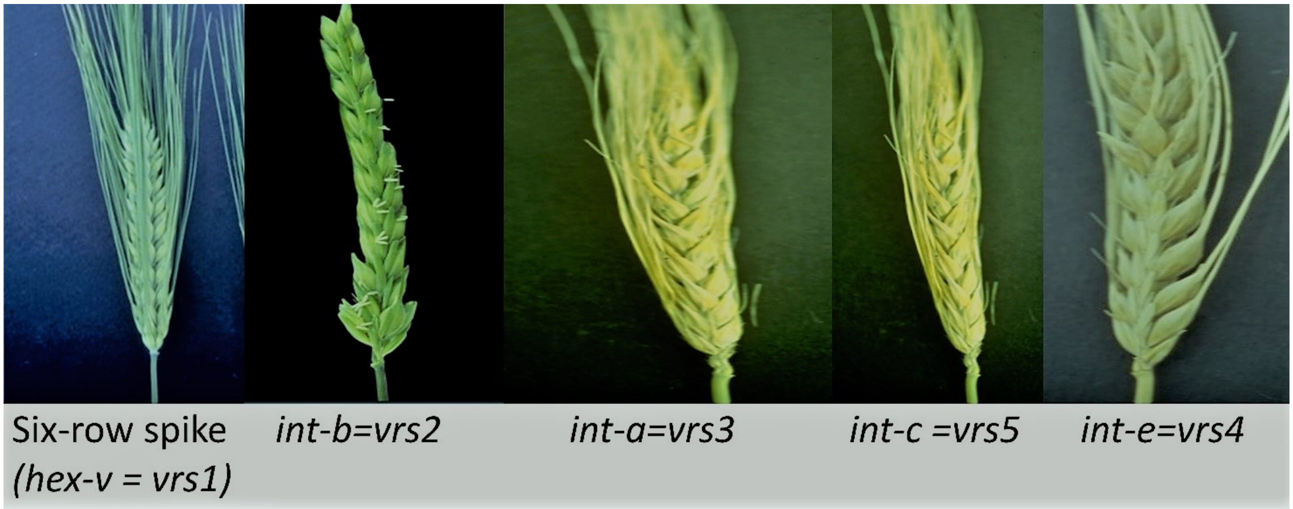
Barley Genetics Newsletter
Volume 48 - 2018

Editorial Committee: P. Bregitzer - U. Lundqvist

A Seasonal View of Barley Research Plots *Photos courtesy of Kathy Satterfield*



Barley *vrs* Mutant Spike Morphology *Photos courtesy of Udda Lundqvist*

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<<Information about the Barley Genetics Newsletter>>

The Barley Genetics Newsletter is published electronically at
https://wheat.pw.usda.gov/ggpages/bgn

The Barley Genetics Newsletter (BGN) was first published in 1971, and in the years since then has served to disseminate to the barley community announcements, memoria, informal research reports, and detailed descriptions of barley genetic stocks.

In recent years, new forms of rapid communication of ideas and data, principally on-line, have reduced the demand for many aspects of BGN. At the 12th International Barley Genetics Symposium, held in Minneapolis, Minnesota, USA June 26-30, 2016, discussion of the fate of BGN resulted in the consensus that a forum for informal communication, memoria, documentation of resources, and any other topic of interest to the community was beneficial.

Thanks to resources provided by GrainGenes, past issues of BGN are preserved and available in electronic format. GrainGenes will serve also as a mechanism for publishing new submissions from the barley community.

Contributions to the Barley Genetics Newsletter can be sent to Phil Bregitzer, phil.bregitzer@usda.gov. Dr. Bregitzer can be reached also at 208-397-4162 ext. 116.

Acknowledgements

BGN has been made possible by the contributors of research reports, the diligence of the many coordinators, and by the special efforts of leaders in the barley genetics community. Of special note, the compilation of the detailed and extensive new and updated barley genetic stock descriptions published in the last several issues of BGN has been made possible by the time and expertise of Jerry Franckowiak and Udda Lundqvist. Special thanks to the USDA-ARS GrainGenes team.

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Diter von Wettstein 1929-2017, In Memoriam

D. von Wettstein

Diter von Wettstein was born in 1929 into the fourth generation of the prominent Austrian scientist family von Kerner – von Wettstein. Several members of the family were professors of Botany or Zoology in Central Europe during the late 19th and early 20th century. His father was, among other things, assistant to the famous geneticist Carl Correns, one of the rediscoverers of Mendel's laws of inheritance, in Berlin. Later, he became Professor of Botany and Genetics in Göttingen where Diter was born. In 1934, the family moved to Berlin, where Diter's father succeeded Correns as Professor of Biology at the Kaiser Wilhelm Institut für Biologie (later called the Max Planck Institute for Biology). His father died in 1945.

During his childhood, Diter was very interested in flora and fauna. He was an avid collector of plants, butterflies and insects, particularly in the alpine areas of Tyrol. He graduated from secondary school in Innsbruck, Austria, in 1947. The same year he began his academic studies in Tübingen, Germany, and in 1950 he continued at the institute of technology ETH in Zürich, Switzerland, studying the moth genus *Solenobia* (part of the bagworm moth family). The following year he moved to Sweden to work with Åke Gustafsson who had become Professor of Genetics at Forest High School in Stockholm. Now Diter encountered the noted Swedish mutation research at Lund University and Swedish Seed Association in Svalöv, where Åke Gustafsson had been based before his recruitment to Stockholm. Here Diter started working on the efficiency of various mutagen treatments, mainly on barley chlorophyll mutants. At the same time, he completed his German doctorate in Tübingen, looking at polarity in moss spores. In 1953 he achieved a Swedish licentiate (degree) in studies of straw stiffness in dense eared barley mutants known as *Erectoides*.

After completing these degrees, Diter wanted to focus on studying the chloroplast development of various chlorophyll mutants in barley, for which new technology was necessary. He contacted Arne Tiselius in Uppsala, and through him gained access to a modern electron microscope that he could use for his work. Later, a new electron microscope could be bought for the Institute of Genetics at Forest High School for continuation of these studies.

The chloroplast research led to a Swedish doctorate in 1957. Diter von Wettstein accepted a position as docent at Stockholm High School (later Stockholm University), and the following year he was awarded a Rockefeller Fellowship to spend a year in the USA at places such as Cold Spring Harbor and Stanford studying the genetics of microorganisms. His knowledge was used to strengthen the education in microbial genetics at the Karolinska Institute, Stockholm, where students from the entire country congregated. At that time, Åke Gustafsson and Diter were also working on the creation of Sweden's first phytotron for growing plants in a controlled environment. It was finished in 1965.

Diter von Wettstein became Professor of Genetics at the University of Copenhagen in 1962. There he contributed to the development of a modern education in genetics, with among other things a microbial direction looking at *Aspergillus* and *Neurospora*. With Mogens Westergaard he began research on the ascomycete fungus *Neottiella rutilans*, which has the interesting peculiarity of having consistently condensing chromosomes. This organism was ideal for cytological examinations of the synaptonemal complex and DNA studies using an electron microscope.

The research on chloroplasts and the biosynthesis of lipids was expanded. Another project started on the large group of *Eceriferum* barley mutants and studies of the chemical steps in surface wax synthesis, which is blocked in the mutants.

In spring of 1966, Diter was invited as a guest professor to the University of California in Davis, where he lectured on the genetics of chloroplasts. In Davis he also met his wife-to-be, Penny, who was working on her PhD. In 1972, Diter became director of the Department of Physiology at the world-famous Carlsberg Laboratory, Copenhagen. At Carlsberg he was granted ample resources to shape the work after his own concepts, and for a couple of decades the Department of Physiology at the Carlsberg Laboratory became a renowned centre for genetic research and plant breeding. Diter von Wettstein worked there until his retirement in 1996.

Several research projects were conducted under Diter von Wettstein's leadership, most prominently on barley. The electron microscopical and genetic studies on chloroplasts continued, but several new areas of research were added, such as thermostability during the malting process of beer, induction of anthocyanidin-free mutants, which are of special importance for the brewing process. One result of this research was the barley cultivar 'Galant.' Other areas of research were chromosome pairing during meiosis in brewery yeast, gluten free wheat cultivars and improved fungus resistance in barley.

Through his extensive international contacts, Diter was offered a guest professorship after his retirement: R.A. Nilan Distinguished Professor at the Department of Crop and Soil Sciences & School of Molecular Biosciences, Washington State University, Pullman, USA. He had this position until 2016.

Diter was always very interested in systematics biology and liked to name different barley mutant groups with Latin and Greek names and symbols. Together with R.A. (Bob) Nilan several such barley groups were created. He was also very interested in establishing Barley Genetics Newsletter and helped with financial support for many years. The first issue was published 1971.

Diter von Wettstein had a great range of work and a very high scientific production. He created constructive environments and good conditions for his colleagues. With his passing we have lost a very brilliant scholar in Scandinavian and international genetics and biological plant research. We all will miss him very much.

Udda Lundqvist *Roland von Bothmer* *Mats Hansson*

Barley Genetics Newsletter (2018) 48:4-8

This is a reprint of Rules for Nomenclature and Gene Symbolization in Barley from Barley Genetics Newsletter (2010) 40:178-182.

Rules for Nomenclature and Gene Symbolization in Barley

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In this volume 48: of the Barley Genetics Newsletter the recommended rules for nomenclature and gene symbolization in barley as reported in BGN 2:11-14, BGN 11:1-16, BGN 21:11-14, BGN 26:4-8, BGN 31:76-79, BGN 34:132-136, BGN 35:114-149, BGN 37:100-104, BGN 38: 165-170, BGN 39:77-81 and BGN 40:178-182 are again reprinted. Also, the current lists of new and revised BGS descriptions are presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in this issue.

Rules for Nomenclature and Gene Symbolization in Barley

1. In naming hereditary factors, the use of languages of higher internationality should be given preference.

2. Symbols of hereditary factors, derived from their original names, should be written in Roman letters of distinctive type, preferably in italics, and be as short as possible.

   AMENDMENT: The original name should be as descriptive as possible of the phenotype. All gene symbols should consist of three letters.

   > COMMENTS: All new gene symbols should consist of three letters. Existing gene symbols of less than three letters should be converted to the three-letter system whenever symbols are revised. When appropriate, one or two letters should be added to existing symbols.
   >
   > For example, add the letters "ap" to "K" to produce the symbol "Kap" to replace "K" as the symbol for Kapuze (hooded). As another example, add the letters "ud" to "n" to produce the symbol "nud" to replace "n" as the symbol for naked caryopsis. Similarly the letter "g" can be added to "ms" to produce the symbol "msg" for genetic male sterility and the letter "e" can be added to "ds" to produce the symbol "des" for desynapsis. When inappropriate or when conflicts arise, questions should be referred to the Committee on Genetic Marker Stocks,

Nomenclature, and Symbolization of the International Barley Genetics Symposium for resolution.

3. Whenever unambiguous, the name and symbol of a dominant begin with a capital letter and those of a recessive with a small letter.

   AMENDMENT: When ambiguous (co-dominance, incomplete dominance, etc.) all symbols should consist of a capital letter followed by two small letters that designate the character, a number that represents a particular locus, and a letter or letters that represents a particular allele or mutational event at that particular locus.

   COMMENTS: As an example, the letters "Mdh" can be used to designate the character malate dehydrogenase, "Mdh1" would represent a particular locus for malate dehydrogenase and "Mdh1a", "Mdh1b", "Mdh1c", etc. would represent particular alleles or mutational events at the "Mdh1" locus. Row number can be used as an example of symbolizing factors showing incomplete dominance. At the present time, the symbol "v" is used to represent the row number in *Hordeum vulgare*, "V" is used to represent the row number in *Hordeum distichum*, and "Vt" is used to represent the row number in *Hordeum deficiens*. According to the amendment to Rule 3, if row number were to be designated by the letters "Vul", the designation of the locus on chromosome 2 would then become "Vul1" and the alleles "v", "V", and "Vt" would be designated "Vul1a", "Vul1b", and "Vul1c".

   SUPPLEMENTARY AMENDMENT (1996): A period should be placed before the allele symbol in the complete gene symbol. COMMENTS: Since DNA sequences similar to those of the original locus may occur at several positions in the *Hordeum vulgare* genome, a three-letter symbol plus a number is inadequate to represent all potential loci. Also, both numbers and letters have been assigned to specific mutants and isozymes in *Hordeum vulgare*. The six-rowed spike locus is used as an example although the symbol “Vul1” for row number in *Hordeum vulgare* is not recommended because the botanical classification of *Hordeum* spp. has changed. The locus symbol “vrs1” and the name six-rowed spike 1 are recommended for the “v” locus. Gene symbols recommended for common alleles at the “vrs1” locus are *vrs1.a*, *vrs1.b*, *vrs1.c*, and *vrs1.t* for the "*v*", "*V*", "v^{lr}", and "V^{t}" genes, respectively.

4. Literal or numeral superscripts are used to represent the different members of an allelic series.

   AMENDMENT: All letters and numbers used in symbolization should be written on one line; no superscripts or subscripts should be used.

5. Standard or wild type alleles are designated by the gene symbols with a + as a superscript or by a + with the gene symbol as a superscript. In formulae, the + alone may be used.

   AMENDMENT: This rule will not be used in barley symbolization.

6. Two or more genes having phenotypically similar effects are designated by a common basic symbol. Non-allelic loci (mimics, polymeric genes, etc.) are distinguished by an additional letter or Arabic numeral either on the same line after a hyphen or as a subscript. Alleles of independent mutational origin may be indicated by a superscript.

