Theoretical and Applied Genetics. DOI: 10.1007/s00122-018-3090-x.
11262.	Gessese M, Bariana H, Wong D, Hayden M and Bansal W 2019 Molecular mapping of stripe rust resistance gene *Yr81* in common wheat landrace AUS27430. Plant Disease 103: 1166-1171. DOI: 10.1094/PDIS-06-18-1055-RE.
11263.	Wang SZ, Asuke S, Vy TTP, Inoue Y, Chuma I, Kato K, Fujita M, and Tosa Y. 2018 Rmg9, a new gene for resistance to Triticum isolates of *Pyricularia oryzae* is combined with *Rmg8* in a common wheat landrace. Phytopathology 108: 1288-1306. DOI: 10.1094/PHYTO-12-17-0400-R.
11264.	Williamson VM, Thomas V, Ferris H and Dubcovsky J 2013 An *Aegilops ventricosa* translocation confers resistance against root-knot nematodes to common wheat. Crop Science 53: 1412-1418. DOI: 10:2135/cropsci2013.120681.
11265.	Cruz CD Peterson GL, Bockus WW, Kankanala P, Dubcovsky J, Jordan KW, Akhunov E, Chumley F, Baldelomar FD and Valent B 2016 The 2NS translocation from *Aegilops ventricosa* confers resistance to the Triticum pathotype of *Magnaporthe oryzae*. Crop Science 56: 990-1000. DOI: 10.2135/cropsci2015.07.0410.
11266.	Qureshi N, Bariana HS, Zhang P, McIntosh RA, Bansal UK, Wong D, Hayden MJ, Dubcovsky J, and Shankar M 2018 Genetic relationship of stripe rust resistance genes *Yr34* and *Yr48* in wheat and identification of linked KASP markers. Plant Disease 102: 443-420. DOI: 10.1094/PDIS-08-17-1144-RE.
11267.	Juliana P, Singh RP, Singh PK, Crossa J, Huerta-Espino J, Lan CX, Bhavani S, Rutkovski JE, Poland JA, Bergstrom GC and Sorrells ME 2017 Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. Theoretical and Applied Genetics 130: 1415-1430. DOI: 10.1007/s00122-017-2897-1.
11268.	Yu GT, Zhang QJ, Friesen TL, Rouse MN, Jin Y, Zhong SB, Rasmussen, Lagudah ES and Xu SS 2015 Identification and mapping of *Sr46* from *Aegilops tauschii* accession CIae 25

	conferring resistance to race TTKSK (Ug99) of wheat stem rust pathogen. Theoretical and Applied Genetics 128: 431-443. DOI: 10.1007/s00122-014-2442-4.
11269.	Tucker EJ, Baumann u, Kouidri A, Suchecki R, Baes M, Garcia M, Okada T, Dong CM, Wu YZ, Sandhu A, Singh M, Langridge P, Wolters P, Albertsen MC, Cigan AM and Whitford R 2017 Molecular identification of the wheat male fertility gene *Ms1* and its prospects for hybrid breeding. Nature Communications 18: 869. DOI: 10.1038/s41467-017-00945-2. SAME AS 11422
11270.	Sanchez-Martin J, Steurnagel B, Ghosh S, Herren G, Hurni G, Adamski N, Vrana J, Kublakova M, Krattinger SG, Wicker T, Dolezel J, Keller B and Wulff BH 2016 Rapid gene isolation in barley and wheat by mutant chromosome sequencing. Genome Biology 17, 221. DOI: 10.1186/s13059-016-1082-1.
11271.	Ren Y, Li SR, Wei YM, Zhou Q, Du XY, He YJ and Zheng YL 2015 Molecular mapping of a stripe rust resistance gene in Chinese wheat cultivar Mianmai 41. Journal of Integrative Agriculture 14: 295-304. DOI: 10.1016/S2095-3119(14)60781-4.
11272.	Anh VL, Inou Y, Asuke S, Vy TTP, Anh NT, Wang SZ, Izumi C and Tosa Y 2017 *Rmg8* and *Rmg7*, wheat genes for resistance to the wheat blast fungus, recognize the same avirulence gene *AVR-Rmg8*. Molecular Plant Pathology 19: 1252-1256. DOI: 10.1111/mpp.12609.
11273.	Lu Y, Xing LP, Xing SJ, Hu P, Cui CF, Zhang MY, Xiao J, Wang HY, Zhang RQ, Wang X Chen PD and Cao AZ 2015 Characterization of a putative new semi-dominant reduced height gene *Rht_Nm9*, in wheat (*Triticum aestivum* L.). Journal of Genetics and Genomics 42: 685-698. DOI: 10.1016/j.jgg.2015.08.007.
11274.	Scofield SR, Huang L, Brandt AS and Gill BS 2005 Development of a virus-induced gene silencing system for hexaploid wheat and its use in functional analysis of the *Lr21*-mediated leaf rust resistance pathway. Plant Physiology 138: 2165-2173. DOI: 10/1104/pp.105.061861.
11275.	Xing LP, Hu P, Liu JQ, Cui CF, Wang H, Di ZC, Zhou SA, Xu JF, Huang ZP and Cao AZ 2017 *NLR1-V*, a CC-NBS-LRR encoding gene is a potential candidate gene of the wheat powdery mildew resistance gene *Pm21*. BioRxiv preprint: DOI: http://dx.doi.org/10.1101/114058.
11276.	Hurni S, Brunner S, Buchmann G, Herren G, Jordan T, Krukowski P, Wicker T, Yahoaoui N, Mago and Keller B 2013 Rye *Pm8* and wheat *Pm3* are orthologous genes and show evolutionary conservation of resistance function against powdery mildew. The Plant Journal 76: 957-969. DOI: 10.1111/tpj.12345.
11277.	Segovia V, Hubbard A, Craze M, Bowden S, Wallington E, Bryant R, Greenland A, Bayles R and Uauy C 2014 *Yr36* confers partial resistance at temperatures below 18°C to U.K. isolates of *Puccinia striiformis*. Phytopathology 104: 871-878. DOI: 10.1094/PHYTO-10-13-0295-R.
11278.	Li Cl, Wang ZH, Bowden R, Bai GH, Li CX and Su ZQ 2017 Mapping of quantitative trait loci for leaf rust resistance in the wheat population Ning 7840 × Clark. Plant Disease 101: 1974-1979. DOI: 10.1094.PDIS-12-16-1743-RE.
11279.	Wu Jh, Wang QL, Kang ZS, Liu SJ, Li HY, Mu JM, Dai MF, Han DJ, Zeng QD and Chen XM 2017 Development and validation of KASP-SNP markers for QTL underlying resistance to stripe rust in common wheat cultivar P10057. Plant Disease 101: 2079-2087. DOI: 10.1094.PDIS-04-14-0468-RE.

11280.	Aoun M, Kolmer JA, Rouse MN, Chao SM, Bubula WD, Elias EM, Acevedo M 2017 Inheritance and bulked segregant analysis of leaf rust and stem rust resistance in durum wheat genotypes. Phytopathology 107: 1496-1506. DOI: 10.1094/PHYTO-12-16-0444-R.
11281.	Kolmer JA, Chao S, Brown-Guedira G, Bansal U and Bariana H 2018 Adult plant leaf rust resistance derived from the soft winter wheat cultivar 'Caldwell' maps to chromosome 3BS. Crop Science 58: 152-158. DOI: 10.2135/cropsci2017.05.0272.
11282.	Ren Y, Li SR, Xia XC, Zhou QA, He YJ, Wei YM, Zheng YL and He ZH 2015 Molecular mapping of a recessive stripe rust resistance gene *YrMY37* in Chinese wheat cultivar Mianmai 37. Molecular Breeding 35, 97. DOI: 10.1007/s11032-015-0293-6.
11283.	Wu JH, Wang QL, Liu SJ, Huang S, Mu JM, Zeng QD, Huang LL, Han DJ and Kang ZS 2017 Saturation mapping of a major effect QTL for stripe rust resistance on wheat chromosome 2B in cultivar Napo 63 using SNP genotyping arrays. Frontiers in Plant Science 6, 653. DOI: 10.3389.fpls.2017.00653.
11284.	Feng JY, Chen GY, Wei YM, Liu YX, Jiang QT, Li W, Pu Z, Lan XJ, Dai SF, Zhang M and Zhenh YL 2015 Identification and mapping stripe rust resistance gene *YrLM168a* using extreme individuals and recessive phenotype class in a complicated genetic background. Molecular and General Genomics 290: 2271-2278. DOI: 10.1007/s00438-015-1077-8.
11285.	Li N, Zong Y, Liu BL, Chen WJ and Zhang B 2017 *TaMYB3*, encoding a functional MYB transcriptor, isolated from the purple pericarp of *Triticum aestivum*. Cereal Research Communications 45: 368-380. DOI: 10.1556/0806.45.2017.027.
11286.	Naruoka Y, Ando K, Bulli P, Muleta KT, Rynearson S and Pumphrey MO 2016 Identification and validation of SNP markers linked to the stripe rust resistance gene *Yr5* in wheat. Crop Science 56: 3055-3065. DOI: 10.2135/cropsci2016.03.0189.
11287.	Wu PP, Xie JZ, Hu JH, Qiu D, Liu ZY, Li JT, Li MM, Zhang Hj, Yang L, Zhou Y Zhang ZJ and Li HJ 2018 Development of molecular markers linked to powdery mildew resistance gene *Pm4b* by combining SNP discovery from transcriptome data with bulked segregant analysis (BSR-Seq) in wheat. Frontiers in Plant Science 9, 95. DOI: 10.3389.fpls.2018.00095.
11288.	Rouse MN and Jin Y 2011 Stem rust resistance in A-genome diploid relatives of wheat. Plant Disease 95: 941-944. DOI: 10.1094/PDIS-04-10-0260.
11289.	Geng MM, Zhang J, Peng FX, Liu X, Lv XD, Mi YY Li YH, Li F, Xie CJ and Sun QX 2016 Identification and mapping of *MLIW30*, a powdery mildew resistance gene derived from wild emmer wheat. Molecular Breeding 36, 130. DOI: 10/s11032-016-0553-0.
11290.	Sun HG, Hu JH, Song W, Qiu D, Cui L, Wu PP, Zhang HJ, Liu HW, Yang L, Qu YF, Li YH, Li T, Cheng W, Zhou Y, Liu ZY, Li JT and Li HJ 2018 *Pm61*: a recessive gene for resistance to powdery mildew in wheat landrace Xuxusanyuehuang identified by comparative genomics analysis. Theoretical and Applied Genetics 131:2085-2097. DOI:10.1007/s00122-018-3135-1.
11291.	Bheema Lingeswaara Reddy IN, Chandresekhar K, Zewdu Y, Dinoor A, Keller B and Ben-David R 2016 Identification and genetic mapping of *PmAF7DS* a powdery mildew resistance gene in bread wheat. Theoretical and Applied Genetics 129: 1127-1137. DOI: 10.1007/s00122-016-2688-0.
11292.	Shi GJ, Friesen TL, Saini J, Xu SS, Rasmussen JB and Faris JD 2015 The wheat *Snn7* gene confers susceptibility on recognition of the *Parastagonospora nodorum* necrotrophic effector SnTox7. Plant Genome 8(2): DOI: 10.3835/plantgenome2015.02.0007.

11293.	Wurschum T, Langer SM, Longin CF, Tucker MR and Leister WL 2017 A modern Green Revolution gene for reduced height in wheat. The Plant Journal 92: 892-903. DOI: 10.1111/tpj.13726.
11294.	Herter CP, Ebmeyer E, Kollers S, Korzun V, Leister WL, Wurschum T and Miedaner T 2018 *Rht24* reduces height in the winter wheat population ‘Solitar × Bussard’ without adverse effects on Fusarium head blight infection. Theoretical and Applied Genetics 131: 1263-1272. DOI: 10.1007/s001222-018-3076-8
11295.	Vikhe P, Patil R, Chavan A, Oak M and Tamhankar S 2017 Mapping gibberellin-sensitive dwarfing locus *Rht18* in durum wheat and development of SSR and SNP markers for selection in breeding. Molecular Breeding 37, 28. DOI 10.1007s11032-017-0641-9.
11296.	Kolmer JA, Garvin DF, Hayden M and Speilmeyer W 2018 Adult plant leaf rust resistance derived from wheat landrace Americano 44d is conditioned by interaction of three QTL. Euphytica 214, 59. DOI: 10.1007/s10681-018-2141-3.
11297.	Ciuca M A preliminary report on the identification of SSR markers for bunt (*Tilletia* sp.) resistance in wheat. Czech Journal of Plant Breeding (Special Issue) 47: S142-S145.
11298.	Singh A, Knox RE, DePauw, Singh AK, Cuthbert RD, Kumar S and Campbell HL 2016 Genetic mapping of common bunt resistance and plant height QTL in wheat. Theoretical and Applied Genetics 129: 243-256. DOI: 10.1007/S00122-015-2624-8.
11299.	Steffen PM, Torp AM, Bergen A, Backes G and Rasmussen SK 2017 Mapping of common bunt resistance gene *Bt9* in wheat. Theoretical and Applied Genetics 130: 1031-1040. DOI: 10.1008/s00122-017-2868-6.
11300.	Mo YJ, Vanzetti L, Hale I, Spagnolo EJ, Guidobaldi G, Al-Obouchi, Odle N, Pearce S, Helguera M and Dubcovsky J 2018 Identification and characterization of *Rht25*, a locus on chromosome arm 6AS affecting wheat plant height, heading time and spike development. Theoretical and Applied Genetics 131:2085-2097. DOI:10.1007/s00122-018-3135-1.
11301.	Ford BA, Foo E, Sharwood R, Karafaitova M, Vrana J, MacMillan C, Nichols DS, Steurnagel B, Uauy C, Dolezel Y, Chandler PM and Spielmeyer W 2018 Rht18 semidwarfism in wheat is due to increased GA 2-oxidaseA9 expression and reduced GA content. Plant Physiology 177: 168-170. DOI: 10.1104/pp18.00023.
11302.	Xie WL, Ben-David R, Zeng B, Distenfeld A, Roder MS, Dinoor A and Fahima T 2013 Identification and characterization of a novel powdery mildew resistance gene *PmG3m* derived from wild emmer wheat, *Triticum aestivum*. Theoretical and Applied Genetics 124: 911-922. DOI: 10.1007s/s00122-011-1756-8.
11303.	Wu JH, Wang QL, Xu LS, Chen XM, Li B, Mu JM, Zeng QD, Huang LL, Han DJ and Kang ZS 2018 Combining single nucleotide polymorphism genotyping array with bulked segregant analysis to map a gene controlling adult plant resistance to stripe rust in wheat line 03031-1-5 H62. Phytopathology 108: 103-113. DOI: 10.1094/PHYTO-04-17-0153-R.
11304.	Yuan CL, Wu JZ, Yan BQ, Hao QQ, Zhang CZ, Lyo B, Ni F, Caplan A, Wu JJ and Fu DL 2018 Remapping of the stripe rust resistance gene *Yr10* in common wheat. Theoretical and Applied Genetics 131: 1353-1262. DOI: 10.1007/s00122-018-3075-9.
11305.	Lukaszewsky AJ and Cowger C 2017 Re-engineering of the *Pm21* transfer from *Haynaldia villosa* to bread wheat by induced homoeologous recombination. Crop Science 57: 2590-2594. DOI: 10.2135/cropsci2017.03.0192.
11306.	Ponce-Molina LJ, Huerta-Espono L, Singh RP, Basnet BR, Alvarado G, Randhawa MS, Lan CX, Aguilar-Rincon VH, Lobata-Ortiz R and Garcia-Zavala JJ 2018 Characterization of leaf rust and stripe rust resistance in spring wheat ‘Chilero’. Plant Disease 102: 421-427. DOI: 10.1094/PDIS-11-16-1545-RE.

11307.	Xue FB, Guo J, Guan CY, Wang HW, Li AF and Kong LR 2015 Molecular mapping of the hybrid necrosis gene *NetJingY176* in *Aegilops tauschii* using microsatellite markers. The Crop Journal 3: 298-304. DOI: 10.1016/j.cj.2015.05.003.
11308.	Wang Y, Zhang HZ, Xie JZ, Guo BM, Chen YX, Zhang HY, Lu P, Wu QH, Li MM, Zhang DY, Guo GH, Yang J, Zhang PP, Zhang Y, Wang XC, Zhao H and Cao TJ 2018 Mapping stripe rust resistance genes by BSR-Seq: *YrMM58* and *YrHy1* on chromosome 2AS in Chinese wheat lines Mengmai 58 and Huaiyang 1 are *Yr17*. The Crop Journal 6: 91-98. DOI: 10.1016/j/cj.2017.03.002.
11309.	Smiley RW, Dababat AA, Iqbal S, Jones MGK, Maafi ZT, Peng DL, Subbotin SA and Waeyenberge L 2017 Cereal cyst nematodes: a complex and destructive group of *Heterodera* species. Plant Disease 101: 1692-1720. DOI: 10.1094/PDIS-03-017-0355-FE.
11310.	Gabrewahid TW, Yao ZJ, Yan XC, Gao P and Li ZF 2017 Identification of leaf rust resistance genes in Chinese common wheat cultivars. Plant Disease 101: 1729-1737. DOI: 10.1094/PDIS-02-17-0247-RE.
11311.	Lu Y, Bowden RL, Zhang GE, Xu XY, Fritz AK and Bai GH 2017 Quantitative trait loci for slow rusting resistance to leaf rust in doubled-haploid wheat population CI13227 × Lakin. Phtopathology 107: 1372-1380. DOI: 10.1094/PHYTO-09-16-0347-R.
11312.	Shoeva OY, Gordeeva EI and Khlestkina EK 2014 The regulation of anthocyanin synthesis in wheat pericarp. Molecules 19: 20166-20279. DOI: 10.3390/molecules191220266.
11313.	Jiang WH, Liu TX, Nan WZ, Jeewani DC, Niu YL, Li CL, Wang Y, Shi X, Wang C, Wang JH, Li Y, Gao X and Wang ZG 2018 Two transcription factors *TaPpm1* and *TaPpb1* co-regulate anthocyanin biosynthesis in purple pericarps of wheat. Journal of Experimental Botany 69: 2555-2567. DOI: 10.1093/jxb/ery101.
11314.	Rinaldo A, Gilbert B, Boni R, Krattinger SG, Singh D, Park RF, Lagudah and Ayliffe M 2016 The *Lr34* adult plant rust resistance gene provides seedling resistance in durum wheat without senescence. Plant Biotechnology Journal 15: 894-905. DOI: 10.1111/pbi.12684.
11315.	Chen SS, Zhang WJ, Bolus S, Rouse MN and Dubcovsky J 2018 Identification and characterization of wheat stem rust resistance gene *Sr21* effective against the UG99 race group at high temperature. PLoS Genetics 14(4):e1007287. DOI:10.137/journal.pgen.1007287.
11316.	Mago R, Zhang P, Vautrin S, Šimková H, Bansal U, Luo M-C, Rouse M, Karaoglu H, Periyannan, Kolmer J, Jin Y, Ayliffe MA, Bariana H, Park RF, McIntosh R, Dolezel T, Berges H, Spielmeyer W, Lagudah ES, Ellis JG and Dodds PN 2015 The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. Nature Plants 15186. DOI: 10.1038/nplants.2015.186.
11317.	Li N, Jia HY, Kong ZX, Tang WB, Ding YX, Liang JC, Ma HQ and Ma ZQ 2017 Identification and marker-assisted transfer of a new powdery mildew resistance gene at the *Pm4* locus in common wheat. Molecular Breeding 37, 79. DOI: 10.1007/s11032-017-0670-4.
11318.	Yu GT, Cai XW, Harris MO, Gu YQ, Luo M-C and Xu SS 2009 Saturation and comparative mapping of the genomic region harboring Hessian fly resistance gene *H26* in wheat. Theoretical and Applied Genetics 118: 1589-1599. DOI: 10.1007/s00122-009-1006-5.
11319.	Yu GT, Klindworth, DL, Friesen TL, Faris JD, Zhong SB, Rasmussen JB and Xu SS 2015 Development of a diagnostic co-dominant marker for stem rust resistance gene *Yr47*

	introgressed from *Aegilops speltoides* into durum wheat. Theoretical and Applied Genetics 118: 1589-1599. DOI: 10.1007/s00122-015-2590-1.
11320.	Wiesma AT, Whetten RB, Zhang GR, Sehgal S, Kolb FL, Poland JA, Mason RE, Carter AH, Cowger C and Olson EL 2018 Registration of two wheat germplasm lines fixed for Pm58. Journal of Plant Registrations. DOI: 10.3198/jpr2017.06.0036crg.
11321.	Zhang RQ, Fan YL, Kong LN, Wang ZJ, Wu JH, Xing LP, Cao AZ and Feng YG 2018 *Pm62*, an adult-plant powdery mildew resistance gene introgressed from *Dasypyrum villosum* chromosome arm 2VL into wheat. Theoretical and Applied Gentics 131: 2613-2620. DOI: 10.1007/s00122-018-3176-5.
11322.	Pakeerathan K, Bariana H, Qureshi N, Wong D, Hayden M and Bansal U 2019 Identification of a new source of stripe rust resistance *Yr82* in wheat. Theoretical and Applied Genetics 132:3169-3176. DOI: 10.1007/s00122-019-03416-y.
11323.	Zhang HY, Ren JD, Quan W, Zhang YB and Zhang SJ 2017 A QTL with major effect on reducing stripe rust severity detected from a Chinese wheat landrace. Plant Disease 101: 1533-1539. DOI: 10.1094/PDIS-08-06-1131-Re.
11324.	Li GQ, Wang Y, Chen MS, Edae E, Poland J, Akhunov E, Chao SM, Bai GH, Carver BF and Yan LL 2015 Precisely mapping a major gene conferring resistance to Hessian fly in bread wheat using genotyping-by-sequencing. BMC Genomics 14, 108. www.biomedcentral.com/1471-2164/14/369.
11325.	Tan CT, Carver BF, Chen M-S, Gu Y-Q and Yan LL 2013 Genetic association of OPR genes with resistance to Hessian fly in hexaploid wheat. BMC Genomics 14, 369.
11326.	Li MM, Li BB, Chen YX, Xie JZ, Lu P, Wu QH, Zheng DY, Zheng HZ, Yang J, Zheng PP, Zhang Y and Liu ZY 2018 Mapping a leaf senescence gene *els1* by BSR-Seq in common wheat. The Crop Journal 6: 236-243. DOI: 10.1016/j.cj.2018.01.004.
11327.	Liu XM, Khajuria C, Li JR, Trick HN, Huang L, Gill BS, Reeck GR, Antony G, White FW and Chen M-S 2013 Wheat *Mds-1* encodes a heat-shock protein and governs susceptibility towards the Hessian fly gall midge. Nature Communications 4, 2070. DOI: 10.1038/ncomms3070.
11328.	Xue SL, Kolmer JA, Wang SW and Yan LL 2018 Mapping of leaf rust resistance genes and molecular characterization of the 2NS/2AS translocation in the wheat cultivar Jagger. Genes, Genomes and Genetics G3 8: 2059-2065. DOI: 10.1534/g3.118.200058.
11329.	Assanga S, Zhang GR, Tan C-T, Rudd JC, Ibrahim A, Xue QW, Chao SM, Fuentealba MP and Liu SY 2017 Saturated genetic mapping of Wheat Streak Mosaic Virus resistance gene *Wsm2* in wheat. Crop Science 57: 332-339. DOI: 10.2135/cropsci2016.04.0233.
11330.	Tan C-T, Assanga S, Zhang GR, Rudd JC, Haley SD, Xue QW, Ibrahim A, Bai GH, Zhang XZ, Bytne P, Fuentealba MP and Liu SY 2017 Develoment and validation of KASP markers for wheat streak mosaic virus resistance gene *Wsm2*. Crop Science 57: 340-349. DOI: 10.2135/cropsci2016.04.0234.
11331.	Tan CC, Li GQ, Cowger C, Carver BF and Xu XY 2018 Characterization of *Pm63*, a powdery mildew resistance gene identified in Iranian landrace PI 628024. Theoretical and Applied Genetics 131: 1137-1144. DOI: 10.1007/s00122-018-3265-5.
11332.	Ghaffary SMT, Chawade A and Singh PK 2018 Practical breeding strategies to improve resistance to Septoria tritici blotch of wheat. Euphytica 214, 122. DOI: 10.1007/s10681-018-2205-4.
11333.	Nicolis V and Venter E 2018 Silencing of a unique integrated domain nucleotide-binding leucine-rich repeat gene in wheat abolishes *Diuraphis noxia* resistance. Molecular Plant-Microbe Interactions 31: 940-950. DOI: 10.1094/MPMI-11-17-0262-R.

