**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* (R2 = 4.4-8.9%) {10071}.

***QPro.inra-3A*** {10071}. 3A {10071}. **v:**  Renan/Recital {10071}. **ma:** *Xcfd79-3A* – *Xfbb250-3A* (R2 = 4.1-8.3%) {10071}.

***QPro.inra-4D*** {10071}. 4D {10071}. **v:**  Renan/Recital {10071}. **ma:**  Linked to *Xcfd71-4D* (R2 = 4.6-10.3%) {10071}.

***QPro.inra-7D*** {10071}. 7D {10071}. **v:**  Renan/Recital {10071}. **ma:** *Xcfd69-7D* – *Pch1* (R2=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*; R2 = 0.09-0.11) and 4B (*Xgwm368-4B* – *Xwmc617-4B*, R2 = 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*, R2 = 17%), 6AS (*Xp39M37*250-6A, R2 = 17%) and 7BL (*Xgwm577-7B*, R2 = 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***v1 {237}. [*Acph-Mv1* {985}, *Aph-v* {237}]. 4Mv {237}. **tr:**  H-93-33 {984}.

***Acph-R1***. 7R {1457}. 7RS {506}. **ad:**  CS/Imperial.

***Acph-S***s1 {1140}. 4Ss {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 (= 7Agi) and L4 (= 4Agi) 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}, *AdhB* {502}]. 4A {502}. 4AL {504}, {516}. **v:**  CS.

***ADH-B1*** {501}, {502}. [Adh1 {501}, AdhA {502}, Adh-A1 {504}]. 4B {502}. 4BS {504},{516}. **v:**  CS.

***Adh-B1a*** {1442}. [*Adh11* {501}, *Adh-A1a* {1442}]. **v:**  CS. **tv:**  PI 226951 {501}; Malavika {1442}.

***Adh-B1b*** {1442}. [*Adh12* {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}. [*AdhD*{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-Agi1*** {560}, {374}. [*Adh-X1* {361}]. 4Agi {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***v1 {984}. [*ADHmu* {984}, *Adh-Mv1* {985}]. 4Mv {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***e1 {1575}. 6Age {1575}. **ad,su:** Rescue/*Th. elongatum*.

***AMP-Ag***i1 {703}. 6Agi {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***i2 {703}. 4Agi {703}. **ad:** Vilmorin27/*Th. intermedium*.

***AMP-E2*** {703}. 4E {703}. **ad:** CS/*E. elongata*.

***AMP-H2*** {703}. 4H {703}. **ad:**  CS/Betzes.

***AMP-H***ch2 {703}. 4Hch {703}. **ad:** CS/*H. chilense*.

***AMP-J2*** {703}. 4J {703}. **ad:** CS/*Th. junceum*.

***AMP-M***v2 {235}. 4Mv {235}. **su:**  H-93-33 {235}.

***AMP-R2*** {703}. 4RS {702}, {93}. 4R {703}. **ad:**  CS/Imperial.

***AMP-S***l2 {703}. 4SlL {703}. **ad:** CS/*Ae. sharonensis* {180}. **tr:** 4DS.4DL-4SlL {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}. [*Amy6A* {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 6A1m* {1084}]. **v:**  Aka.

***a-AMY-B1***

***a-Amy-B1a*** {7}. [*Amy 4* {1084}, *Amy 6B2o* {1084}, *Amy 6B1* {1084}]. **v:**  CS {7}; Rare.

***a-Amy-B1b***{7}. [*Amy 4m* {1084}, *Amy 6B1o* {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 4m* {1084}, *Amy6B2o* {1084}, *Amy 6B1o* {1084}]. **v:**  Sicco {7}; Rare.

***a-Amy-B1e*** {7}. [*Amy 6B2o* {1084}, *Amy 6B14'* {1084}, *Amy 4m* {1084}]. **v:**  Cappelle-Desprez {7}.

***a-Amy-B1f*** {7}. [*Amy 6B14* {1084}, *Amy 6B2o* {1084}, *Amy4m* {1084}]. **v:**  Sappo {7}.

***a-Amy-B1g*** {7}. [*Amy 4* {1084}, *Amy 6B2o* {1084}, *Amy 6B14* {1084}]. **v:**  Cheyenne {7}.

***a-Amy-B1h*** {7}. [*Amy 6B2o*{1084}, *Amy 6B1o* {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***i1 {374}. 6Agi {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***m1 {13}. 6RmL {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 41* 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*o, and *Amy 6B1*4', considered to be mutually exclusive {1084}] and *Amy 6B2* [with forms *Amy 62* and *Amy 6B2*o {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}. [*Amy7A* {1082}]. 7AL {412, 1082}.

***a-AMY-B2*** {7}. [*Amy7B* {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 7B2m* {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***. [*Amy7D* {1082}]. 7DL {412, 1082}. **v:**  CS.

***a-Amy-D2a*** {412}. [*Amy 7D1* {1084}]. **v:**  CS.

***a-Amy-D2b*** {417}. [*Amy 7D1o* {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***i2 {374}. 7Agi {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***ch2 {1015}. 7Hchbeta {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***b2 {13}. 7Sb{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*t1 alleles were predominant in 60 accessions of *T. tauschii* {1578}.