   AMENDMENT: Barley gene symbols should consist of three letters that designate the character, a number that represents a particular locus, and a letter or letters that represents a particular allele or mutational event at that particular locus. All letters and numbers should be written on the same line without hyphens or spaces. Alleles or mutational events that have not been assigned to a locus should be symbolized by three letters that designate the character followed by two commas used to reserve space for the locus number when determined, followed by a letter or letters representing the particular allele or mutational event. After appropriate allele testing, the correct locus number will be substituted for the commas. Where appropriate (when assigning new symbols or when revising existing symbols) letters representing alleles or mutational events should be assigned consecutively without regard to locus number or priority in discovery or publication.

   > COMMENTS: The use of the proposed system of symbolization can be illustrated by the desynaptic mutants. Two loci are known: *lc* on chromosome 1 (7H) and *ds* on chromosome 3 (3H). These will be resymbolized as *des1a* and *des2b*. A large number of desynaptic mutants have been collected. They will be designated *des,,c*, *des,,d*, *des,,e*, etc. If allele tests show that *des,,c* is at a different locus than *des1* and *des2*, *des,,c* will become *des3c*. If allele tests show that *des,,d* is at the same locus as *des2*, *des,,d* will become *des2d*. In practical use, the symbol *des* will be used when speaking of desynapsis in general or if only one locus was known for the character. The symbol *des2* will be used when speaking of that particular locus, and the symbol *des2b* will be used only when speaking of that particular allele or mutational event. If additional designation is needed in particular symbolization, it can be obtained by adding numbers behind the allele letters, and, if still further designation is needed, letters can be added to the symbol behind the last number. Symbolization consisting of alternation of letters and numbers written on the same line without hyphens or spaces will allow for the expansion of the symbol as future needs arise. In any work with large numbers of polymeric gene mutants, every mutant has to be given a designation not shared by any other mutant of this polymeric group and this designation should become a part of the permanent symbol representing that particular allele or mutational event. This requirement can be met by assigning allele designations in consecutive order without regard to locus number.

   SUPPLEMENTARY AMENDMENT (1996): A period should be used instead of two commas in gene symbols for mutants within a polymeric group that cannot be assigned to a specific locus. COMMENTS: The “des” symbol should be used when referring to desynapsis in general; *des1* and *des2*, for specific loci; *des1.a* and *des2.b* for specific genes or alleles at their respective loci; and *des.c*, *des.d*, *des.e*, etc., for desynaptic mutants not assigned to a specific locus.

SUPPLEMENTARY AMENDMENT 2 (2004): Even if the locus in question is the only one known that affects a given phenotype, the three-letter basic symbol is followed by a serial number starting with 1.

7. Inhibitors, suppressors, and enhancers are designated by the symbols *I*, *Su*, and *En*, or by *i*, *su*, and *en* if they are recessive, followed by a hyphen and the symbol of the allele affected.

   AMENDMENT: This rule is no longer applicable and will not be used in barley symbolization.

8. Whenever convenient, lethals should be designated by the letter *l* or *L* and sterility and incompatibility genes by *s* or *S*.

   AMENDMENT: This rule will not be used in barley symbolization.

   > COMMENT: J.G. Moseman (BGN 2:145-147) proposed that the first of the three letters for designating genes for reaction to pests should be R. The second and third letters will be the genus and species names of the pest.
   > SUPPLEMENTARY COMMENT (1986): A motion was passed during the workshop on "Linkage Groups and Genetic Stock Collections" at the Fifth International Barley Genetics Symposium in 1986 (Barley Genetics V:1056-1058, BGN 17:1-4), that the International Committee for Nomenclature and Symbolization of Barley Genes should "recommend use of *Ml* as the designation of genes for resistance to powdery mildew."

9. Linkage groups and corresponding chromosomes are preferably designated by Arabic numerals.

   AMENDMENT (1996): The current wheat homoeologous group numbering scheme (the Triticeae system) is recommended for *Hordeum vulgare* chromosomes. Arabic numerals followed by an H will indicate specific barley chromosomes. The *H. vulgare* chromosomes should be 7H, 2H, 3H, 4H, 1H, 6H, and 5H instead of 1, 2, 3, 4, 5, 6, and 7, respectively.

10. The letter *X* and *Y* are recommended to designate sex chromosomes.

    AMENDMENT: This rule will not be used in barley symbolization.

11. Genic formulae are written as fractions with the maternal alleles given first or above. Each fraction corresponds to a single linkage group. Different linkage groups written in numerical sequence are separated by semicolons. Symbols of unlocated genes are placed within parenthesis at the end of the formula. In euploids and aneuploids, the gene symbols are repeated as many times as there are homologous loci.

12. Chromosomal aberrations should be indicated by abbreviations: *Df* for deficiency, *Dp* for duplication, *In* for inversion, *T* for translocation, *Tp* for transposition.

13. The zygotic number of chromosomes is indicated by 2n, the gametic number by n, and basic number by x.

14. Symbols of extra-chromosomal factors should be enclosed within brackets and precede the genic formula.

Recommendations made by the International Committee for Nomenclature and Symbolization of Barley Genes at the Fourth International Barley Genetics Symposium in 1981 (Barley Genetics IV:959-961) on gene and mutation designations were as follows.

> AMENDMENT (1981): A. Present designations for genes and mutations. - Most of the present designations should be maintained. However, new designations may be given, when additional information indicates that new designations would aid in the identification of genes and mutations.
>
> AMENDMENT (1981): B. New designations for genes and mutations. - New genes or mutations will be designated by characteristic, locus, allele, and then the order of identification or mutational event. Three letters will be used to identify new characteristics. Consecutive numbers will be used to identify the order of identification or mutational event. Loci will be designated by numbers and alleles by letters when they are identified. For example, *des-6* indicates that this is the sixth gene or mutation identified for the characteristic *des* (desynaptic). *des1-6* and *des2-7* indicate that gene or mutational events 6 and 7 for the desynaptic characteristic have been shown to be at different loci and those loci are then designated 1 and 2, respectively. *des1a6* and *des1b8*, indicate that the gene or mutational events 6 and 8 for the characteristic desynaptic have been shown to be at different alleles at locus 1 and those alleles are then designated a and b.

SUPPLEMENTARY COMMENT (1986):

> A motion was passed during the workshop of the "Nomenclature and Gene Symbolization Committee" at the Fifth International Barley Genetics Symposium in 1986 (Barley Genetics V:1056-1058) that "the recommended systems for Nomenclature and Gene Symbolization of the International Committee be published annually in the Barley Genetics Newsletter."

SUPPLEMENTARY COMMENT 2 (1996):

> At the workshop for ”Recommendations of Barley Nomenclature” held at Saskatoon, July 31, 1996 and adopted at the General Meeting of the Seventh International Barley Genetics Symposium, it was recommended that a period instead of a dash be used to designate the allele portion of the gene symbol. Consequently, the first gene symbol for the characteristic “des” (desynapsis) should be expressed as *des1.a*. The code *des1* identifies a specific locus. The period indicates that the symbol a identifies a specific allele or mutational event that produces a desynaptic phenotype. (The allele symbol “*a*” will be always associated with this specific desynaptic mutant even if the locus symbol is changed based on subsequent research results.

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Descriptions of Barley Genetic Stocks for 2018

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In this volume of the Barley Genetics Newsletter eighty-two revised and new Barley Genetic Stock (BGS) descriptions are published (Table 1). The current lists of new and revised BGS descriptions, including those in Table 1, are presented by BGS number order (Table 2) and by locus symbol or code in alphabetic order (Table 3) in another section of this issue. Information on the description location, recommended locus name, chromosomal location, other gene symbols or codes, and the primary genetic stock (GSHO number and/or NGB number) are included in these lists. The GSHO stocks are held in the USDA-ARS Barley Genetic Stocks collection at the National Small Grains Collection (U.S. Department of Agriculture, Agricultural Research Service, National Small Grains Germplasm Research Facility, 1691 S 2700 W, Aberdeen, ID 83210, USA. The NGB stocks are held in the Nordic Genetic Resource Center (NordGen), Smedjevägen 3, SE-230 53 Alnarp, Sweden. This information is available through the Internet at the following addresses:

(1) https://www.ars.usda.gov/pacific-west-area/aberdeen-id/small-grains-and-potato-germplasm-research/

(2) https://www.ars.usda.gov/pacific-west-area/aberdeen-id/small-grains-and-potato-germplasm-research/docs/barley-wheat-genetic-stocks-collections-1/

(3) http://wheat.pw.usda.gov/ggpages/bgn/

(4) http:/www.nordgen.org/sesto

(5) http://www.nordgen.org/bgs

Table 1. A listing of new and revised Barley Genetic Stock (BGS) descriptions published in volume 48 of the Barley Genetics Newsletter, giving recommended locus symbols or codes and names, chromosomal locations, and stock source information.

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
2	fch12	f_c, clo-fc	7HS	Chlorina seedling 12	48:57	36
14	des5	des5, HvDMC1	5H	Desynapsis 5	48:59	596
15	blx1	bl, HvMpc1	4HL	Non-blue aleurone xenia 1	48:61	185
19	blx2	bl2	7HS	Non-blue aleurone xenia 2	48:63	209
25	Xnt1	X_a, xan-h	7HL	Xantha seedling 1	48:65	1606
26	sbn1	sb	7HS	Subnodal dwarf 1	48:67	1217
33	ant1	rs, rub-a, HvMpc1	7HS	Anthocyanin less 1	48:68	1620
35	rsm1	sm	7HS	Reaction to barley stripe mosaic virus (RSMV) 1	48:71	2492
52	fch15	or	2HS	Chlorina seedling 15	48:72	49
55	fch1	f, lg	2HS	Chlorina seedling 1	48:73	112
62	sbk1	sk, cal-a	2HS	Subjacent hood 1	48:75	267
76	Pre2	Re2, P	2HL	Red lemma and pericarp 2	48:77	234
80	ant2	pr, rub, HvHLH1	2HL	Anthocyanin less 2	48:80	1632
81	gsh7	gs7	2HL/ 5H	Glossy sheath 7	48:83	1759
111	dsp10	l_c	3HS	Dense spike 10	48:84	71
117	fch2	f2, lg5. HvCAO	3HL	Chlorina seedling 2	48:86	107
146	cal-d	cal-d	3H	Calcaroides-d	48:88	1698
150	scl-b	scl-5	3HL/ 6HS	Scirpoides leaf-b	48:90	
157	brh2	br, ari-l, HvTUD1	4HL	Brachytic 2	48:91	573
173	blx3	bl3, bly, HvMyc2	4HL	Non-blue aleurone xenia 3	48:93	2506
174	blx4	bl4, HvMpc1	4HL	Non-blue (pink) aleurone xenia 4	48:95	2507
186	sld3	ant17.567	4HS	Slender dwarf 3	48:97	2467
190	tfm1	tfm1	1HL	Thick filament 1	48:99	2477
191	fch17	vy3	1HL/ 3HL	Chlorina seedling 7	48:100	1079

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
200	ari-z	ari-189	4HL	Breviaristatum-z	48:101	
203	Blp1	B	1HL	Black lemma and pericarp 1	48:102	988
220	fch3	f3	1HS	Chlorina seedling 3	48:104	853
223	Zeb3	zb$_c$. zb3	1HL	Zebra stripe 3	48:105	1451
224	ert-b	ert-2	1HL	Erectoides-b	48:107	470
225	clh1	clh	7HL	Curled leaf dwarf 1	48:109	1212
226	rvl1	rvl	1HL	Revoluted leaf 1	48:110	608
227	sls1	sls1	1HL	Small lateral spikelet 1	48:111	2492
228	Sil1	Sil	1H	Subcrown internode length 1	48:112	1604
232	Lys4	Lys4d, sex5g	1HS	High lysine 4	48:113	2475
241	Acr3	Acr, Lax	1HL	Accordion rachis 3	48:115	1071
242	sld6	sld.g	1H	Slender dwarf 6	48:117	2482
251	mu12	mlt2	6HL	Multiflorus 2	48:119	1394
276	gpc1	HvNAM-1	6HS	Grain protein content 1	48:120	
301	fst1	fs	5HL	Fragile stem 1	48:122	629
329	ari-h	ari-127	5HL	Breviaristatum-h	48:124	
336	glo-b	glo-b	5HL	Globosum-b	48:125	1327
342	glo-f	glo-e	5HL	Globosum-f	48:127	
366	msg10	ms10	7HS	Male sterile genetic 10	48:128	1811
382	sex1	se6f, lys5	6HL	Shrunken endosperm xenia 1	48:130	755
385	msg24	msg,,v	4HL	Male sterile genetic 24	48:132	2376
389	des10	des,,p, HvMlh3	5HL	Desynapsis 10	48:134	601
400	cer-e	cer-8	1HL	Eceriferum-e -/+ ++ ++	48:136	1518
401	cer-f	cer-9	1H	Eceriferum-f + + ++	48:138	1523
422	cer-zd	cer-67	3H	Eceriferum-zd ++ ++ -	48:140	463
425	cer-zg	cer-214	4HL	Eceriferum-zg ++ ++ +	48:142	454
433	cer-zp	cer-313	5HL	Eceriferum-zg ++ ++ +	48:144	463
434	cer-zq	cer-248		Eceriferum-zg ++ ++ +	48:146	1524
454	blx5	bl5	7HL	Non-blue aleurone xenia 5	48:148	2509
455	seg8	seg8	7H	Shrunken endosperm genetic 8	48:149	2469
477	Lax-f	Lax-61		Laxatum-f	48:151	
496	Lax-mf	Lax-302		Laxatum-fm	48:152	
512	Rpg2	T2	2HL	Reaction to Puccinia graminis (wheat stem rust) 2	48:153	1584
519	mnd1	m	2HS	Many noded dwarf 1	48:155	253
533	cer-yt	cer-yt	1HL	Eceriferum-yt - ++ ++	48:156	1553