11334.	Dieguez MJ, Petignot C, Ferella L, Fiorentino G, Silva M, Dabove MA, Yanez GIR, Lopez M, Pergolesi MF, Ingala L, Cuyeu AR and Saccvo F 2018 Mapping a gene on wheat chromosome 4BL involved in a complementary interaction with adult plant leaf rust resistance gene *LrSV2*. Theoretical and Applied Genetics 131: 2333-2344. DOI: 10.1007/s00122-018-3155-x.
11335.	Ullah KN, Li N, Shen Y, Wang PS, Tang WB, Ma SW, Zheng ZM, Jia HY, Kong ZX and Ma ZQ 2018 Fine mapping of powdery mildew resistance gene *Pm4e* in bread wheat (*Triticum aestivum* L.). Planta 248: 1319-1328. DOI: 10.1007/s00425-018-2990-y.
11336.	Qureshi N, Kandiah P, Gessese MK, Nsabiyera V, Wells V, Babu P, Wong D, Hayden M, Bariana H and Bansal U 2018 Development of co-dominant KASP markers co-segregating with effective stem rust resistance gene *Sr26* in wheat. Molecular Breeding 38, 7. DOI: 10.1007/s11032-018-0854-6.
11337.	Singh RP and McIntosh RA 1987 Genetics and cytogenetics of resistance to *Puccinia graminis tritici* in three South African wheats. Genome 29: 664-670.
11338.	Mago R, Zhang P, Xia XD, Zhang JP, Hoxa S, Lagudah E, Graner A and Dundas I 2018 Transfer of stem rust resistance gene *SrB* from *Thinopyrum ponticum* into wheat and development of a closely linked PCR-marker. Theoretical and Applied Genetics 132: 371-382. DOI: 10.1007/s00122-018-3224-1.
11339.	Bassi FM, Kumar A, Zhang Q, Paux E, Huttnet E, Kilian A, Dizon R, Feuillet C, Xu SS and Kianian SF 2013 Radiation hybrid QTL mapping of *Tdes* involved in first meiotic division of wheat. Theoretical and Applied Genetics 126: 1977-1990. DOI: 10.1007/s00122-013-2111-z.
11340.	Mundt CC 2018 Pyramiding for resistance durability: Theory and practice. Phytopathology 108: 792-802. DOI: 10.1094/PHYTO-12-17-0426-RVW.
11341.	Shi GJ, Zhang ZC, Friesen TL, Raats D, Fahima T, Brueggerman RS, Lu SW, Trick HN, Liu ZH, Chao W, Frenkel Z, Xu SS, Rasmussen and Faris JD 2016 The highjacking of a receptor kinase-driven pathway by a wheat fungal pathogen leads to disease. Science Advances 2:e1600822. DOI: 10.1126/sciadv.160082.
11342.	Kandel DR, Glover KD, Berzonsky WA, Gonzalez-Hernandez JL, Ali S, Chao S and Bhusal SJ 2017 Flanking SSR markers for alleles involved in the necrosis of hybrids between hexaploid bread wheat and synthetic hexaploid wheat. Journal of Crop Improvement 31: 879-893. DOI: 10.1080/1542728.2017.1365794.
11343.	Zhang ZC, Belcram H, Gornicki P, Charles M, Just J, Huneau C, Magdelenat G, Couloux, Samain S, Gill BS, Rasmussen JB, Barbe V, Faris JD and Chalhoub B 2018 Duplication and partitioning in evolution and function of homoeologous *Q* loci governing domestication characters in polyploid wheat. Proceedings of the National Academy of Sciences of the United States of America 108: 18737-18742. DOI:
11344.	Greenwood JR, Finnegan EJ, Watanabe N, Trevaskis B and Swain SM 2017 New alleles of the wheat domestication gene *Q* reveal multiple roles in growth and reproductive development. Development 144: 1959-1965. DOI: 10.1242/dev.146407.
11345.	Zhao KJ, Xiao J, Chen SL, Yuan CX, Cao AH, You FM, Yang DL, An SM, Wang HY and Wang Xe 2018 *Rht23* (5Dq') likely encodes a Q homeologue with pleiotropic effects on plant height and spike compactness. Theoretical and Applied Genetics 131: 1825-1834. DOI: 10.1007/s00122-018-3115-5.
11346.	Zhang DY, Zhu KY, Dong LL, Liang Y, Li GQ, Fang TL, Guo GH, Wu QH, Xie JZ, Chen YX, Lu P, Li MM, Zhang HZ, Wang ZXZ, Zhang Y, Sun QX and Liu ZY 2019 Wheat powdery mildew resistance gene *Pm64* derived from wild emmer (*Triticum turgidum* var.

	dicoccoides) is tightly linked in repulsion with stripe rust resistance gene *Yr5*. The Crop Journal 7: 761-770. DOI: 10.1016/j.cj.2019.03.003.
11347.	Zurn JD, Rouse MN, Chao S, Aoun M, Marcharia G, Hiebert CW, Pretorius ZA, Bonman JM and Acevedo M 2018 Dissection of the multigenic wheat stem rust resistance present in Montenegran spring wheat accession PI 362698. BMC Genomics 19,67. DOI: 10.1186/s12864-018-4438-y.
11348.	Mandoulakami BA, Yaniv E, Kalendar R, Raats D, Bariana HS, Bihanta MZ and Schuman AH 2015 Development of IRAP- and REMAP-derived SCAR markers for marker-assisted selection of the stripe rust resistance gene *Yr15* derived from wild emmer wheat. Theoretical and Applied Genetics 128: 211-218. DOI: 10.1007/s00122-014-2422-8.
11349.	Qie YM, Liu Y, Wang MN, Li X, See DR, An DG & Chen XM 2019 Development, validation, and re-selection of wheat lines with pyramided genes *Yr64* and *Yr15* linked on the short arm of chromosome 1B for resistance to stripe rust. Plant Disease 103: 51-58. DOI: 10.1094/PDIS-03-18-0470-RE.
11350.	Wu JH, Zeng QD, Wang QL, Liu SJ, Mu JM, Huang S, Sela H, Distelfeld A, Huang LL, Han DJ and Kang ZS 2018 SNP-based pool genotyping and haplotype analysis accelerate fine-mapping of the wheat genomic region containing stripe rust resistance gene *Yr26*. Theoretical and Applied Genetics 131: 1481-1496. DOI: 10.1007/s00122-018-3092-8.
11351.	Marchal C, Zhang J, Zhang, P, Fenwick P, Steuernagel B, Adamski NM, Boyd L, McIntosh R, Wulff BBH, Berry S, Lagudah E and Uauy C 2018 BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. Nature Plants 4: 662-668. DOI: 10.1038/s41477-018-0236-4.
11352.	He HG, Ji YY, Zhu SY, Li B, Zhao RH, Jiang ZN and Bie TD 2017 Genetic, physical and comparative mapping of the powdery mildew resistance gene *Pm21* originating from *Dasypyrum villosum*. Frontiers in Plant Science 8, 1914. DOI: 10.3389/fpls.2017.01914.
11353.	He HG, Zhu SY, Zhao RH, Jiang ZN, Ji YY, Ji JA, Qui D, Li HJ and Bie TD 2018 *Pm21*, encoding a typical CC-NBS-LRR protein, confers broad-spectrum resistance to wheat powdery mildew disease. Molecular Plant 11: 879-882. DOI: 10.1016/j.molp.2018.03.004.
11354.	Hurni S, Brunner S, Buchmann G, Herren G, Jorden T, Krukowski P, Wicker T, Yahiaoui N, Mago R and Keller B 2013 Rye *Pm8* and *Pm3* are orthologous genes and show evolutionary conservation of resistance function against powdery mildew. The Plant Journal 76: 957-969. DOI: 1111/tpj.12345.
11355.	Singh SP, Hurni S, Ruinelli M, Brunner S, Sanchez-Martin J, Krukowski P, Peditto D, Buchmann G, Zbinden H and Keller B 2018 Evolutionary divergence of the rye *Pm17* and *Pm8* genes reveal ancient diversity. Plant Molecular Biology 98: 249-260. DOI: 10.1007/s11103-018-0780-3.
11356.	Li GQ, Cowger C, Wang XW, Carver BF and Xu XY 2019 Characterization of *Pm65*, a new powdery mildew resistance gene on chromosome 2AL of a facultative wheat cultivar. Theoretical and Applied Genetics 132: 2625-2632. DOI: 10.1007/s00122-019-03377.
11357.	Zhang JP, Zhang P, Hewitt T, Li JB, Dundas I, Schnippenkoetter W, Hoxha S, Chen CH, Park R and Lagudah E 2019 A strategy for identifying markers linked with stem rust resistance in wheat harbouring an alien chromosome introgression from a non-sequenced genome. Theoretical and Applied Genetics 132: 125-135. DOI: 10.1007/s0122-018-3201-8.
11358.	Ren JD, Wang Z, Du ZY, Che MZ, Zhang YB, Quan W, Wang YJ, Jiang X and Zhang ZJ 2019 Detection and validation of a novel major QTL for resistance to Fusarium head blight from *Triticum aestivum* in the terminal region of chromosome 7DL. Theoretical and Applied Genetics 132:241-255. DOI: 10.1007/s0122-018-3213-4.

11359.	Gyawali Y, Zhang W, Chao SM, Xu S and Cai ZW 2019 Delimitation of wheat *ph1b* deletion and development of *ph1b*-specific markers. Theoretical and Applied Genetics 132: 195-204. DOI: 10.1007/s00122-018-3207-2.
11360.	Yang NN, McDonald MC, Solomon PS and Milgate AW 2018 Genetic mapping of *Stb19*, a new resistance gene to *Zymoseptoria tritici* in wheat. Theoretical and Applied Genetics 131: 2765-2773. DOI: 10.1007/s00122-018-3189-0.
11361.	Brown JKM, Chatrian L, Lasserre-Zuber P and Saintenac C 2015 Genetics of resistance to *Zymosseptoria tritici* and applications to wheat breeding. Fungal Genetics and Wheat Breeding 79: 33-41. DOI: 10.1016/j.fgb.2015.04.017.
11362.	Kariyawasam GK, Carter A, Rasmussen, Faris J, Xu SS, Mergoum M and Liu ZH 2016 Genetic relationships between race-nonspecific and race-specific interactions in the wheat-*Pyrenophora tritici-repentis* pathosystem. Theoretical and Applied Genetics 129: 897-908.
11363.	Faris JD, Overlander ME, Kariyawasam G.K., Carter A, Xu SS and Liu ZH 2020 Identification of a major dominant gene for race-nonspecific tan spot resistance in wild emmer wheat. Theoretical and Applied Genetics (2020) 133:829. 10.1007/s00122-019-03509-8.
11364.	Li HH, Dong ZJ, Ma C, Xia Q, Tian XB, Sehgal S, Koo D-H, Friebe B, Ma PT and Liu WX 2020 A spontaneous wheat-*Aegilops longissima* translocation carrying *Pm66* confers resistance to powdery mildew. Theoretical and Applied Genetics 133: 1149-1159. DOI: 10.1007/s00122-020-03538-8.
11365.	Mu JM, Huang S, Liu SJ, Zeng QD, Dai MF, Wang QL, Wu JH, Yu SH, Kang ZS and Han DJ 2019 Genetic architecture of wheat stripe rust resistance revealed by combining QTL mapping using SNP-based genetic maps and bulked segregant analysis. Theoretical and Applied Genetics 132: 443-455. DOI: 10.1007/s00122-018-3231-2.
11366.	Wang Z, Ren JD, Du ZY, Che MZ, Zhang YB, Quan W, Jiang X, Ma Y, Zhao Y and Zhang ZY 2019 Identification of a major QTL on chromosome arm 2AL for reducing rust severity from a Chinese wheat landrace with evidence for durable resistance. Theoretical and Applied Genetics 132: 457-471. DOI: 10.1007/s001222-018-3232-1.
11367.	Soresi D, Zappacosta D, Garayalde A, Irigoyen I, Basualdo J and Carrera A 2017 A valuable QTL for Fusarium head blight resistance from *Triticum turgidum* ssp. dicoccoides has a stable expression in durum wheat cultivars. Cereal Research Communications 45: 234-247. DOI: 20.1556/0806.45.2017.007.
11368.	Zhang RQ, Singh RP, Lillemo M, He XY, Randhawa MS, Huerta-Espino J, Singh PK, Li ZK and Lan CX 2019 Two main stripe rust resistance genes identified in synthethic-derived wheat line Soru#1. Phytopathology 109: 120-126. DOI: 10.1094/PHYTO-04-18-0141-R.
11369.	Kolmer JA, Su Z, Bernardo A, Bai G and Chao S 2019 A backcross line of Thatcher wheat with adult plant resistance from Duster wheat has *Lr46* and *Lr77*. Phytopathology 109: 127-132. DOI: 10.1094/PHYTO-04018-0184-R.
11370.	Nishimura K, Moriyama R, Katsura K, Saito H, Takisawa R, Kitajima A and Nakazaki T 2018 The early flowering trait of an emmer wheat accession (*Triticum turgidum* L. ssp. *dicoccum*) is associated with the cis-element of the *Vrn-A3* locus. Theoretical and Applied Genetics 131: 20137-2053. DOI: 10.1007/s00122-018-3131-5.
11371.	Zeng QD, Wu JH, Huang S, Yuan FP, Liu SJ, Wang QL, Mu JH, Yu SZ, Chen L, Han DJ and Kang ZS 2019 SNP-based linkage mapping for validation of adult plant resistance QTL in common wheat cultivar Chakwal 86. The Crop Journal 7: 176-186. DOI: 10.1016.j.cj.2018.12.002.

11372.	Vikhe P, Venkatesan S, Chavan, Tamhankar S and Patil R 2019 Mapping of dwarfing gene *Rht14* in durum wheat and its effect on seedling vigor, internode length and plant height. The Crop Journal 7: 187-197. DOI: 10.1016.j.cj.2018.11.004.
11373.	Huang S, Wu JH, Wang XT, Mu JM, Xu Z, Zeng QD, Liu SJ, Wang QL, Kang ZD and Han DJ 2019 Utilization of the genomewide wheat 55K SNP array for genetic analysis of stripe rust resistance in common wheat line P0036. Phytopathology 109: 819-827. DOI: 10.1084/PHTO-10-18-0388-R.
11374.	Chao KX, Su WW, Wu L, Li Q, Wang BT and MA DF 2019 Molecular mapping of a recessive powdery mildew resistance gene in wheat cultivar Tian Xuan 45 using bulked segregant analysis with polymorphic relative ratio distribution. Phytopathology 109: 838-838. DOI: 10.1094/PHYTO-03-18-0092-R.
11375.	Kumar S, Roder MS, Tripathi SB, Kumar S, Chand R, Joshi AK and Kumar U 2015 Mendelization and fine mapping of a bread wheat spot blotch disease resistance QTL. Molecular Breeding 35, 218. DOI: 10.1007/s11032-015-0411-5.
11376.	Friesen TL, Holmes DJ, Bowden RL and Faris JD 2018 ToxA is present in the U.S. *Bipolaris sorokiniana* population and is a significant virulence factor on wheat harbouring *Tsn1*. Plant Disease 102: 2446-2452. DOI: 10.1094/PDIS-03-18-0521-RE.
11377.	Zeng QD, Wu JH, Liu SJ, Chen XM, Yuan FP, Su PP, Wang QL, Huang S, Mu KM, Han DJ and Kang ZS 2019 Genome-wide mapping for stripe rust resistance loci in common wheat cultivar Qinnong 142. Plant Disease 103: 439-447. DOI: 10.1094/PDIS-05-18-0846-RE.
11378.	Xu XY, Li GQ, Carver BF and Scott Armstrong JS 2020 *Gb8*, a new gene conferring resistance to economically important greenbug biotypes in wheat. Theoretical and Applied Genetics 133: 615-622. DOI: 10.1007/s00122-019-03491-1.
11379.	Zhou XL, Hu T, Li X, Yu YY, Yang SZ, Huang KB Han DJ and Kang ZS 2019 Genome-wide mapping of adult plant stripe rust resistance in wheat cultivar Toni. Theoretical and Applied Genetics 132: 1693-1704. DOI: 10.1007/s00122-03308-1.
11380.	Ma PT, Xu HX, Xu YF, Song LP, Liang SS, Han GH, Zhang XT and An DG 2018 Characterization of a powdery mildew resistance gene in wheat breeding line 10V-2 and its application in marker-assisted selection. Plant Disease 103: 925-931. DOI: 10.1094/PDIS-02-17-0199-RE.
11381.	Chao KX, Yang JY, Liu H, Jing JX, Li Q, Wang BT and Ma DF 2018 Genetic and physical mapping of a putative Leymus mollis-derived stripe rust resistance gene on wheat chromosome 4A. Plant Disease 102: 1001-1007. DOI: 10.1094/PDIS-05-17-0671-RE.
11382.	Pirseyedi SM, Kumar A, Ghavami F, Hegstad JB, Mergoum M, Mazaheri M, Kianian SF and Elias EM 2019 Mapping QTL for Fusarium head blight resistance in a Tunisian-derived durum wheat population. Cereal Research Communications 47: 78-87. DOI: 10.1556/0806.46.2018.053.
11383.	Kuzay S, Xu Y, Zhang J, Katz A, Pearce S, Su Z, Frazer M, Anderson JA, Brown-Guedira G, DeWitt N, Peters Haugrud A, Faris JD, Akhunov E, Bai G and Dubcovsky J 2019 Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping. Theoretical and Applied Genetics 132: 2689-2705. DOI: 10.1007/s00122-019-03382-5.
11384.	Li C, Lin H, Chen A, Lau M, Jernstedt J and Dubcovsky J 2019 Wheat RN1, FUL2 and FUL3 play critical and redundant roles in spikelet meristem identity and spike determinacy. Development. In press (also available in BioRxiv BIORXIV/2019/510388).

11385. Chen S, Rouse MN, Zhang W, Zhang X, Guo Y, Briggs J and Dubcovsky J 2019 Wheat gene *Sr60* encodes a protein with two putative kinase domains that confers resistance to stem rust. New Phytologist 225: 948–959. DOI: 10.1111.nph.16169.

11386. Cobo N, Wanjugi H, Lagudah and Dubcovsky J 2019 High-resolution map of wheat *QYr.ucw-1BL*, an adult-plant stripe rust resistance locus in the same chromosomal region as *Yr29*. The Plant Genome 12, 180055. DOI: 10.3835/plantgenome20-18.08.0055.

11387. McIntosh RA, Dubcovsky J, Rogers WJ, Xia XC and Raupp J 2019 Catalogue of gene symbols for wheat: 2019 supplement.

11388. Ni F, Qi J, Hao QQ, Lyo B, Luo M-C, Wang Y, Chen FJ, Wang SY, Zhang CZ, Epstein L, Zhao XY, Wang HG, Zhang XS, Chen CX, Sun LZ and Fu DL 2017 Wheat *Ms2* encodes for an orphan protein that confers male sterility in grass species. Nature Communications 8, 15121. DOI: 10.1038/ncomms15121.

11389. Xia C, Zhang LC, Zou C, Gu YQ, Duan JL. Zhao GY, Wu JJ, Liu Y, Fang XH, Gao LF, Jiao YN, Sun JQ, Pan YH, Liu X, Jia JZ and Kong XY 2017 A TRIM insertion in the promoter of *Ms2* causes male sterility in wheat. Nature Communications 8, 15407. DOI: 10.1038/ncomms15407.

11390. Wu J, Kong XY, Wan JM, Liu XY, Zhang X, Guo XP, ZhouRH, Zhao GY, Jing RL, Fu XD and Jia JZ 2011 Dominant and pleiotropic effects of a GAI gene in wheat results from lack of interaction between *DELLA* and *GID1*. Plant Physiology 157: 2120-2130. DOI: 10.1104/pp111.185272.

11391. McIntosh R, Mu JM, Han DJ and Kang ZS 2018 Wheat stripe rust resistance gene *Yr34/Yr26* A retrospective review. The Crop Journal 6: 321-329. DOI: 10.1016.j.cj.2018.02.001.

11392. Klymiuk V, Yaniv E, Huang L, Raats D, Fatiukha A, Chen SS, Feng LH, Frenkel Z, Krugman T, Lidzbarsky G, Chang W, Jaaskelainen MJ, Schudoma C, Paulin L, Laine P, Bariana H, Sela H, Saleem K, Sorensen CK, Hovmoller MS, Distenfeld A, Chalhoub B, Dubcovsky J, Korol AB, Schulman AH and Fahima T 2018 Cloning of the wheat *Yr15* resistance gene sheds light on the plant tandom kinase-pseudokinase family. Nature Communications 9, 3735. DOI.1038/s41467-018-06138-9.

11393. Liu MY, Lei L, Powers C, Liu ZY, Campbell KG, Chen XM, Bowden RL, Carver BF and Yan LL 2016 *TaXa21-A1* on chromosome 5AL is associated with resistance to multiple pests in wheat. Theoretical and Applied Genetics 129:345-355. DOI: 10.1007/s00122-015-2631-9.

11394. Cui L, Qiu D, Sun L, Sun Y, Ren YK, Zhang HJ, Li JT, Zou JW, Wu PP, Hu JH, Xie JZ, Liu HW, Yang L, Zhou Y, Wang Y, Lv Y, Liu ZY , Murray TD and Li HJ 2019 Resistance to *Heterodera filipjevi* and *H. avenae* in winter wheat is conferred by different QTL. Phytopathology, in review.

11395. Ando K, Krishnan V, Rynearsa S, Rouse MN, Danilova T, Friebe B, See D and Pumphrey M 2019 Introgression of a novel Ug-99-effective stem rust resistance gene into wheat and development of *Dasypyrum villosum* chromosome-specific markers via genotyping-by-sequencing (GBS). Plant Disease 103: 1068-1074. DOI: 10.1094/PDIS-05-18-0831-RE.

11396. Li JB, Dundas I, Dong CM, Li GR, Trethowan R, Yang ZJ, Hoxha S and Zhang P 2020 Identification and characterization of a new stripe rust resistance gene *Yr83* on rye chromosome 6R in wheat. Theoretical and Applied Genetics 133: 1095-1107. DOI: 10.1007/s00122-020-03534-y.

11397. Zhang JP, Hewitt TC, Boshoff WHP, Dundas I, Upadhyaya N, Li JB, Patpour M, Chandramohan S, Pretorius ZA, Hovmøller M, Schnippenkoetter W, Park RF, Mago R,

	Periyannan S, Bhatt D, Hoxha S, Chakraborty S, Luo M, Dodds P, Steuernagel B, Wulff BH, Ayliffe M, McIntosh RA, Zhang P and Lagudah ES 2021 A recombined *Sr26* and *Sr61* disease resistance gene stack in wheat encodes unrelated NLR genes. Nature Communications 12, 3378 | https://doi.org/10.1038/s41467-021-23738-0.
11398.	Singh SP, Hurni S, Ruinelli M, Brunner S, Sanchez-Martin J, Krukowski P, Peditto D, Buchmann G, Zbinden H and Keller B 2018 Evoluionary divergence of the rye *Pm17* and *Pm8* genes reveals ancient diversity. Plant Molecular Biology 98: 249-260. DOI: 10.1007/s11103-018-0780-3.
11399.	Kolmer JA, Bernardo A, Bai G, Hayden MJ and Anderson JA 2019 Thatcher wheat line RL6149 carries *Lr64* and a second leaf rust resistance gene on chromosome 1DS. Theoretical and Applied Genetics 132: 2809-2814. DOI: 10.1007/s00122-019-03389-y.
11400.	Wang R, Gordon T, Hole D, Zhao WD, Isham K, Bonman JM, Goates B and Chen JL 2019 Identification and assessment of two major QTLs for dwarf bunt resistance in winter wheat line 'ID085'. Theoretical and Applied Genetics 132: 2755-2766. DOI: 10.1007/s00122-019-03385-2.
11401.	Liu KY, Cao J, Yu KH, Liu XY, Gao YJ, Chen Q, Zhang WJ, Peng HR, Du JK, Xin MM, Hu ZR, Guo WL, Rossi V, Ni ZF, Sun QX and Yao YY 2019 Wheat *TaSPL8* modulates leaf angle through auxin and brassinosteroid signalling. Plant Physiology 181: 179-194. DOI: 10.1104/pp.19.00248.
11402.	Qiu YC, Zhou RH, Kong XY, Zhang SS and Jia JZ 2005 Microsatellite mapping of a *Triticum urartu* Tum. derived powdery mildew resistance gene transferred to common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 111: 1424-1531. DOI: 10.1007/s00122-005-0081-5.
11403.	Mago R, Zhang P, Vautrin S, Simkova H, Bansal U, Luo M-C, Rouse M, Karaoglu H, Periyannan S, Kolmer J, Jin Y, Ayliffe MA, Bariana H, Park R, McIntosh R, Dolezel J, Berges H, Spielmeyer W, Lagudah ES, Ellis JG and Dodds P 2015 The wheat *Sr50* gene reveals rich diversity at a cereal disease resistance locus. Nature Plants 1, 15186. DOI: 10.1038/nplants.2015.186.
11404.	Steuernagel B, Periyannan SK, Hernandez-Pinzon I, Witek K, Rouse MN, Yu GT, Hatta A, Ayliffe M, Bariana H, Jones JDG, Lagudah ES and Wulff BH 2016 Rapid cloning of disease resistance genes in plants using mutagenesis and sequence capture. Nature Biotechnology 34: 652-655. DOI: 10.1038/nbt.3543.
11405.	Arora S, Steuernagel B, Gaurav K, Chandramohan S, Long YM, Matny O, Johnson R, Enk J, Periyannana S, Singh N, Hatta MAM, Athiyannan N, Cheema J, Yu GT, Kangara N, Gosh S, Szabo LJ, Poland J, Bariana H, Jones JDG, Bentley AR, Ayliffe M, Olsen E, Xu SS, Steffenson BJ, Lagudah E and Wulff BBH 2019 Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nature Biotechnology 37: 139-143. DOI: 10.1038/s41587-018-0007-9.
11406.	Thambugala D, Menzies JM, Knox RE, Campbell H and McCartney C 2020 Genetic analysis of loose smut (*Ustilago tritici*) resistance in Sonop spring wheat. BMC Plant Biology 20, 314. DOI: 10.1186/s12870-020-02525-x.
11407.	Zhang L, Zhao YL, Gao LF, Zhao GY, Zhou RH and Zhang BS 2012 TaCKX6-D1, the ortholog of rice *OsCKX2*, is associated with grain weight in hexaploid wheat. New Phytologist 195: 574-584. DOI:
11408.	Lin M, Cai SB, Wang S, Liu SH and Zhang GR 2018 Genotyping-by-sequencing (GBS) identified SNP tightly linked to QTL for ore-harvest sprouting resistance. Theoretical and Applied Genetics 128: 1385-1395. DOI:10.1007/s00122-015-2513-1.