***b-AMY-Ag***i1 {168}, {13}. 4Agi {168}. **ad:** Vilmorin27/*Th. intermedium*.

***b-AMY-C1*** {1278}. *B* {1278}. **ad:** *Aestivum* cv. Alcedo /*Ae. caudata* line B.

***b-AMY-Eb1*** {661}. 5EbL {661}. **tr:** 5AS.5EbL.

***b-AMY-H1***. 4H {1153}. **ad:**  CS/Betzes.

***b-AMY-Hch1*** {13}. 4Hch {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-Sl1*** {13}. *D* {13}. 4Sl {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-Hch1*** {708}. 7Hch {708}. **su:** CS/*H. chilense*.

***EP-Ht1*** {1037}. 7HtS {1037}. **ad:** CS/*E. trachycaulus*.

***EP-Mv1*** {985}. [*Ep-Mv1* {985}]. 7MvL. **su:** 7Mv.

***EP-R1***{92}, {708}, {266}. 6RL {92}. **ad:**  CS/Imperial.

***EP-Sb1*** {708}. 7Sb {708}. **su:** Holdfast/*Ae. bicornis*.

***EP-Sl1*** {517}. 4Sl {517}. **ad:** CS/*Ae. longissima*.

***EP-Ss1*** {1140}. 7Ss {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***. [*EstA*{61}]. 3AS {60}. **v:**  CS.

***EST-B1***. [*EstB*{61}]. 3BS {100}. 3B {60}. **v:**  CS.

***EST-D1***. [*EstD*{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***. [*EstR* {61}]. 3R {1254,60}. **ad:**  CS/Imperial {60}; Holdfast/King II {100}; Kharkov/Dakold {100}.

***EST-S11*** {814}. 3S1 {814}. **ad:** CS/*Ae. longissima*.

**EST-2**

EST-2 is a coleoptile-specific monomeric enzyme that electrofocuses at low pI.

***EST-A2***. [*Est-2A* {585}]. 3A {585}. **v:**  CS.

***EST-B2***. [*Est-2B* {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-2D* {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-3B* {585}]. 7BS {585}. **v:**  CS.

***EST-D3***. [*Est-3D* {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-4A* {585}]. 6AL {585, 919}. **v:**  CS.

***EST-B4***. [*Est-4B* {585}]. 6BL {585, 919}. **v:**  CS.

***EST-D4***. [*Est-4D* {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 (= 6Agi) 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*t5 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*t5 (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 designaged *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-Agi5*** {374}. 3Agi {374}. **ad:** Vilmorin 27/*Th. intermedium*.

***EST-H5*** {10}. 3H {10}. **ad:**  CS/Betzes.

***EST-Hch5*** {10}. 3Hch {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-Rm5*** {10}. [*EstB* {737}]. 6RmL {737}. 6Rm {10}. **ad:** CS/*S. montanum*.

***EST-Sb5*** {10}. 3Sb {10}. **su,ad:** CS/*Ae. bicornis*.

***EST-Sl5*** {10}. 3Sl {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}. 2E {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-Rm7*** {812}. 2Rmalpha {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*t1 was found in 60 accessions of *Ae. tauschii* {1578}.

***GPI-Agi1***. [*Gpi-X1* {361}]. 1Agi {361}. **ad:** Vilmorin 27/*Th. intermedium*.

***GPI-E1*** {518}. 1ES {518}. **ad:** CS/*E. elongata*.

***GPI-H1*** {1153}. 1HS {1153}. **ad:**  CS/Betzes.

***GPI-Hch1*** {195}. 1Hch {195}. **ad:** CS/*H. chilense*.

***GPI-R1*** {195}. 1R {195}.1RS {779}. **ad:**  CS/King II {195}. **al:**  2a, 2b, and R14 {779}.

***GPI-Rm1*** {195}. 1R {195}. **ad:** CS/*S. montanum*.

***GPI-Sl1*** {1228}. 1S1S {1228}.1S1 {517}. **ma:**  In *Ae. longissima 2 x Ae. longissima 10, GPI-Sl1*, two glutenin loci, and three gliadin loci were mapped relative to one another as follows: *GLU-Sl1*– 15.9 cM– *GPI-Sl1*– 38 cM– *GLI-Sl4*– 7.1 cM– *GLU-Sl3*– 0.9 cM– *GLU-Sl1*– 5.6 cM– *GLI-Sl5*{1228}; *GLU-Sl1* is located in 1SlL and the other loci are in 1SlS.

***GPI-Ss1*** {1140}. 1Ss {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-Age2*** {1575}. 6Age {1575}. **ad,su:** Rescue/*Th. elongatum*.

***GOT-E2*** {518}. 6EBeta {518}. **ad:** CS/*E. elongata*.

***GOT-H2*** {520}. 6H {520}. **ad:**  CS/Betzes.

***GOT-Ht2*** {1037}. 6Ht {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-Age3*** {521}. 3AgeL {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-Hch3*** {351}. 3Hch {351}. **ad:** MA/*H. chilense*.