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
534	cer-yu	cer-yu	1HS	Eceriferum-yu ++ ++ -	48:157	1554
535	cer-yx	cer-yx	1HL/5HL	Eceriferum-yx + + ++	48:158	1555
536	Cer-yy	Gle1	1HS	Eceriferum-yy - ++ ++	48:159	1556
548	Fol-b	Ang	1H	Angustifolium-b	48:161	17
560	ert-f	ert-18	1H	Erectoides-f	48:162	478
563	ert-l	ert-12	5HL	Erectoides-l	48:163	486
564	ert-p	ert-44	5HL	Erectoides-p	48:164	490
565	ert-s	ert-50	7H	Erectoides-s	48:165	493
569	ert-y	ert-69		Erectoides-y	48:166	499
570	ert-z	ert-71	5H	Erectoides-z	48:167	500
596	ant5	rs2, rub-a	2HL	Anthocyanin less 5	48:168	1643
623	eli-a	lig-a, eli-3	2HS	Eligulum-a	48:170	3647
661	dub1	dub1	5HL	Double seed 1	48:172	
676	fch16	clo.117	2HS	Chlorina seed 16	48:173	
716	ibl1	en-Bl, Ibl	7HL	Intense blue aleurone 1	48:174	2508
746	ant23	ant-3	2HL/5HL	Anthocyanin-deficient 23	48:176	
747	ant24	ant-10		Anthocyanin-deficient 24	48:177	
748	Rpg3	Rpg3	5HL	Reaction to Puccinia graminis 3	48:178	
750	rpg6	rpg6	6HS	Reaction to Puccinia graminis 6	48:179	
751	Rpg7	Rpg7	3HL	Reaction to Puccinia graminis 7	48:180	
752	Qsd1	SD1	5HL	Quantitative seed dormancy 1	48:181	
753	Qsd2	SD2	3HL	Quantitative seed dormancy 2	48:184	
754	Qsd3	qsd3	3HL	Quantitative seed dormancy 3	48:188	

* Recommended locus symbols or codes that are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

† Chromosome numbers and arm designations for barley that are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

‡ The seed stock associated with each BGS number, which are held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Grains Germplasm Research Facility, Aberdeen, Idaho, USA.4

Descriptions of Barley Genetic Stocks
Tables 2 and 3 (2018)

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In this section of the Barley Genetics Newsletter volume 48, you will find two updated tables with new and revised barley locus descriptions. The descriptions are listed by BGS numbers (Table 2) and by alphabetic order using the existing and recommended locus symbols or codes (Table 3). As research in barley is proceeding rapidly, it is necessary to update the latest research and findings about specific barley genes.

Table 2. A listing of Barley Genetic Stock (BGS) descriptions in volume 48 and recent issues of the Barley Genetics Newsletter providing recommended locus symbols or codes, recommended locus names, chromosome locations, description citation, and stock location information.

Table 3. An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on recommended locus names, recommended locus symbols or codes, chromosomal locations, description citation, and original cultivars.

Table 2. A listing of Barley Genetic Stock (BGS) descriptions in recent issues of the Barley Genetics Newsletter providing recommended locus symbols or codes, recommended locus names, chromosome locations, description citation, and stock location information.

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
1	brh1	br, ari-i	7HS	Brachytic 1	47: 50	25
2	fch12	f_c, clo-fc	7HS	Chlorina seedling 12	48: 57	36
3	yvs2	y_c	7HS	Virescent seedling 2	26: 46	41
4	abo8	a_{c2}, alb-m	7HS	Albino seedling 8	26: 47	61
5	fch8	f8	7HS	Chlorina seedling 8	41: 62	40
6	vrs1	v, Int-d	2HL	Six-rowed spike 1	37:192	196
7	nud1	n, h	7HL	Naked caryopsis 1	44: 51	115
9	dsp1	l	7HS	Dense spike 1	43: 50	1232
10	lks2	lk2, lk4	7HL	Short awn 2	45: 80	566
11	ubs4	lks2, ari-d	7HL	Unbranched style 4	45: 84	567
12	des1	lc	7H	Desynapsis 1	42: 58	592
13	des4	des4	7H	Desynapsis 4	44: 54	595
14	des5	des5, HvDMC1	5H	Desynapsis 5	48: 59	596
15	blx1	bl	4HL	Non-blue aleurone xenia 1	48: 61	185
16	wax1	wx, glx	7HS	Waxy endosperm 1	42: 65	908
17	fch4	f4, yv	7HL	Chlorina seedling 4	43: 54	1214
18	fch5	f5, yv2	7HS	Chlorina seedling 5	43: 56	1215
19	blx2	bl2	7HS	Non-blue aleurone xenia 2	48: 63	209
20	Rym2	Ym2	7HL	Reaction to BaYMV 2	26: 66	984
21	Run1	Un	7HS	Reaction to *Ustilago nuda* 1	26: 67	1324
22	Rsg1	Grb	7H	Reaction to *Schizaphis graminum* 1	37:199	1317
23	wnd1	wnd	4HL	Winding dwarf 1	42: 74	2499
24	fst3	fs3	7HS	Fragile stem 3	41: 74	1746
25	Xnt1	X_a, xan-h	7HL	Xantha seedling 1	48: 65	1606
26	sbn1	sb	7HS	Subnodal dwarf 1	48: 67	1217
27	lbi3	lb3	7HL	Long basal rachis internode 3	42: 79	536
28	ert-a	ert-a	7HS	Erectoides-a	41: 76	468
29	ert-d	ert-d	7HS	Erectoides-d	42: 82	475
30	ert-m	ert-m	7HS	Erectoides-m	46: 47	487
31	sex6	ssIIa	7HS	Shrunken endosperm xenia 6	45: 86	2476
32	Rph9	Pa9, Pa12	5HL	Reaction to *Puccinia hordei* 9	37:201	1601

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
33	ant1	rs, rub-a, HvMpc1	7HS	Anthocyanin less 1	48: 68	1620
34	msg50	msg,,hm	7HL	Male sterile genetic 50	45: 88	2404
35	rsm1	sm	7HS	Reaction to barley stripe mosaic virus (RSMV) 1	48: 71	2492
36	xnt4	x_{c2}	7HL	Xantha seedling 4	26: 85	42
37	xnt9	xan,,i	7HL	Xantha seedling 9	26: 86	584
38	smn1	smn	3H/5H	Seminudoides 1	43: 58	1602
39	mss2	mss2	7HS	Midseason stripe 2	44: 59	2409
40	prm1	prm	7HS	Premature ripe 1	44: 60	2429
41	brh7	brh.w	7H	Brachytic 7	42: 98	1687
42	Pyr1	Pyr.g, Pyr.i	3HL	Pyramidatum 1	41: 78	1581
43	mov1	mo5	7HL	Multiovary 1	43: 59	3641
44	brh16	brh.v, ari-o	7HL	Brachytic 16	45: 89	1686
45	sdw4		7HL	Semidwarf 4	46: 51	
48	Rpt4	QRpt7	7HL	Reaction to *Pyrenophora teres* f. *maculata* 4	43: 61	
49	sld8	sld.i	7HS/ 4HL	Slender dwarf 8	43: 63	2484
51	rtt1	rt	2HS	Rattail spike 1	47: 53	216
52	fch15	or	2HS	Chlorina seedling 15	48: 72	49
53	abo2	a2	2HS	Albino seedling 2	26: 89	70
55	fch1	f, lg	2HS	Chlorina seedling 1	48: 73	112
56	wst4	wst4	2HL	White streak 4	44: 61	568
57	eog1	e, lep-e	2HL	Elongated outer glume 1	43: 64	29
58	vrs1	lr, v^{lr}	2HL	Six-rowed spike 1	26: 94	153
59	gpa1	gp, gp2	2HL	Grandpa 1	45: 91	1379
60	lig1	li, aur-a	2HL	Liguleless 1	45: 93	6
61	trp1	tr	4HL	Triple awned lemma 1	41: 82	210
62	sbk1	sk, cal-a	2HS	Subjacent hood 1	48: 75	267
62	sbk1	sk, cal-a	2HS	Subjacent hood 1	40: 51	267
63	yvs1	y_x, alb-c.7	2HS	Virescent seedling 1	26: 99	68
64	des7	des7	3H	Desynapsis 7	43: 67	598
65	Eam1	Ea, Ppd-H1	2HS	Early maturity 1	47: 54	1316
66	vrs1	V^d	2HL	Two-rowed spike 1	26:103	346
67	vrs1.t	V^t	2HL	Deficiens 1	47: 57	684
68	Pvc 1	P_c	2HL	Purple veined lemma 1	44: 67	132

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
69	Gth 1	G	2HL	Toothed lemma 1	47: 59	309
70	Rph1	Pa	2H	Reaction to *Puccinia hordei* 1	26:107	1313
71	com2	bir2	2HS	Compositum 2	45: 95	1700
74	flo-c	flo-a	6HL	Extra floret-c	45: 97	1743
75	Lks1	Lk	2HL	Awnless 1	41: 84	44
76	Pre2	Re2, P	2HL	Red lemma and pericarp 2	48: 77	234
77	hcm1	h	2HL	Short culm 1	26:113	2492
78	mtt4	mtt,,e, mt	2HL	Mottled leaf 4	41: 86	1231
79	wst7	rb	2HL	White streak 7	47: 61	247
80	ant2	pr, rub, HvHLH1	2HL	Anthocyanin less 2	48: 80	1632
81	gsh7	gs7	2HL/ 5H	Glossy sheath 7	48: 83	1759
82	Zeo1	Knd, Ert-r	2HL	Zeocriton 1	47. 63	1613
83	sld2	sld2	2HS	Slender dwarf 2	44: 74	2491
84	mss1	mss	5H	Midseason stripe 1	44: 75	1404
85	yst4	yst4	2HL	Yellow streak 4	44: 76	2502
86	fch13	f13	5HL	Chlorina seedling 13	44: 77	16
87	fch14	f14	2HL	Chlorina seedling 14	44: 78	1739
88	Rph2	Pa2, A	5HS	Reaction to *Puccinia hordei* 2	37:212	1593
89	ari-g	lk10	2H	Breviaristatum-g	47: 66	1655
90	ert-j	ert-j	2H	Erectoides-j	43: 70	484
91	ert-q	ert-q	6H	Erectoides-q	43: 71	1562
92	ert-u	br5, ari-o	7HL	Erectoides-u	45:100	496
93	ert-zd	br7, ari-o	7HL	Erectoides-zd	45:102	504
94	abo4	a4	2H	Albino seedling 4	26:133	167
95	abo13	alb,,p	2HL	Albino seedling 13	26:134	585
96	Rph15	Rph16	2HS	Reaction to *Puccinia hordei* 15	37:214	1586
97	acr1	acr, ril	2HL	Accordion rachis 1	47: 68	1617
98	Eam6	Ea6, Ea, HvCEN	2HS	Early maturity 6	46: 57	
99	lin1	s, rin	2HL	Lesser internode number 1	41: 92	2492
100	sld4	sld.d	2HS	Slender dwarf 4	43: 72	2479
101	als1	als	3HL	Absent lower laterals 1	43: 74	1065
102	uzu1	uz, ert-ii, HvBRI1	3HL	Uzu 1 or semi brachytic 1	47: 70	1300
104	yst1	yst, ys	3HS	Yellow streak 1	42:178	1140
105	xnt3	x_c, vir-l	3HS	Xantha seedling 3	26:139	66
106	abo6	a_c	3HS	Albino seedling 6	46: 60	30

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
107	wst1	wst, wst3	3HL	White streak 1	41: 97	159
108	alm1	al, ebu-a	3HS	Albino lemma 1	46: 61	270
109	yst2	yst2	3HS	Yellow streak 2	44: 81	570
111	dsp10	l_c	3HS	Dense spike 10	48: 84	71
112	abo9	a_n	3HS	Albino seedling 9	26:146	348
113	xnt6	x_s	3HS	Xantha seedling 6	26:147	117
114	cur2	cu2	3HL	Curly 2	44: 82	274
115	btr1	bt1	3HS	Non-brittle rachis 1	43: 78	1233
116	btr2	bt2	3HS	Non-brittle rachis 2	43: 80	842
117	fch2	f2, lg5. HvCAO	3HL	Chlorina seedling 2	48:86	107
119	des2	ds	3H	Desynapsis 2	43: 84	593
120	zeb1	zb	3HL	Zebra stripe 1	43: 86	1279
121	Rph3	Pa3	7HL	Reaction to *Puccinia hordei* 3	26:156	1316
122	Rph5	Pa5, Pa6	3HS	Reaction to *Puccinia hordei* 5	37:224	1597
123	Ryd2	Yd2	3HL	Reaction to BYDV 2	26:158	1315
124	vrs4	v4, int-e, HvRA2	3HL	Six-rowed spike 4	47: 76	775
125	lzd1	dw4	3H	Lazy dwarf 1	43: 87	1787
126	sld1	dw1	3HL	Slender dwarf 1	41:103	2488
127	Pub1	Pub	3HL	Pubescent leaf blade 1	44: 84	1576
128	sca1	sca	3HS	Short crooked awn 1	44: 85	2439
129	wst6	wst,,j	3HL	White streak 6	41:105	2500
130	eam10	ea_{sp}	3HL	Early maturity 10	44: 86	2504
131	gra-a	gran-a	7H	Granum-a	47: 79	1757
132	ari-a	ari-a, lk7	3HS	Breviaristatum-a	41:106	1648
133	sdw2	sdw-b	3HL	Semidwarf 2	45:108	2466
134	ert-c	ert-c	3HL	Erectoides-c	41:108	471
135	ert-ii	uzu1	3HL	Erectoides-ii	45:104	483
136	Rph7	Pa7, Pa5	3HS	Reaction to *Puccinia hordei* 7	37:228	1318
137	Rph10	Rph10	3HL	Reaction to *Puccinia hordei* 10	26:174	1588
138	nec4	nec4	3H	Necrotic leaf spot 4	43: 88	
139	nec5	nec5	3H	Necrotic leaf spot 5	43: 89	
140	xnt8	xan,,h	3HS	Xantha seedling 8	26:177	582
141	rym5	Ym	3HL	Reaction to barley yellow mosaic virus 5	32: 90	
142	brh8	brh.ad	3HL	Brachytic 8	42:232	1671
143	sex8	sex.j	3HS	Shrunken endosperm xenia 8	43: 90	2471