11409. Lin M, Zhang DD, Liu SB, Zhang GR, Yu JM, Fritz AK and Bai GH 2016 Genome-wide association analysis on pre-harvest sprouting resistance and grain color in U.S. winter wheat. BMC Genetics: 17, 794. DOI:10.1186/s12864-016-3148-6.

11410. Jiang H, Zhao LX, Chen XJ, Cao JJ, Wu ZY, Liu K, Zhang C, Wei WX, Xie HY, Li L, Gan YG, Lu J, Chang C, Zhang HP, Xia XC, Xiao SH and Ma CX 2018 A novel 33-bp insertion in the promoter of *TaMFT-3A* is associated with pre-harvest sprouting resistance in common wheat. Molecular Breeding 38, 69. DOI: 10.1007/s11032-018-0830-1.

11411. Kerber ER and Green GJ 1980 Suppression of stem rust resistance in the hexaploid wheat cv. Canthatch by chromosome 7DL. Canadian Journal of Botany 58: 1347-1350. DOI: 10.1139/g91-144.

11412. Hiebert CW, Moscou MJ, Hewitt T, Steuernagel B, Hernández-Pinzón I, Green P, Pujol V, Zhang P, Rouse MN, Jin Y, McIntosh RA, Upadhyaya N, Bhavani S, Vrána J, Karafiátová M, Huang L, Fetch T, Doležel J, Wulff BH, Lagudah E and Spielmeyer W 2020 Stem rust resistance in wheat is suppressed by a subunit of the Mediator complex. Nature Communications 11, 1123. DOI: 10.1038/s41467-02014937-2.

11413. Wang ZZ, Li HW, Zhang DY, Guo L, Chen JJ, Chen YX, Wu QH, Xie JZ, Xie JZ, Zhang Y, Sun QX, Dvorak J, Luo M-C and Liu ZY 2015 Genetic and physical mapping of powdery mildew resistance gene *MlHLT* in Chinese landrace Hulutou. Theoretical and Applied Genetics 128: 365-373, DOI: 10.1007/s00122-014-2436-2.

11414. Lu P, Guo L, Wang ZZ, Li BB, Li J, Li YH, Qiu D, Shi WQ, Yang LJ, Wang N, Guo GH, Xie JZ, Wu QH, Chen YX, Li MM, Zhang HZ, Dong LL, Zhang PP, Zhu KY, Yu DZ, Zhang Y, Deal KR, Huo NX, Liu CM, Luo M-C, Dvorak J, Gu YQ, Li HJ and Liu ZY 2020 A rare gain of function mutation in a wheat tandem kinase confers resistance to powdery mildew. Nature Communications 11, 680. DOI: 10.1038/s41467-020-14294-0.

11415. Cheng XJ, Xin MM, Xu RB, Chen ZY, Cai WL, Chai LL, Xu HW, Jia L, Feng ZY, Wang ZH, Peng HR, Yao YY, Hu ZR, Ni ZF and Sun QX 2020 A single amino acid substitution in STKc_GSK3 kinase conferring semisphaerical grains and its implications for the origin of *Triticum sphaerococcum* Perc. The Plant Cell 32: 923-034. DOI: 10.1105/tpc.19.00580.

11416. Guerrero-Chavez R, Glover KD, Rouse MN and Gonzalez-Hernandez JL 2015 Mapping of two loci conferring resistance to wheat stem rust pathogen races TTKSK (Ug99) and TRTTF in the elite hard red spring wheat line SD4279. Molecular Breeding 35, 8. DOI: 10.1007/s11032-015-0198-4.

11417. Kerber ER 1991 Stem-rust resistance in 'Canthatch' hexaploid wheat induced by a nonsuppressor mutation on chromosome 7DL. Genome 34: 935-939. DOI: org/10.1139/g91-144

11418. Hiebert CW, Rouse MN, Nirmala J and Fetch T 2017 Genetic mapping of stem rust resistance to *Puccinia graminis* f. sp. *tritici* race TRTTF in the Canadian wheat cultivar Harvest. Phytopathology 107: 192-197. DOI: 10.1095/PHYTO-05-16-0186-R.

11419. Babiker EM, Gordon TC, Chao S, Rouse MN, Wanyera R, Brown-Guedira and Bonman JM 2017 Molecular mapping of stem rust resistance loci effective against the Ug99 race group of the stem rust pathogen and validation of a single nucleotide polymorphism marker linked to rust resistance gene *Sr28*. Phytopathology 107: 208-215. DOI: 10.1094/PHYTO-08-160294-R.

11420. Turner MK, Jin Y, Rouse MN and Anderson JA 2016 Stem rust resistance in 'Jagger' winter wheat. Crop Science 56: 1719-1725. DOI: 10.2135/cropsci2015.11.0683.

11421. Wang Z, Li JI, Chen SX, Heng YF, Chen Z, Yang J, Zhou KJ, Pei JW, He H, Deng XW and Ma LG 2017 Poaceae-specific Ms1 encodes a phospholipid-binding protein for male

	fertility in bread wheat. Proceedings of the National Academy of Sciences of the United States of America 114: 12614-12609. DOI:10.1073/pnas.1715570114.
11422.	Tucker EJ, Baumann U, Kouidri A, Suchecki R, Baes M, Garcia M, Okada T, Dong CM, Wu YZ, Sandhu A, Singh M, Langridge P, Wolters P, Albertsen MC, Cigan AM and Whitford R 2017 Molecular identification of the wheat male fertility gene *Ms1* and its prospects for hybrid breeding. Nature Communications 8, 869. DOI: 10.1038/s41467-017-00945-2. SAME AS 11269
11423.	Li XJ, Ding WH, Chen XD, Li G, Jiang XL, Dong N, Xiao YJ, Ren CC, Gao XH and Ru ZG 2018 Genetics and mapping of the novel leaf-colour mutant gene *yglw-1* on wheat chromosome arm 2BS. Crop & Pasture Science 69: 955-965. DOI: 10.1071/CPI18321.
11424.	Ma JA, Ding PY, Liu JJ, Li T, Zou YY, Habib A, Mu Y, Tang HP, Jiang QT, Liu YX, Chen GY, Wang JR, Deng M, Qi PF, Li W, Pu ZE, Zheng YL, Wei, YM and Lan XJ 2019 Identification and validation of a major and stably expressed QTL for spikelet number per spike in bread wheat. Theoretical and Applied Genetics 132: 3155-3167. DOI: 10.1007/ss00122-019-03415-z.
11425	Zhang LJ, Geng MM, Zhang Z, Zhang Y, Yan GJ, Wen SM, Liu GR and Wang RH 2020 Molecular mapping of major QTL conferring resistance to orange wheat blossom midge (*Sitodiplosis mosellana*) in Chinese wheat varieties with selective populations. Theoretical and Applied Genetics 133: 491-502. DOI: 10.1007/s00122-019-03480-4.
11426.	Zhang RQ, Xiong CX, Mu HQ, Yao RN, Meng XR, Kong LN, Xing LP, Wu JH, Feng YG and Cao AZ 2020 *Pm67*, a new powdery mildew resistance gene transferred from *Dasypyrum villosum* chromosome 1V to common wheat (*Triticum aestivum* L.). The Crop Journal 9: 882-888. DOI: 10.1016/j.cj.2020.09.012.
11427.	Pallotta MA, Warner P, Kouidri A, Tucker EJ, Baes M, Suchecki R, Watson-Haigh N, Okada T, Garcia M, Sandhu A, Singh M, Wolters P, Albertsen MC, Cigan AM, Baumann U and Whitford R 2019 Wheat *ms5* male-sterility is induced by recessive homoeologous A and D genome non-specific lipid transfer proteins. The Plant Journal 99: 673-68. DOI: 10.1111/tpj.14350.
11428.	Sun LH, Yang WL, Li YF, Shan QQ, Ye XB, Wang DZ, Yu K, Lu WW, Xin PY, Pei Z, Guo XL, Liu DC, Sun JZ, Zhan KH, Chu JF and Zhang AM 2019 A wheat dominant dwarfing line with *Rht12*, which reduces stem cell length and affects gibberellic acid synthesis, is a terminal deletion line. The Plant Journal 97: 887-900. DOI: 10.1111/tpj.14168.
11429.	Klymiuk V, Fatiukha A, Raats D, Bocharova V, Huang L, Feng LH, Jaiwar S, Pozniak C, Coaker G, Dubcovsky J and Fahima T 2020 Three previously characterized resistances to yellow rust are encoded by a single locus *Wtk1*. Journal of Experimental Botany 71: 2561-2572. DOI: 10.1093/jxb/eraa020.
11430.	Karlstedt F, Kopahnke D, Perovic D, Jacobi A, Pillen K and Ordan F 2019 Mapping of quantitative trait loci (QTL) for resistance against *Zymoseptora tritici* in the winter spelt accession HTR11410 (*Triticum aestivum* subsp. *spelta*). Euphytica 215, 108. DOI: 10.1007/s10681-019-2432-3.
11431.	Paull JG, Nable RO and Rathjen AJ 1992 Physiological and genetic control of the tolerance of wheat to high concentrations of boron and implications for plant breeding. Plant and Soil 146: 251-260.
11432.	Pallota M, Schnurbusch T, Hayes J, Hay A, Baumann U, Langridge P and Sutton T 2014 Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. Nature 514: 88-9. DOI: 10.1038/nature13538.

11433. Shi GJ, Zheng ZC, Friesen TL, Raats D, Fahima T, Brueggeman RS, Lu SW, Trick HN, Liu ZH, Chao W, Frenkel Z, Xu SS, Rasmussen JB and Faris JD 2016 The hijacking of a receptor-driven pathway by a wheat fungal pathogen leads to disease. Science Advances 2:e1600822. DOI: 10.1126/sciadv.1600822.

11434. Saintenac C, Lee W-S, Cambon F, Rudd JJ, King RC, Marande W, Powers SJ, Berges H, Phillips AL, Uauy C, Hammond-Kosack KE, Langin T and Kanyaka K 2018 Wheat receptor-kinase-like resistance to fungal pathogen *Zymoseptoria tritici*. Nature Genetics 50: 368-374. DOI: 10.1038/s41588-018-0051-x.

11435. Liu SB, Yang XP, Zhang DD, Bai GH, Chao SM and Bockus W 2014 Genome-wide association analysis identified SNPs closely linked to a gene resistant to soil-borne wheat mosaic virus. Theoretical and Applied Genetics 127: 1039-1047. DOI: 10.1007/s00122-014-2277-z.

11436. Yu YC, Ren SZ, Zhao LF, Guo J, Bao YG, Ma YX, Wan HW, Ohm HW, Yu DZ, Li HJ and LR Kong 2018 Molecular mapping of a novel wheat powdery mildew resistance gene *Ml9214E8-9* and its application in wheat breeding by marker-assisted selection. The Crop Journal 6: 621-627. DOI: 10.1016/j.cj.2018.04.cn.

11437. Metakovsky E, Melnik V, Rodriquez-Quijana M, Upelniek V, and Carillo JL 2018 A catalog of gliadin alleles: Polymorphism of 20th century common wheat germplasm. The Crop Journal 6: 628-641. DOI: 10.1016/j.cj.2018.02.003.

11438. Zhang CZ, Huang L, Zhang HF, Hao QQ, Lyo B, Wang MN, Epstein L, Liu MA, Kou CL, Qi JA, Li MK, Gao G, Ni F, Zhang LQ, Gao M, Wang JR, Chen XM, Luo M-C, Zheng YL, Wu JJ, Liu DC and Fu DL 2019 An ancestral NB-LRR with duplicated 3'UTRs confers stripe rust resistance in wheat and barley. Nature Communications 19, 4023. DOI: 10.1038/s41467-019-11872-9.

11439. Brown JKM, Chartrain L, Lasserre-Zuber P and Saintenac C 2015 Genetics of resistance to *Zymoseptoria tritici* and applications to wheat breeding. Fungal Genetics and Biology 79: 33-41. DOI: 10.1016/j.fgb.2015.04.017.

11440. Lan CX, Zhang SA, Herrera-Foesse SA, Basney BR, Huerta-Espina J, Lagudah ES and Singh RP 2015 Identification and characterization of pleiotropic and co-located resistance loci to leaf rust and stripe rust in bread wheat cultivar Sujata. Theoretical and Applied Genetics 128: 549-561.DOI: 10.1007/s00122-015-2454-8.

11441. Ponce-Molina LJ, Huerta-Espina J, Singh RP, Basnet BR, Lagudah ES, Aguilar-Rincon VH, Alvarado G, Lobato-Ortiz R, Garcia-Zavala J and Lan CX 2018 Characterization of adult plant resistance to leaf rust and stripe rust in Indian wheat cultivar 'New Pusa 876'. Crop Science 58: 630-638. DOI: 10.2135/cropsci2017.06.0396.

11442. Pinto da Silva GB, Zanella CM, Martinelli JÁ, Chaves MS, Hiebert CW, McCallum BD and Boyd LA 2018 Quantitative trait loci conferring leaf rust resistance in hexaploid wheat. Phytopathology 108: 1344-1354. DOI: 10.1094/PHYTO-016-18-0208-RVW.

11443. Yu JS, Miao YZ, Shi ZB, Miao NN, Ding MQ, Zhang H, Jiang YR, and Rong JK 2019 Identification and mapping of a photoperiod response gene (*QPpd.zafu-4A*) on wild emmer wheat (*Triticum turgidum* L.) chromosome 4AL. Euphytica 125, 146. DOI: 10.1007/s10681-019-2469-3.

11444. Boehm JD, Zhang MY, Cai XW and Morris CF 2017 Molecular and cytogenetic characterization of the 5DS-5BS chromosome translocation conditioning soft kernel texture in durum wheat. The Plant Genome 10, 3. DOI: 10.3835/plant genome2017.04.0031.

11445. Jia MS, Xu HX, Liu C, Mao RX, Li HS, Liu JJ, Du WX, Wang WR, Zhang X, Han R, Wang XL, Wu LR, Liang X, Song JC, He HG and Ma PT 2020 Characterization of the

	powdery mildew resistance gene in the elite wheat cultivar Jimai 23 and its application in marker-assisted selection. Frontiers in Genetics 11, 241. DOI: 10.3389/fgene.2020.00241.
11446.	Jing H-C, Lovell D, Gutteridge R, Jenk D, Kornyukhin D, Mitrofanova OP, Kema GHJ and Hammond-Kosack KE 2008 Phenotypic and genetic analysis of the *Triticum monococcum – Mycosphaella graminicola* interaction. New Phytologist 179: 1121-1132. DOI: 10.1111/j.1469-8137.2008.02526.x.
11447.	Qie YM, Sheng YA, Xu HX, Jin YL, Ma FF, Li LH, Li XQ and An DG 2019 Identification of a new powdery mildew resistance gene *pmDHT* at or closely linked to the *pm5* locus in the Chinese wheat landrace Dahongtou. Plant Disease 103: 2645-2651. Doi: 10.1094/PDIS-02-0401-RE.
11448.	Riaz A, Athiyannan N, Periannan S, Afanasenko O, Mitrafanova O, Aitken EAB, Lagudah E and Hickey LT 2017 Mining Vavilov's treasure chest of wheat diversity for adult plant resistance to *Puccinia triticina*. Plant Disease 101: 317-323. DOI: 10.1094/PDIS-05-16-0614-RE.
11449.	Buerstmayer M, Matiasch L, Mascher F, Vida G, Ittu M, Robert O, Holdgate S, Flath K, Neumayer A and Buerstmayer H 2014 Mapping of quantitative adult plant field resistance to leaf rust and stripe rust in two European winter wheat populations reveals co-location of three QTL conferring resistance to both rusts. Theoretical and Applied Genetics 127: 2011-2028. DOI: 10.1007/s00122-014-2357-0.
11450.	Li Q, Huang J, Hou H, Liu P, Jing JX, Wang BT and Kang ZS 2012 Genetic and molecular mapping of stripe rust resistance gene in wheat-*Psathyrostachys huashanica* translocation line H9020-1-6-8-3. Plant Disease 96: 1482-1487. DOI: 10.1094/PDIS-03-11-0204-RE.
11451.	Wan WT, Xiao J, Li ML, Tang Xo, Wen MX, Cheruiyot AK, Li YB, and Wang HY 2020 Fine mapping of wheat powdery mildew resistance gene *Pm6* using 2B/2G homoeologous recombinants induced by the *ph1b* locus. Theoretical and Applied Genetics 133: 1265-1275. DOI: 10.1007/s00122-020-03546-8.
11452.	Xie JZ, Wang LL, Wang Y, Zhang HZ, Zhou SH, Wu QH, Chen YX, Wang ZZ, Wang GX, Zhang DY, Zhang Y, Hu TZ and Liu ZY 2017 Fine mapping of powdery mildew resistance gene *PmtM4* in wheat using comparative genomics. Journal of Integrative Agriculture 16: 540-550. DOI: 10.1016/S2095-3119(16)61377-1.
11453.	Xu XD, Li QA, Ma Zh, Fan JR and Zhou YL 2018 Molecular mapping of powdery mildew resistance gene *PmSGD* in Chinese wheat landrace Shangeda using RNA-seq with bulk segregant analysis. Molecular Breeding 38, 23. DOI: 10.1007/s11032-018-0783-4.
11454.	Li MM, Dong LL, Li BB, Wang ZZ, Xie JZ, Qiu D, Li YH, Shi WQ, Yang LJ, Wu QH, Chen YX, Lu P, Guo GH, Zhang HZ, Zhang PP, Zhu DZ, Li UYW, Zhang Y, Wang TG, Yuan CG, Liu W, Yu DZ, Luo M-C, Fahima T, Nevo E, Li HJ and Liu ZY 2020 A CNL protein in wild emmer wheat confers powdery mildew resistance. New Phytologist 228: 1027-1037. DOI: 10.1111/nph.16761.
11455.	Wang J, Li WL and Wang W 2014 Fine mapping and metabolic and physiological characterization of the glume glaucousness inhibitor locus *Iw3* derived from wild wheat. Theoretical and Applied Genetics 127: 831-841. DOI: 10.1007/s00122-014-2260-8.
11456.	Zhang ZZ, Wei WJ, Zhu HL, Challa GS, Bi CL, Trick HN and Li WL 2015 *W3* is a new wax locus that is essential for biosynthesis of beta-diketone, development of glaucousness, and reduction of cuticle permeability in common wheat. PLoS One 10(10)e0140524. DOI: 10.1371/journal.pone.0140524.

11457.	Nishijima R, Tanaka C, Yoshida K and Takumi S 2018 Genetic mapping of a novel recessive allele for non-glaucousness in wild diploid wheat *Aegilops tauschii*: implications for the evolution of common wheat. Genetica 146: 249-254.
11458.	Hen-Avivi S, Savin O, Racovita RC, Lee W-S, Adamski NM, Malitsky S, Almekias E, Levy M, Vautrin S, Berges H, Friedlander G, Kartvelishily E, Ben-Zvi G, Alkan N, Uauy C, Kanyuka K, Jetter R and Distelfeld A 2016 A metabolic gene cluster in the wheat *W1* and barley *Cer-cqu* loci determines beta-diketone biosynthesis and glaucousness. The Plant Cell 28: 1440-1460.
11459.	Huang DQ, Feurtado JA, Smith MA, Flatman LK, Koh C and Cutler AY 2017 Long noncoding miRNA gene represses wheat beta-diketone waxes. Proceedings of the National Academy of Sciences of the United States of America 114: E3149-E3158. DOI: 10.10-73/pnas.1617483114.
11460.	Bennett D, Izanloo, Edwards J, Kuchel H, Chambers K, Tester M, Reynolds M, Schnurbusch T and Langridge P 2012 Identification of novel quantitative trait loci for days to ear emergence and flag leaf glaucousness in a bread wheat (*Triticum aestivum*) population adapted to southern Australian conditions. Theoretical and Applied Genetics 124: 697-611. DOI: 10.1007/s00122-011-1740-3.
11461.	Li YH, Shi XH, Hu JH, WU PP, Qiu D, Qu YF, Xie JH, Wu QH, Zhang HJ, Yang L, Liu HW, Zhou Y, Liu ZY and Li HJ 2020 Identification of a recessive gene *PmQ* conferring resistance to powdery mildew in wheat landrace Qingxinmai using BSR-Seq analysis. Plant Disease 104: 743-751. DOI: 10.1094/PDIS-08-19-1745-RE.
11462.	Zhang JP, Wu J, Liu WH, Lu XA, Yang XM, Gao AN, Li XQ, Lu YQ and Li LH 2013 Genetic mapping of a fertile tiller inhibition gene, *ftin*, in wheat. Molecular Breeding 31: 441-449. DOI: 10.1007/s11032-012-9801-0.
11463.	Xu T, Bian NF, Wen MX, Xiao J, Yuan CX, Cao Az, Zhang SZ, Wang XE and Wang HY 2017 Characterization of a common wheat (*Triticum aestivum*) high-tillering dwarf mutant. Theoretical and Applied Genetics 130: 483-404. DOI: 10.1007/s00122-016-2826-6.
11464.	Kumar S, Bhardwaj SC, Gangwar OP, Sharma A, Qureshi N, Kumaran VV, Khan H, Prasad P, Miah H, Singh GP, Sharma K, Verma H, Forrest KL, Trethowan RM, Bariana HS and Bansal U 2021 *Lr80*: A new and widely effective source of leaf rust resistance of wheat for enhancing diversity of resistance among modern cultivars. DOI: 10.1007/s00122-020-03735-5.
11465.	Wang ZQ, Liu YX, Shi HR, Mo HJ, Wu FK, Lin Y, Gao S, Wang JR, Wei YM, Liu CJ and Zheng YL 2016 Identification and validation of low-tiller number QTL in common wheat. Theoretical and Applied Genetics 129: 603-612. DOI: 10.1007/s00122-015-2653-4.
11466.	He HG, Liu RK, Zhang HH, Du HN, Ma PT 3 and Zhu SY 2020 Characterization of *Pmxx*, a new broad-spectrum powdery mildew resistance gene on chromosome 2BS, in Greek durum wheat accession TRI 1796. Manuscript.
11467.	Wang CF, Yin GH, Xia XC, He ZH, Zhang PP, Yao ZJ, Qin JY, Li ZF and Liu DQ 2016 Molecular mapping of a new temperature-sensitive gene *LrZH22* for leaf rust resistance in Chinese wheat cultivar Zhoumai 22. Molecular Breeding 36, 18. DOI: 101007/s11032-016-043703.
11468.	Qiu LN, Wang HF, Li YH, Wang WD, Liu YJ, Mu JY, Geng MM, Guo WL, Hu ZR, Ma J, Sun QX and Xie CJ 2020 Fine mapping of the wheat leaf rust resistance gene *LrLC10* (*Lr13*) and validation of its co-segregation markers. Frontiers in Plant Science 11, 470. DOI: 10.3389/fpls.2020.00470.