***GOT-R3*** {1457}. [Got3 {1559}]. 3R {1457}. **ad:**  CS/Imperial {1457}; Holdfast/ King II {1253}; Kharkov/Dakold {1253}.

***GOT-Ss3*** {1140}. 3Ss {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-Ss2*** {1140}. 5Ss {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-Hch1*** {352}. 1Hch {352}. **ad:** MA/*H. chilense*.

***MDH-R1***. [*Mdh2-1* {1252}]. 1RL {1252}. **ad:**  CS/Imperial 1R; Kharkov/Dakold 1R; Holdfast/King II 1RL.

***MDH-Ss1*** {1140}. 1Ss {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-Hch1*** {12}. 1Hch {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-Age4***. 7AgeS {694}. **tr:** Certain CS 7D/*Ag*e lines.

***PER-Agi4***. [*Per-Agi3* {374}]. 7Agi {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-Sl5*** {816}. 2Sl {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-Sl1***. 3SlS {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}]. 7AmS {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}, 1Hch {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-Agi1***. [*Pgm-X1* {361}]. 4Agi {361}. **ad:** Vilmorin 27/*Th. intermedium*.

***PGM-H1***. [*Pgm-b1* {90}]. 4H {90}. **ad:**  CS/ Betzes.

***PGM-Hch1*** {351}. 4Hch {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-Ht1*** {1037}. 5Ht {1037}. **ad:** CS/*E. trachycaulus*.

***SKDH-Mv1*** {985}. [*Skdh-Mv1* {985}]. 5Mv. **su:** 5Mv(5A), 5Mv(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-Sl1*** {85}. 5SlS {85}. **ad:**  CS/ *Ae. longissima*.

***SKDH-Ss1*** {1140}. 5Ss {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-Ss1*** {1140}. 2Ss {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-Sl1*** {1139}. 3Sl {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-Agi2*** {374}. 5Agi {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-Sl2*** {1139}. 5Sl {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-Age2*** {1575}. 6Age {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-Age1*** {1575}. 6Age {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-Sl1*** {189}. 6Sl {189}. **ad:** CS/*Ae. longissima*.

***ACO-Ss1*** {1140}. 6Ss {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-Mv2*** {1341}. [*Aco-Mv2* {985}]. 5Mv. **ad:** 5Mv(5A),5Mv(5D).

***ACO-R2*** {189}. 5RL {189}. **ad:**  CS/King II 5R; Holdfast/ King II 5RL.

***ACO-Ss2*** {1140}. 4Ss {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-Hch1*** {813}. 4Hch {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****11* {813}. 4Sl {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* F2 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-Sl3*** {813}. 3SlL {813}. **ad:** CS/*Ae. longissima*; CS/*Ae. sharonesis* (3Sl).

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-Mv1*** {985}. [*Adk-Mv1* {985}]. 7MvL. **su:** 7Mv(7D).

***ADK-R1*** {91}. 7RL {91}. **ad:**  CS/Imperial; Holdfast/King II.

***ADK-U1*** {91}. *E* {91}. **ad:** CS/*Ae. umbellulata*.

***ADK-Agi1*** {91}. 7Agi {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* F2 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}. 2AmL {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– *Xgwm1070-2ª* {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-A1ma* {10805}]. **dv:**  PI 191146, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A1aa*** {10805}. [*Glu-A1mb* {10805}]. **dv:**  PI 190946, *T. monococcum* L. ssp. *monococcum* {10805}.

***Glu-A1ab*** {10805}. [*Glu-A1mc* {10805}]. **dv:**  PI 191098, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A1ac*** {10806}. [*Glu-Au1-I* {10806}]. **dv:**  PI 428319 {10806}.