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
144	sld5	sld5	3HS	Slender dwarf 5	44: 90	2483
146	cal-d	cal-d	3H	Calcaroides-d	48: 88	1698
147	mov2	mo	3HS	Multiovary 2	43: 91	3642
148	brh14	brh.q, ari-o	7HL	Brachytic 14	45:111	1682
149	Rpc1		3H	Reaction to *Puccinia coronata* var. *hordei* 1	37:232	1601
150	scl-b	scl-5	3HL/ 6HS	Scirpoides leaf-b	48: 90	
151	fch9	f9	4HS	Chlorina seedling 9	44: 92	571
152	Kap1	K	4HS	Hooded lemma 1	26:179	985
155	glf1	gl, cer-zh	4HL	Glossy leaf 1	47: 81	98
156	lbi2	lb2, ert-i	4HS	Long basal rachis internode 2	44: 93	572
157	brh2	br, ari-l, HvTUD1	4HL	Brachytic 2	48: 91	573
158	yhd1	yh	4HL	Yellow head 1	42:250	574
160	min2	en-min		Enhancer of minute 1	26:186	266
161	min1	min	4HL	Semi-minute dwarf 1	44: 97	987
163	sgh1	sh1	4HL	Spring growth habit 1	26:188	575
164	Hln1	Hn	4HL	Hairs on lemma nerves 1	44: 99	576
165	glf3	gl3, cer-j	4HL	Glossy leaf 3	47: 86	577
166	msg25	msg,,r	4HL	Male sterile genetic 25	45:113	744
167	rym1	Ym	4HL	Reaction to barley yellow mosaic virus 1	32: 96	
168	glo-a	glo-a	4H	Globosum-a	45:115	1328
169	lgn2	lg2	4HS	Light green 2	42:264	171
170	lgn3	lg3, lg7	1HL	Light green 3	44:103	171
171	lgn4	lg4, lg1	4HL	Light green 4	44:105	681
172	lks5	lk5, ari-c	4HL	Short awn 5	47: 89	1297
173	blx3	bl3, bly, HvMyc2	4HL	Non-blue aleurone xenia 3	48: 93	2506
174	blx4	bl4, HvMpc1	4HL	Non-blue (pink) aleurone xenia 4	48: 95	2507
176	ovl1	ovl	4H	Ovaryless 1	35:191	
177	fch10		4H	Chlorina seedling 10	43: 95	1737
178	int-c	i, vrs5 HvTB1	4HS	Intermedium spike-c	47: 91	776
179	Hsh1	Hs	4HL	Hairy leaf sheath 1	44:107	986
180	sid1	nls	4HL	Single internode dwarf 1	43: 97	2477

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
181	eam9	ea,,c	4HL	Early maturity 9	26:204	1732
182	flo-a	flo-a	6HL	Extra floret-a	45:116	1741
183	Ynd1	Yn	4HS	Yellow node 1	44:109	1607
184	Zeo3	Zeo2, cly1.c	4HL	Zeocriton 3	47: 95	1611
185	brh5	brh.m	4HS	Brachytic 5	44:110	1678
186	sld3	ant17.567	4HS	Slender dwarf 3	48: 97	2467
187	brh9	brh.k	4HL	Brachytic 9	43: 99	1676
188	Alp1	Alp, Pht	4HL	Aluminum tolerance 1	47: 98	
189	Acr2	acr, lax	4HL	Accordion rachis 2	47:101	1071
190	tfm1	tfm1	1HL	Thick filament 1	48: 99	2477
191	fch17	vy3	1HL/ 3HL	Chlorina seedling 7	48:100	1079
193	viv-b	viv-6	4HS	Viviparoides-b	43:100	
194	sld7	sld.f	4HL	Slender dwarf 7	43:101	2481
195	sex9	sex.l	4HL	Shrunken endosperm xenia 9	43:102	2473
196	sdw7	sdw.u	4HL	Semidwarf 7	43:103	2462
197	nec34	nec.k	4HS	Necroticans 34	43:104	
198	Rpt8	QRpts4	4HS	Reaction to *Pyrenophora teres* f. *maculata* 8	43:105	
200	ari-z	ari-189	4HL	Breviaristatum-z	48:101	
201	fch7	f7, clo-f7	1HL	Chlorina seedling 7	41:113	4
202	trd1	t, bra-c	1HL	Third outer glume 1	46: 65	227
203	Blp1	bl, HvMpc1-H3	1HL	Black lemma and pericarp 1	48:102	988
207	abo1	a_t	1HL	Albino seedling 1	26:210	51
208	fst2	fs2	1HL	Fragile stem 2	41:114	578
213	Sgh3	Sh3	1HL	Spring growth habit 3	26:212	764
214	eam8	ea_k, mat-a	1HL	Early maturity 8	46: 69	765
215	des6	des6	1HL/ 5HL	Desynapsis 6	43:106	597
218	Rph4	Pa4	1HS	Reaction to *Puccinia hordei* 4	42:302	1314
220	fch3	f3	1HS	Chlorina seedling 3	48:104	853
221	wst5	wst5	1HL	White streak 5	46: 73	591
222	nec1	sp,,b	1HL	Necrotic leaf spot 1	43:108	989
223	Zeb3	zb_c. zb3	1HL	Zebra stripe 3	48:105	1451
224	ert-b	ert-2	1HL	Erectoides-b	48:107	470
225	clh1	clh	7HL	Curled leaf dwarf 1	48:109	1212
226	rvl1	rvl	1HL	Revoluted leaf 1	48:110	608

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
227	sls1	sls1	1HL	Small lateral spikelet 1	48:111	2492
228	Sil1	Sil	1H	Subcrown internode length 1	48:112	1604
229	cud2	cud2	1HL	Curly dwarf 2	47:103	1712
230	glo-e	glo-e	3HL	Globosum-e	45:117	1755
231	cur5	cu5	2HS	Curly 5	41:120	1710
232	Lys4	Lys4d, sex5g	1HS	High lysine 4	48:113	2475
233	xnt7	xan,,g	1HL	Xantha seedling 7	26:231	581
234	mov3	mo-a	1H	Multiovary 3	32:102	
235	lel1	lel	2H	Leafy lemma 1	46:74	1780
237	Rpt2	Rpt2c	1HS	Reaction to *Pyrenophora teres* f. *teres* 2	43:110	
238	ari-t	ari-25	1H	Breviaristatum-t	47:104	
239	sci-b	sci-4	1H/6H	Scirpoides-b	46: 76	
240	sdw6	sdw.f	1H/7H	Semidwarf 6	46:77	2449
241	Acr3	Acr, Lax	1HL	Accordion rachis 3	48:115	1071
242	sld6	sld.g	1H	Slender dwarf 6	48:117	2482
244	dsp11	dsp.am, dsp.ao	1HL	Dense spike 11	41:121	1722 1723
251	mul2	mlt2	6HL	Multiflorus 2	48:119	1394
252	eam7	HvCO7	6HS	Early maturity 7	45:118	579
253	cul2	uc2	6HL	Uniculm 2	43:112	531
254	rob1	o, rob-o	6HS	Orange lemma 1	46: 78	707
255	xnt5	x_n	6HL	Xantha seedling 5	26:237	43
257	raw5	r,,e	6HL	Smooth awn 5	44:112	785
258	dsp9	l9, ert-e	6HL	Dense spike 9	47:107	1774
260	fch11	f11	6HL	Chlorina seedling 11	45:120	1738
261	nec2	nec2	6HS	Necrotic leaf spot 2	26:241	1224
262	cur1	cu1	3HL	Curly 1	46: 81	1705
263	cur3	cu3	6HL	Curly 3	41:125	1707
264	mtt5	mt,,f	6HL	Mottled leaf 5	41:126	2410
265	nec3	nec3	6HS	Necrotic leaf spot 3	43:116	1330
266	ert-e	l9, dsp9	6HL	Erectoides-e	47:109	477
267	Rph11	Rph11	6HL	Reaction to *Puccinia hordei* 11	26:247	1589
268	lax-b	lax-b	6HL	Laxatum-b	44:113	1776
269	lys6	lys6	6H	High lysine 6	44:114	1786
270	abo14	alb,,q	6HL	Albino seedling 14	26:250	586
271	abo15	alb,,t	6HS	Albino seedling 15	26:251	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
272	Rpt5	Pt$_{a}$	6HL	Reaction to *Pyrenophora teres* f. *teres* 5	43:120	
274	ari-x	ari-22	6H	Breviaristatum-x	43:124	
275	lfl1	lfl, lfs	6HL	Leafless 1	47:111	609
276	gpc1	HvNAM-1	6HS	Grain protein content 1	48:120	
301	fst1	fs	5HL	Fragile stem 1	48:122	629
302	mtt2	mt2	5HL	Mottled leaf 2	41:127	1398
303	var3	va3	5HL	Variegated 3	44:115	1277
304	wst2	wst2	5HL	White streak 2	46: 83	766
305	crm1	cm	5HL	Cream seedling 1	26:256	20
306	var1	va	5HL	Variegated 1	37:259	1278
308	lbi1	lb, rac-a	5HL	Long basal rachis internode 1	43:125	580
309	Sgh2	Sh2	5HL	Spring growth habit 2	26:259	770
311	dex1	sex2	5HS	Defective endosperm xenia 1	26:260	
312	raw1	r	5HL	Smooth awn 1	46: 84	27
313	fch6	f6, yv	5HL	Chlorina seedling 6	44:116	1390
314	vrs2	v2, int-b	5HL	Six-rowed spike 2	47:113	773
315	vrs3	v3, int-a	1HL	Six-rowed spike 3	47:115	774
317	ddt1	ddt	5HS	Reaction to DDT 1	26:266	331
319	rpg4	rpg4	5HL	Reaction to *Puccinia graminis* 4	26:267	2438
320	int-b	vrs2	5HL	Intermedium spike-b	47:118	1764
321	srh1	s, l	5HL	Short rachilla hair 1	46: 86	27
322	dsk1	dsk	5HL	Dusky 1	41:128	1714
323	nld1	nld	5HL	Narrow leafed dwarf 1	46: 88	769
324	cud1	cud	5HL	Curly dwarf 1	26:272	
325	crl1	crl, cl	6H	Curly lateral 1	41:129	
326	blf1	bb	5HL	Broad leaf 1	46: 90	
327	flo-b	flo-a	6HL	Extra floret-b	45:121	
328	ari-e	lk9, GPert	5HL	Breviaristatum-e	47:121	
329	ari-h	ari-127	5HL	Breviaristatum-h	48:124	
330	ert-g	ert-g, br3	1HL	Erectoides-g	41:133	
331	ert-n	ert-n	5HL	Erectoides-n	44:120	488
332	Ert-r	Zeo1	2HL	Erectoides-r	47:123	492
333	Rph12	Pa12, Pa9	5HL	Reaction to *Puccinia hordei* 12	26:281	1590
334	raw6	r6	5HL	Smooth awn 6	26:282	2437
335	msg49	msg,,jw	5HL	Male sterile genetic 49	45:122	2402
336	glo-b	glo-b	5HL	Globosum-b	48:125	1327

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
337	blf2	bb2, nlh	5HL	Broad leaf 2	41:137	1667
338	lys1	lys	5HL	High lysine 1	26:286	1784
339	lys3	sex3	5HL	High lysine 3	43:127	1785
340	raw2	r2	5HL	Smooth awn 2	46: 92	27
341	abo12	alb,,o	5HS	Albino seedling 12	26:290	583
342	glo-f	glo-e	5HL	Globosum-f	48:127	
343	Lfb1	Lfb	5HL	Leafy bract 1	41:140	1577
344	var2	va2	5HL	Variegated 2	32:104	2496
345	rym3	ym3	5HS	Reaction to barley yellow mosaic virus 3	32:105	
346	yst5	yst5	7HS	Yellow streak 5	43:130	2501
347	mnd4	m4	5HL	Many noded dwarf 4	44:122	1798
348	Eam5	HvPhyC-e	5HL	Early maturity 5	45:123	
349	brh4	brh.j	2HL	Brachytic 4	42:407	1675
350	brh6	brh.s	5HS	Brachytic 6	42:408	1683
351	gsh1	gs1, cer-q	2HS	Glossy sheath 1	46: 94	735
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	47:125	736
353	gsh3	gs3, cer-a	7HS	Glossy sheath 3	41:143	737
354	gsh4	gs4, cer-x	6HL	Glossy sheath 4	41:146	738
355	gsh5	gs5, cer-s	2HL	Glossy sheath 5	47:128	739
356	gsh6	gs6, cer-c	2HS	Glossy sheath 6	46:101	740
357	msg1	ms1	1HL	Male sterile genetic 1	45:126	1810
358	msg2	ms2	2HL	Male sterile genetic 2	45:128	2371
359	msg3	ms3	2HS	Male sterile genetic 3	45:130	1130
360	msg4	ms4	1H	Male sterile genetic 4	45:132	2392
361	msg5	ms5	3HS	Male sterile genetic 5	45:133	2403
362	msg6	ms6	6HS	Male sterile genetic 6	45:135	2405
363	msg7	ms7	5HL	Male sterile genetic 7	45:137	2406
364	msg8	ms8	5HL	Male sterile genetic 8	45:139	2407
365	msg9	ms9	2HS	Male sterile genetic 9	45:141	2408
366	msg10	ms10	7HS	Male sterile genetic 10	48:128	1811
367	msg11	ms11	5HS	Male sterile genetic 11	45:144	1812
368	msg13	ms13	3HL	Male sterile genetic 13	45:146	1813
369	msg14	ms14	7HS	Male sterile genetic 14	45:147	1814
370	msg15	ms15		Male sterile genetic 15	45:149	1815
371	msg16	ms16	5HS	Male sterile genetic 16	45:150	1816
372	msg17	ms17	5HL	Male sterile genetic 17	45:152	1817