11469.	Muellner AE, Eshonkulnov B, Hagenguth J, Pachler B, Michel S, Buerstmayr M, Hole D and Buerstmayr H 2020 Genetic mapping of the common and dwarf bunt resistance gene *Bt12* descending from the wheat landrace PI119333. Euphytica 216, 83. DOI: 10.1007/s10681-020-02614-w.
11470.	Inoue Y, Vy TTP, Yoshida K, Asano H, Mitsuoka C, Asuke S, Anh VL, Cumagun CJR, Chuma I, Terauchi R, Kato K, Mitchell, Valent B, Farman M and Tosa Y 2017 Evolution of the wheat blast fungus through functional losses in a host specificity determinant. Science 357: 80-83. DOI: 10.1126/science.aam9654.
11471.	Hao M, Luo JT, Zeng DY, Zhang L, Ning SZ, Yuan ZW, Yan ZH, Zhang HG, Zheng YL, Feuillet C, Choulet F, Yen Y, Zhang LQ and Liu DC 2014 *QTug.sau-3B* is a major quantitative trait locus for wheat hexaploidization. G3: 4: 1943-1953. DOI:10.1534/g3.114.013078.
11472.	Wang N, Xie YZ, Li YZ, Wu SN, Wei HS and Wang CS 2020 Molecular mapping of a novel early leaf-senescence gene *els2* in common wheat by SMP genotyping arrays. Crop & Pasture Science 71: 356-367. DOI: 10.1071/CP19435.
11473.	Mukai Y and Tsunewak K 1979 Basic studies on hybrid wheat breeding. Theoretical and Applied Genetics 54: 153-160.
11474.	Sinha P, Tomar SMS, Vinod, Singh VK and Balyan HS 2013 Genetic analysis and molecular mapping of a new fertility restorer gene *Rf8* for *Triticum timopheevi* cytoplasm in wheat (*Triticum aestivum* L.) using SSR markers. Genetica 141:431-441. DOI: 10.1007/s10709-013-9742-5.
11475.	Shahinnia F, Geyer M, Block A, Mohler M and Hartl L 2020 Identification of a new gene *Rf9* and unravelling the genetic complexity for controlling fertility restoration in hybrid wheat. BioRxiv, DOI: 10.1101/2020.06.20.162644.
11476.	Geyer M, Bund A, Albrecht T, Hartl L and Mohler V 2016 Distribution of the fertility-restoring gene *Rf3* in common and spelt wheat determined by an informative SNP marker. Molecular Breeding 36, 167. DOI: 10.1007/s11032-016-0592-6.
11477.	Tsunewaki K 2015 Fine mapping of the first multi-fertility-restoring gene, *Rfmulti*, of wheat for three *Aegilops* plasmons, using 1BS-1RS recombinant lines. Theoretical and Applied Genetics 128:723-732. DOI: 10.1007/s00122-015-2467-3.
11478.	Hohn CE and Lukaszewsk AJ 2016 Engineering the 1BS chromosome arm in wheat to remove the *Rfmulti* locus restoring male fertility in cytoplasms of *Aegilops kotschyi*, *Ae. uniaristata* and *Ae. mutica*. Theoretical and Applied Genetics 129: 1769-1774. DOI: 10.1007/s00122-016-2738-7.
11479.	Xie WL, Ben-David R, Zeng B, Distelfeld A, Roder MS, Dinoor A and Fahima T 2012 Identification and characterization of a novel powdery mildew resistance gene *PmG3M* derived from wild emmer wheat, *Triticum dicoccoides*. Theoretical and Applied Genetics 124: 911-922. DOI: 10.1007/s00122-011-1756-8.
11480	Lodhi S, Bariana H, Randhawa M, Gul A, John P and Bansal U 2019 Identification of recombinants carrying stripe rust resistance gene *Yr57* and adult plant stem rust resistance gene *Sr2* through marker-assisted selection. Plant Breeding 138: 148-153. DOI: 10.1111/pbr.12674.
11481.	Liu YA, Zhang QJ, Salsman E, Fiedler JD, Hegstad JB, Liu ZH, Faris JD, Xu SS and Li XH 2020 QTL mapping of resistance to tan spot induced by race 2 of *Pyrenophora tritici-repentis* in tetraploid wheat. Theoretical and Applied Genetics 133: 433-442. DOI: 10.10087/s00122-019-03474-2.

11482.	Würschum T, Langer SM, Longin CFH, Tucker MR and·Leiser WL 2020 Refining the genetic architecture of flag leaf glaucousness in wheat. Theoretical and Applied Genetics 133: 981-991. DOI: 10.1007/s00122-019-03522-x.
11483.	Wang HW, Sun SL, Ge WY, Zhao LF, Hou BQ, Wang K, Lyu ZF, Chen LY, Xu SS, Guo J, Li M, Su PS, Li XF, Wang GP, Bo CY, Fang XJ, Zhuang WW, Cheng XX, Wu JW, Dong LH, Chen WY, Li W, Xiao GL, ZhaoJX, Hao YC, Xu Y, Gao Y, Liu WJ, Liu YH, Yin HY, Li JZ, Li X, Zhao Y, Wang XQ, Ni F, Ma X, Li AF, Xu SS, Bai GH, Nevo E, Gao CX, Ohm H and Kong LR 2020 Horizontal gene transfer of *Fhb7* from fungus underlies Fusarium head blight resistance in wheat. Science 368, eaba5435. DOI: 10.1126/science.368.6487.122.
11484.	Nsabiyera V, Baranwal D, Qureshi N, Kay P, Forrest K, Valarik M, Dolezel J, Hayden MJ, Bariana HS and Bansal UK 2020 Fine mapping of *Lr49* using 90K NNP chip array and flow-sorted chromosome sequencing in wheat. Frontiers in Plant Science 19, 1787. DOI: 10.3389/fpls.2019.01787.
11485.	Zurn JD, Newcomb M, Rouse MN, Jin Y, Chao SM, Sthapit J, See DR, Wanyera R, Njau P, Bonman JM, Brueggeman and Acevedo M 2014 High-density mapping of a resistance gene to Ug99 from the Iranian landrace PI 626573. Molecular Breeding 34: 871-0881. DOI: 10.1007/s11032-014-0081-8.
11486.	Wessels E, Prins R, Boshoff WHP, Zurn JD, Acevedo M and Pretorius ZA 2019 Mapping a resistance gene to *Puccinia graminis* f. sp. *tritici* in the bread wheat cultivar 'Matlabas'. Plant Disease 102: 2327-2344.
11487.	Steiner B, Buerstmayr M, Wagner C, Danler A, Eshonkulov B, Ehn M and Buerstmayr H 2019 Fine-mapping of the Fusarium head blight resistance QTL *Qfhs.ifa-5A* identifies two QTL associated with anther extrusion. Theoretical and Applied Genetics 132: 2039-2053. DOI: 10.1007/s00122-019-03336-x.
11488.	Zhao RH, Wang HY, Xiao J, Bie TD, Cheng SH, Jia Q, Yuan CX, Zhang RQ, Cao AH, Chen PD and Wang XE 2013 Induction of 4VS chromosome translocations and mapping of the wheat yellow mosaic virus resistance gene from *Haynaldia villosa* 2013 Theoretical and Applied Genetics 126: 2921-2930. DOI: 10.1007/s00122-013-2181-y.
11489.	Ibba MI, Zhang MY, Cai XW and Morris CF 2019 Identification of a conserved *ph1b*-mediated 5DS-5BS crossing over site in soft-kernel durum wheat (*Triticum turgidum* subsp. *durum*) lines. Euphytica 215, 200. DOI: 10.1007/s10681-019-2518-y.
11490.	Hernández-Espinosa N, Payne T, Huerta-Espino J, Cervantes F, Gonzalez-Santoyo H, Ammar K and Guzmán C 2019 Preliminary characterization for grain quality traits and high and low molecular weight glutenins subunits composition of durum wheat landraces from Iran and Mexico. Journal of Cereal Science 88: 47-56. DOI:10.1016/j.jcs.2019.05.007.
11491.	Alvarez JB and Guzmán C 2019 Recovery of wheat heritage for traditional food: genetic variation for high molecular weight glutenin subunits in neglected/underutilized wheat. Agronomy 9: 755. DOI:10.3390/agronomy9110755.
11492.	Ruiz M, Bernal G and Giraldo P 2018 An update of low molecular weight glutenin subunits in durum wheat relevant to breeding for quality. Journal of Cereal Science 83: 236–244. DOI:10.1016/j.jcs.2018.09.005.
11493.	Chegdali Y, Ouabbou H, Essamadi A, Cervantes F, Ibba MI and Guzmán C 2020 Assessment of the glutenin subunits diversity in a durum wheat (*T. turgidum* ssp. *durum*) collection from Morocco. Agronomy 10: 957. DOI:10.3390/agronomy10070957.

11494.	Wang Hu, Zou SH, Li YW, Lin FY and Dingzhong Tang 2020 An ankyrin-repeat and WRKY-domain-containing immune receptor confers stripe rust resistance in wheat. Nature Communications 11:1353. DOI: 10.1038/s41467-020-15139-6.
11495.	Shaw LM, Li C, Woods DP, Alvarez MA, Lin H, Lau MY, Chen A and Dubcovsky J 2020 Epistatic interactions between PHOTOPERIOD-1, CONSTANS 1 and CONSTANS 2 modulate the photoperiodic response in wheat. PLoS Genetics. In press. bioRxiv preprint DOI: 10.1101/2020.04.29.067959.
11496.	Deleted: Duplicate of 11383.
11497.	Zhang Y, Schonhofen A, Zhang W, Hegarty J, Carter C, Vang T, Laudencia-Chingcuanco D and Dubcovsky J 2020 Contributions of individual and combined *Glu-B1x* and *Glu-B1y* high-molecular-weight glutenin subunits to semolina functionality and pasta quality. Journal of Cereal Science 93, 102943. DOI: 10.1016/j.jcs.2020.102943.
11498.	Kolmer JA 2020 Personal communication.
11499.	Piredi S-M, Somo M, Poudel RS, Cai XW, McCallum B, Saville B, Fetch T, Chao SM and Marais F 2015 Characterization of recombinants of the *Aegilops preregrina*-derived *Lr59* translocation of common wheat. Theoretical and Applied Genetics 124: 2403-2413. DOI: 10.1007s00122-015-2594-x.
11500.	Bayles R, O'Sullivan D, Lea V, Freeman S, Budge G, Walsh K, and Henry C 2007 Controlling soil-borne cereal mosaic virus in the UK by developing resistant cultivars. Progress Report no 418 to the Home-Grown Cereals Authority, UK.
11501.	Linsell KJ, Rahman MS, Taylor JD, Davey RS, Gogel BJ, Wallwork H, Forrest KL, Hayden MJ, Taylor SP and Aldach KH 2014 QTL for resistance to root lesion nematode (*Pratylenchus thornei*) from a synthetic hexaploid wheat source. Theoretical and Applied Genetics127: 1409-1421. DOI: 10.1007/s00122-014-2308-9.
11502.	Rahman MS, Linsell KJ, Taylor JD, Hayden MJ, Collins NC and Oldach KH 2020 Fine mapping of root lesion nematode (*Pratylenchus thornei*) resistance loci chromosome 6D and 2B of wheat. Theoretical and Applied Genetics 133: 635-652. DOI: 10.1007/s00122-019-03495-x.
11503.	Chen F, Jia HY, Zhang XJ, Qiao LY, Li X, Zheng J, Guo HJ, Powers C, Yan LL and Chang ZJ 2019. Positional cloning of *PmCH1357* reveals the origin and allelic variation of the *Pm2* gene for powdery mildew resistance in wheat The Crop Journal 7: 771-783. DOI: 10.1016/j.cj.2019.08.004.
11504.	Asuke S, Umehara Y, Inoue Y, Vy TTP, Iwakawa M, Matsuoka Y, Kato K and Tosa Y 2021 Origin and dynamics of *Rwt6*, a wheat gene for resistance to non-adapted pathotypes of *Pyricularia oryzae*. Phytopathology. 10.1094/PHYTO-02-21-0080-R.
11505.	Ansari MJ, Al-Ghamdi A, Usmani S, Jumar R, Naru A, Singh K, Dhaliwal HS 2013 Characterization and gene mapping of a brittle culm mutant of diploid wheat (*Triticum monococcum* L.) with irregular xylem vessels development. Acta Physiologiae Plantarum 35: 2407-2419. DOI 10.1007/s11738-013-1275-0.
11506.	Sapkota S, Hao HF, Johnson J, Lopez B, Bland D, Chen ZB, Sutton S, Buck J, Youmans J and Mergoum M 2019 Genetic mapping of a major gene for leaf rust resistance in soft red winter wheat cultivar AGS 2000 . Molecular Breeding 39, 8. DOI, 10.1007/s11032-018-0909-8.
11507.	Sapkota S, Mergoum M, Kumay A, Fiedler JD, Johnson J, Bland D, Lopez b, Sutton S, Ghirmire B, Buck J, Chen ZB and Harrison S 2020 A novel adult plant leaf rust resistance gene *Lr2K38* mapped on wheat chromosome 1AL. The Plant Genome 13:e20061. DOI: 10.1002/tpg2.20061.

11508. Wu PP, Yang L, Guo GH, Qiu JH, Li YH, Shi XH, Zhang HJ, Liu HW, Zhao JT, Sun GH, Liu ZY and Li HJ 2021 Molecular mapping and identification of a candidate gene for new locus *Hg2* conferring hairy glume in wheat. Plant Science 307, 110879. DOI: 10.1016/j.plantsci.2021.110879.

11509. Hewitt, T, Muller MC, Molnar I, Mascher M, Holusova K, Simkova H, Kunz L, Zhang JP, Li JB, Bhatt D, Sharma R, Schudel S, Yu GT, Steurnagel B, Periyannan S, Wulff B, Ayliffe M, McIntosh R, Keller B, Lagudah E and Zhang P 2021 A highly differentiated region of wheat chromosome 7AL encodes a *Pm1a* immune receptor that recognizes its corresponding *AvrPm1a* effector from *Blumeria graminis*. New Phytologist 229: 2812-2826. DOI: 10.1111/nph.17075

11510. Bassi FM, Brahmi H, Sabraoui A, Amri A, Nsarellah N, Nachit MA, Al-Abdallat A, Chen MS, Lazraq A and El Bouhssini M 2019 Genetic identification of loci for Hessian fly resistance in durum wheat. Molecular Breeding 39, 24. DOI: 10.1007/s11032-019-0927-1.

11511. Liu GX, Liu XM, Xu YF, Bernardo A, Chen MS, Li YG, Niu FA, Zhao LF and Bai GH 2020 Reassigning Hessian fly resistance genes *H7* and *H8* to chromosomes 6A and 2B of wheat cultivar ‘Seneca’ using genotype-by-sequencing. Crop Science 60: 1488-1498. DOI: 10.1002/csc2.20148.

11512. Zhao LF, Abdelsalem NR, Xu YF, Chen M-S, Feng Y, Kong LR and Bai GH 2020 Identification of two novel Hessian fly resistance genes *H35* and *H36* in a hard red winter wheat line SD06165. Theoretical and Applied Genetics 133: 2343-1253. DOI: 10.1007/s00122-020-03602-3.

11513. Winn ZJ, Acharya R, Merrill K, Lyerly J, Brown-Guedira G, Cambron S, Harrison SH, Reisig D and Murphy JP 2021 Mapping of a novel major effect Hessian fly field partial-resistance locus in southern soft red winter wheat line LA03136E71. Theoretical and Applied Genetics. DOI: 10.1007/s00122-021-02936-6.

11514. Luo J, Rouse MN, Hua L, Li HN, Li BS, Li TY, Zhang WJ, Gao CX, Wang YP, Dubcovsky J and Chen SS 2022. Identification and characterization of *Sr22b*, a new allele of the wheat stem rust resistance gene *Sr22* effective against the Ug99 race group. Plant Biotechnology Journal 20: 554-563. DOI: 10.1111/pbi.13737.

11515. Lukaszewski AJ, Porter DR, Antonelli EF and Dubcovsky J 2000 Registration of URCBW98-1 and ICRBW98-2 wheat germplasms with leaf rust and greenbug resistance genes. Crop Science 40: 590. DOI: 10.2135/cropsci2000.0022rgp.

11516. Xu XY, Li GQ, Bai GH, Bernardo A, Carver BF and Amand PS 2010 Development of KASP markers for wheat greenbug resistance gene *Gb5*. Crop Science 61: 490-499. DOI: 10.1002/csc2.20339.

11517. Si YWQ, Zheng SS, Niu JQ, Tian SQ, Shi XL, He YL, Li YW and Ling H-Q 2021 Fine mapping of hybrid necrosis gene *Ne1* in common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 134: 2603-2611. DOI: 10.1007/s00122-021-03846-7.

11518. Li N, Tan QY, Ding JH, Pan XL and Ma ZQ 2021 Fine mapping of *Ne1*, the hybrid necrosis gene complementary to *Ne2* in common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 134: 2813-1821. DOI: 10.1007/s00122-021-03860.

11519. Millet E, Steffenson BJ, Prins R, Sela H, Przewieslik-Allen AM and Pretorius ZA 2017 Genome targeted introgression of resistance to African stem rust from *Aegilops sharonensis* into bread wheat. Plant Genome 10: 1–11. DOI: 10.3835/plantgenome2017.07.0061

11520. Milec Z, Tomkova L, Sumikova T and Pankova K 2012 A new multiplex PCR test for determination of *Vrn-B1* alleles in bread wheat (*Triticum aestivum*). Molecular Breeding 30: 317-323. DOI: 10.1007/s11032-011-9621-7.

11521.	Shcherban AB, Efremova TT and Salina EA 2012 Identification of a new *Vrn-B1* allele using two near-isogenic wheat lines with difference in heading time. Molecular Breeding 29, 675-685. DOI: 10.1007/S11032-011-9581-y.
11522.	Zhang B, Wang XG, Wang XL, Wang, Ma L, Wang ZH and Zhang XK 2018 Molecular characterization of a novel vernalization allele *Vrn-B1d* and its effect on heading time in Chinese wheat (*Triticum aestivum*) landrace Hongchunmai. Molecular Breeding 38, 127. DOI: 10.1007/211032-018-0870-6.
11523.	Milec Z 2021 Personal communication.
11524.	Yu GT, Matny O, Champouret N, Steuernagel S, Moscou MJ, Hernández-Pinzón I, Green P, Hayta S, Smedley M, Harwood W, Kangara N, Yue YZ, Gardener C, Banfield MJ, Olivera PD, Welchin C, Simmons J, Millet E, Minz-Dub A, Ronen M, Avni R, Sharon A, Patpour M, F. Justesen AF, Jayakodi M, Himmelbach A, Stein N, Wu ZY, Poland J, Ens J, Pozniak C, Karafiátová M, Molnár I, Doležel J, Ward ER, Reuber TL, Jones JDG, Mascher M, Steffenson BJ and Wulff BBH 2022 *Aegilops sharonensis* genome-assisted identification of stem rust resistance gene *Sr62*. Nature Communications 13,1607. DOI: 1-.1038/s41467-022-29132-8.
11525.	Sanchez-Martín J, Widrig V, Herren G, Wicker T, Zbinden H, Gronnier J, Sporri L, Praz CR, Heuberger M, Kolodziej MC, Isaksson J, Steuernagel B, Karafiatova M, Dolezel J, Zipfel C and Keller B 2021 Wheat *Pm4* resistance to powdery mildew is controlled by alternative splice variants encoding chimeric proteins. Nature Plants 7: 327–341. DOI: 10.1038/s41477-021-00869-2.
11526.	Svacina V, Karafiatova M, Malurova M, Serra H, Vitek D, Endo TR, Sourdille P and Bartos J 2020 Development of deletion lines for chromosome 3D of bread wheat. Frontiers in Plant Science 10, 1776. 10.3389/fpls.2019.01756.
11527.	Serra H, Svacina R, Baumann U, Whitford R, Sutton T, Bartos J, and Sourdille P 2021 *Ph2* encodes the mismatch repair protein MSH7-3D that inhibits wheat homoeologous recombination. Nature Communications 12, 803. DOI: 10.1038/s41467-021-21127-1.
11528.	Zhang JP, Hewitt TC, Boshoff WHP, Dundas I, Upadhyaya N, Li JB, Patpour M, Chandramohan S, Pretorius ZA, Hovmoller M, Schnippenkoetter W, Park RF, Mago R, Periyannan S, Bhatt D, Hoxha S, Chakraborty S, Luo M, Dodds P, Steuernagel B, Wulff BBH, Ayliffe M, McIntosh RA, Zhang P and Lagudah ES 2021 A recombined *Sr26* and *Sr61* disease resistance gene stack in wheat encodes unrelated NLR genes. Nature Communications 12, 3378. DOI: 10.1038/s41467-021-23738-0.
11529.	Qiu LN, Wang HF, Li YH, Wang WD, Liu YJ, Mu JY, Geng MM, Guo WL, Hu ZR, Ma J, Sun QX and Xie CJ 2020 Fine mapping of the wheat leaf rust resistance gene *LrLC10* (*Lr13*) and validation of its co-segregation markers. Frontiers in Plant Science 11, 470. DOI: 10.3389/fpls.2020.00470.
11530.	Hewitt T, Zhang JP, Li H, Upadhyaya N, Li JB, Park RF, Hoxha S, McIntosh R, Lagudah E and Zhang P 2021 Wheat leaf rust resistance gene *Lr13* is a specific *Ne2* allele for hybrid necrosis. Molecular Plant 14: 1025-1028. DOI: 10.1016/j.molp2121.05.010.
11531.	Yan XC, Li MM, Zhang PP, Yin GH, Zhang HZ, Gebrewalid TW, Zhang JP, Dong LL, Liu DQ, Liu ZY and Li ZF 2021 High-temperature wheat leaf rust resistance gene *Lr13* exhibits pleiotropic effects on hybrid necrosis. Molecular Plant 14: 1029-1032. DOI: 10.1016/j.molp.2021.05.009.
11532.	Si YQ, Zheng SS, Niu JQ, Tian SQ, Gu MJ, Lu Q, He YL, Zhang J, Shi XL, Li YW and Ling H-Q 2021 *Ne2*, a typical CC-NBS-LRR-type gene, is responsible for hybrid necrosis in wheat. New Phytologist. DOI: 10.1111/nph.17575.