***Glu-A1ad*** {10806}. [*Glu-Au1-II* {10806}]. **dv:**  PI 428232 {10806}.

***Glu-A1ae*** {10806}. [*Glu-Au1-III* {10806}]. **dv:**  PI 428240 {10806}.

***Glu-A1af*** {10806}. [*Glu-Au1-IV* {10806}]. **dv:**  PI 428335 {10806}.

***Glu-A1ag*** {10806}. [*Glu-Au1-V* {10806}]. **dv:**  PI 538741 {10806}.

***Glu-A1ah*** {10806}. [*Glu-Au1-VI* {10806}]. **dv:**  PI 428230 {10806}.

***Glu-A1ai*** {10806}. [*Glu-Au1-VII* {10806}]. **dv:**  PI 428253 {10806}.

***Glu-A1aj*** {10806}. [*Glu-Au1-VIII* {10806}]. **dv:**  PI 427328 {10806}.

***Glu-A1ak*** {10806}. [*Glu-Au1-IX* {10806}]. **dv:**  PI 428327 {10806}.

***Glu-A1al*** {10806}. [*Glu-Au1-X* {10806}]. **dv:**  PI 428256 {10806}.

***Glu-A1am*** {10806}. [*Glu-Au1-XI* {10806}]. **dv:**  PI 428224 {10806}.

***Glu-A1an*** {10806}. [*Glu-Au1-XII* {10806}]. **dv:**  PI 428228 {10806}.

***Glu-A1ao*** {10806}. [*Glu-Au1-XIII* {10806}]. **dv:**  PI 538724 {10806}.

***Glu-A1ap*** {10806}. [*Glu-Au1-XIV* {10806}]. **dv:**  TRI 6734 {10806}.

***Glu-A1aq*** {10806}. [*Glu-Au1-XV* {10806}]. **dv:**  TRI 11494 {10806}.

***Glu-A1ar*** {10806}. [*Glu-Au1-XVI* {10806}]. **dv:**  TRI 11495 {10806}.

***Glu-A1as*** {10806}. [*Glu-Au1-XVII* {10806}]. **dv:**  PI 428217 {10806}.

***Glu-A1at*** {10806}. [*Glu-Au3-XVIII* {10806}]. **dv:**  PI 428225 {10806}.

***Glu-A1au*** {10806}. [*Glu-Au3-XIX* {10806}]. **dv:**  PI 538733 {10806}.

***Glu-A1av*** {10806}. [*Glu-Au3-XX* {10806}]. **dv:**  PI 428196 {10806}.

***Glu-A1aw*** {10806}. [*Glu-Au3-XXI* {10806}]. **dv:**  PI 538724 {10806}.

***Glu-A1ax*** {10806}. [*Glu-Au3-XXII* {10806}]. **dv:**  PI 428191 {10806}.

***Glu-A1ay*** {10806}. [*Glu-Au3-XXIII* {10806}]. **dv:**  TRI 6734 {10806}.

***Glu-A1az*** {10806}. [*Glu-Au3-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}. 7OE+7OE+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+7OE+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}. 7OE {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}. 7OE+8 {10808}. **v:**  ACA 303 {10808}; Courtot {10808}; Demai 3 {10808}; Shinchunaga {10808}.

***Glu-B1cc*** {10808}. 7OE+8a\* {10808}. **v:**  Klein Jabal 1 {10808}; Pioneer {10808}; ProINTA {10808}; Redemon {10808}.

***Glu-B1cd*** {10808}. 7OE+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 2t denoting its origin in the *Ae. tauschii* genome) +T1+T2), *Glu-D1af* (encoding 3 (or 3t)+T1+T2) and *Glu-D1ag* (encoding 1.5 (or1.5t)+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 12.4t (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}.2t+12.2t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1y*** {755}. 3t+12.2t {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}. 2.1t+12.2t {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}. 1.5t+12.2t {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}. 1.5t+10.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1ar*** {03124}. 2t+10.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1as*** {03124}. 1.5t+10.2t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1at*** {03124}. 3t+10.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1au*** {03124}. 2.1t+10.2t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1av*** {03124}. 2t+12.3t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1aw*** {03124}. 1t+10t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1ax*** {03124}. 1t+12t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1ay*** {03124}. 1t+10.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1az*** {03124}. 4t+12.2t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1ba*** {03124}. 1t+12.3t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bb*** {03124}. 1.5t+11t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bc*** {03124}. 1.5t+10.3t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bd*** {03124}. 1t+11t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1be*** {03124}. 2.1t+12.4t {3124}. **dv:** *Ae. tauschii*.

***Glu-D1bf*** {03124}. 2t+12.1t {03124}. **dv:** *Ae. tauschii* {03124}.

***Glu-D1bg*** {03124}. 3t+10.2t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bh*** {03124}. 4t+10.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bi*** {03124}. 4t+10.2t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bj*** {03124}. 5t+11t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bk*** {03124}. 5t+10.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1bl*** {03124}. 5t+12.2t {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+10.1t {10426}. **tv:** *Ae. tauschii* TD81 {10426}.   
Subunit 10.1t 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}. 1.6t+12.3t {10642}. **dv:** *Ae. tauschii* TD16 {10642}.

***Glu-D1bt*** {10568}. 2.1t+12t {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-Agi1*** {374}. 1Agi {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* (Ee 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-Hch1***. 1Hch {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 1Hch, 2Hch and 3Hch were previously referred to as Hcha, Hchb and Hchc {03112}.

***Glu-Hch1a*** {03114}. 1Hch {03114}. **al:** *H. chilense* accession H1 {03114}.

***Glu-Hch1b*** {03114}. 2Hch {03114}. **al:** *H. chilense* accession H11 {03114}.

***Glu-Hch1c*** {03114}. 3Hch {03114}. **al:** *H. chilense* accession H7 {03114}.

***Glu-Hch1d*** {03114}. 4Hch {03114}. **al:** *H. chilense*  accesion H16{03114}.

***Glu-Hch1e*** {03114}. 5Hch {03114}. **al:** *H. chilense*  accession H47 {03114}.

***Glu-Hch1f*** {03114}. 6Hch {03114}. **al:** *H. chilense*  accession H220 {03114}.

***Glu-Hch1g*** {03114}. 7Hch {03114}. **al:** *H. chilense* accession H293 {03114}.

***Glu-Hch1h*** {03114}. 8Hch {03114}. **al:** *H. chilense* accession H297 {03114}.

***Glu-Hch1i*** {03114}. 9Hch {03114}. **al:** *H. chilense* accession H252 {03114}.

***Glu-Hch1j*** {03114}. 10Hch {0 3114}. **al:** *H. chilense* accession H210 {03114}.

***GLU-Ht1*** {1037}. 1HtL {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}. 1r-4r {03116}. **v:**  Indiana hexaploid triticale {03116}.