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
373	msg18	ms18	5HL	Male sterile genetic 18	45:153	1818
374	msg19	ms19	5HS	Male sterile genetic 19	45:155	1819
375	msg20	msg,,ad	4H	Male sterile genetic 20	45:156	2372
376	msg21	ms21	1HL	Male sterile genetic 21	45:157	2373
377	seg1	se1	7HL	Shrunken endosperm genetic 1	45:158	750
378	seg2	se2	7HS	Shrunken endosperm genetic 2	26:326	751
379	seg3	se3, ant17	3H	Shrunken endosperm genetic 3	45:160	752
380	seg4	se4	7HL	Shrunken endosperm genetic 4	37:267	753
381	seg5	se5	7HS	Shrunken endosperm genetic 5	26:329	754
382	sex1	se6f, lys5	6HL	Shrunken endosperm xenia 1	48:130	755
383	msg22	ms22	7H	Male sterile genetic 22	45:162	741, 2374
384	msg23	ms23	7HL	Male sterile genetic 23	45:163	2375
385	msg24	msg,,v	4HL	Male sterile genetic 24	48:132	2376
386	des3	des3	2H/ 5HL	Desynapsis 3	43:140	594
387	des8	des8	3H	Desynapsis 8	41:151	599
388	des9	des9	7HL	Desynapsis 9	44:131	600
389	des10	des,,p, HvMlh3	5HL	Desynapsis 10	48:134	601
390	des11	des11	3HL	Desynapsis 11	44:132	602
391	des12	des12	3H	Desynapsis 12	44:133	603
392	des13	des13	3H	Desynapsis 13	44:134	604
393	des14	des14	7H	Desynapsis 14	44:135	605
394	des15	des15	3HL	Desynapsis 15	44:136	606
395	msg26	msg,,u	7HS	Male sterile genetic 26	45:166	745
396	seg6	se6	3HL	Shrunken endosperm genetic 6	44:138	2467
397	seg7	se7		Shrunken endosperm genetic 7	37:269	2468
399	cer-d	cer-5	5HL	Eceriferum-d + ++ ++	41:153	425
400	cer-e	cer-8	1HL	Eceriferum-e -/+ ++ ++	48:136	1518
401	cer-f	cer-9	1H	Eceriferum-f + + ++	48:138	1523
402	cer-g	cer-10	2HL	Eceriferum-g + + ++	47:131	428
403	cer-h	cer-13	4HS	Eceriferum-h - ++ ++	41:157	429
404	cer-i	cer-16	5HL	Eceriferum-i - ++ ++	41:158	430
405	cer-k	cer-39	4HL	Eceriferum-k + ++ ++	41:160	432
406	cer-l	cer-14	3HL	Eceriferum-l + ++ ++	44:142	433
407	cer-m	cer-15	1HL/ 3HL	Eceriferum-m +/++ + ++	41:161	434

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408	cer-n	gs9,cer-20	2HL	Eceriferum-n - - ++ & - +/- ++	44:143	435
409	cer-o	cer-28	1HL	Eceriferum-o -/+ ++ ++	40:106	436
410	cer-p	cer-37	7HL	Eceriferum-p ++ ++ +	41:162	437
411	cer-r	cer-19	3HL	Eceriferum-r +/- + ++	45:168	439
412	cer-t	cer-22	5HL	Eceriferum-t +/- ++ ++	41:162	441
413	gsh8	cer-u, gs8	2HS	Glossy sheath 8	46:105	442
414	cer-v	cer-v	2HS	Eceriferum-w +/- ++ ++	44:147	443
415	cer-w	cer-w	5HL	Eceriferum-w +/- ++ ++	41:166	1519
417	cer-y	cer-y	1HS	Eceriferum-y + +/++ ++	44:149	446
418	cer-z	cer-z	7HS	Eceriferum-z - - ++	44:150	447
419	cer-za	cer-za	5HL	Eceriferum-za ++ ++ -	43:144	1521
420	cer-zb	cer-zb	5HS	Eceriferum-zb - ++ ++	42:508	1522
421	cer-zc	cer-zc	4HL/ 2HS	Eceriferum-zc +/- ++ ++	42:510	450
422	cer-zd	cer-zd	3H	Eceriferum-zd ++ ++ -	48:140	463
423	cer-ze	gl5	7HS	Eceriferum-ze ++ ++ -	44:152	452
424	cer-zf	cer-zf	3H/ 7HS	Eceriferum-zf ++ ++ +	42:516	453
425	cer-zg	cer-zg	4HL	Eceriferum-zg ++ ++ +	48:142	454
427	cer-zi	cer-zi	1HL	Eceriferum-zi + + ++	41:168	456
428	cer-zj	cer-zj	5HL	Eceriferum-zj ++ ++ -	42:520	457
429	cer-zk	cer-zk	2H	Eceriferum-zk + + +/-	43:146	458
430	cer-zl	cer-zl		Eceriferum-zl - - ++	26:382	459
431	cer-zn	cer-zn	1H	Eceriferum-zn +/- ++ ++	40:112	1523
432	cer-zo	cer-zo	3HS	Eceriferum-zo - ++ ++	44:154	462
433	cer-zp	cer-zp	5HL	Eceriferum-zp ++ ++ -	48:144	463
434	cer-zq	cer-zq		Eceriferum-zq ++ ++ -	48:146	1524
435	cer-zr	cer-zr	5HL	Eceriferum-zr +/- ++ ++	44:155	1525
436	cer-zs	cer-zs		Eceriferum-zs + ++ ++	44:156	1526
437	cer-zt	cer-zt	2HS	Eceriferum-zt + ++ ++	44:157	1527
438	cer-zu	cer-zu	1HS	Eceriferum-zu - + ++	41:170	1528
439	cer-zv	cer-zv	4HL	Eceriferum-zv - - -	47:133	1529
440	cer-zw	cer-zw		Eceriferum-zw + + ++	26:392	1530
441	cer-zx	cer-zx	3H	Eceriferum-zx + + ++	46:109	1531
442	cer-zy	cer-zy	1HS	Eceriferum-zy ++ ++ +	40:116	1532
443	cer-zz	cer-zz	3HL	Eceriferum-zz ++ ++ -	44:159	1533
444	cer-ya	cer-ya	3HS	Eceriferum-ya ++ ++ -	26:396	1534

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
445	cer-yb	cer-yb	2HL	Eceriferum-yb ++ ++ -	41:171	1535
446	cer-yc	cer-yc	6H/7HS	Eceriferum-yc - ++ ++	41:172	1536
447	cer-yd	cer-yd	3HS	Eceriferum-yd - ++ ++	26:399	1537
448	cer-ye	cer-ye	4H	Eceriferum-ye ++ ++ -	43:149	1538
449	cer-yf	cer-yf	7H	Eceriferum-yf ++ ++ +	44:160	1539
450	cer-yg	cer-yg	7HS	Eceriferum-yg - - -	44:161	1540
451	cer-yh	cer-yh	3HS	Eceriferum-yh - ++ ++	26:403	1541
453	fer1			Few roots 1	46:112	2538
454	blx5	bl5	7HL	Non-blue aleurone xenia 5	48:148	2509
455	seg8	seg8	7H	Shrunken endosperm genetic 8	48:149	2469
460	cur4	cu4, glo-d	2HL	Curly 4	45:172	1708
461	zeb2	zb2, fch10	4HS	Zebra stripe 2	43:152	93
462	yst3	yst,,c	3HS	Yellow streak 3	44:163	48
463	gig1	gig, sf	2HL	Gigas 1	44:164	1650
464	msg27	msg,,ae	2HS	Male sterile genetic 27	45:174	2379
465	msg28	msg,,as	2HS	Male sterile genetic 28	45:175	2380
466	msg29	msg,,a	5HL	Male sterile genetic 29	45:176	2381
467	msg30	msg,,c	7HL	Male sterile genetic 30	45:177	2382
468	msg31	msg,,d	1HL	Male sterile genetic 31	45:178	2383
469	msg32	msg,,w	7H	Male sterile genetic 32	45:179	2384
470	msg33	msg,,x	2HS	Male sterile genetic 33	45:180	2385
471	msg34	msg,,av	6HS/ 7HS	Male sterile genetic 34	45:181	2386
472	abr1	abr	2HL	Accordion basal rachis internode 1	26:419	1563
473	com1	lax-270, bir1	5HL	Compositum 1	47:135	
474	lax-a	lax-a	5HL	Laxatum-a	46:113	
475	lax-c	lax-21	6HL	Laxatum-c	47:137	
476	lax-d	lax-83		Laxatum-d	47:139	
477	Lax-f	Lax-61		Laxatum-f	48:151	
478	lax-g	lax-25		Laxatum-g	47:141	
479	lax-h	lax-26	3H	Laxatum-h	47:142	
480	lax-i	lax-50		Laxatum-i	47:144	
481	lax-j	lax-49	2H	Laxatum-j	47:145	
482	lax-k	lax-84	2H/3H	Laxatum-k	47:147	
483	lax-l	lax-60	1H	Laxatum-l	47:148	
484	lax-m	lax-80		Laxatum-m	47:149	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
485	lax-n	lax-67	2H/4HL/5H	Laxatum-n	47:150	
486	lax-o	lax-79		Laxatum-o	47:152	
487	lax-df	lax-204		Laxatum-df	47:153	
488	lax-ef	lax-225	2H	Laxatum-ef	47:154	
489	lax-ff	lax-216		Laxatum-ff	47:156	
490	lax-gf	lax-217		Laxatum-gf	47:157	
491	lax-hf	lax-244	2H/3HL/5H	Laxatum-hf	47:158	
492	lax-if	lax-246		Laxatum-if	47:160	
493	Lax-jf	lax-253	4HS	Laxatum-jf	47:161	
494	lax-kf	lax-295		Laxatum-kf	47:163	
495	lax-lf	lax-274		Laxatum-lf	47:164	
496	Lax-mf	Lax-302		Laxatum-fm	48:152	
497	lax-nf	lax-322	2HL/4H	Laxatum-nf	47:166	
498	msg35	msg,,dr	2HL	Male sterile genetic 35	45:183	2387
499	msg36	msg,,bk	6HS	Male sterile genetic 36	45:184	2388
500	msg37	msg,,hl	3HL	Male sterile genetic 37	45:186	2389
501	msg38	msg,,jl	3H	Male sterile genetic 38	45:187	2390
502	msg39	msg,,dm	3H	Male sterile genetic 39	45:188	2391
503	msg40	msg,,ac	6HL	Male sterile genetic 40	45:190	2393
504	msg41	msg,,aj	6HS	Male sterile genetic 41	45:191	
505	msg42	msg,,db	3H	Male sterile genetic 42	45:193	
506	msg43	msg,,br	2HL	Male sterile genetic 43	45:194	
507	msg44	msg,,cx	5HL	Male sterile genetic 44	45:195	
508	msg45	msg,,dp	5HL/ 7HS	Male sterile genetic 45	45:196	
509	msg46	msg,,ec	2H/6H	Male sterile genetic 46	45:197	
510	msg47	msg,,ep	3HS/ 7HS	Male sterile genetic 47	45:198	
511	Rpg1	T	7HS	Reaction to *Puccinia graminis* (wheat stem rust) 1	26:437	
512	Rpg2	T2	2HL	Reaction to Puccinia graminis (wheat stem rust) 2	48:153	1584
513	xnt2	x_b		Xantha seedling 2	26:440	
515	Rsp1	Sep		Reaction to *Septoria passerinii* 1	26:441	2510
516	Rsp2	Sep2		Reaction to *Septoria passerinii* 2	37:275	2511
517	Rsp3	Sep3		Reaction to *Septoria passerinii* 3	37:276	2512
518	sdw1	denso, Hv20ox$_2$	3HL	Semidwarf 1	47:168	2513
519	mnd1	m	2HS	Many noded dwarf 1	48:156	253