11533.	Xie JZ, Guo GG, Wang Y, Hu AZ, Li JT, Qiu D, Li JH, Wu QH, Lu P, Chen YX, Dong LL, Li MM, Zhang HZ, Zhang PP, Zhu KY, Li BB, Deal KR, Huo NX, Zhang Y, Luo M-C, Liu SZ, Gu YQ, Li HJ and Liu ZY 2020 A rare single nucleotide variant in *pm5e* confers powdery mildew resistance in common wheat. New Phytologist 228: 1011-1026. DOI: 10.111/nph.16762.
11534.	Li QQ, Zhao QS, Jiang HB, Geng JF, Liu LX, Zhang XY, Xie YZ and Wang CS 2017 Characteristics and genetic analysis of wheat mutant I30 with white stripe pattern. Journal of Triticeae Crops 37: 871-879. DOI: 10.7606/j.issn.1009-1041.2017.07.03. In Chinese with English summary.
11535.	Li HJ, Jiao ZX, Ni YJ, Jiang YM, Li JC, Pan C, Zhang J, Sun YL, An JH, Liu HJ, Li QY and Niu JS 2021 Heredity and gene mapping of a novel *white stripe leaf* mutant in wheat. Journal of Integrative Agriculture 20: 1743-1752. DOI: 10.1016/S2095-3119(20)63345-7.
11536.	Zhang Q,Wei WX, Zuansun XX, Zhang SN, Wang C, Liu NN, Qiu LN, Wang WD, Guo WL, Ma J, Peng HR, Hu ZR, Sun QX and Xie CJ 2012 Fine mapping of the leaf rust resistant gene *Lr65* in spelt wheat ‘Altgold’. Frontiers in Plant Science 12, 666921. DOI: 10.3389/fpls.2021.666921.
11537.	Li N, Tan QY, Ding JH, Pan XL and Ma ZQ 2021 Fine mapping of *Ne1*, the hybrid necrosis gene complementary to *Ne2* in common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 134: 2813-2821. DOI: 10.1007/s00122-021-03860-9.
11538.	Abrouk M, Athiyannan N, Muller T, Pailles Y, Stritt C, Roulin AC, Chu CG, Liu SY, Morita T, Handa H, Poland J, Keller B and Krattinger SG 2012 Population genomics and haplotype analysis in spelt and bread wheat identifies a gene regulating glume color. Communications Biology 4, 375. DOI: 10.1038/s42003-021-01908-6.
11539.	Aguiriano E, Ruiz M, Fité R and Carrillo JM 2008 Genetic variation for glutenin and gliadins associated with quality in durum wheat (*Triticum turgidum* L. ssp. *turgidum*) landraces from Spain. Spanish Journal of Agricultural Research 6: 599-609. DOI: 10.5424/sjar/2008064-353.
11540.	Chacón EA, Vázquez FJ, Giraldo P, Carrillo JM, Benavente E and Rodríguez-Quijano M 2020 Allelic variation for prolamins in Spanish durum wheat landraces and its relationship with quality traits. Agronomy 10, 136. DOI: 10.3390/agronomy10010136.
11541.	Fahima T 2021 Personal communication.
11542.	Li HY, Baraina HS, Dingh D, Zhang LQ, Dillon S, Whan A, Bansal U and Ayliffe M 2020 A durum wheat adult plant resistance QTL and its relationship with the bread wheat *Yr80* locus. Theoretical and Applied Genetics 133: 3049-3066. DOI: 10.1008/s00172-020-03643-5.
11543.	Tariq M, Mirza JI, Hussain S, Qureshi N, Forrest K, Bariana H and Bansal U 2021 Molecular mapping of all stage stripe rust resistance gene *YrPak* in wheat landrace PI 388231. Euphytica 217, 121. DOI: 10/s10681-021-02856-2.
11544.	Xu XY, Li GQ, Bai GH, Bernardo A, Carver BF, St Amand P and Bian RL 2021 Characterization of an incomplete leaf rust resistance gene on chromosome 1RS and development of KASP markers for *Lr47* in wheat. Phytopathology 111: 649-658. DOI: 10.1094/PHYTO-07-20-02-308-R.
11545.	Gebrewahid TW, Zhou Y, Zhang PP, Ren Y, Gao P, Xia XC, He ZH, Li ZF, and Liu DQ 2020 Mapping of stripe rust and leaf rust quantitative trait loci in the Chinese spring wheat line Mianyang351-15. Phytopathology 111: 1074-1081. DOI: 10.1094/PHYTO-08-19-0316-R.

11546.	Shorinola O, Balcarkova B, Hyles J, Tibbits JFG, Hayden MJ, Holusova K, Valarik M, Distelfeld A, Torada A, Barrero JM and Uauy C 2017 Haplotype analysis of the pre-harvest sprouting resistance locus *Phs-A1* reveals a causal role of *TaMKK3-A* in global germplasm. Frontiers in Plant Science 8, 1555. DOI: 10.3389/fpls.2017.01555.
11547.	Mares D and Himi E 2021 The role of *TaMYB10-A1* of wheat (*Triticum aestivum* L) in determining grain coat color and dormancy phenotype. Euphytica 217, 89. DOI: 10.1007/s10681-021-02826-8.
11548.	Yang X, Pan YB, Singh PK, He XY, Ren Y, Zhao L, Zhang N, Cheng SH, and Chen F 2019 Investigation and genome-wide association study for Fusarium crown rot resistance in Chinese common wheat. BMC Plant Biology 19, 153. DOI: 10.1186/s12870-019-17858-2.
11549.	Kolodziej MC, Singla J, Sanchez-Martin J, Zbinden H, Simkova H, Karafiatova M, Dolezel J, Gronnier J, Poretti M, Glauser G, Zhu WS, Koster P, Zipfel C, Wicker T, Krattinger SG and Keller B 2021 A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. Nature Communications 12, 956. DOI: 10.1038/s41467-020-20777-x.
11550.	Zhao F, Li Y, Yang B, Yuan H, Jin C, Zhou L, Pei H, Zhao L, Li Y, Zhou Y, Xie J and Shen Q 2020 Powdery mildew disease resistance and marker-assisted screening at the *Pm60* locus in wild diploid wheat *Triticun urartu*. The Crop Journal 8: 252-259. DOI: doi.org/10.1016/j.cj.2019.09.007
11551.	Li YH, Wei Z-Z, Fatiukha A, Jaiwar S, Wang HC, Hasan S, Liu ZY, Sela H, Krugman T and Fahima F 2021 *TdPm60* identified in wild emmer wheat is an ortholog of *Pm60* and constitutes a strong candidate for *PmG16* powdery mildew resistance. Theoretical and Applied Genetics 134: 2777-2793. DOI: 10.1007/s0122-021-03858-3.
11552.	Bansal M, Adamski NM, Toor PI, Kaur S, Molnar I, Holusova K, Vrana J, Dolezel J, Valarik M, Uauy C and Chhuneja P 2020 *Aegilops umbellulata* introgression carrying leaf rust and stripe rust resistance genes *Lr76* and *Yr70* located to 9.47-Mb region on 5DS telomeric end through a combination of chromosome sorting and sequencing. Theoretical and Applied Genetics 133: 903-915. DOI: 10.1007/s00122-019-03514-x.
11553.	Steadman J, Schulden T, Kalia B, Koo D-H, Gill BS, Bowden R, Yadav IS, Chhuneja P, Erwin J, Tiwari V and Rawat N 2021 An approach for high-resolution genetic mapping of distant wild relatives of bread wheat: example of fine mapping of *Lr57* and *Yr40* genes. Theoretical and Applied Genetics 134: 2671-2686. DOI: 10.1007/s0122-021-03851-w.
11554.	Mago R, Chen RH, Xia XD, Whan A, Forrest K, Basnet BR, Perera G, Chandramohan S, Randhawa M, Upadhyaya N, Hayden M, Bansal U, Huerta-Espino J, Singh RP, Bariana H and Lagudah E (2021) Adult plant stem rust resistance in durum wheat Glossy Huguenot: mapping, marker development and validation. Theoretical and Applied Genetics 135:1541-1550. DOI: 10.1007/s00122-022-04052-9.
11555.	Liu SJ, Huang S, Zeng QD, Wang XT, Yu R, Wang QL, Singh RP, Bhavani S, Kang ZS, Wu JH and Han DJ 2021 Refined mapping of stripe rust resistance gene *YrP10090* with a desirable haplotype for wheat improvement on chromosome 6A. Theoretical and Applied Genetics 134: 2005-2021. DOI: 10.1007/s0021-03801-6.
11556.	Lu N, Lu MX, Liu P, Xu HX, Qiu XL, Hu SS, Wu YA, Bai SL, Wu JH and Xue SL 2020 Fine mapping a broad spectrum powdery mildew resistance gene in Chines landrace Datoumai, *PmDTM*, and its relationship with *Pm24*. Plant Disease 104: 1709-1714. DOI: 10.1094/PDIS-11-19-2431-RE
11557.	Zhou XL, Zhong X, Roter J, Li X, Yao QA, Yan JH, Yang SZ, Guo QY, Distelfeld A, Selo H and Kong ZS 2020 Genome wide mapping of loci for adult-plant resistance to stripe rust

	in durum wheat Svevo using the 90-K SNP array Plant Disease 105: 879-888. DOI: 10.1094/PDIS-09-20-1933-RE.
11558.	Yang MY, Li GR, Wan HS, Li LP, Li J, Yang WY, Pu ZJ, Yang ZY and Yang EN 2019 Identification of QTLs for stripe rust resistance in a recombinant inbred line population. International Journal of Molecular Science 20, 3410. DOI: 10.3390/ijms20143410.
11559.	Zeng QD, Wu JH, Liu SJ, Chen XM. Yuan FP, Su PP, Wang QL, Huang SO, Mu JM, Han DJ and Kang ZS 2019 Genome-wide mapping for stripe rust resistance loci in common wheat cultivar Qinnong 142. Plant Disease 103: 439-447. DOI: 10.1094/PDOS-05-18-0846-RE.
11560.	Liu L, Wang MN, Feng JY, See DR and Chen XM 2019 Whole-genome mapping of stripe rust resistance quantitative trait loci and race-specificity related to resistance reduction in winter wheat cultivar Eltan. Phytopathology 109: 1226-1235. DOI: 10.1094/PHYTO-10-0385-R.
11561.	Upadhyaya NM, Mago R, Panwar V, Hewitt T, Luo M, Chen J, Sperschneider J, Nguyen-Phuc H, Wang AH, Ortiz D, Hac L, Bhatt D, Li F, Zhang JP, Ayliffe M, Figuerosa M, Kanyuka K, Ellis JG and Dodds P 2021 Genomics accelerated isolation of a new stem rust avirulence gene-wheat resistance gene pair. Nature Plants 7: 1220-1228. DOI: 10.1038/s41477-021-00971-5.
11562.	Wu Y, Wang YQ, Yao FJ, Long L, Li J, Pu ZE, Li W, Jiang QT, Wang JR, Wei YM, Ma JA, Kang HY, Qi PF, Dai SF, Deng M, Zheng YL, Jiang YF and Chen GY 2021 Molecular mapping of a novel quantitative trait locus conferring adult plant resistance to stripe rust in Chinese wheat landrace Guantoumai. Plant Disease 105: 1919-1925. DOI: 10.1094/PDIS-07-20-1544-RE.
11563.	Wang Y, Xie JZ, Zhang HZ, Guo BM, Ning SZ, Chen YX, Lu P, Wu QH, Li MM, Zhang DY, Guo GH, Zhang Y, Liu DC, Zou SK, Tang JW, Zhou G, Wang XC, Li J, Yang WY, Cao TJ, Yin GH and Liu ZY (2017) Mapping stripe rust resistance gene *YrZH22* in Chinese wheat cultivar Zhoumai 22 by bulked segregant RNA-Seq (BSR-Seq) and comparative genomics analyses. Theoretical and Applied Genetics 130: 2191-2201. DOI: 10.1007/s00122-017-2950-0.
11564.	Duplicate reference- deleted.
11565.	Xue SL, Lu MX, Hu SS, Xu HX, Ma YY, Lu N, Bai SL, Gu AY, Wan HS and Li SP 2021 Characterization of *PmHHXM*, a new broad-spectrum powdery mildew resistance gene in Chinese wheat landrace Honghuaxiaomai. Plant Disease 105: 2089-2096. DOI: 10.1094/PDIS-10-20-2296-RE.
11566.	Hu YL, Huang XH, Wang F, He Y, Feng LH, Jiang B, Hao M, Ning SZ, Yuan ZW, Wu JJ, Zhang LQ, Wu BH, Liu DC and Huang L 2021 Development and validation of gene-specific KASP markers for *YrAS2388* conferring stripe rust resistance in wheat. Euphytica 217, 206. DOI: 10.1007/s10681-021-02937-2.
11567.	Bokore FE, Knox RE, Hiebert CW, Cuthbert RD, DePauw RM, Meyer B, N'Diaye A, Pozniak CJ and McCallum BD 2022 A combination of leaf rust resistance genes, including *Lr34* and *Lr46*, is the key to the durable resistance of the Canadian wheat cultivar, Carberry. Frontiers in Plant Science 12, 775383. DOI: 10.3389/fpls.2021.775383.
11568.	ElDoliefy AEA, Kumar A, Anderson JA, Glover KD, Mamidi S, Elias EM, Seetan R, Alamri MS, Kianian SF, Sapkota S, Green A and Mergoum M 2020 Genetic dissection of Fusarium head blight resistance in spring wheat cv. Glenn. Euphytica 216, 71. DOI: 10.1007/s10681-020-02610-0.

11569.	Vetch JM, Stougaard RN, MartinJM, and Giroux MJ 2019 Review: Revealing the genetic mechanisms of pre-harvest sprouting in hexaploid wheat (*Triticum aestivum* L.). Plant Science 281: 180-185. DOI: 10.1016/j.plantsci.2019.01.004.
11570.	Huang DQ, Zheng QA, Melchkart T , Bekkaoui Y, Konkin DJF, Kagale S , Martucci M, You FM , Clarke M, Adamski NM , Chinoy C, Steed A, McCartney CA , Cutler AJ, Nicholson P and Feurtado JA 2019 Dominant inhibition of awn development by a putative zinc-finger transcriptional repressor expressed at the *B1* locus in wheat. New Phytologist 225: 340-355. DOI: doi: 10.1111/nph.16154.
11571.	DeWitt N, Guedira M, Lauer E, Sarinelli M, Tyagi P, Fu D, Hao Q, Murphy JP, Marshall D, Akhunova A, Jordan K, Akhunov E and Brown-Guedira G 2020. Sequence based mapping identifies a candidate transcription repressor underlying awn suppression at the *B1* locus in wheat. New Phytologist 225: 326-339. doi: 10.1111/nph.16152.
11572.	Qin Yao, Ronghua Zhou, Tihua Fu, Weiren Wu, Zhendong Zhu, Aili Li and Jizeng Jia 2009 Characterization and mapping of complementary lesion-mimic genes *lm1* and *lm2* in common wheat. Theoretical and Applied Genetics 119: 1005-1012. DOI 10.1007/s00122-009-1104-4.
11573.	Wang F, Wu W, Wang D, Yang W, Sun J, Liu D and Zhang AM 2016 Characterization and genetic analysis of a novel light-dependent lesion mimic mutant, lm3, showing adult-plant resistance to powdery mildew in common wheat. PLoS ONE 11: e0155358. DOI: 10.1371/journal.pone.0155358.
11574.	Wang ZQ, Liu YX, Shi HR, Mo HJ, Wu FK, Lin Y, Gao S, Wang JR, Wei YM, Liu CJ and Zheng YL 2016 Identification and validation of novel low-tiller number QTL in common wheat. Theoretical and Applied Genetics 129: 603-612. DOI 10.1007/s00122-015-2652-4.
11575.	Wang ZQ, Wu FK, Chen XD, Zhou WL, Shi HR, Lin Y, Hou S, Yu SF, Zhou H, Li CX and Liu YX 2022 Fine mapping of the tiller inhibition gene *TIN4* contributing to ideal plant architecture in common wheat . Theoretical and Applied Genetics 135: 527-535. DOI: 10.1007/s00122-021-03981-1.
11576.	Li C, Liu H, Wang JA, Pan Q, Wang Y, Wu KY, Jia PY, Mu Y, Tang HP, Xu QA, Jiang QT, Liu YX, Qi PF, Zhang XJ, Huang L, Chen GY, Wang JR, Wei · Zheng YL, Gou LL, Yao QF, Lan XJ and Ma JA 2022 Characterization and fine mapping of a lesion mimic mutant (*Lm5*) with enhanced stripe rust and powdery mildew resistance in bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 135: 421-438. DOI: 10.1007/s00122-021-03973-1
11577.	Liu R, Lu J, Zheng SG, Du M, Zhang CH, Wang MX, Li YF, Xing JY, Wu Y and Zhang L 2021 Molecular mapping of a novel lesion mimic gene (*lm4*) associated with enhanced resistance to stripe rust in bread wheat. BMC Genomic Data 221, 1. DOI: 10.1186/s12863-021-00963-6.
11578.	Xing LO, Yuan L, Lv ZS, Wang QA, Yin CH, Huang ZP, Liu JQ, Cao SQ, Zhang RQ, Chen PD, Karafiatova M, Vrana J, Bartos J, Dolezel J and Cao AZ 2021 Long-range assembly of sequences helps to unravel the genome structure and small variation of the wheat–*Haynaldia villosa* translocated chromosome 6VS.6AL. Plant Biotechnology Journal 19: 1567–1578. DOI: 10.1111/pbi.13570.
11579.	Walkowiak S, Gao L, Monat C, Haberer G, Kassa MT, Brinton J, Ramirez-Gonzalez RH, Kolodziej MC, Delorean E, Thambugala D, Klymiuk V, Byrns B, Gundlach H, Bandi V, Siri JN, Nilsen K, Aquino C, Himmelbach A, Copetti D, Ban T, Venturini L, Bevan M, Clavijo B, Koo DH, Ens J, Wiebe K, N'Diaye A, Fritz AK, Gutwin C, Fiebig A, Fosker C, Fu BX, Accinelli GG, Gardner KA, Fradgley N, Gutierrez-Gonzalez J, Halstead-Nussloch

	G, Hatakeyama M, Koh CS, Deek J, Costamagna AC, Fobert P, Heavens D, Kanamori H, Kawaura K, Kobayashi F, Krasileva K, Kuo T, McKenzie N, Murata K, Nabeka Y, Paape T, Padmarasu S, Percival-Alwyn L, Kagale S, Scholz U, Sese J, Juliana P, Singh R, Shimizu-Inatsugi R, Swarbreck D, Cockram J, Budak H, Tameshige T, Tanaka T, Tsuji H, Wright J, Wu J, Steuernagel B, Small I, Cloutier S, Keeble-Gagnere G, Muehlbauer G, Tibbets J, Nasuda S, Melonek J, Hucl PJ, Sharpe AG, Clark M, Legg E, Bharti A, Langridge P, Hall A, Uauy C, Mascher M, Krattinger SG, Handa H, Shimizu KK, Distelfeld A, Chalmers K, Keller B, Mayer KFX, Poland J, Stein N, McCartney CA, Spannagl M, Wicker T and Pozniak CJ 2020 Multiple wheat genomes reveal global variation in modern breeding. Nature 588: 277-283.
11580.	Nirmala J, Saini J, Newcomb M, Olivera P, Gale S, Klindworth D, Elias E, Talbert L, Chao SM, Faris J, and Xu S, Jin Y, and Rouse MN 2017 Discovery of a novel stem rust resistance allele in durum wheat that exhibits differential reactions to Ug99 solates. G3: 7: 3481-3490. DOI: /10.1534/g3.117.300209.
11581.	Wang DZ, Yu K, Jin D, Sun LH, Chu JF, Wu WY, Xin PY, Gregov E, Li X, Sun JZ, Yang WL, Zhan KH, Zhang AM and Liu DC 2020 Natural variations in the promoter of *Awn Length Inhibitor 1* (*ALI-1*) are associated with awn elongation and grain length in common wheat. The Plant Journal 101: 1075-1090. doi: 10.1111/tpj.14575.
11582.	Wurschum T, Jahne F, Phillips AL, Langer SM, Longin CFH, Tucker MR and Leister WL 2020 Misexpression of a transcriptional repressor candidate provides a molecular mechanism for the suppression of awns by *Tipped 1* in wheat. Journal of Experimental Botany 71: 3428-3236 DOI: 10.1093/jxb/eraa106.
11583.	Xu X, Kolmer J, Li G, Tan C, Carver BF, Bian R, Bernardo A and Bai G 2022 Identification and characterization of the novel leaf rust resistance gene *Lr81* in wheat. Theoretical and Applied Genetics 135: 2725-2734. DOI: 10.1007/s00122-022-04145-5.
11584.	Gill BK, Klindworth DL, Rouse MN, Zhang JL, Zhang QJ, Sharma JS, Chu CG, Long YM, Chao SM, Olivera PD, Friesen TL, Zhong SB, Jin Y, Faris JD, Fiedler JD, Elias EM, Liu SY, Cai XW and Xu SS 2021 Function and evolution of allelic variations of *Sr13* conferring resistance to stem rust in tetraploid wheat (*Triticum turgidum* L.). The Plant Journal 106: 1674-1691. DOI: 10.1111/tpj.15263.
11585.	Klymiuk V, Chawla HS, Wiebe K, Ens J, Fatiukha A, Govta L, Fahima T and Pozniak CJ (2022) Discovery of stripe rust resistance with incomplete dominance in wild emmer wheat using bulked segregant analysis sequencing. Communications Biology 5, 826. DOI: 10.1038/s42003-022-03773-3.
11586.	Bariana HS, Babu P, Forrest KL, Park RF and Bansal UK et al. 2022 Discovery of the new leaf rust resistance gene *Lr82* in wheat: Molecular mapping to marker development. Genes 13, 964. DOI: 10.3390/genes13060964.
11587.	Chai SY, Yao Q, Liu R, Xiang WH, Xiao XE, Fan X, Zeng JA, Sha LN, Kang HY, Zhang HQ, Long D, Wu DD, Zhou YH and Wang Y 2022 Identification and validation of a major gene for kernel length at the *P1* locus in *Triticum polonicum*. The Crop Journal 10: 387-396. DOI: 10.1016/j.cj.2021.07.006.
11588.	Pourkhorshid Z, Dadkhodaie A and Niazi A 2022 Moleculr mapping of the *Aegilops speltoides*-derived leaf rust resistance gene *Lr36* in common wheat (*Triticum aestivum* L.) Euphytica 218, 26. DOI: 10.1007/s10681-022-02975-4.
11589.	Zhu KY, Li MM, Wu HB, Zhang DY, Dong LL, Wu QH, Chen YX, Xie JZ, Lu P, Guo GH, Zhang HZ, Zhang PP, Li BB, Wu WL, Dong L, Wang QF, Zhu JH, Hu WL Guo LQ, Wang Rg, Yuan CG, Li HJ, Liu ZY and Hua W 2022 Fine mapping of powdery mildew

	resistance gene *MlWE74* derived from wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) in an NBS-LRR gene cluster. Theoretical and Applied Genetics 135: 1235-1245. DOI: 10.1007/s00122-021-04027-2.
11590.	Li HN, Hua L, Rouse MN, Li TY, Pang SY, Bai SS, Shen Y, Luo J, Li HY, Zhang WJ, Wang XD, Dubcovsky J and Chen SS 2021 Mapping and characterization of a wheat stem rust resistance gene in durum wheat “Kronos”. Frontiers in Plant Sciience 12: 751398. DOI: 10.3389/fpls.2021.751398.
11591.	Dang C, Zhang JL and Dubcovsly J 2022 High-resolution mapping of *Yr78*, an adult plant resistance gene to wheat stripe rust. Plant Genome 15;e20212. DOI: DOI: 10.1002/tpg2.20212.
11592.	Zhang PP, Guo GH, Wu QH, Chen X, Xie JZ, Lu P, Li BB, Dong LL, Li MM, Wang RG, Yuan CG, Zhang HZ, Zhu KY, Li WL and Liu ZY 2020 Identification and fine mapping of spot blotch (*Bipolaris sorokiniana*) resistance gene *Sb4* in wheat. Theoretical and Applied Genetics 133:2451-2459. DOI: 10.1007/s00122-020-03610-3.
11593.	Athiyannan N, Abroiuk M, Boshoff WHP, Cauet S, Rodde N, Kudra D, Mohammed N, Bettgenhaeuser J, Botha KS, Derman SS, Wing RA, Prins R and Krattinger. 2022 Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. Nature Genetics 54: 227-231. DOI: 10.1038/s41588-022-01022-1.
11594.	Zhang M, Lv SK, Wang YZ, Wang SW, Chen CH, Wang CY, Wang YJ, Zhang H and Li WQ 2022 Fine mapping and distribution analysis of hybrid necrosis genes *Ne1* and *Ne2* in wheat in China. Theoretical and Applied Genetics 135: 1177-1189. DOI: 10.1007/s00122-021-04023-6.
11595.	Vetch JM, Stougaard RN, Martin JM and Giroux MJ 2019 Review: Revealing the genetic mechanisms of pre-harvest sprouting in hexaploid wheat (*Triticum aestivum* L.). Plant Science 281: 180-185. DOI: 10.1016/j.plantsci.2019.01.004.
11596.	Niu JQ, Zheng SS, Shi XL, Si YQ, Tian SQ, He YL and Ling H-Q 2020 Fine mapping and characterization of the inhibitor *B1* locus in common wheat (*Triticum aestivum* L. The Crop Journal 8: 613-622. DOI: 10.1016/j.cj.2019.12.005.
11597.	Tian XB, Chen QF, Ma C, Men WQ, Liu QQ, Zhao Y, Qian JJ, Fan ZW, Miao JN, He JQ, Sehgal SK, Li HH and Liu WX 2022 Development and characterization of *Triticum aestivum-Aegilops longissima* $6S^{l}$ recombinants harboring a novel powdery mildew resistance gene *Pm6Sl.* Frontiers in Plant Science 13,918508. DOI: 10.3389/fpls.2022.918508.
11598.	Wang WR, He HG, Gao HM, Xu HX, Song WY, Zhang X, Zhang LP, Song JC, Liu C, Liu KC and Ma PT 2021 Characterization of thye powdery mildew resistance gene in wheat breeding line KN0816 and its evaluation in marker-assisted selection. Plant Disease 105: 4042-4050. DOI: 10.1094/PDIS-05-21-0896-RE.
11599.	Lin GF, Chen H, Tian B, Sehgal SK, Singh L, Xie JZ, Rawat N, Juliana P, Singh N, Shrestha S, Wilson DL, Shult H, Lee H, Scoen AW, Tiwari VK, Singh RP, Huttieri MJ, Trick HN, Poland J, Bowden RL, Bai GH, Gill B and Liu SZ 2022 Cloning of the broadly effective wheat leaf rust resistance gene *Lr42* transferred from *Aegilops tauschii*. Nature Communications 13, 3044. DOI: 10.1038/s41467-022-30784-9.
11600.	Lan CX, Basnet BR, Singh RP, Huerta-Espino J, Herrera-Foessel SA, Ren Y and Randhawa MS 2017 Genetic analysis and mapping of adult plant resistance loci to leaf rust in durum wheat cultivar Bairds. Theoretical and Applied Genetics 130: 609-619. DOI: 10.1007/s00122-016-2839-3.