***Glu-R1b*** {03116}. 2r-6.5r {03116}. **v:**  Graal hexaploid triticale {03116}.

***Glu-R1c*** {03116}. 6r-13r {03116}. **v:**  Almao hexaploid triticale {03116}.

***Glu-R1d*** {03116}. 2r-9r {03116}. **v:**  Olympus hexaploid triticale {03116}.

***Glu-R1e*** {03116}. 6.5r {03116}. **v:**  Clercal hexaploid triticale {03116}.

***Glu-R1f*** {03115}. 0.8r-6r {03115}. **v:**  Carmara hexaploid triticale {03115}.

***Glu-R1g*** {03115}. 5.8r {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 6.5r (*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 6r 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-Rm***1 {1339}. 1RmL {1340, 1339}. **ad:** CS/*S. montanum* {1340, 1339}.

***GLU-Sl1*** {1228}. 1SlL {1228}. **ma:**  In *Ae. longissima 2 /Ae. longissima 10, GLU-S*l1, G*LU*-*Sl3*, one glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one and other {1228} as follows: *GLU-S*l1– 15.9 cM– *GPI-S*l1– 38 cM– *GLI-S*l4– 7.1 cM– *GLU-S*l3– 0.9 cM– *GLI-S*l1– 5.6 cM– *GLI-S*l5. *GLU-S*l1 is located in 1SlL and the other loci are in 1SlS.

***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}. 7OE {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}. Dtx1.5 {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 Dty10 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}. 1t {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}. [1.6t {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}. 12.1t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1-2s*** {03124}. 12.3t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1-2t*** {03124}. 12.4t {03124}. **dv:** *Ae. tauschii*.

***Glu-D1-2u*** {10306}. Dty10 {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 Dtx1.5 {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}. 1r {03116}. **v:**  Indiana hexaploid triticale {03116}.

***Glu-R1-1b*** {03116}. 2r {03116}. **v:**  Graal hexaploid triticale {03116}.

***Glu-R1-1c*** {03116}. 6r {03116}. **v:**  Alamo hexaploid triticale {03116}.

***Glu-R1-1d*** {03115}. 0.8r {03115}. **v:**  Carmara hexaploid triticale {03115}.

***Glu-R1-1e*** {03115}. 5.8r {03115}. **v:**  Arrayan hexaploid triticale {03115}.

***Glu-R1-2***. 1R, 1RL.

***Glu-R1-2a*** {03116}. 4r {03116}. **v:**  Indiana hexaploid triticale {03116}.

***Glu-R1-2b*** {03116}. 6.5r {03116}. **v:**  Graal hexaploid triticale {03116}.

***Glu-R1-2c*** {03116}. 13r {03116}. **v:**  Alamo hexaploid triticale {03116}.

***Glu-R1-2d*** {03116}. 9r {03116}. **v:**  Olympus hexaploid triticale {03116}.   
There was difficulty in assigning subunit 6r 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 (Mr 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 Mr 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 F6 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 1Am 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-A3ma* {10805}]. **dv:**  PI 190947, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A3u*** {10805}. [*Glu-A3mb* {10805}]. **dv:**  PI 190946, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A3v*** {10805}. [*Glu-A3mc* {10805}]. **dv:**  BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A3w*** {10805}. [*Glu-A3md* {10805}]. **dv:**  PI 191097, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A3x*** {10805}. [*Glu-A3me* {10805}]. **dv:**  BGE-013624, *T. monococcum* ssp. *Monococcum* {10805}.