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519	mnd1	m	2H	Many-noded dwarf 1	43:154	253
520	msg48	msg,,jt	1H	Male sterile genetic 48	45:199	2401
521	mtt1	mt. mt3	1HL	Mottled leaf 1	41:179	622
522	cer-yi	cer-yi	2H	Eceriferum-yi ++ ++ -	41:180	1542
523	cer-yj	cer-yj	1HS	Eceriferum-yj ++ ++ -	40:124	1543
524	cer-yk	cer-yk	7HL	Eceriferum-yk + + ++	44:167	1544
525	cer-yl	cer-yl	4HL	Eceriferum-yl - - ++	47:171	1545
526	cer-ym	cer-ym	4HL	Eceriferum-ym - - -	47:173	1546
527	cer-yn	cer-yn	1H	Eceriferum-yn + + ++	40:125	1547
528	cer-yo	cer-yo	4HS	Eceriferum-yo ++ ++ +	44:168	1548
529	cer-yp	cer-yp	5HS	Eceriferum-yp ++ ++ +	44:169	1549
530	cer-yq	cer-yq	5H	Eceriferum-yq ++ ++ -	44:170	1550
531	cer-yr	cer-yr	5HL	Eceriferum-yr -/+ + ++	44:171	1551
532	cer-ys	cer-ys	2HL	Eceriferum-ys ++ ++ -	44:172	1552
533	cer-yt	cer-yt	1HL	Eceriferum-yt - ++ ++	48:156	1553
534	cer-yu	cer-yu	1HS	Eceriferum-yu ++ ++ -	48:157	1554
535	cer-yx	cer-yx	1HL/5HL	Eceriferum-yx + + ++	48:158	1555
536	Cer-yy	Gle1	1HS	Eceriferum-yy - ++ ++	48:159	1556
537	cer-yz	cer-yz	1H/5H	Eceriferum-yz + + ++	44:173	1557
538	cer-xa	cer-xa	2HL/4H/ 5HL	Eceriferum-xa ++ ++ -	44:174	1558
539	cer-xb	cer-xb	4H	Eceriferum-xb - ++ ++	44:175	1559
540	cer-xc	cer-xc	1H	Eceriferum-xc + + ++	44:176	1560
541	cer-xd	cer-xd	4H/ 5HL	Eceriferum-xd	44:177	1561
542	Dwf2	Dwf2		Dominant dwarf 2	24:170	
543	int-f	int-20	2HS/ 3HL	Intermedium spike-f	44:178	1767
544	int-h	int-h	5H	Intermedium spike-h	44:179	1768
545	int-i	int-i	2HS	Intermedium spike-i	41:181	1769
546	int-k	int-k	7H	Intermedium spike-k	44:180	1770
547	int-m	int-m	5HL	Intermedium spike-m	44:181	1772
548	fol-b	Ang	1H	Angustifolium-b	48:161	17
549	Lga1	Log	7HS	Long glume awn 1	44:183	835
550	ari-b	ari-b		Breviaristatum-b	44:185	1649
551	ari-f	ari-21	7H	Breviaristatum-f	41:182	1654
552	ari-j	ari-32		Breviaristatum-j	44:186	1658
553	ari-k	ari-504	3H	Breviaristatum-k	44:187	1659
554	ari-m	brh1	7HS	Breviaristatum-m	47:175	1661

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
555	ari-n	ari-45	7H	Breviaristatum-n	41:185	1662
556	ari-o	ert-u, ert-zd	7HL	Breviaristatum-o	45:200	1663
557	ari-p	ari-27		Breviaristatum-p	46:120	1664
558	ari-q	ari-271	4H	Breviaristatum-q	44:188	1665
559	ari-r	ari-14	5H	Breviaristatum-r	41:187	1666
560	ert-f	ert-18	1H	Erectoides-f	48:162	478
561	ert-h	ert-h	5HL	Erectoides-h	44:189	481
562	ert-k	ert-k	6H	Erectoides-k	46:121	485
563	ert-l	ert-12	5HL	Erectoides-l	48:163	486
564	ert-p	ert-44	5HL	Erectoides-p	48:164	490
565	ert-s	ert-50	7H	Erectoides-s	48:165	493
566	ert-t	brh3	2HS	Erectoides-t	45:203	494
567	ert-v	ert-v	6H	Erectoides-v	41:188	497
568	ert-x	ert-x	1H/7H	Erectoides-x	40:136	498
569	ert-y	ert-69		Erectoides-y	48:166	499
570	ert-z	ert-71	5H	Erectoides-z	48:167	500
571	ert-za	ert-za	5H	Erectoides-za	44:190	501
572	ert-zb	ert-zb	7HL	Erectoides-zb	45:205	502
573	ert-zc	ert-zc	7HS	Erectoides-zc	45:206	503
574	ert-ze	ert-ze	5HS	Erectoides-ze	45:207	505
575	Rph6	Pa6		Reaction to *Puccinia hordei* 6	26:501	1598
576	Rph8	Pa8		Reaction to *Puccinia hordei* 8	26:502	1600
577	Rsg2	Rsg2		Reaction to *Schizaphis graminum* 2	37:283	2513
578	mat-b	mat-b	7HL	Praematurum-b	46:123	1788
579	mat-c	Eam6, HvCEN	2H	Praematurum-c	46:125	1789
580	mat-d	mat-d	4Hl/ 6HL	Praematurum-d	45:208	1790
581	mat-e	mat-e		Praematurum-e	26:508	1791
582	mat-f	mat-f	1H	Praematurum-f	45:210	1792
583	mat-g	mat-g		Praematurum-g	26:510	1793
584	mat-h	mat-h	4HL	Praematurum-h	45:212	1794
585	mat-i	mat-i	7HL	Praematurum-i	45:214	1795
586	bra-d	bra-d	1HL	Bracteatum-d	40:139	1696
587	abo3	a2, alb-za		Albino seedling 3	26:514	165
588	abo10	a_{t2}		Albino seedling 10	26:515	57

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
589	abo11	a_{t3}, alb^{t}		Albino seedling 11	26:516	233
590	Rph13	Rph13		Reaction to *Puccinia hordei* 13	28: 31	1591
591	Rph14	Rph14		Reaction to *Puccinia hordei* 14	28: 32	1592
592	yhd2	yh2		Yellow head 2	45:215	757
593	adp1	adp	3HL	Awned palea 1	43:158	1618
594	ant3	rub		Anthocyanin-deficient 3	29: 82	1641
595	ant4	ant4	4H	Anthocyanin-deficient 4	45:216	1642
596	ant5	rs2, rub-a	2HL	Anthocyanin less 5	48:168	1643
597	ant6	ant6		Anthocyanin-deficient 6	29: 85	1644
598	ant13	ant13	6HL	Proanthocyanin-free 13	29: 86	1624
599	ant17	ant17	3HS	Proanthocyanin-free 17	46:128	1628
600	ant18	ant18		Proanthocyanin-free 18	45:221	1630
601	ant19	ant19		Proanthocyanin-free 19	29: 92	1631
602	ant20	ant20		Anthocyanin-rich 20	29: 93	1633
603	ant21	ant21	6H	Proanthocyanin-free 21	29: 94	1634
604	ant22	ant22	2HL	Proanthocyanin-free 22	41:191	1635
605	ant25	ant25		Proanthocyanin-free 25	29: 96	1638
606	ant26	ant26		Proanthocyanin-free 26	29: 97	1639
607	ant27	ant27		Proanthocyanin-free 27	29: 98	1640
608	ant28	ant28	3HL	Proanthocyanin-free 28	46:131	
609	ant29	ant29		Proanthocyanin-free 29	29:100	
610	ant30	ant30		Proanthocyanin-free 30	29:101	
611	Nec6	Sp	7HS	Necrotic leaf spot 6	43:159	977
612	gig2	gig2	4HL	Gigas 2	44:191	1750
613	brc1	brc-5, com2	2HS	Branched 1	45:224	
614	Zeo2	cly1.b, HvAP2	2HL	Zeocriton 2	47:177	637
615	wxs1	wxs1	7H/ 2HL	Waxy spike 1	43:160	3649
616	cul3	cul3	3HL	Uniculme 3	43:161	2494
617	cul4	uc-5, uc-3	3HL	Uniculme 4	46:132	2495
618	mnd3	mn3, m3	4HS	Many noded dwarf 3	44:194	1797
619	bra-a	bra-a	7H	Bracteatum-a	44:196	1693
620	cal-b	cal-b	5HL	Calcaroides-b	44:197	1697
621	Cal-c	Cal-c	5HL	Calcaroides-c	41:195	1567
622	cal-e	cal-23	5HS	Calcaroides-e	32:123	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
623	eli-a	lig-a, eli-3	2HS	Eligulum-a	48:170	3647
624	ops1	op-3	7HS	Opposite spikelets 1	45:226	2427
625	sci-a	sci-3	5H	Scirpoides 1	44:200	
626	scl-a	scl-6	1HL	Scirpoides leaf-a	44:201	
627	viv-a	viv-5	2H	Viviparoides-a	45:227	2498
628	sex7	sex.i	5HL	Shrunken endosperm 7	32:129	2470
629	mtt6	mtt6	7HS	Mottled leaf 6	45:228	2411
630	Ari-s	ari-265	5H/7H	Breviaristatum-s	41:197	
631	brh3	brh.g, ert-t	2HS	Brachytic 3	45:229	1672
632	mnd5	mnd5	7HL	Many noded dwarf 5	44:202	
633	mnd6	den-6	5HL	Many noded dwarf 6	44:203	1713
634	pmr2	nec-50		Premature ripe 2	32:135	2421
635	nec7	nec-45	1H/6H /7H	Necroticans 7	43:166	2420
636	tst2		4HL	Tip sterile 2	43:167	1781
637	nar1	nar1	6HS	NADH nitrate reductase-deficient 1	35:194	2431
638	nar2	nar2	5HL	NADH nitrate reductase-deficient 2	35:195	2415
639	nar3	nar3	7HS	NADH nitrate reductase-deficient 3	35:196	2416
640	nar4	nar4	2Hl	NADH nitrate reductase-deficient 4	35:197	
641	nar5	nar5	5HL	NADH nitrate reductase-deficient 5	35:198	2417
642	nar6	nar6	2HL	NADH nitrate reductase-deficient 6	35:199	
643	nar7	nar7	6HL	NADH nitrate reductase-deficient 7	35:200	2418
644	nar8	nar8	6HS	NADH nitrate reductase-deficient 8	35:201	
645	bsp1			Bushy spike 1	43:168	3652
646	ovl2	ovl2		Ovaryless 2	43:169	3655
647	tst1	tst1	6HL	Tip sterile 1	43:170	3644
648	mov4	mo8		Multiovary 4	43:171	3643
649	asp1	asp1		Aborted spike 1	43:172	3654
650	sun1	sun1		Sensitivity to *Ustilago nuda* 1	43:173	3650
651	lam1	lam1		Late maturity 1	43:174	3653
652	ylf1	ylf1	7HS	Yellow leaf 1	43:175	
653	brh10	brh.l	2HS	Brachytic 10	45:231	1677

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
654	brh11	brh.n	5HS	Brachytic 11	45:232	1679
655	brh12	brh.o	5HS	Brachytic 12	45:233	1680
656	brh13	brh.p	5HS	Brachytic 13	45:234	1681
657	brh15	brh.u	2HL	Brachytic 15	44:205	1685
658	brh17	brh.ab	5HS	Brachytic 17	45:236	1669
659	brh18	brh13	5HS	Brachytic 18	45:237	1670
660	nld2		5H/6H /7H	Narrow leafed dwarf 2	43:176	3645
661	dub1	dub1	5HL	Double seed 1	48:172	
663	sdw3	gai	2HS	Semidwarf 3	46:134	
667	Rpt1	Pt	3HL	Reaction to *Pyrenophora teres* 1	43:177	
671	nec8	nec.w	5HL	Necrotic leaf spot 8	43:179	3600
672	nec9		3HL	Necrotic leaf spot 9	43:181	3599
673	cst1	cs	5HL	Corn stalk 1	41:199	
674	mtt8	Mut 1661		Mottled leaf 8	43:182	3597
675	mtt9	Mut 2721		Mottled leaf 9	44:207	3598
676	fch16	clo.117	2HS	Chlorina seed 16	48:173	
676	fch16	clo.117	2HS	Chlorina seedling 16	40:144	
677	mtt7	mtt.h	2HS	Mottled leaf 7	42:753	
678	ari-u	ari-245	2HS	Breviaristatum-u	45:239	
679	acr4	acr-3	2H/ 6HL	Accordion rachis 4	47:181	
680	ari-v	ari-137	5HS	Breviaristatum-v	41:202	
681	nec10	necS 1-1	3H	Necroticans 10	43:184	3607
682	nec11		1H	Necroticans 11	43:185	3610
683	nec12			Necroticans 12	43:186	3613
684	nec13			Necroticans 13	43:187	3616
685	nec14			Necroticans 14	43:188	3619
686	nec15			Necroticans 15	43:189	3620
687	nec16			Necroticans 16	43:190	3621
688	nec17			Necroticans 17	43:191	3622
689	nec18			Necroticans 18	43:192	3623
690	nec19			Necroticans 19	43:193	3624
691	nec20			Necroticans 20	43:194	3625
692	nec21			Necroticans 21	43:195	3626
693	Nec22			Necroticans 22	43:196	3627
694	nec23			Necroticans 23	43:197	3628
695	Nec24			Necroticans 24	43:198	3629
696	nec25			Necroticans 25	43:199	3630