11601.	Chhetri M, Bariana H, Wong D, Sohail Y, Hayden H and Bansal U 2017 Development of robust molecular markers for marker-assisted selection of leaf rust resistance gene *Lr23* in common and durum wheat breeding programs. Molecular Breeding 37, 21. DOI: 10.1007/s11032-017-0628-6.
11602.	Chen SS, J Hegarty J, Shen T, Hua L, Li HN, Luo J, Li HY, Bai SS. Zhang CZ and Dubcovsky J. 2021 Stripe rust resistance gene *Yr34* (synonym *Yr48*) is located within a distal translocation of *Triticum monococcum* chromosome $5A^{m}L$ into common wheat. Theoretical and Applied Genetics 134:2197. DOI: 10.1007/s00122-021-03816-z.
11603.	Kuzay S, Lin H, Li C, Chen S, Woods D, Zhang J and Dubcovsky J 2022. *WAPO-A1* is the causal gene of the 7AL QTL for spikelet number per spike in wheat. PLoS Genetics 18: e1009747. DOI: 10.1371/journal.pgen.1009747.
11604.	Shaw L, Lyu B, Turner R, Li C, Chen F, Han X, Fu D and Dubcovsky J 2019. *FLOWERING LOCUS T2* (*FT2*) regulates spike development and fertility in temperate cereals. Journal of Experimental Botany 70: 193-204. DOI: 10.1093/jxb/ery350/.
11605.	Glenn P, Zhang J, Brown-Guedira G, DeWitt N, Cook JP, Li K and Dubcovsky J 2022. Identification and characterization of a natural polymorphism in *FT-A2* associated with increased number of grains per spike in wheat. Theoretical and Applied Genetics 135: 679-692. DOI: 10.1007/s00122-021-03992-y.
11606.	Adamski NM, Simmonds J, Brinton JF, Backhaus AE, Chen Y, Smedley M Hayta S, Florio T, Crane P, Scott P, Pieri A, Hall O, Barclay JE, Clayton M, Doonan JH, Nibau C and Uauy C 2021. Ectopic expression of *Triticum polonicum VRT-A2* underlies elongated glumes and grains in hexaploid wheat in a dosage-dependent manner. The Plant Cell 33; 2296-2319. DOI: 10.1093/plcell/koab119.
11607.	Li K, Debernardi JM, Li CX, Lin HQ, Zhang CZ, Jernstedt J, von Korff M, Zhong JS, and Dubcovsky J 2021 Interactions between SQUAMOSA and SHORT VEGETATIVE PHASE MADS-box proteins regulate meristem transitions during wheat spike 11108development. The Plant Cell 2021: 33: 3621–3644. DOI:10.1093/plcell/koab243.
11608.	Wu QH, Zhao F, Chen YX, Zhang PP, Zhang HZ, Guo GH, Xie JZ, Dong LL, Lu P, Li MM, Ma SW, Fahima T, Nevo E, Li HJ, Zhang YJ, and Liu ZY 2021 Bulked segregant CGT-Seq-facilitated map-based cloning of a powdery mildew resistance gene originating from wild emmer wheat (*Triticum dicoccoides*). Plant Biotechnology Journal 19: 1288-1290. doi: 10.1111/pbi.13609.
11609.	Wu QH, Chen YX, Li BB, Li J, Zhang PP, Xie JZ, Zhang HZ, Guo GH, Lu P, Li MM, Zhu KY, Li WL, Fahima T, Nevo E, Li HJ, Dong LL and Liu ZY 2022 Functional characterization of powdery mildew resistance gene *MlIW172*, a new *Pm60* allele and its allelic variation in wild emmer wheat. Journal of Genetics and Genomics 49: 787-795. DOI: 10.1016/j.jgg.2022.01.01.
11610.	Jia AL, Ren Y, Gao FM, Yin GH, Liu JD, Guo L, Zheng JZ, He ZH and Xia XC 2018 Mapping and validation of a new QTL for adult plant resistance to powdery mildew in Chinese elite bread wheat line Zhou8425B. Theoretical and Applied Genetics 131:1063-1071. DOI: 10.1007/s00122-018-3058-x.
11611.	Dong Y, Xu DA, Xu XW, Ren Y, Gao FM, Song J, Jia AL, Hao YF, He ZH, and Xia XC 2022 Fine mapping of *QPm.caas-3BS*, a stable QTL for adult-plant resistance to powdery mildew in wheat (*Triticum aestivum* L.) Theoretical and Applied Genetics 135: 1083 1099. DOI: 10.1007/s00122-021-04019-2.
11612.	Gaurav K, Arora S, Silva P, Sánchez-Martín S, Horsnell R, Gao LL, Brar GS, Widrig V, Raupp WJ, Singh N, Wu SY, Kale SM, Chinoy C, Nicholson P, Quiroz-Chávez J,

	Simmonds J, Hayta S, Smedley MA, Harwood W, Pearce S, Gilbert D, Kangara N, Gardener C, Forner-Martíne M, Liu JQ, Yu GT, Boden SA, Pascucci A, Ghosh S, Hafeez AN, O'Hara T, Waites J, Cheema J, Steuernagel B, Patpour M, Fejer Justesen A, Liu SY, Rudd JC, Avni R, Sharon A, Steiner S, Pasthika Kirana R, Buerstmayr H, Mehrabi AA, Nasyrova FY, Chayut N, Matny O, Steffenson BJ, Sandhu N, Chhuneja P, Lagudah E, Elkot AF, Tyrrell S, Bian XD, Davey RP, Simonsen M, Schauser L, Tiwari VK, Kutcher HR, Hucl P, Li Al, Liu DC, Mao L, Xu S, Brown-Guedira G, Faris J, Dvorak J, Luo MC, Krasileva K, Lux L, Artmeier S, Mayer KFX, Uauy C, Mascher, Bentley AR, Keller B, Poland J and Wulff BBH. 2022. Population genomic analysis of *Aegilops tauschii* identifies targets for bread wheat improvement. Nature Biotechnology 40: 422-431. DOI: 10.1038/s41577-021-01058-4.
11613.	Toor PI, Kaur S, Bansal M, Yadav B and Chhuneja P 2016 Mapping of stripe rust resistance gene in an *Aegilops caudata* introgression line in wheat and its genetic association with leaf rust resistance. Journal of Genetics 95: 933-938. DOI: 10.1007/s12041-016-0718-y.
11614.	Narang D, Kaur S, Steuernage B, Ghosh S, Dhillon D, Bansal M, Uauy C, Wulff BBH and Chhuneja P 2019 Fine mapping of *Aegilops peregrina* co-segregating leaf and stripe rust resistance genes to distal-most end of 5DS. Theoretical and Applied Genetics 132: 1473-1485. DOI: 10.1007/s00122-019-03293-5.
11615.	Bansal M, Adamski NM, Toor PI, Kaur S, Sharma A, Srivastava P, Bansal U, Uauy C and Chhuneja P 2021 A robust KASP marker for selection of four pairs of linked leaf rust and stripe rust resistance genes introgressed on chromosome arm 5DS from different wheat genomes. Molecular Biology Reports 48: 5209-5216. DOI: 10.1007/s11033-021-06525-4.
11616.	Feng JY, Yao FJ, Wang MN, See DR and Chen XM 2023 Molecular mapping of *Yr85* and comparison with other genes for resistance to stripe rust on wheat chromosome 1B. Plant Disease 107: 3585-3591. DOI: 10.1094/PDIS-11-22-2600-RE.
11617.	Luo W, Zhou JG Liu JJ, Liu YL, Mu Y, Tang HP, Xu QA, Deng M, Jiang QT, Chen GY, Qi PF, Wang JR, Jiang YF, Chen ZX, Zheng Z, Wei Y, Zheng YM, Lan XJ and Ma JA 2022 Fine mapping of the hairy glume (*Hg*) gene in a chromosome variation region at the distal terminus of 1AS. Frontiers in Plant Science 13, 1006510. DOI: 10.3389/fpls.2022.1006510.
11618.	Qie YM, Liu Y, Wan MN, Li X, See DR, An DG and Chen XM 2019 Development, validation, and re-selection of wheat lines with pyramided genes *Yr64* and *Yr15* linked on the short arm of chromosome 1B for resistance to stripe rust. Plant Disease 103: 51-58. DOI: 10.1094/PDIS-03-18-0470-RE.
11619.	Bokore, F Knox RE, DePauw RM, Cuthbert RD, Valereio IP, Clarke FR, Beres BL, Ruan YF and Campbell HL. 2019 Validation of the effects of the *Gpc-B1* high grain protein locus from Lillian hard red spring wheat (*Triticum aestivum* L.) using locus specific markers. Euphytica 215, 2. DOI: 10.1007/s10682-018-2322-0.
11620.	Li AX, Yang WL, Lou XY, Liu DC, Sun JZ, Guo XL, Wang J, Li YW, Zhan KH, Ling H-Q, and Zhang AM 2013 Novel natural variation at the *Rht-1* loci in wheat. Journal of Integrative Plant Biology 55: 1026-1037. DOI: 10.1111/jipb.12103.
11621.	Bazhenov MS, Divashuk MG, Amagai Y, Watanabe N and Karlov GI 2015 Isolation of the dwarfing *Rht-B1p* (*Rht17*) gene from wheat and the development of an allele-specific PCR marker. Molecular Breeding 35, 213. DOI: 10.1007/s11032-015-0407-1.
11622.	Buss W, Ford BA, Foo E, Schnippenkoetter W, Borrill P, Brooks B, Ashton AR, Chandler PM and Spielmeyer W 2020 Overgrowth mutants determine the causal role of gibberellin

	GA2oxidaseA13 in *Rht12* dwarfism of wheat. Journal of Experimental Botany 71: 7171-7178. DOI: 10.1093/jxb/eraa443.
11623.	Tian XL, Xia XC, Xu DA, Liu YQ, Xie L, Hassan MA, Song J, Li FJ, Wang DS, Zhang Y, Hao YF, Li GY, Chu CC, He ZH and Cao SH 2022 *Rht24b*, an ancient variation of *TaGA2ox-A9*, reduces plant height without yield penalty in wheat. New Phytologist 233: 738-750. DOI: 10.1111/nph.170808.
11624.	Chai LL, Xin MM, Dong CQ, Chen ZY, Zhai HJ, Zhuang JH, Cheng XJ, Wang NJ, Geng J, Wang XB, Bian RL, Yao YY, Guo WL, Hu ZR, Peng HR, Bai GH, Sun QX, Su ZQ, Liu J and Ni ZF 2022 A natural variation in Ribonuclease H-like gene underlies *Rht8* to confer ‘‘Green Revolution’’ trait in wheat. Molecular Plant 15: 377-380. DOI: 10.1016/j.molp.2022.01.013.
11625.	Cui CG, Lu QM, Zhao ZC, Lu S, Duan S, Yang Y, Qiao Y, Chen LA and Hu Y-G 2022. The fine mapping of dwarf gene *Rht5* in bread wheat and its effects on plant height and main agronomic traits. Planta 255, 114. DOI: 10.1007/s00425-022-03888-1.
11626.	Borrill P, Mago R, Xu TY, Ford B, Williams SJ, Derkx A, Bovill WD, Hyles J, Bhatt D, Xia XD, MacMillan C, White R, Buss W, Molnár I, Walkowiak S, Olsen O-A, Doležel J, Pozniak CJ and Spielmeyer W 2022 An autoactive NB-LRR gene causes *Rht13* dwarfism in wheat. Proceedings of the National Academy of the United States of America 48, e22098785119. DOI: 10.1073/pnas.2209875119.
11627.	Li YH, Wei ZZ, Sela H, Govta L, Klymiuk V, Roychowdhury R, Chawla HS, Ens J, Wiebe K, Bocharova V, Ben-David R, Pawar PB, Zhang UQ, Jaiwar S, Molnár I, Doležel Y, Coaker G, Pozniak CJ and Fahima T 2023 Dissection of a rapidly evolving wheat resistance gene cluster by long-read genome sequencing accelerated the cloning of *Pm69*. Plant Communications 5, 1006465. DOI: 10.1016/j.xplc.2023.100646.
11628.	Muterko A, Balashova I, Cockram J, Kalendar R and Sivolap Y 2015 The new wheat vernalization response allele *Vrn-D1s* is caused by DNA transposon insertion in the first intron. Plant Molecular Biology Reporter 33: 294-303. DOI: 10.1007/s11105-014-0750-0.
11629.	Wu LR, Zhu T, He HG, Cao XY, Li HS, Xu HX, Jia MS, Zhang LP, Song JC, Mirzaghaderi G, Liu Cc, Ma PT 2022 Genetic dissection of the powdery mildew resistance in wheat breeding line LS5082 using BSR-Seq. The Crop Journal 10: 1120-1130. DOI: 10.1016/j.cj.2021.12.008.
11630.	Wang Y, Abrouk M, Gourdoupis S, Koo D-H, Karafiátová M, Molnár I, Holusova K, Doležel J, Athiyannan N, Cavalet-Giorsa, E, Jaremko Ł, Poland J and Krattinger SG 2023 An unusual tandem kinase fusion protein confers leaf rust resistance in wheat. Nature Genetics 55: 914–920. DOI: 10.1038/s41588-023-01401-2.
11631.	Yu GT, Matny O, Gourdoupis S, Rayapuram N, Aljedaani FR, Wang YL, Nürnberger T, Johnson R, Crean EE, Saur IM-L, Gardener C, Yue YJ, Kangara N, Steuernagel B, Hayta H, Smedley M, Harwood W, Patpour M, Wu SY, Poland J, Jones JDG, Reuber TL, Ronen M, Sharon A, Rouse MN, Xu S, Holušová K, Bartoš J, Molnár I, Karafiátová M, Hirt H, Blilou I, Jaremko L, Doležel J, Steffenson BJ and Wulff BBH 2023 The wheat stem rust resistance gene *Sr43* encodes an unusual protein kinase. Nature Genetics 55: 921-926. DOI: 1038/s41588-023-01402-1.
11632.	Arora S, Steed A, Goddard R, Gaurav K, O’Hara T, Schoen A, Rawat N, Elkot AF, Korolev AV, Chinoy C, Nicholson MH, Asuke S, Antoniou-Kourounioti R, Steuernagel B, Yu JT, Awal R, Forner-Martínez M, Wingen L, Baggs E, Clarke J, Saunders DGO, Krasileva KV, Tosa Y, Jones JDG, Vijay K, Tiwari VK, Wulff BBH and Nicholson P 2022 A wheat

	kinase and immune receptor form the host-specificity barriers against the blast fungus. Nature Plants 9: 385-392. DOI: 10.1038/s41477-023-01357-5.
11633.	Tan C-T, Yu HJ, Yang, Xu XY, Chen MS, Rudd JC, Xue QW, Ibrahim AMH, Garza L, Wang SC, Sorrells ME and Liu SY 2017 Development and validation of KASP markers for the greenbug resistance gene *Gb7* and the Hessian fly resistance gene *H32* in wheat. Theoretical and Applied Genetics 130: 1867-1864. DOI: 10.1007/s00122-017-2930-4.
11634.	Niu FU, Xu YF, Liu XM, Zhao LF, Bernardo A, Li YG, Liu GX, Chen M-S, Cao LM, Hu ZB, Xu XY and Bai GH 2020 The Hessian fly recessive resistance gene *h4* mapped to chromosome 1A of the wheat cultivar 'Java' using genotyping-by-sequencing. Theoretical and Applied Genetics 133: 2927-2935. DOI: 10.1007/s00122-020-03624-9.
11635.	Zhang LR, Xu YF, Chen M-S, Su ZQ, Liu Y, Xu YZ, La GX and Bai GH 2022 Identification of a major QTL for Hessian fly resistance in wheat cultivar 'Chokwang'. The Crop Journal 10: 775-782. DOI: 10.1016/j.cj.2021.08.004.
11636.	Mahlandt A, Rawat N, Leonard J, Venglat P, Datla R, Meier N, Gill BS, Riera-Lizarazu O, Coleman G, Murphy AS and Tiwari VK 2021 High-resolution mapping of the *Mov-1* locus in wheat by combining radiation hybrid (RH) and recombination-based mapping approaches. Theoretical and Applied Genetics 134: 2302-2314. DOI: 10.1007/s00122-021-03827-w.
11637.	Zhang ZC, Friesen TL, Xu SS, Shi GJ, Liu ZH, Rasmussen JB and Faris JD 2011 Two putatively homoeologous wheat genes mediate recognition of SnTox3 to confer effector-triggered susceptibility to *Stagonospora nodorum*. The Plant Journal 65, 27–38. DOI: 10.1111/j.1365-313X.2010.04407.x.
11638.	Kolmer JA, Bajgain P, Rouse MN, Li J and Zhang P 2023 Mapping and characterization of the recessive leaf rust resistance gene *Lr83* on wheat chromosome arm 1DS. Theoretical and Applied Genetics 136, 115. DOI: 10.1007/s00122-023-04361-7.
11639.	Li ZK, Yuan C, Herrera-Foessel SA, Randhawa MS, Huerta-Espino J, Liu DM, Dreisigacker S, Singh RP and Lan CX 2019. Four consistent adult plant resistance loci confer resistance to leaf rust in two durum wheat lines Heller#1 and Dunkler. Phytopathology 110: 892-899. DOI: 10.1094/PHYTO-09-19-0348-R.
11640.	Li, Lan CX, et al. 2022 Rapid cloning and functional gene analysis for a leaf rust resistance locus in durum wheat. Submitted.
11641.	Zhu ZW, Cao QA, Han DJ, Wu JH, Wu L, Tong JY, Xu XW, Yan J, Zhang Y, Xu KJ, Wang FJ, Dong YC, Gao CB, He ZH, Xia XC and Hao YF 2023 Molecular characterization and validation of adult-plant stripe rust resistance gene *Yr86* in Chinese wheat cultivar Zhongmai 895. Theoretical and Applied Genetics (2023) 136, 142. DOI: 10.1007/s00122-023-04374-2.
11642.	Xiong HC, Zhou CY, Fu MY, Guo HJ, Xie SR, Zhao LS, Li YT, Zhang JZ, Wang K, Li XJ and Liu LX 2022: Cloning and functional characterization of *Rht8*, a "Green Revolution" replacement gene in wheat. Molecular Plant 15: 373-376. DOI: 10.1016/j.molp.2022.01.014.
11643.	Guttieri MJ, Bowden RL, Zhang G, Haley S, Frels K, Hein GL and Jordan KW 2022 Agronomic and quality impact of a shortened translocation for wheat streak mosaic virus resistance. Crop Science 63: 622-634. DOI: 10.1002/csc2.20876.
11644.	Bowden R et al. 2023 Personal communication.
11645.	Chen YM, Ji JL, Kong DH, Tang XO, Wen MX, Wang GQ, Dai KL, Shi PY, Zhang X, Zhang HL, Jiao CX, Wang ZK, Sun L, Yuan CX, Wang HY, Zhang ZY, Sun BJ, Fei XR, Guo H, Xiao J and Wang XE 2023 Resistance of *QYm.nau-2D* to wheat yellow mosaic

	virus was derived from an alien introgression into common wheat. Theoretical and Applied Genetics 136, 3 DOI: 10.1007/s00122-023-04286-1.
11646.	Zhao MH, Su B, Zhang XX, Zhang XM, Li RB, Cheng P, Wang BT and Li QA 2022 Molecular mapping of a recessive gene for stripe rust resistance at the *YrCf75* locus using bulked segregant analysis combined with single nucleotide polymorphism genotyping arrays and bulked segregant analysis. Plant Disease 106: 2090-2096. DOI: 10.1094/PDIS-11-21-2564-RE.
11647.	Liang X, Xu HX, Zhu SY, Zheng YS, Zhong W, Li HS, Niu LP, Wu LR, Zhang LP, Song JC, He HG, Liu C and Ma PT 2022 Genetically detecting the novel powdery mildew resistance gene in wheat breeding line PBDH1607. Plant Disease 106: 2145-2154. DOI: 10.1094/PDIS-12-2771-RE.
11648.	Li X, Xiang ZP, Chen WQ, Huang QL, Liu TG, Li Q, Zhong SF, Zhang M, Guo JW, Lei L and Luo PG 2017 Reevaluation of two quantitative trait loci for type II resistance to Fusarium head blight in wheat germplasm PI 672538. Phytopathology 107: 92-99. DOI: 10.1094/PHYTO-04-16-0170-R.
11649.	Guo JW, Shi GJ, Kalil A, Friskop A, Elias E, Xu SS, Faris JD and Liu ZH 2020 *Pyrenophora tritici-repentis* race 4 isolates cause disease on tetraploid wheat. Phytopathology 110: 1781-1790. DOI: 10.1094/PHYTO-05-20-0179-R
11650.	Dong CH, Zhang LC, Zhang QA, Yang YX, Li DP, Xie ZC, Cui GQ, Chen YY, Wu LF, Li Z, Liu GX, Zhang XY, Liu CM, Chu JF, Zhao GY, Xia CA, Jia JZ, Sun JQ, Kong XY and Liu X 2023 Tiller Number1 encodes an ankyrin repeat protein that controls tillering in bread wheat. Nature Communications 14, 836. DOI: 10.1038/s41467-023-36271-z
11651.	Zhang Q, Li Y, Li Y, Fahima T, Shen Q and Xie C 2021 Introgression of the powdery mildew resistance genes *Pm60* and *Pm60b* from *Triticum urartu* to common wheat using durum as a 'bridge'. Pathogens 11, 25. DOI: 10.3390/pathogens11010025.
11652.	Wang SZ, Asuke S, Vy TTP, Inoue Y, Chuma I, Win J, Kato K and Tosa Y 2018 A new resistance gene in combination with *Rmg8* confers strong resistance against *Triticum* isolates of *Pyricularia oryzae* in a common wheat landrace. Phytopathology 108: 1299-1306. DOI: 10.1094/PHYTO-12-17-0400-R.
11653.	Nsabiyera V, Qureshi N, Li J, Randhawa M, Zhang P, Forrest K, Bansal U and Bariana H 2023 Relocation of *Sr48* to chromosome 2D using an alternative mapping population and development of a closely linked marker using diverse molecular technologies. Plants 12, 1601. DOI: 10.3390/plants12081601.
11654.	Xie YC, Nachappa P, Nalam VJ and Pearce S 2022 Genomic and molecular characterization of wheat streak mosaic virus resistance locus 2 (*Wsm2*) in common wheat (*Triticum aestivum* L.) Frontiers in Plant Science 13, 928949. DOI: 10.3389/flps.2022.928949.
11655.	Bapela T, Shimelis H, Terefe T, Bourras S, Sánchez-Martín J, Douchkov D, Desiderio F and Tsilo TJ 2023 Breeding wheat for powdery mildew resistance: Genetic resources and methodologies - A review. Agronomy 13, 1173. DOI: 10.3390/agronomy13041173.
11656.	Singh K, Wegulo SN, Skoracka A and Kunmar Kundu J 2018 Wheat *streak mosaic virus*: a centuries old virus with rising importance worldwide. Molecular Plant Pathology 19: 2193-2206 DOI: 10.1111.mpp.12683.
11657.	Hyles J, Vautrin S, Pettolino F, MacMillan C, Stachurski Z, Breen J, Berges H, Wicker T and W. Spielmeyer W 2017 Repeat-length variation in a wheat cellulose synthase-like gene is associated with altered tiller number and stem cell wall composition. Journal of Experimental Botany 68: 1519-1529. DOI: 10.1093/jxb/erx051.