***Glu-A3y*** {10805}. [*Glu-A3mf* {10805}]. **dv:**  PI 191094, *T. monococcum* ssp. *monococcum* {10805}.

***Glu-A3z*** {10806}. [*Glu-Au3-I* {10806}]. **dv:**  PI 428139, *T. urartu* {10806}.

***Glu-A3aa*** {10806}. [*Glu-Au3-II* {10806}]. **dv:**  PI 428327, *T. urartu* {10806}.

***Glu-A3ab*** {10806}. [*Glu-Au3-III* {10806}]. **dv:**  PI 428340, *T. urartu* {10806}.

***Glu-A3ac*** {10806}. [*Glu-Au3-IV* {10806}]. **dv:**  PI 428322, *T. urartu* {10806}.

***Glu-A3ad*** {10806}. [*Glu-Au3-V* {10806}]. **dv:**  PI 428188, *T. urartu* {10806}.

***Glu-A3ae*** {10806}. [*Glu-Au3-*VI {10806}]. **dv:**  PI 428203, *T. urartu* {10806}.

***Glu-A3af*** {10806}. [*Glu-Au3-VII* {10806}]. **dv:**  PI 428255, *T. urartu* {10806}.

***Glu-A3ag*** {10806}. [*Glu-Au3-VIII* {10806}]. **dv:**  PI 428328, *T. urartu* {10806}.

***Glu-A3ah*** {10806}. [*Glu-Au3-IX* {10806}]. **dv:**  PI 428256, *T. urartu* {10806}.

***Glu-A3ai*** {10806}. [*Glu-Au3-X* {10806}]. **dv:**  PI 428217, *T. urartu* {10806}.

***Glu-A3aj*** {10806}. [*Glu-Au3-XI* {10806}]. **dv:**  PI 428335, *T. urartu* {10806}.

***Glu-A3ak*** {10806}. [*Glu-Au3-XII* {10806}]. **dv:**  PI 428186, *T. urartu* {10806}.

***Glu-A3al*** {10806}. [*Glu-Au3-XIII* {10806}]. **dv:**  PI 428183, *T. urartu*{10806}.

***Glu-A3am*** {10806}. [*Glu-Au3-XIV* {10806}]. **dv:**  TRI 11563, *T. urartu* {10806}.

***Glu-A3an*** {10806}. [*Glu-Au3-XV* {10806}]. **dv:**  PI 427328, *T. urartu* {10806}.

***Glu-A3ao*** {10806}. [*Glu-Au3-XVI* {10806}]. **dv:**  PI 428253, *T. urartu* {10806}.

***Glu-A3ap*** {10806}. [*Glu-Au3-XVII* {10806}]. **dv:**  PI 538735, *T. urartu* {10806}.

***Glu-A3aq*** {10806}. [*Glu-Au3-XVIII* {10806}]. **dv:**  PI 428225, *T. urartu* {10806}.

***Glu-A3ar*** {10806}. [*Glu-Au3-XIX* {10806}]. **dv:**  PI 538733, *T. urartu* {10806}.

***Glu-A3as*** {10806}. [*Glu-Au3-XX* {10806}]. **dv:**  PI 428196, *T. urartu* {10806}.

***Glu-A3at*** {10806}. [*Glu-Au3-XXI* {10806}]. **dv:**  PI 538724, *T. urartu* {10806}.

***Glu-A3au*** {10806}. [*Glu-Au3-XXII* {10806}]. **dv:**  PI 428191, *T. urartu* {10806}.

***Glu-A3av*** {10806}. [*Glu-Au3-XXIII* {10806}]. **dv:**  TRI 6734, *T. urartu* {10806}.

***Glu-A3aw*** {10806}. [*Glu-Au3-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-Sl3*** {1228}, {480}. 1Sl {480}. 1S1S {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*l1– 15.9 cM – *GPI-S*l1– 38 cM– *GLI-S*l4– 7.1 cM– *GLU-S*l3– 0.9 cM– *GLI-S*l1– 5.6 cM– *GLI-S*l5. *GLU-S*l1 is located in 1SlL and the other loci are in 1S1S.

***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-A1ma* {10805}]. **dv:**  PI 191146, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1y*** {10805}. [*Gli-A1mb* {10805}]. **dv:**  PI 190947 *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1z*** {10805}. [*Gli-A1mc* {10805}]. **dv:**  PI 190946, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1aa*** {10805}. [*Gli-A1md* {10805}]. **dv:**  PI 191097, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1ab*** {10805}. [*Gli-A1me* {10805}]. **dv:**  BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1ac*** {10805}. [*Gli-A1mf* {10805}]. **dv:**  BGE-013626, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1ad*** {10805}. [*Gli-A1mg* {10805}]. **dv:**  BGE-013628, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A1ae*** {10811}. [*Gli-Au1-I* {10811}]. **dv:**  PI-428333, *T. urartu* {10811}.