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
697	Nec26			Necroticans 26	43:200	3631
698	nec27			Necroticans 27	43:201	3633
699	nec28			Necroticans 28	43:202	3635
700	nec29			Necroticans 29	43:203	3636
701	nec30			Necroticans 30	43:204	3637
702	nec31			Necroticans 31	43:205	3638
703	nec32			Necroticans 32	43:206	3639
704	nec33			Necroticans 33	43:207	3640
707	Rpr1		4H	Required for *Puccinia graminis* resistance 1	42:757	
711	Rpt3	QRptt2	2HS	Reaction to *Pyrenophora teres* f. *teres* 3	43:208	
713	Rpt6		5HL	Reaction to *Pyrenophora teres* f. *maculata* 6	43:210	
714	Rpt7	Qrpts4	4HL	Reaction to *Pyrenophora teres* f. *teres* 7	43:211	
716	ibl1	en-Bl, Ibl	7HL	Intense blue aleurone 1	48:174	2508
718	ops2	op-2	5HL	Opposite spikelets 2	43:213	2426
719	ops3	op-1	5HS	Opposite spikelets 3	43:214	2425
720	viv-c	viv-1	5H	Viviparoides-c	43:215	2497
721	ari-w	ari-153	7H	Breviaristatum-w	43:216	
722	ari-y	ari-9	5H	Breviaristatum-y	43:217	
723	mov5	mov.o		Multiovary 5	43:218	3671
724	lks6	lks.q	1H/5H /6H	Short awn 6	43:219	3674
725	ovl3			Ovaryless 3	43:220	3687
726	mnd7			Many noded dwarf 7	43:221	3686
727	ubs5			Unbranched style 5	43:222	3675
728	fxp1			Fenoxaprop-p-ethyl reaction 1	43:223	3684
729	dsk2	msg,,df	7HL	Dusky 2	44:208	
730	lab1		5HL	Labile1	46:137	
731	rpr2	γ08-118; R43-22#1	6H	Required for *Puccinia graminis* resistance 2	46:139	
732	rpr3	γ08-112; R12-31#3		Required for *Puccinia graminis* resistance 3	46:141	3696
733	rpr4	γ08-114; R36-37#1		Required for *Puccinia graminis* resistance 4	46:142	3697
734	rpr5	γ08-117; R42-33#5		Required for *Puccinia graminis* resistance 5	46:143	3699
735	rpr6	γ08-119;		Required for *Puccinia graminis*	46:144	3700

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
		R47-23#1		resistance 6		
736	rpr7	γ08-115; R3-18#3		Required for *Puccinia graminis* resistance 7	46:145	3701
737	rcr1	γ08-122; (R4-29)		Required for resistance to *Cochliobolus sativus* 1	45:249	3703
738	rcr2	γ08-123; (R4-40)		Required for resistance to *Cochliobolus sativus* 2	45:250	3704
739	rcr3	γ08-124		Required for resistance to *Cochliobolus sativus* 3	45:251	3705
740	Pbg1	Pbg	7H	Pubescence on glume 1	47:182	
741	stb1	stb		Stubble1	47:183	
743	twk1	tw	7H	Tweaky spike 1	47:185	
744	acr5	acr-2	7H	Accordion rachis 5	47:187	
746	ant23	ant-3	2HL/5HL	Anthocyanin-deficient 23	48:176	
747	ant24	ant-10		Anthocyanin-deficient 24	48:177	
748	Rpg3	Rpg3	5HL	Reaction to Puccinia graminis 3	48:178	
750	rpg6	rpg6	6HS	Reaction to Puccinia graminis 6	48:179	
751	Rpg7	Rpg7	3HL	Reaction to Puccinia graminis 7	48:180	
752	Qsd1	SD!	5HL	Quantitative seed dormancy 1	48:181	
753	Qsd2	SD2	3HL	Quantitative seed dormancy 2	48:184	
754	Qsd3	qsd3	3HL	Quantitative seed dormancy 3	48:188	

* Recommended locus symbols or codes are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 5 1996.

† Chromosome numbers and arm designations for barley that are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on August 05 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

‡ The seed stock associated with each BGS number, which are held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Small Grains Germplasm Research Facility, Aberdeen, ID 83210, USA.

Table 3. An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on recommended locus names, recommended locus symbols or codes, chromosomal locations, description citation, and original cultivars.

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
abo1	a_t	207	1HL	Albino seedling 1	26:210	Trebi
abo2	a2	53	2HS	Albino seedling 2	26: 89	Nilsson-Ehle No 2
abo3	alb-za	587		Albino seedling 3	26:514	Unknown cultivar
abo4	a4	94	2H	Albino seedling 4	26:133	Unknown cultivar
abo6	a_c	106	3HS	Albino seedling 6	46: 60	Colsess
abo8	a_{c2}	4	7HS	Albino seedling 8	26: 47	Coast
abo9	a_n	112	3HS	Albino seedling 9	26:146	Nigrinudum
abo10	a_{t2}	588		Albino seedling 10	26:515	Canadian Thorpe
abo11	a_{t3}	589		Albino seedling 11	26:516	Trebi
abo12	alb,,o	341	5HS	Albino seedling 12	26:290	Titan
abo13	alb,,p	95	2HL	Albino seedling 13	26:134	Titan
abo14	alb,,q	270	6HL	Albino seedling 14	26:250	Shabet
abo15	alb,,t	271	6HS	Albino seedling 15	26:251	Betzes
abr1	abr	472	2HL	Accordion basal rachis internode 1	26:419	Bonus
acr1	acr, ril	97	2HL	Accordion rachis 1	47: 68	ACBV89B2 29
Acr2	acr, lax	189	4HL	Accordion rachis 2	47:101	CIho 6164
Acr3	Acr, Lax	241	1HL	Accordion rachis 3	48:117	Burma Girl
acr4	acr-3	679	2H/ 6HL	Accordion rachis 4	47:181	Bonus
acr5	acr-2	744	7H	Accordion rachis 5	47:187	
adp1	adp	593	3HL	Awned palea 1	43:158	Unknown line
alm1	al	108	3HS	Albino lemma 1	46: 61	Russia 82
Alp1	Alp, Pht	188	4HL	Aluminum tolerance 1	47: 98	
als1	als	101	3HL	Absent lower laterals 1	43: 74	Montcalm
ant1	rs, rub-a, HvMpc1	33	7HS	Anthocyanin-less 1	48: 68	Bonus
ant2	pr, rub, HvHLH1	80	2HL	Anthocyanin-less 2	48: 80	Foma

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
ant3		594		Anthocyanin-deficient 3	29: 82	Bonus
ant4		595	4H	Anthocyanin-deficient 4	45:216	Foma
ant5	rs2, rub-a	596	2HL	Anthocyanin-deficient 5	48:168	Bonus
ant6		597		Anthocyanin-deficient 6	29: 85	Foma
ant13		598	6HL	Proanthocyanidin-free 13	29: 86	Foma
ant17		599	3HS	Proanthocyanidin-free 17	46:128	Nordal
ant18		600	3H	Proanthocyanidin-free 18	45:221	Nordal
ant19		601		Proanthocyanidin-free 19	29: 92	Alf
ant20		602		Anthocyanidin-rich 20	29: 93	Foma
ant21		603	6H	Proanthocyanidin-free 21	29: 94	Georgie
ant22		604	2HL	Proanthocyanidin-free 22	41:191	Hege 802
ant23	ant-3	746	2HL/ 5HL	Anthocyanin- deficient 23	48:176	Bonus
ant24	ant-10	747		Anthocyanin-defient 24	48:177	Foma
ant25		605		Proanthocyanidin-free 25	29: 96	Secobra 18193
ant26		606		Proanthocyanidin-free 26	29: 97	Grit
ant27		607		Proanthocyanidin-free 27	29: 98	Zebit
ant28		608	3HL	Proanthocyanidin-free 28	46:131	Grit
ant29		609		Proanthocyanidin-free 29	29:100	Ca 708912
ant30		610		Proanthocyanidin-free 30	29:101	Gunhild
ari-a	ari-1	132	3HS	Breviaristatum-a	41:106	Bonus
ari-b	ari-11	550		Breviaristatum-b	44:185	Bonus
ari-e	lk9, GPert	328	5HL	Breviaristatum-e	47:121	Bonus
ari-f	ari-21	551	7H	Breviaristatum-f	41:182	Bonus
ari-g	lk10	89	2H	Breviaristatum-g	47: 66	Bonus
ari-h	ari-127	329	5HL	Breviaristatum-h	48:124	Foma
ari-j	ari-32	552		Breviaristatum-j	44:186	Bonus
ari-k	ari-504	553	3H	Breviaristatum-k	44:187	Bonus
ari-m	brh1	554	7HS	Breviaristatum-m	47:175	Bonus
ari-n	ari-45	555	7H	Breviaristatum-n	41:185	Bonus
ari-o	ert-u, ert-zd	556	7HL	Breviaristatum-o	45:200	Bonus
ari-p	ari-27	557		Breviaristatum-p	46:120	Foma
ari-q	ari-271	558	4H	Breviaristatum-q	44:188	Kristina
ari-r	ari-14	559	5H	Breviaristatum-r	41:187	Bonus

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Ari-s	ari-265	630	5H/ 7H	Breviaristatum-s	41:197	Kristina
ari-t	ari-25	238	1H	Breviaristatum-t	47:104	Bonus
ari-u	ert-t	678	2HS	Breviaristatum-u	45:100	Foma
ari-v	ari-137	680	5HS	Breviaristatum-v	41:202	Foma
ari-w	ari-153	721	7H	Breviaristatum-w	43:216	Foma
ari-x	ari-22	274	6H	Breviaristatum-x	43:124	Bonus
ari-y	ari-9	722	5H	Breviaristatum-y	43:217	Bonus
ari-z	ari-189	200	4HL	Breviaristatum-z	48:101	Foma
asp1		649		Aborted spike 1	43:172	Steptoe
blf1	bb	326	5HL	Broad leaf 1	46: 90	Bonus
blf2	bb2, nlh	337	5HL	Broad leaf 2	41:137	Hannchen
Blp1	B	203	1HL	Black lemma and pericarp 1	48:102	Nigrinudum
blx1	bl, HvMpc1	15	4HL	Non-blue aleurone xenia 1	48: 61	Goldfoil
blx2	bl2	19	7HS	Non-blue aleurone xenia 2	48: 63	Nepal
blx3	bl3, bly, HvMyc2	173	4HL	Non-blue aleurone xenia 3	48: 93	Blx
blx4	bl4, HvMpc1	174	4HL	Non-blue (pink) aleurone xenia 4	48: 95	Ab 6
blx5	bl5	454	7HL	Non-blue aleurone xenia 5	48:148	BGM 122
bra-a		619	7H	Bracteatum-a	44:196	Bonus
bra-d		586	1HL	Bracteatum-d	40:139	Foma
brc1	brc-5, com2	613	2HS	Branched 1	45:224	BGRC 13145
brh1	br	1	7HS	Brachytic 1	47: 50	Himalaya
brh2	br, ari-l, HvTUD1	157	4HL	Brachytic 2	48: 91	Svanhals
brh3	brh.g, ert-t	631	2HS	Brachytic 3	45:229	Birgitta
brh4	brh.j	349	2HL	Brachytic 4	42:407	Birgitta
brh5	brh.m	185	4HS	Brachytic 5	44:110	Birgitta
brh6	brh.s	350	5HL	Brachytic 6	42:408	Akashinriki
brh7	brh.w	41	7H	Brachytic 7	42: 98	Volla
brh8	brh.ad	142	3HL	Brachytic 8	42:232	Birgitta
brh9	brh.k	187	4HL	Brachytic 9	43: 99	Birgitta
brh10	brh.l	653	2HS	Brachytic 10	45:231	Birgitta
brh11	brh.n	654	5HS	Brachytic 11	45:232	Birgitta

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
brh12	brh.o	655	5HS	Brachytic 12	45:233	Birgitta
brh13	brh.p	656	5HS	Brachytic 13	45:234	Birgitta
brh14	ari-o	148	7HL	Brachytic 14	45:111	Akashinriki
brh15	brh.u	657	2HL	Brachytic 15	44:205	Julia
brh16	brh.v	44	7HL	Brachytic 16	45: 89	Korál
brh17	brh.ab	658	5HS	Brachytic 17	45:236	Morex
brh18	brh13	659	5HS	Brachytic 18	45:237	Triumph
bsp1		645		Bushy spike 1	43:168	Morex
btr1	bt1	115	3HS	Non-brittle rachis 1	43: 78	A 222
btr2	bt2	116	3HS	Non-brittle rachis 2	43: 80	Sakigoke
cal-b		620	5HL	Calcaroides-b	44:197	Bonus
Cal-c		621	5HL	Calcaroides-c	41:195	Bonus
cal-d		146	3H	Calcaroides-d	48: 88	Foma
cal-e		622	5HS	Calcaroides-e	32:123	Semira
cer-d	cer-5	399	5HL	Eceriferum-d + ++ ++	41:153	Bonus
cer-e	cer-8	400	1HL	Eceriferum-e -/+ ++ ++	48:136	Bonus
cer-f	cer-9	401	1H	Eceriferum-f + + ++	48:138	Bonus
cer-g	cer-10	402	2HL	Eceriferum-g + + ++	47:131	Bonus
cer-h	cer-13	403	4HS	Eceriferum-h - ++ ++	41:157	Bonus
cer-i	cer-16	404	5HL	Eceriferum-i - ++ ++	41:158	Bonus
cer-k	cer-39	405	4HL	Eceriferum-k + ++ ++	41:160	Bonus
cer-l	cer-14	406	3HL	Eceriferum-l + ++ ++	44:142	Bonus
cer-m	cer-15	407	1H/ 3H	Eceriferum-m +/++ + ++	41:161	Bonus
cer-n	gs9, cer-20	408	2HL	Eceriferum-n - - ++ & - +/- ++	44:143	Bonus
cer-o	cer-28	409	1HL	Eceriferum-o -/+ ++ ++	40:106	Bonus
cer-p	cer-37	410	7HL	Eceriferum-p ++ ++ +	41:162	Bonus
cer-r	cer-19	411	3HL	Eceriferum-r +/- + ++	45:168	Bonus
cer-t	cer-22	412	5HL	Eceriferum-t +/- ++ ++	41;164	Bonus
cer-v	cer-49	414	2HS	Eceriferum-v +/- ++ ++	44:147	Bonus
cer-w	cer-48	415	5HL	Eceriferum-w +/- ++ ++	41:166	Bonus
cer-xa	cer-585	538	2HL/ 4H/ 5HL	Eceriferum-xa ++ ++ -	44:174	Foma
cer-xb	cer-943	539	4H	Eceriferum-xb - ++ ++	44:175	Bonus
cer-xc	cer-1371	540	1H	Eceriferum-xc + + ++	44:176	Bonus