11658.	Bouvet L, Percival-Alwyn L, Berry S, Fenwick P, Holdgate S, Mackay IJ and Cockram J 2022 Genetic resistance to yellow rust infection of the wheat ear is controlled by genes controlling foliar resistance and flowering time. Crop Science 62: 1758-1770. DOI: 10.1002/csc2.20768.
11659.	Zhang JL, Li CX, Zhang WJ, Zhang XQ, Mo YJ, Tranquilli GE, Vanzetti LS, and J Dubcovsky J 2023 Wheat plant height locus *RHT25* encodes a PLATZ transcription factor that interacts with DELLA (*RHT1*). Proceedings of the National Academy of Sciences of the United States of America 120: e2300203120. DOI: 10.1073/pnas.2300203120.
11660.	Kobayashi F, Kojima H, Tanaka T, Saito M, Kiribuchi-Otobe and Nakamura T 2020 Characterization of the *Q.Ymym* region on wheat chromosome 2D associated with wheat yellow mosaic virus resistance. Plant Breeding 139: 93-106. DOI:10.1111/pbr.12759.
11661.	Yao DY, Ijaz W, Liu Y, Hu JH, Peng WT, Zhang BW, Wen XL, Wang JA, Qiu D, Li HJ, Xiao SH and Sun GZ 2022 Identification of a *Pm4* allele as a powdery mildew resistance gene in wheat line Xiaomaomai. International Journal of Molecular Science 23, 1194. DOI: 10.3390/ijms23031194.
11662.	Li HQ, Fan ZW, Ma C, Zhao Y, Wang CL, Tian XB, Chen QF, Miao JN, He JQ, Qian JJ, Sehgal SK, Li HH, and Liu WX 2022 Mapping of the novel powdery mildew resistance gene *Pm2Mb* from *Aegilops biuncialis* based on *ph1b*-induced homoeologous recombination. Theoretical and Applied Genetics 135: 2993-3003. DOI: 10.1007/s00122-022-04162-4.
11663	Zou SH, Shi WQ, Ji JH, Tang YS, Yu D and Tang DZ 2022 Diversity and similarity of wheat powdery mildew resistance among three allelic functional genes at the *Pm60* locus. The Plant Journal 110: 1781-1790. DOI: 10.1111/15771.
11664.	Athiyannan N, Zhang P, McIntosh R, Chakraborty S, Hewitt, Bhatt D, Forrest K, Upadhyaya, Steuernagel B, Arora S5, Huerta J, Hayden M, Wulff BDH5, Ayliffe M, Hickey LT, Lagudah E and Periyannan 2022 Haplotype variants of the stripe rust resistance gene *Yr28* in *Aegilops tauschii*. Theoretical and Applied Genetics 135: 4327-4336. DOI: 10.1007/s00122-022-04221-w.
11665.	Zhu KY, Li MM, Wu HB, Zhang DY, Dong LL, Wu QH, Chen YX, Xie JZ, Lu P, Guo G , Zhang HZ, Zhang PP, Li BB, Li WL, Dong L, Wang QF, Zhu JH, Hu WL6, Guo LQ, Wang RG, Yuan CG, Li HJ, Liu ZY and Hua W 2022 Fine mapping of powdery mildew resistance gene *MlWE74* derived from wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) in an NBS-LRR gene cluster. Theoretical and Applied Genetics 135:1235-1245. DOI: 10.1007/s00122-021-04027-2.
11666.	Yin HY, Fang XJ, Li PH, Yang YH, Hao YC, Liang XM, Bo CY, Ni F, Ma X, Du XY, Li AF, Wang HW, Nevo E and Kong LR 2021 Genetic mapping of a novel powdery mildew resistance gene in wild emmer wheat from “Evolution Canyon” in Mt. Carmel Israel. Theoretical and Applied Genetics 134: 909-921. DOI: 10.1007/s00122-020-03741-7.
11667.	Bi C, Wei CX, Tian S, Li JH, Zhang YF, Ma J and You MS 2023 Dosage effect of anthocyanin biosynthesis in purple-grained wheat (*Triticum aestivum* L.). Euphytica 219, 55. DOI: 10.1007/s10681-023-03183-4.
11668.	Chumanova E, Efremova T and Vavilova V 2023. Characterization of the *Vrn-A1* allele introgressed from *T. aestivum* ssp. *petropavlovsky* that influences the heading time in bread wheat. Euphytica 219, 53. DOI: 10.1007/s10681-023-03178-1.
11669.	Kaur S, Pennington T, Conley EM, Green A, Kolmer j, Anderson J, Gupta R and Gill U 2023 High-resolution melting-based marker development for wheat leaf rust resistance gene *Lr34*. Phytopathology 113: 508-515. DOI: 10.1094/PHYTO-08-22-0313-R.

11670. Kanwal M, Qureshi N, Gessese M, Forrest K, Babu P, Bariana H and Bansal U 2021 An adult plant stripe rust resistance gene maps on chromosome 7A of Australian wheat cultivar Axe. Theoretical and Applied Genetics 134: 2213-2220. DOI: 10.1007/s00122-021-03818-x.

11671. Jiang YF, Duan LY, Guan FN, Yao FJ, Long L, Wang YQ, Zhao XY, Li H, Li W, Xu QA, Jiang QT, Wang JR, Wei YM, Ma JA, Hang HY, Qi PF, Deng M, Zheng YL and Chen GY 2022. Exome sequencing from bulked segregant analysis identifies a gene for all-stage resistance on chromosome 1AL in Chinese wheat landrace 'Xiaohemai'. Plant Disease 106: 1209-1215. DOI: 10.1094/PDIOS-08-21-1618-RE.

11672. Yang X, Jiang YF, Yu XH, Zhang HP, Wang YQ, Guan FN, Long L, Li H, Li W, Jiang QT, Wang JR, Wei YM, Ma JA, Kang HY, Qi PF, Xu QA, Deng M, Zhang YZ, Zheng YL, Zhou YH and Chen GY 2023. Fine mapping and transcriptome sequencing reveal candidate genes conferring all-stage resistance to stripe rust on chromosome arm 1AL in Chinese wheat landrace AS1676. The Crop Journal 11: 1501-1511. DOI: 10.1016/j.cj.2023.04.011.

11673. Li HN, Luo J, Zhang WJ, Hua L, Li K, Wang JA, Xu BY, Yang C, Wang GP, Rouse MN, Dubcovsky J and Chen SS 2023 High-resolution mapping of *SrTm4*, a recessive resistance gene to wheat stem rust. Theoretical and Applied Genetics 136, 120. DOI: 10.1007/s00122-023-04369-z.

11674. Hou S, Lin Y, Yu SF, Yan N, Chen H, Shi HR, Li CX, Wan ZQ and Liu YX 2023 Genome-wide association analysis of Fusarium crown rot resistance in Chinese wheat landraces. Theoretical and Applied Genetics 136, 101. DOI: 10.1007/s00122-023-04289-y.

11675. Li YH, Lin RM, Hu JH, Shu XH, Qiu D, Wu PP, Goitom GH, Wang SQ, Zhang HJ, Yang L, Liu HW, Wu QH, Xie JZ, Zhou Y, Liu ZY and Li HJ 2022 Mapping of wheat stripe rust resistance gene *Yr041133* by BSR-Seq analysis. The Crop Journal 10: 447-455. DOI: 10.1016/j.cj2021.06.009.

11676. Wang X, Li GQ, Jia, HY, Cheng R, Zhong JK, Shi JX, Chen RT, Wen, YX and Ma ZQ 2024 Breeding evaluation and precise mapping of *Fhb8* for Fusarium head blight resistance in wheat (*Triticum aestivum*). Plant Breeding 143: 26-33. DOI: 10.1111/pbr.13113.

11677. Wang PS, Huang J, Li N, Zhang J, Gu CM, Yuan Y, Wen ZR, Jia HY, Kong ZX and Ma ZQ 2023 Identification and fine mapping of *PmNJ3946* for powdery mildew resistance in einkorn wheat. The Crop Journal 11: 1846-1851. DOI: 10.1016/j.cj.2023.05.010.

11678. Wu JZ, Jia HY, Qiao LY, Fu BS, Brown-Guedira G, Nagarajan R and Yan LL 2023 Genetic basis of resistance against powdery mildew in the wheat cultivar "Tabasco". Molecular Breeding 43, 56. https://doi.org/10.1007/s11032-023-01402-3.

11679. Chen C, Hao WH, Wu JC, Si HQ, Xia XC and Ma CX 2022 Fine mapping of stripe-rust-resistance gene *YrJ22* in common wheat by BSR-Seq and MutMap-based sequencing. Plants 11, 3244. DOI: 10.3390/plants1123324.

11680. Sheng DC, Qiao LY, Zhang XJ, Li X, Chang LF, Guo HJ, Zhang SW, Chen F and Chang ZJ 2022 Fine mapping of a recessive leaf rust resistance locus on chromosome 2BS in wheat accession CH1539. Molecular Breeding 42, 52. DOI: 10.1007/s11032-022-01318-4.

11681. Graybosch RA, Peterson, CJ, Baenziger PS, Baltensperger DD, Nelson LA, Jin Y, Kolmer J, Seabourn B, French R, Hein G, Martin TJ, Beecher B, Schwarzacher T and Heslop-Harrison P 2009 Registration of 'Mace' hard red winter wheat. Journal of Plant Registrations 3: 51-56. DOI: 10.3198/jpr2008.06.0345crc.

11682. Norman M, Chen CH, Miah H, Patpour M, Sørensen C, Hovmøller M, Forrest K, Kumar5 S, Prasad P, Gangwar OP, Bhardwaj S, Bariana H, Periyannan S and Bansal U 2024 *Sr65*:

	a widely effective gene for stem rust resistance in wheat. Theoretical and Applied Genetics 137, 1. DOI: 10.1007/s00122-023-04507-7.
11683.	Millet E, Manisterski J, Ben-Yehuda P, Distelfield A, Deek J, Wan A, Chen X and Stefffenson BJ 2014. Introgression of leaf rust and stripe rust resistance from Sharon goatgrass (*Aegilops sharonensis* Eig) into bread wheat (*Triticum aestivum* L.) Genome 57. DOI: 10.1139/gen-2014-0004.
11684.	Khazan S, Minz-Dub A, Sela H, Manisterski J, Ben-Yehuda P, Sharon A and Millet E 2020 Reducing the size of an alien segment carrying leaf rust and stripe rust resistance in wheat. BMC Plant Biology 20,153. DOI: 10.1186/s12870-020-2306-9.
11685.	Cavalet-Giorsa E, Gonza-Munoz A, Athiyannan N, Holden S, Salhi A, Gardener C, Quiroz-Chavez J, Rustamova SM, Elkot AF, Patpour M, Rasheed A, Mao L, Lagudah ES, Periyannan SK, Sharon S, Himmelbach A, Reif JC, Knauft M, Mascher M, Stein N, Chayut N, Ghosh S, Perovic D, Putra A, Perera AB, Hu C-Y, Yu GT, Ahmed HI, Laquai KD, Rivera LF, Chen RJ, Wang YJ, Gao X, Liu SZ, Raupp WJ, Olson EL, Lee J-Y, Chhuneja P, Kaur S, Zhang P, Park RF, Ding Y, Liu D-C, Li WL, Nasyrova FY, Dvorak J, Abbasi M, Li M, Kumar N, Meyer WB, Boshoff WHP, Steffenson BJ, Matny O, Sharma PK, Tiwari VK, Grewal S, Pozniak C, Chawla HS, Ens J, Dunning LT, Kolmer JA, Lazo GR, Xu S, Gu YQ, Xu XY, Uauy C, Abrouk M, Bougouffa S, Brar GS, Wulff BBH and Krattinger SG 2024. Origin and evolution of the bread wheat D genome. Nature XXXX DOI: 10.1038/s41586-024-07808-z.
11686.	Han G, Liu H, Zhu S, Gu T, Ca, L, Ya, H, Jin Y, Wang J, Liu S, Zhou Y, Shi Z, He H and An D 2023 Two functional CC-NBS-LRR proteins from rye chromosome 6RS confer differential age-related powdery mildew resistance to wheat. Plant Biotechnology Journal 22: 66-81. DOI: 10.1111/pbi.14165.
11687.	Che MZ, Hiebert CW, McCartney CA, Zhang ZJ and McCallum BD 2019 Mapping and DNA marker development for *Lr33* from the leaf rust resistant line KU168-2. Euphytica 215, 29. DOI: 1007/s10681-019-2343-
11688.	Sharma JS, Che MZ, Fetch T, McCallum BD, Xu SS and, Hiebert CW 2024 Identification of *Sr67*, a new gene for stem rust resistance in KU168-2 located close to the *Sr13* locus in wheat Theoretical and Applied Genetics 137, 30. DOI: 10.1007/s00122-023-04530-8.
11689.	Lin X, N'Diaye A, Walkowiak S, Nilsen KT, Cory AT, Haile J, Kutcher HR, Ammar K, Loladze A, Huerta-Espino J, Clarke JM, Ruan YF, Knox R, Fobert P, Sharpe AG and Pozniak CJ 2018 Genetic analysis of resistance to stripe rust in durum wheat (*Triticum turgidum* L. var. durum). PLoS ONE 13: e0203283. DOI: 10.1371/journal.pone.0203283.
11690.	Simmonds J, Scott P, Brinton J, Mestre TC, Bush M, del Blanco A, Dubcovsky J and·Uauy C 2016 A splice acceptor site mutation in TaGW2-A1 increases thousand grain weight in tetraploid and hexaploid wheat through wider and longer grains. Theoretical and Applied Genetics 129: 1099–1112. DOI 10.1007/s00122-016-2686-2.
11691.	Rivera-Burgos L, VanGesse C, Guedira M, Smith J, Marshall D, Jin Y, Rouse M and Brown-Guedira G. 2024 Fine mapping of stem rust resistance derived from soft red winter wheat cultivar AGS2000 to an NLR gene cluster on chromosome 6D. Theoretical and Applied Genetics 137, 206. DOI:10.1007/s00122-024-04702-0.
11692.	Ni F, Zheng YY, Liu XK, Yu Y, Zhang GQ, Epstein L, Mao XE, Wu JZ, Yuan CL, Lv B, Yu HX, Li JL, Zhao Q, Yang QY, Liu, JJ, Qi JA, Fu DL and Wu JJ 2023 Sequencing trait-associated mutations to clone wheat rust-resistance gene *YrNAM*. Nature Communications 14, 4253. DOI:10.1038/s41467-023-39993-2.

11693.	Lunzer M, Buerstmayr M, Grausgruber H, Müllner AE, Fallbacher I·and Buerstmayr H 2023 Wheat (*Triticum aestivum*) chromosome 6D harbours the broad spectrum common bunt resistance gene *Bt11*. Theoretical and Applied Genetics 136, 207. DOI:10.1007/s00122-023-04452-5.
11694.	Gaurav G, Arora S, Silva P, Sánchez-Martín J, Horsnell R, Gao LL, Brar GS, Widrig V, Raupp WJ, Singh N, Wu SY, Kale SM, Chinoy C, Nicholson P, Quiroz-Chávez J, Simmonds J, Hayta S, Smedley MA, Harwood W, Pearce S, Gilbert D, Kangara N, Gardener C, Forner-Martínez M, Liu JQ, Yu GT, Boden SA, Pascucci A, Ghosh S, Hafeez AN, O'Hara T, Waites J, Cheema J, Steuernagel B, Patpour M, Justesen AF, Liu SY, Rudd JC, Avni R, Sharon A, Steiner B, Kiranam RP, Buerstmayr H, Firuza M, Nasyrova Y, Chayut N, Matny O, Steffenson BJ, Sandhu N, Chhuneja P, Lagudah E, Elkot AF, Tyrrell S, Bian XD, Davey RP, Simonsen M, Schauser L, Tiwari VK, Kutcher HR, Hucl P, Li AL, Liu D-C, Mao L, Xu S, Brown-Guedira G, Faris J, Dvorak J, Luo M-C, Krasileva K, Lux T, Artmeier S, Mayer KFX, Uauy C, Mascher M, Bentley AR, Keller B, Poland J and Wulff BBH 2022. Population genomic analysis of *Aegilops tauschii* identifies targets for bread wheat improvement. Nature Biotechnology 40: 422-431. DOI: 10.1038/s41587-021-01058-4.
11695.	Tang XO, Dai FX, Hao YL, Chen YM, Zhang JP, Wang GQ, Li, XY Peng XJ, Tao Xu, Yuan CX, Sun L, Xiao J, Wang HY, Shi WQ, Yang LJ, Wang XK and Wang XE 2023 Fine mapping of two recessive powdery mildew resistance genes from *Aegilops tauschii* accession CIae8. Theoretical and Applied Genetics 136, 206. DOI: 10.1007/s00122-023-04454-3.
11696.	Liu SJ, Liu D, Zhang CL, Zhang WJ, Wang XT, Mi ZW, Gao X, Ren Y, Lan CX, Liu XK, Zhao ZD, Liu JJ, Li HS, Yuan FP, Su BF,·Kang ZS, Li CL, Han DJ, Wang CF, Cao XY and Wu JH 2023 Slow stripe rusting in Chinese wheat Jimai 44 conferred by *Yr29* in combination with a major QTL on chromosome arm 6AL. Theoretical and Applied Genetics 136, 175 DOI: 10.1007/s00122-023-04420-z.
11697.	Lim AS, WL, Lou XY, Liu DC, Sun JZ, Guo XL, J, Zhan KH, Ling H-Q and Zhang AM 2013 Novel natural allelic variations at the *Rht*-1 loci in wheat. Journal of Integrative Plant Biology 65: 1026-1037. DOI: 10.1111/jipb12103.
11698.	Narang D1, Kaur S, Steuernagel B, Ghosh S, Bansal M, Li JB, Zhang P, Bhardwaj S, Uauy C, Wulff BBH and Chhuneja P 2020 Discovery and characterization of a new leaf rust resistance gene introgressed in wheat from wild wheat *Aegilops peregrina*. Scientific Reports 10, 7573. DOI: 10.1038/s41598-020-64166-2.
11699.	Xu SS, Lyu ZF, Zhang N, Li MZ, Wei XY, Gao YH, Cheng XX, Ge WY,·Li ZF, Bao YG, Yang ZJ, Ma X, Wang HW and Kong LR 2023 Genetic mapping of the wheat leaf rust resistance gene *Lr19* and development of translocation lines to break its linkage with yellow pigment. Theoretical and Applied Genetics 136, 200. DOI: 10.1007/s00122-023-04425-8.
11700.	Thambugala D, Lewarne MK, McCallum BD, Bilichak A, Hiebert CW and· McCartney CA 2023 Genetic mapping of the wheat leaf rust resistance gene *Lr2a* and its importance in Canadian wheat cultivars. Theoretical and Applied Genetics (2023) 136, 198. DOI: 10.1007/s00122-023-04440-9.
11701.	Su FY, Han GH, Yu ZY, Li HS, Wang XL, Chang L, Xiao LN, Mu YJ, Bian QZ, Wang Ft, Jin YL and Ma PT 2023 Identification of a *Pm4* allele conferring powdery mildew resistance in wheat breeding line GR18-1. Plant Disease 107: 2104-2111. DOI: 10.1094/PDIS-11-22-2627-RE./-

11702.	Hu JH, Gebremariam GG, Zhang P, Qu YF, Qiu D, Shi ZH, Li YH, Wu QH, Luo M, Yang LJ, Liu HW, Zhou Y, Liu ZH and Wang BT 2023 Resistance to powdery mildew is conferred by different genetic loci at the adult-plant and seedling stages in winter wheat line Tianmin 668. Plant Disease 107: 2133-2143. DOI: 10.1094/PDIS-11-22-2633-RE.
11703.	Zhao RH, Liu BL, Jiang ZN, Chen TT, Wang L, Ji YY, Hu ZB, He HG and Bie TD 2019. Comparative analysis of genetic effects of wheat-*Dasypyrum villosum* translocations T6V#2S·6AL and T6V#4S·6DL. Plant Breeding 138:503-512. DOI: 10.1111/pbr.12711.
11704.	Zhang X, Wang WR, Liu C, Zhu SY, Gao HM, Xu HX, Zhang LP, Song JC, Song WY, Liu KC, He HG and Ma PT 2021 Diagnostic kompetitive allele-specific PCR markers of wheat broad-spectrum powdery mildew resistance genes *Pm21*, *PmV* and *Pm12* developed for high-throughput marker-assisted selection. Plant Disease 105: 2844-2850. DOI: 10.1094/PDIS-02-21-0308-RE.
11705.	Wu YA, Yu XT, Zhang X, Yan LJ, Gao L, Hao YQ, Wang XY, Xue XL, Qu YF, Hu TZ, Fu BS, Li SP, Li HJ, Li CX, Ma PT and Xu HX 2021 Characterization of *PmDGM* conferring powdery mildew resistance in Chinese wheat landrace Duanganmang. Plant Disease 105: 3127-3133. DOI: 10.1094/PDIS-12-20-2719-RE.
11706.	Li YX, Liu L, Wang MN, Ruff T, See DR, Hu XP and Chen XM 2023 Characterization and molecular mapping of a gene conferring high-temperature adult-plant resistance to stripe rust originally from *Aegilops ventricosa*. Plant Disease 107: 431-442. DOI: 10.1094/PDIS-06-22-1419-RE.
11707.	Qiu D, Huang JA, Guo GH, Hu JH, Li YH, Zhang HJ, Liu HW, Yang L, Zhou Y, Yang BZ, Zhang YD, Liu ZY and Li HJ 2022 The *Pm5e* gene has no negative effect on wheat agronomic performance: Evidence from newly established near-isogenic lines. Frontiers in Plant Science 13, 918559. DOI: 10.3389/fpls.2022.918559.
11708.	Han GH, Yan HW, Gu TT, Cao LJ, Zhou YL, Liu W, Liu DC and An DG 2023 Identification of a wheat powdery mildew dominant resistance gene in the *Pm5* locus for high-throughput marker-assisted selection. Plant Disease 107: 450-456. DOI: 10.1094/PDIS-07-22-1545-RE.
11709.	Nigro D, Blanco A, Piarulli L, Signorile MA, Colasuonno P, Blanco E, and Simeone R. 2022 Fine mapping and candidate gene analysis of *Pm36*, a wild emmer-derived powdery mildew resistance locus in durum wheat. International Journal of Molecular Sciences 23, 13659. DOI:10.3390/ijms232113659.
11710.	Zhong SF, Ma LX, Fatima SA, Yang JZ, Chen WQ, W, Liu TG, Hu YT, Li Q, Guo JW, Zhang M, Lei L, Li X, Tang SW and Luo PG. 201 Collinearity analysis and high-density genetic mapping of the wheat powdery mildew resistance gene *Pm40* in PI 672538. PLoS ONE 11: e0164815. DOI: 10.1371/journal.pone.0164815.
11711.	Yang H, Zhong SF, Chen C, Yang H, Chen W, Tan FQ, Zhang M, Chen WQ, Ren TH, Li and Luo P 2021 Identification and cloning of a CC-NBS-NBS-LRR gene as a candidate of *Pm40* by integrated analysis of both the available transcriptional data and published linkage mapping. International Journal of Molecular Sciences 22, 10239. DOI: 10.3390/ijms221910239.
11712.	Sharma D, Avni R, Gutierrez-Gonzalez J, Kumar R, Sela H, Ranjan R, Prusty M, Cohen A, Molnár I, Holušová K, Said M, Doležel J, Millet E, Khazan-Kost S, Landau U, Bethke G, Ezrati S, Ronen M, Maatuk O, Eilam T, Manisterski J, Ben-Yehuda P, Anikster Y, Matny O, Steffenson BJ, Mascher M, Brabham HJ, Moscou MJ, Liang Y, Yu GT, Wulff BBH, Muehlbauer G, Minz-Dub A and Sharon A 2023 A single NLR gene confers resistance to leaf and stripe rust in wheat, Research Square. DOI: 10.21203/rs.3.rs-3146908/v1.