***Gli-A1af*** {10811}. [*Gli-Au1-II* {10811}]. **dv:**  PI-428319, *T. urartu* {10811}.

***Gli-A1ag*** {10811}. [*Gli-Au1-III* {10811}]. **dv:**  PI-428335, *T. urartu* {10811}.

***Gli-A1ah*** {10811}. [*Gli-Au1-IV* {10811}]. **dv:**  PI-428323, *T. urartu* {10811}.

***Gli-A1ai*** {10811}. [*Gli-Au1-V* {10811}]. **dv:**  PI-428231, *T. urartu* {10811}.

***Gli-A1aj*** {10811}. [*Gli-Au1-VI* {10811}]. **dv:**  PI-428194, *T. urartu* {10811}.

***Gli-A1ak*** {10811}. [*Gli-Au1-VII* {10811}]. **dv:**  PI-428256, *T. urartu* {10811}.

***Gli-A1al*** {10811}. [*Gli-Au1-VIII* {10811}]. **dv:**  PI-428234, *T. urartu* {10811}.

***Gli-A1am*** {10811}. [*Gli-Au1-IX* {10811}]. **dv:**  PI-428320, *T. urartu* {10811}.

***Gli-A1an*** {10811}. [*Gli-Au1-X* {10811}]. **dv:**  PI-428255, *T. urartu* {10811}.

***Gli-A1ao*** {10811}. [*Gli-Au1-XI* {10811}]. **dv:**  PI-428241, *T. urartu* {10811}.

***Gli-A1ap*** {10811}. [*Gli-Au1-XII* {10811}]. **dv:**  PI-428235, *T. urartu* {10811}.

***Gli-A1aq*** {10811}. [*Gli-Au1-XIII* {10811}]. **dv:**  PI-428183, *T. urartu* {10811}.

***Gli-A1ar*** {10811}. [*Gli-Au1-XIV* {10811}]. **dv:**  PI-428317, *T. urartu* {10811}.

***Gli-A1as*** {10811}. [*Gli-Au1-XV* {10811}]. **dv:**  PI-427328, *T. urartu* {10811}.

***Gli-A1at*** {10811}. [*Gli-Au1-XVI* {10811}]. **dv:**  PI-428327, *T. urartu* {10811}.

***Gli-A1au*** {10811}. [*Gli-Au1-XVII* {10811}]. **dv:**  PI-428253, *T. urartu* {10811}.

***Gli-A1av*** {10811}. [*Gli-Au1-XVIII* {10811}]. **dv:**  PI-428224, *T. urartu* {10811}.

***Gli-A1aw*** {10811}. [*Gli-Au1-XIX* {10811}]. **dv:**  PI-538727, *T. urartu* {10811}.

***Gli-A1ax*** {10811}. [*Gli-Au1-XX* {10811}]. **dv:**  PI-428211, *T. urartu* {10811}.

***Gli-A1ay*** {10811}. [*Gli-Au1-XXI* {10811}]. **dv:**  PI-538724, *T. urartu* {10811}.

***Gli-A1az*** {10811}. [*Gli-Au1-XXII* {10811}]. **dv:**  PI-428191, *T. urartu* {10811}.

***Gli-A1ba*** {10811}. [*Gli-Au1-XXIII* {10811}]. **dv:**  TRI-6735, *T. urartu* {10811}.

***Gli-A1bb*** {10811}. [*Gli-Au1-XXIV* {10811}]. **dv:**  TRI-11494, *T. urartu* {10811}.

***Gli-A1bc*** {10811}. [*Gli-Au1-XXV* {10811}]. **dv:**  TRI-6734, *T. urartu* {10811}.

***Gli-A1bd*** {10811}. [*Gli-Au1-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-Agi1***. 1Agi {168}. **ad:** Vilmorin 27/*Th. intermedium*.

***GLI-E1*** {781}. 1ES {781}. **ad:** CS/*E. elongata*. ***GLI-Ht1*** {1037}. 1Htp {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-Rm1*** {1340}. 1RmS {1340}. **ad:** CS/*S. montanum*.

***GLI-Sl1*** {573}. 1Sl {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-Dt1*) and *GLU-D1* (strictly *GLU-Dt1*), 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-Dt1* 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-Sl4* 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-A2ma* {10805}]. **dv:**  BGE-013630, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2al*** {10805}. [*Gli-A2mb* {10805}]. **dv:**  PI 094740, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2am*** {10805}. [*Gli-A2mc* {10805}]. **dv:**  PI 190942, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2an*** {10805}. [*Gli-A2md* {10805}]. **dv:**  PI 190947, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2ao*** {10805}. [*Gli-A2me* {10805}]. **dv:**  PI 190946, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2ap*** {10805}. [*Gli-A2mf* {10805}]. **dv:**  BGE-013626, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2aq*** {10805}. [*Gli-A2mg* {10805}]. **dv:**  PI 191095, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2ar*** {10805}. [*Gli-A2mh* {10805}]. **dv:**  BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2as*** {10805}. [*Gli-A2mi* {10805}]. **dv:**  PI 191096, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2at*** {10805}. [*Gli-A2mj* {10805}]. **dv:**  BGE-020466, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2au*** {10805}. [*Gli-A2mk* {10805}]. **dv:**  BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2av*** {10805}. [*Gli-A2ml* {10805}]. **dv:**  BGE-029108, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2aw*** {10805}. [*Gli-A2mm* {10805}]. **dv:**  BGE-013627, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2ax*** {10805}. [*Gli-A2mn* {10805}]. **dv:**  BGE-001937, *T. monococcum* ssp. *monococcum* {10805}.

***Gli-A2ay*** {10811}. [*Gli-Au2-I* {10811}]. **dv:**  PI-428333, *T. urartu* {10811}.

***Gli-A2az*** {10811}. [*Gli-Au2-II* {10811}]. **dv:**  PI-428320, *T. urartu* {10811}.

***Gli-A2ba*** {10811}. [*Gli-Au2-II* {10811}]. **dv:**  PI-428230, *T. urartu* {10811}.

***Gli-A2bb*** {10811}. [*Gli-Au2-IV* {10811}]. **dv:**  PI-428319, *T. urartu* {10811}.

***Gli-A2bc*** {10811}. [*Gli-Au2-V* {10811}]. **dv:**  PI-428239, *T. urartu* {10811}.

***Gli-A2bd*** {10811}. [*Gli-Au2-VI* {10811}]. **dv:**  PI-428336, *T. urartu* {10811}.

***Gli-A2be*** {10811}. [*Gli-Au2-VII* {10811}]. **dv:**  PI-428235, *T. urartu* {10811}.

***Gli-A2bf*** {10811}. [*Gli-Au2-VIII* {10811}]. **dv:**  PI-428234, *T. urartu* {10811}.

***Gli-A2bg*** {10811}. [*Gli-Au2-IX* {10811}]. **dv:**  PI-428183, *T. urartu* {10811}.

***Gli-A2bh*** {10811}. [*Gli-Au2-X* {10811}]. **dv:**  PI-428256, *T. urartu* {10811}.

***Gli-A2bi*** {10811}. [*Gli-Au2-XI* {10811}]. **dv:**  PI-428255, *T. urartu* {10811}.

***Gli-A2bj*** {10811}. [*Gli-Au2-XII* {10811}]. **dv:**  PI-428224, *T. urartu* {10811}.

***Gli-A2bk*** {10811}. [*Gli-Au2-XIII* {10811}]. **dv:**  PI-428208, *T. urartu* {10811}.

***Gli-A2bl*** {10811}. [*Gli-Au2-XIV* {10811}]. **dv:**  PI-428202, *T. urartu* {10811}. ]

***Gli-A2bm*** {10811}. [*Gli-Au2-XV* {10811}]. **dv:**  PI-428217, *T. urartu* {10811}.

***Gli-A2bn*** {10811}. [*Gli-Au2-XVI* {10811}]. **dv:**  PI-427328, *T. urartu* {10811}.

***Gli-A2bo*** {10811}. [*Gli-Au2-XVII* {10811}]. **dv:**  PI-428317, *T. urartu* {10811}.

***Gli-A2bp*** {10811}. [*Gli-Au2-XVIII* {10811}]. **dv:**  PI-428253, *T. urartu* {10811}.

***Gli-A2bq*** {10811}. [*Gli-Au2-XIX* {10811}]. **dv:**  PI-538742, *T. urartu* {10811}.

***Gli-A2br*** {10811}. [*Gli-Au2-XX* {10811}]. **dv:**  PI-428232, *T. urartu* {10811}.

***Gli-A2bs*** {10811}. [*Gli-Au2-XXI* {10811}]. **dv:**  PI-428188, *T. urartu* {10811}.

***Gli-A2bt*** {10811}. [*Gli-Au2-XXII* {10811}]. **dv:**  PI-428244, *T. urartu* {10811}.

***Gli-A2bu*** {10811}. [*Gli-Au2-XXIII* {10811}]. **dv:**  PI-538733, *T. urartu* {10811}.

***Gli-A2bv*** {10811}. [*Gli-Au2-XXIV* {10811}]. **dv:**  PI-428212, *T. urartu* {10811}.

***Gli-A2bw*** {10811}. [*Gli-Au2-XXV* {10811}]. **dv:**  TRI-6734, *T. urartu* {10811}.

***Gli-A2bx*** {10811}. [*Gli-Au2-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-Agi2*** {374}. 6Agi {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-Rm2*** {1339}. 6Rm {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-Sl2*** {573}. 6Sl {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-Sl3*** {1228}. 1S1S {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*l1– 15.9 cM– *GPI-S*l1– 38 cM– *GLI-S*l4– 7.1 cM– *GLU-S*l3– 0.9 cM– *GLI-S*l1– 5.6 cM– *GLI-S*l5. *GLU-S*l1 is located in 1SlL and the other loci are in 1SlS.

***Gli-V3*** {111}. 4VL {111}. **ad:** Creso/*D. villosum*.

**GLI-4**

It is not clear how *GLI-Sl4* and *GLI-Sl5* 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 1Am 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-DtT1* locus (currently included in the Catalogue as locus (*GLI-DT1*). *GLI-A7* was located 0.69 cM from *GLI-Dt1* {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-Sl2*** {701}. 1Sl {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 4Hch and 7Hch {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-Agi2*** {699}. 5Agi {699}. **ad:**  Vilmorin 27/ *Th. intermedium*.

***TI-Mt2*** {699}. 5Mt {699}. **ad:** CS/*Ae. mutica*.

***TI-R2*** {699}. 5RL {699}. **ad:**  CS/Imperial. **su:**  CS/King II.

***TI-Sl2*** {699}. 5SlL {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}. 5Agi {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-Sl1*** {818}. 5Sl {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 5AmS.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-Am1*** {0083}. 5AmS {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-Am1* is completely linked to *GSP-Am1* {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-Sb1***{03108}. **dv:** *Ae. bicornis* spp. *typica* TA1954, TA1942 {03108}.

***Pina-Sl1*** {03108}. **dv:** *Ae. longissima* spp. *longissima* TA1912 (GenBank AY622790) {3108}; *Ae. longissima* spp. *nova* TA1921 (GenBank AY622791) {03108}.

***Pina-Ss1***{03108}. **dv:** *Ae. searsii* TA1837, TA1355 (GenBank AY622792) {03108}.

***Pina-Ssh1***{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-Hch1*** {817}. 7Hch {817}. **ad:** CS/*H. chilense*.

***WSP-Sl1*** {817}. 7Sl {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-BS1g*** {10587}. **al:** *Ae. speltoides* 33 {10587}.

***Wx-BSL1h*** {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-DDN1g*** {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}.