11713.	Crawford AC and Francki MG. 2013 Lycopene-e-cyclase (e-LCY3A) is functionally associated with quantitative trait loci for flour b* colour on chromosome 3A in wheat (*Triticum aestivum* L.) Molecular Breeding 31: 737-741. DOI 10.1007/s11032-012-9812-x.
11714.	Wu PP, Hu JH, Zou JW, Qiu D, Qu YF, Li YH, Li T, Zhang HJ, Yang L, Liu HW, Zhou Y, Zhang ZJ, Li JT, Liu ZY and Li HJ 2019 Fine mapping of the wheat powdery mildew resistance gene *Pm52* using comparative genomics analysis and the Chinese Spring reference genomic sequence. Theoretical and Applied Genetics 132: 1451-1461. DOI: 10.1007/s00122-019-03291-7.
11715.	Qu YF, Wu PP, Hu JH, Chen YX, Shi ZL, Qiu D, Li YH, Zang HJ, Zhou Y, Yang L, Liu HW, Zhu TQ, Liu ZY, Zhang YM and Li HJ 2020 Molecular detection of the powdery mildew resistance genes in winter wheats DH51302 and Shimai 26. Journal of Integrative Agriculture 19: 931-940 DOI: 10.1016/S2095-3119(19)62644-4.
11716.	Shi XH, Wu PP, Hu JH, Qiu D, Qu YF, Li YH, Liu Y, Gebremariam YG, Xie JH, Wu QH, Zhang HJ, Liu HW, Li Y, Sun GH, Zhou Y, Liu ZH and Li HJ 2021 Molecular characterization of all-stage and adult-plant resistance loci against powdery mildew in winter wheat cultivar Liangxing 99 using BSR-Seq technology. Plant Disease 105: 3443-3450. DOI: 10.1094/PDIS-03-21-0664-RE.
11717.	Hanzalova A, Dumalasova V and Zelba O 2021 Virulence in the *Puccinia triticina* population in the Czech Republic and resistance genes in registered cultivars 1966-2019. Euphytica 217, 4. DOI10.1007/s10681-020-02733-4.
11718.	Wei B, Jing RL, Wang CS, Chen JB, Mao XG, Chang XP and Jia JZ 2009 *Dreb1* genes in wheat (*Triticum aestivum* L.): Development of functional markers and gene mapping based on SNPs. Molecular Breeding 23: 13-22. DOI: 10.1007/s11032-008-9209-z.
11719.	Li H, Zhang F, Zhao J, Bai G, Amand PS, Bernardo A, Ni Z, Sun Q, and Su Z 2022 Identification of a novel major QTL from Chinese wheat cultivar Ji5265 for Fusarium head blight resistance in the greenhouse. Theoretical and Applied Genetics 135: 1867-1877. DOI: 10.1007/s00122-022-04080-5.
11720.	Gessese M, Miah H, Bansal U and Bariana H. 2021 Genetics of stripe rust resistance in a common wheat landrace Aus27492 and its transfer to modern wheat cultivars. Canadian Journal of Plant Pathology 43: S256 – S262. DOI: 10.1080/07060661.2021.1979657.
11721.	Li HN, Hua L, Zhao SQ, Hao M, Song R, PangSY, Liu YN, Chen H, Zhang WJ, Shen T, Gou J-Y, Mao HL, Wang GP, Hao XH, LiJA, Song BX, Lan CX, Li ZF, Deng XW, Dubcovsky J, Wang XD and Chen SS 2023 Cloning of the wheat leaf rust resistance gene *Lr47* introgressed from *Aegilops speltoides*. Nature Communications |14, 6072. DOI: 10.1038/s41467-023-41833-2.
11722.	Chemonges M, Herselman L. Pretorius ZA, Mare A and Boshoff WHP 2022 Characterization of stem rust resistance in the South African winter wheat cultivar PAN 3161. Euphytica 218, 139. DOI: 10.1007/s10681-022-02087-9.
11723.	Mago R, Tabe L, McIntosh RA, Pretorius Z, Kota R, Paux E, Wicker T, Breen J, Lagudah ES, Ellis JG and Spielmeyer W 2011 A multiple resistance locus on chromosome arm 3BS in wheat confers resistance to stem rust (*Sr2*), leaf rust (*Lr27*) and powdery mildew. Theoretical and Applied Genetics 123: 615–623. DOI: 10.1007/s00122-011-1611-y.
11724.	Mago R 2023. By request.
11725.	Chemonges M, Herselman L, Pretorius ZA, Rouse MN, Mare A and Boshoff WHP 2023 Mapping and validation of all-stage resistance to stem rust in four South African winter wheat cultivars. Euphytica 219, 11. DOI: 10.1007/s10681-022-03143-4.

11726.	Xu XY, Li GQ, Bai GH, Bian RL, Bernardo A, Wolabu TW, Carver BF, Wu YQ and Elliott N 2024. Characterization of a new greenbug resistance gene *Gb9* in a synthetic hexaploid wheat. Theoretical and Applied Genetics 137, 140. DOI. 10.1007/s00122-024-04650-9.
11727.	Zhang FP, Zhang HJ, Liu JL, Ren XM, Ding YP, Sun FY, Zhu ZZ, He X, Zhou Y, Bai GH, Ni ZF, Sun QX, and Su ZQ 2024 *Fhb9*, a major QTL for Fusarium head blight resistance improvement in wheat. Journal of Integrative Agriculture XXXX DOI: 10.1016/j.jia.2024.03.045.
11728.	Zhao Y, Dong ZJ, Miao JN, Liu QW, Ma C, Tian XB, He JQ, Bi HB, Yao W, Li T, Gill HS, Zhang ZB, Cao AZ, Liu B, Li HH, Sehgal SK, and Liu WX 2024. *Pm57* from *Aegilops searsii* encodes a tandem kinase protein and confers wheat powdery mildew resistance. Nature Communications 15, 4796 DOI: 10.1038/s41467-024-49257-2.
11729.	Kassa Mt, Menzies JG and McCartney CA 2015 Mapping of a resistance gene to loose smut (*Ustilago tritici*) from the Canadian wheat breeding line BW278. Molecular Breeding 35, 1180. DOI: 10.1007/s11032-015-0369-3.
11730.	Cao QA, Zhu ZW, Xu DA, Wu JH, Xu XW, Dong Y, Bian YJ, Ding FG, Zhao DH, Tu Y, Wu L, Dejun DJ, Lan CX, Xia XC, He ZH and Hao YF 2024 Characterization of a 4.1 Mb inversion harboring the stripe rust resistance gene *YR86* on wheat chromosome 2AL. The Crop Journal 12: 1168-1175. DOI: 10.1016/j.cj.2024.05.011.
11731.	Xu XY, Li GQ, Bai GH, Carver BF, Bian RL, Bernardo A, Scott Armstrong J. 2023 Genomic location of *Gb1*, a unique gene conferring wheat resistance to greenbug biotype F. The Crop Journal 11: 1595- 1599. DOI: 10.1016/j.cj.2023.02.002.
11732.	Fu BS, Zhang ZL, Zhang QF, Wu XY, Wu JZ and Cai SB 2017 Identification and mapping of a new powdery mildew resistance allele in the Chinese wheat landrace Hongyoumai. Molecular Breeding 37, 133. DOI 10.1007/s11032-017-0728-3.
11733.	Mackenzie A, Norman M, Gessese M, Chen CH, Sorensen C, Hovmoller M, Ma LN, Forrest K, Hickey L, Bariana H, Bansal U and Periyannan S 2023 Wheat stripe rust resistance locus *YR63* is a hot spot for evolution of defence genes – a pangenome discovery. BMC Plant Biology 23, 590. DOI: 10.1186/s12870-023-04576-2.
11734.	Qian ZJ, Han GH, Yu NN, Liu C, Han R, Jameson PE, Wang JJ, Zhao Y, Xiao B, LiuRS, Zhang JD, Jin YL, Li HJ and Ma PT 2024 Fine mapping of the powdery mildew resistance gene *PmXQ-0508* in bread wheat. The Crop Journal 12: 1176-1184. doi.org/10.1016/j.cj.2024.05.016
11735.	Asuke S, Morita K, Shimizu M, Abe F, Terauchi R, Nago C, Takahashi Y, Shibata M, Yoshioka M, Iwakawa M, Kishi-Kaboshi M, Su ZO, Nasuda S, Handa H, Fujita M, Tougou M, Hatta K, Mori N, Matsuoka Y, Kato K and Tosa Y 2024 Evolution of wheat blast gene *Rmg8* accompanied by differentiation of variants recognizing the powdery mildew fungus. Nature Plants 10: 971-983. DOI: 10.1101/2023.09.26.559445.
11736.	Yoshioka M, Kishii M, Singh PK, Inoue Y, Vy TTP, Tosa Y and Asuke S 2024 *Rmg10*, a novel wheat blast resistance gene derived from *Aegilops tauschii*. Phytopathology Draft manuscript. /DOI: 10.1094/PHYTO-01-24-0018-R
11737.	Torada A, Koike M, Ogawa T, Takenouchi Y, Tadamura K, Wu JZ, Matsumoto T, Kawaura T and Ogihara Y 2016 A causal gene for seed dormancy on wheat chromosome 4A encodes a MAP kinase kinase. Current Biology 26: 782-787. DOI: 10.1038/s41477-024-01711-1.
11738.	Abe F, Haque E, Hisano H, Tanaka T, Kamiya Y, Mikami M, Kawaura K, Endo M, Onishi K, Hayashi T and Sato K 2019 Genome-edited triple-recessive mutation alters seed dormancy in wheat. Cell Reports 28: 1362–1369. DOI: 10.1016/j.celrep.2019.06.090.

11739. Song J, Li L, Liu BY, Dong YC, Dong Y, Li FJ, Liu SY, Luo XM, Sun MJ, Ni ZQ, Fei SP, Xia XC, Ni ZF, He ZH and Cao ZH 2023 Fine mapping of reduced height locus *RHT26* in common wheat Theoretical and Applied Genetics 136, 62. DOI: 10.1007/s00122-023-04331-z.

11740. Liu XL, Zheng SS, Tian SQ, Si YQ, Ma SW, Ling H-Q and J Niu JQ 2024 Natural variant of *Rht27*, a dwarfing gene, enhances yield potential in wheat. Theoretical and Applied Genetics 137, 128 DOI: 10.1007/s00122-024-04636-7.

11741. Xu DA, Jia CF, Lyu XR, Yang, Qin HM, Wang YL, Hao QL, Liu WX, Dai XH, Zeng JB, Zhang HS, Xia XC, He ZH, Cao SH and Ma WJ 2023 In silico curation of QTL-rich clusters and candidate gene identification for plant height of bread wheat. The Crop Journal 11: 1480–1490. DOI: 10.1016/j.cj.2023.05.007.

11742. Lu CT, Du J, Chen HY, Gong SJ, Jin YY, Meng XR, Zhang T, Fu BS, Molnár I, Holušová K, Said M, Xing LP, Kong LN, Doležel J, Li GY, Wu JZ, Chen PD, Cao AZ and Zhang RQ 2024 Wheat *Pm55* alleles exhibit distinct interactions with an inhibitor to cause different powdery mildew resistance. Nature Communications 15, 503. DOI:10.1038/s41467-024-44796-0.

11743. Elliott C, Zhou FS, Spielmeyer W, Panstruga R and Schultze-Lefert P 2002 Functional conservation of wheat and rice *Mlo* orthologs in defense modulation to the powdery mildew fungus. Molecular Plant Microbe Interactions 15: 1069–1077. DOI: 10.1094/MPMI.2002.15.10.1069.

11744. Wang YP, Cheng X, Shan QW, Zhang Y, Liu JX, Gao CX and Qiu JL 2014. Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. Nature Biotechnology 32: 947-951. DOI: 10.1038/nbt.2969.

11745. Li SN, Lin DX, Zhang YW, Deng M, Chen YX, Lv B, Li BS, Lei Y, Wang YP, Zhao L, Liang YT, Liu JX, Chen KL, Liu ZY, Xiao J, Qiu J-L and Gao CX 2022 Genome-edited powdery mildew resistance in wheat without growth penalties. Nature 602: 455-460. DOI: 10.1038/s41586-022-04395-9.

11746. Wang J, Li HY, Shen T, Lyu SK, ur Rehman S, Li HN, Wang GP, Xu BY, Wang Q, Hub WY, Li KR, Bai SS, Mac J, Yu HT, Rouse MN and Chen SS 2023 High-resolution genetic mapping and identification of candidate genes for the wheat stem rust resistance gene *Sr8155B1*. The Crop Journal 11: 1852–1861. DOI: 10.1016/j.cj.2023.09.006.

11747. Zhang JP, Nirmala J, Chen SS, Jost M, Steuernagel B, Karafiatova M, Hewitt T, Li HN, Edae E, Sharma K, HoxhaS, Bhatt D, Antoniou-Kourounioti R, Dodds P, Wulff BBH, Dolezel J, Ayliffe M, Hiebert C, McIntosh R, Dubcovsky J, Zhang P, Rouse MN, and Lagudah E 2023 Single amino acid change alters specificity of the multi-allelic wheat stem rust resistance locus *SR9*. Nature Communications 14, 7354. DOI: 10.1038/s41467-023-42747-9.

11748. Xue SL, Huan Wang HA, Ma YY, Sun TP, Wang YX, Meng F, Wang XT, Yang ZH,·Zhang JL, Du JX, Li SP and Li ZF 2024 Fine mapping of powdery mildew resistance gene *PmXNM* in a Chinese wheat landrace Xiaonanmai, Theoretical and Applied Genetics 137, 3510. DOI: 1007/s00122-024-04544-w.

11749. Xue SL, Hu SS, Chen XA, Ma YY, Lu MX, Bai SL, Wang XT, Sun TP, Wang YX, Wan HS, An X and Li SP. 2022 Fine mapping of *Pm58* from *Aegilops tauschii* conferring powdery mildew resistance. Theoretical and Applied Genetics 135:1657–1669. DOI: 10.1007/s00122-022-04061-8.

11750. Corsi, B, Percival-Alwyn L, Downie RC, Venturini L, Iagallo EM, Campos Mantello M, McCormick-Barnes C, Theen See P, Oliver RP, Moffat CS and Cockram J 2020 ·Genetic

	analysis of wheat sensitivity to the ToxB fungal effector from *Pyrenophora tritici-repentis*, the causal agent of tan spot. Theoretical and Applied Genetics 133:935–950. DOI: 10.1007/s00122-019-03517-8.
11751.	Running KLD, Momotaz A, Kariyawasam GK, Zurn JD, Acevedo M, Carter AH, Liu Z and Faris JD 2022 Genomic analysis and delineation of the tan spot susceptibility locus *Tsc1* in wheat. Frontiers in Plant Science 13,793925. DOI: 0.3389/fpls.2022.793925.
11752.	Xu XY, Li GQ, Cowger C, Bai GH, Carver BF, Bian RL and Bernardo A 2023 Identification of a novel *Pm65* allele conferring a wide spectrum of resistance to powdery mildew in wheat accession PI 351817. Phytopathology 113: 1979-1984. DOI: 10.1094/Phyto-01-23-0032-R.
11753.	Xu XT, Ni ZQ, Zou XY, Zhang YL, Tong JY, Xu XW, Dong YC, Han B, Li SM, Wang DS, Xia XC, He ZH and Hao YF 2023 QTP mapping reveals both all-stage and adult plant resistance to powdery mildew in Chinese elite cultivars. Plant Disease 107: 3230-3237. DOI: 10.1094/PDIS-02-23-0399-RE.
11754.	Li HN, Luo J, Zhang WJ, Hua L, Li K, Wang JA, Xu BY, Yang C, Wang GP, Rouse MN, Dubcovsky J and Chen SS 2023 High-resolution mapping of *SrTm4*, a recessive resistance gene to wheat stem rust. Theoretical and Applied Genetics 136:120 DOI: 10.1007/s00122-023-04369-z.
11755.	Islam MT, Nago C, Yoshioka M, Vy TTP, Tosa Y and Asuke S. 2024. Identification of *Rmg11* in tetraploid wheat as a new blast resistance gene with tolerance to high temperature. Phytopathology XXXX. DOI: 10.1094/PHYTO-02-24-0074-R.
11756.	Li HH, Men WQ, Ma C, Liu QW, Dong ZJ, Tian XB, Wang CL, Liu C, Gill HS, Ma PT, Zhang ZB, Liu B, Zhao Y, Sehgal SK and Liu WX 2024 Wheat powdery mildew resistance gene *Pm13* encodes a mixed lineage kinase domain-like protein. Nature Communications 15, 2449. DOI:10.1038/s41467-024-46814-7.
11757.	Gao P, Zhou Y, Gebrewahid TW, Zhang PP, Wang SM, Liu DQ and Li ZF 2024 QTL mapping for adult-plant resistance to leaf rust in Italian wheat cultivar Libellula. Plant Disease 108: 13-19. DOI: 10.1094/PDIS-01-23-0105-SR.
11758.	Saini J, Faris JD Zhang QD, Rouse, MN, Jin Y, Long YM, Klindworth DL, Elias EM, McClean PE, Edwards MC and Xu SS 2018. Identification, mapping, and marker development of stem rust resistance genes in durum wheat 'Lebsock'. Molecular Breeding 38, 77. DOI: 10.1007/s11032-018-0833-y.
11759.	Deng M, Long L, Cheng YK, Yao FJ, Guan FN, Wang YQ, Li H, Zhien Pu, Li W, Jiang QT, Wei YM, Ma JA, Kang HY, Qi PF, Wang JR, Zheng YL, Jiang YR and Chen GY 2022 Mapping a stable adult-plant stripe rust resistance QTL on chromosome 6AL in Chinese wheat landrace Yibinzhuermai. Crop J 10: 1111-1119. DOI: 10.1016/j.cj.2021.10.011.
11760.	Wang YQ, Gao MR, Jiang YF, Huang WZ, Zhao X, Zhu W, Li H, Y,· Zeng JA, Wu DD, Wei YM, Zhou YH, Zheng YL, Zhang P, Chen GY and Kang HY 2024 Identification of candidate genes for adult plant stripe rust resistance transferred from *Aegilops ventricosa* $2N^{v}S$ into wheat via fine mapping and transcriptome analysis. Theoretical and Applied Genetics (2024) 137, 116. DOI: 10.1007/s00122-024-04620-1.
11761.	
11762.	Naz AA, Bungartz A, Serfling A, Kamruzzaman M, Schneider M, Wulff BBH, Pillen, Ballvora A, Oerke E-C, Ordon F and Léon J 2021. *Lr21* diversity unveils footprints of wheat evolution and its new role in broad-spectrum leaf rust resistance. Plant, Cell & Environment 44, 3445-3458. DOI: 10.1111/pce.141443458

11763.	Dibley K, Jost M, McIntosh R, Lagudah E and Zhang P 2024. The wheat stripe rust gene Yr_{CG} is *Yr10*. Nature Communications 15, 3291. DOI: 10.1038/s41467-024-47513-z.
11764.	Alfares W, Bouguennec A, Balfourier F, Gay G, Berges H, Vautrin S, Sourdille S, Bernard M and Feuillet C. 2009 Fine mapping and marker development for the crossability gene *SKr* on chromosome 5BS of hexaploid wheat (*Triticum aestivum* L.). Genetics 183: 469–481. DOI: 10.1534/genetics.109.107706.
11765.	Rey M-D, Martín AC, Higgins J, Swarbreck D, Uauy C, Shaw P and Moore 2017 Exploiting the *ZIP4* homologue within the wheat *Ph1* locus has identified two lines exhibiting homoeologous crossover in wheat-wild relative hybrids. Molecular Breeding 37: 95. DOI: 10.1007/s11032-017-0700-2.
11766.	Boden SA, Langridge P, Sprangenberg G and Able JA 2009 *TaASY1* promotes homologous chromosome interactions and is affected by deletion of *Ph1*. The plant Journal 57: 487-497. DOI: 10.1111/j.1365-313x.2008.03701.
11767.	Di Dio C, Serra H, Sourdille P and Higgins JD 2023 ASYNAPSIS 1 ensures crossover fidelity in polyploid wheat by promoting homologous recombination and suppressing non-homologous recombination. Frontiers in Plant Science XXXX. DOI: 10.3389/fpls.2023.1188347
11768.	Manan F, Shi GJ, Gong HM, Hou HY, Khan H, Leng YQ, Castell-Miller C, Ali S, Faris JD, Zhong SB, Steffenson BJ and Liu ZH 2023 Prevalence and importance of the necrotrophohic effector gene *ToxA* in *Bipolaris sorokiniana* populations collected from spring wheat and barley. Plant Disease 107: 2424-2430. DOI: 10.1094/PDIS-08-22-2011-RE.
11769.	Krolow K 1970 Investigations on compatibility between wheat and rye. Zeitschrift fur Pflanzenzuchtung, 64, 44-72. DOI: NOT AVAILABLE.
11770.	
11771.	Muterko A, Kalendar R and Salina E 2016 Allelic variation at the VERNALIZATION-A1, VRN-B1, VRN-B3, and PHOTOPERIOD-A1 genes in cultivars of *Triticum durum*. Planta 244:1253-1263. DOI: 10.1007/s00425-016-2584-5.
11772.	Xie ZC, Zhang QA, Xia CV, Dong CH, Li DP, Liu X, Kong XY and Zhang 2024 Identification of the early leaf senescence gene *ELS3* in bread wheat (*Triticum aestivum* L.). Planta 259, 5. DOI: 10.1007/s00425-023-04278-x.
11773.	Wang XT, Xiang MJ, Li HZ, Li XX, Mu KQ, Huang S, Zhang YB, Cheng XR, Yang SQ, Yuan XY, Singh RP, Bhavani S, Zeng QD, Wu JH, Kang ZS, Liu SJ and Han DJ 2024 High-density mapping of durable and broad-spectrum stripe rust resistance gene *Yr30* in wheat. Theoretical and Applied Genetics 137, 152. DOI: 10.1007/s00122-024-04654-5.
11774.	Yao DY, Ijaz W, Li Y, Hu JH, Peng WT, Zhang BW, Wen XL, Wang J, Qiu D, Li HI, Xiao SH and Sun GZ 2022. Identification of a *Pm4* allele as a powdery mildew resistance gene in wheat line Xiaomaomai. International Journal of Molecular Science 23, 1194. DOI: 10.3390/ijms23031194.
11775.	O'Hara T, Steed A, Goddard R, Gaurav K, Arora S, Quiroz-Chávez J, Ramírez-González R, Badgami R, Gilbert D, Sánchez-Martín J, Wingen L, Feng C, Jiang M, Cheng SF, Dreisigacker S, Keller B, Wulff BBH, Uauy C and Nicholson P 2024 The wheat powdery mildew resistance gene *Pm4* also confers resistance to wheat blast. Nature Plants 10: 894-993. DOI: 10.1038/s41477-024-01718-8.
11776.	Singh PK, Gahtyari NC, Roy C, Roy KK, He XY, Tembo B, Xu KJ, Juliana P, Sonder K, Kabir MR and Chawade A (2021) Wheat blast: A disease spreading by intercontinental

	jumps and its management strategies. Frontiers in Plant Science 12, 710707. DOI: 10.3389/fpls.2021.710707.
11777.	Klymiuk V, Wiebe K, Chawla HS1, Ens J, Subramaniam R and Pozniak CJ 2024 Coordinated function of paired NLRs confers *Yr84*-mediated stripe rust resistance in wheat. bioXiv11689 DOI: 10.1101/2024.06.14.599041.
11778.	Xu BY, Shen T, Chen H, Li HN, ur Rehman, Lyu SK, Hua L, Wang GP, Zhang CZ, Li KR, Hao Li H, Lan CX, Chen G-Y, Hao M and Chen SS. 2024 Mapping and characterization of rust resistance genes *Lr53* and *Yr35* introgressed from *Aegilops* species. Theoretical and Applied Genetics 137, 113. DOI: 10.1007/s00122-024-04616-x.
11779.	Mago R, Verlin D, Zhang P, Bansal U, Bariana H, Jin Y, Ellis J, Hoxha S and Dundas I 2013 Development of wheat–*Aegilops speltoides* recombinants and simple PCR-based markers for *Sr32* and a new stem rust resistance gene on the 2S#1 chromosome. Theoretical and Applied Genetics 126: 2943-2955. DOI: 10.1007/s00122-013-2184-8.
11780.	Li HY, Li KR, Li HN, Yang C, Perera G, Wang GP, Lyu LK, Hua L, ur Rehman S, Zhang YZ, Ayliffe M, Yu HT and Chen SS 2024. Mapping and candidate gene analysis of an all-stage stem rust resistance gene in durum wheat landrace PI 94701. DOI: 10.20944/preprints202407.0406.v1.
11781.	Wu CJ, Ma KJ, Chen WB, Li JB, Liu MJ, Cheng P, Wang BT and Li QA 2023 Identification and molecular mapping of the gene *YrF* in wheat cultivar Flanders with durable resistance to stripe rust. Plant Disease 107: 2716-2723. DOI: 10.1094/PDIS-11-22-2683-RE.
11782.	
11783.	Yang GT, Boshoff WHP, Li HW, Pretorius ZA, Luo QL, Li B, Li ZS and Zheng Q 2021 Chromosomal composition analysis and molecular marker development for the novel Ug99-resistant wheat–*Thinopyrum ponticum* translocation line WTT34. Theoretical and Applied Genetics 134: 1587-1599. DOI: 10.1007/s00122-021-03796-0.