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
cer-xd	cer-1455	541	4H/5HL	Eceriferum-xd + + ++	44:177	Bonus
cer-y	cer-72	417	1HS	Eceriferum-y + +/++ ++	44:149	Bonus
cer-ya	cer-180	444	3HS	Eceriferum-ya ++ ++ -	26:396	Bonus
cer-yb	cer-200	445	2HL	Eceriferum-yb ++ ++ -	41:171	Bonus
cer-yc	cer-135	446	6H/7HS	Eceriferum-yc - ++ ++	41:172	Bonus
cer-yd	cer-139	447	3HS	Eceriferum-yd - ++ ++	26:399	Bonus
cer-ye	cer-267	448	4H	Eceriferum-ye ++ ++ -	43:149	Foma
cer-yf	cer-652	449	7H	Eceriferum-yf ++ ++ +	44:160	Bonus
cer-yg	cer-1014	450	7HS	Eceriferum-yg - - -	44:161	Carlsberg II
cer-yh	cer-116	451	3HS	Eceriferum-yh - ++ ++	26:403	Bonus
cer-yi	cer-254	522	2H	Eceriferum-yi ++ ++ -	41:180	Foma
cer-yj	cer-667	523	1HS	Eceriferum-yj ++ ++ -	40:124	Bonus
cer-yk	cer-627	524	7HL	Eceriferum-yk + + ++	44:167	Bonus
cer-yl	cer-187	525	4HL	Eceriferum-yl - - ++	47:171	Bonus
cer-ym	cer-753	526	4HL	Eceriferum-ym - - -	47:173	Bonus
cer-yn	cer-1112	527	1H	Eceriferum-yn + + ++	40:125	Kristina
cer-yo	cer-647	528	4HS	Eceriferum-yo ++ ++ +	44:168	Bonus
cer-yp	cer-949	529	5HS	Eceriferum-yp ++ ++ +	44:169	Bonus
cer-yq	cer-1246	530	5H	Eceriferum-yq ++ ++ -	44:170	Kristina
cer-yr	cer-492	531	5HL	Eceriferum-yr -/+ + ++	44:171	Foma
cer-ys	cer-680	532	2HL	Eceriferum-ys ++ ++ -	44:172	Bonus
cer-yt	cer-758	533	1HL	Eceriferum-yt - ++ ++	48:156	Bonus
cer-yu	cer-158	534	1HS	Eceriferum-yu ++ ++ -	48:157	Bonus
cer-yx	cer-421	535	1H/3H/5H	Eceriferum-yx + + ++	40:128	Foma
Cer-yy	Gle1	536	1HS	Eceriferum-yy - ++ ++	48:159	Bonus
cer-yz	cer-1452	537	1H/5H	Eceriferum-yz + + ++	44:173	Bonus
cer-z	cer-52	418	7HS	Eceriferum-z - - ++	44:150	Bonus
cer-za	cer-126	419	5HL	Eceriferum-za ++ ++ -	43:144	Foma
cer-zb	cer-38	420	5HS	Eceriferum-zb - ++ ++	42:508	Bonus
cer-zc	ccer-65	421	4HL/2HS	Eceriferum-zc +/- ++ ++	42:510	Bonus
cer-zd	cer-67	422	3H	Eceriferum-zd ++ ++ -	48:142	Bonus
cer-ze	gl5	423	7HS	Eceriferum-ze ++ ++ -	44:152	Bonus

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
cer-zf	cer-70	424	3H/ 7HS	Eceriferum-zf ++ ++ +	42:516	Bonus
cer-zg	cer-214	425	4HL	Eceriferum-zg ++ ++ +	48:142	Foma
cer-zi	cer-68	427	1HL	Eceriferum-zi + + ++	41:168	Bonus
cer-zj	cer-78	428	5HL	Eceriferum-zj ++ ++ -	42:520	Bonus
cer-zk	cer-85	429	2H	Eceriferum-zk + + +/-	26:381	Bonus
cer-zl	cer-17	430		Eceriferum-zl - - ++	26:382	Bonus
cer-zn	cer-244	431	1H	Eceriferum-zn +/- ++ ++	40:112	Foma
cer-zo	cer-229	432	3HS	Eceriferum-zo - ++ ++	44:154	Foma
cer-zp	cer-313	433	5HL	Eceriferum-zp ++ ++ -	48:144	Bonus
cer-zq	cer-248	434		Eceriferum-zq ++ ++ -	48:146	Foma
cer-zr	cer-260	435	5HL	Eceriferum-zr +/- ++ ++	44:155	Foma
cer-zs	cer-467	436		Eceriferum-zs + ++ ++	44:156	Foma
cer-zt	cer-389	437	2HS	Eceriferum-zt + ++ ++	44:157	Foma
cer-zu	cer-122	438	1HS	Eceriferum-zu - + ++	41:170	Foma
cer-zv	cer-268	439	4HL	Eceriferum-zv - - -	47:133	Foma
cer-zw	cer-286	440		Eceriferum-zw + + ++	26:392	Foma
cer-zx	cer-100	441	3H	Eceriferum-zx + + ++	46:111	Bonus
cer-zy	cer-118	442	1HS	Eceriferum-zy ++ ++ +	40:116	Bonus
cer-zz	cer-615	443		Eceriferum-zz ++ ++ -	44:159	Bonus
clh1	clh	225	7H/5 H	Curled leaf dwarf 1	48:109	Hannchen
com1	lax-270, bir1	473	5HL	Compositum 1	47:135	Foma
com2	bir2	71	2HS	Compositum 2	45: 95	CIMMYT freak
crl1	cl	325	6H	Curly lateral 1	41:129	Montcalm
crm1	cm	305	5HL	Cream seedling 1	26:256	Black Hulless
cst1	cs	673	5HL	Corn stalk 1	41:199	Husky
cud1	cud	324	5HL	Curly dwarf 1	26:272	Akashinriki
cud2		229	1HL	Curly dwarf 2	47:103	Akashinriki
cul2	uc2	253	6HL	Uniculm 2	43:112	Kindred
cul3	cul3	616	3HL	Uniculme 3	43:161	Donaria
cul4	uc-5	617	3HL	Uniculme 4	46:132	Bonus
cur1	cu1	262	3HL	Curly 1	46: 81	48-cr cr-17
cur2	cu2	114	3HL	Curly 2	44: 82	Choshiro
cur3	cu3	263	6HL	Curly 3	41:125	Akashinriki

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cur4	glo-d	460	2HL	Curly 4	45:172	Asahi 5
cur5	cu5	231	2HS	Curly 5	41:120	Glenn
ddt1	ddt	317	5HS	Reaction to DDT 1	26:266	Spartan
des1	lc	12	7H	Desynapsis 1	42: 58	Mars
des2	ds	119	3H	Desynapsis 2	43: 84	Husky
des3		386	2H/ 5HL	Desynapsis 3	43:140	Betzes
des4		13	7H	Desynapsis 4	44: 54	Betzes
des5	des5, HvDMC 1	14	7HL	Desynapsis 5	48: 59	Betzes
des6		215	1HL	Desynapsis 6	43:106	Betzes
des7		64	3H	Desynapsis 7	43: 67	Betzes
des8		387	3H	Desynapsis 8	41:151	Betzes
des9		388	7HL	Desynapsis 9	44:131	Betzes
des10	des,,p, HvMlh3	389	3HL	Desynapsis 10	48:134	Betzes
des11		390	3HL	Desynapsis 11	44:132	Betzes
des12		391	3H	Desynapsis 12	44:133	Betzes
des13		392	3H	Desynapsis 13	44:134	Betzes
des14		393	7H	Desynapsis 14	44:135	Betzes
des15		394	3HL	Desynapsis 15	44:136	Ingrid
dex1	sex2	311	5HS	Defective endosperm xenia 1	26:260	BTT 63-j-18-17
dsk1	dsk	322	5HL	Dusky 1	41:128	Chikurin-Ibaraki 1
dsk2		729	7HL	Dusky 2	44:208	Betzes
dsp1	l	9	7HS	Dense spike 1	43: 50	Honen 6
dsp9	l9, ert-e	258	6HL	Dense spike 9	47:107	Akashinriki
dsp10	l_c	111	3HS	Dense spike 10	48: 84	Club Mariout
dsp11	dsp	244	1HL	Dense spike 11	41:121	Akashinriki
dub1		661	6HL	Double seed 1	48:172	Bonus
Dwf2		542		Dominant dwarf 2	24:170	Klages / Mata
Eam1	Ea, Ppd-H1	65	2HS	Early maturity 1	47: 54	Estate
Eam5	HvPhyC-e	348	5HL	Early maturity 5	45:123	Higuerilla*2/ Gobernadora

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Eam6	Ea6, Ea, HvCEN	98	2HS	Early maturity 6	46: 57	Morex
eam7	HvCO7	252	6HS	Early maturity 7	45:118	California Mariout
eam8	ea$_k$, mat-a	214	1HL	Early maturity 8	46: 69	Kinai 5
eam9	ea,,c	181	4HL	Early maturity 9	26:204	Tayeh 8
eam10	ea$_{sp}$	130	3HL	Early maturity 10	44: 86	Super Precoz
eli-a	lig-a	623	2HS	Eligulum-a	48:170	Foma
eog 1	e, lep-e	57	2HL	Elongated outer glume 1	43: 64	Triple Bearded Club Mariout
ert-a	ert-6	28	7HS	Erectoides-a	41: 76	Gull
ert-b	ert-2	224	1HL	Erectoides-b	48:107	Gull
ert-c	ert-1	134	3HL	Erectoides-c	41:108	Gull
ert-d	ert-7	29	7HS	Erectoides-d	42: 82	Gull
ert-e	l9, dsp9	266	6HL	Erectoides-e	47:109	Bonus
ert-f	ert-18	560	1H	Erectoides-f	48:162	Bonus
ert-g	ert-g	330	1HL	Erectoides-g	41:133	Bonus
ert-h	ert-25	561	5HL	Erectoides-h	44:189	Bonus
ert-ii	uzu1	135	3HL	Erectoides-ii	45:109	Bonus
ert-j	ert-31	90	2H	Erectoides-j	43: 70	Bonus
ert-k	ert-32	562	6H	Erectoides-k	46:121	Bonus
ert-l	ert-12	563	5HL	Erectoides-l	48:163	Maja
ert-m	ert-34	30	7HS	Erectoides-m	46: 47	Bonus
ert-n	ert-51	331	5HL	Erectoides-n	44:120	Bonus
ert-p	ert-44	564	5HL	Erectoides-p	48:164	Bonus
ert-q	ert-101	91	6H	Erectoides-q	43: 71	Bonus
Ert-r	Ert-52	332	2HL	Erectoides-r	47:123	Bonus
ert-s	ert-50	565	7H	Erectoides-s	48:165	Bonus
ert-t	brh3	566	2HS	Erectoides-t	45:203	Bonus
ert-u	ari-o	92	7HL	Erectoides-u	45:100	Bonus
ert-v	ert-57	567	6H	Erectoides-v	41:188	Bonus
ert-x	ert-58	568	1H/ 7H	Erectoides-x	40:136	Bonus
ert-y	ert-69	569		Erectoides-y	48:166	Bonus
ert-z	ert-71	570	5H	Erectoides-z	48:167	Bonus

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
ert-za	ert-102	571	5H	Erectoides-za	44:189	Bonus
ert-zb	ert-132	572	7HL	Erectoides-zb	45:205	Bonus
ert-zc	ert-149	573	7HS	Erectoides-zc	45:206	Bonus
ert-zd	ari-o	93	7HL	Erectoides-zd	45:102	Bonus
ert-ze	ert-105	574	5HS	Erectoides-ze	45:207	Bonus
fch1	f, lg	55	2HS	Chlorina seedling 1	48: 73	Minn 84-7
fch2	f2, lg5, HvCAO	117	3HL	Chlorina seedling 2	48: 86	28-3398
fch3	f3	220	1HS	Chlorina seedling 3	48:104	Minn 89-4
fch4	f4	17	7HL	Chlorina seedling 4	43: 54	Montcalm
fch5	f5	18	7HS	Chlorina seedling 5	43: 56	Gateway
fch6	f6	313	5HL	Chlorina seedling 6	44:116	Himalaya
fch7	f7	201	1HL	Chlorina seedling 7	41:113	Smyrna
fch8	f8	5	7HS	Chlorina seedling 8	41: 62	Comfort
fch9	f9	151	4HS	Chlorina seedling 9	44: 92	Ko A
fch10		177	4H	Chlorina seedling 10	43: 95	Unknown cultivar
fch11	f11	260	6HL	Chlorina seedling 11	45:207	Himalaya
fch12	f_c, clo-fc	2	7HS	Chlorina seedling 12	48: 57	Colsess
fch13	f13	86	5HL	Chlorina seedling 13	44: 77	Nigrinudum
fch14	f14	87	2HL	Chlorina seedling 14	44: 78	Shyri
fch15	or	52	2HS	Chlorina seedling 15	48: 72	Trebi IV
fch16	clo.117	676	2HS	Chlorina seedling 16	48:173	Bonus
fch17	vy	191	1HL/ 3HL	Chlorina seedling 17	48:100	Himalaya / Ingrescens
fer1		453		Few roots 1	46:112	Bomi Abed
flo-a		182	6HL	Extra floret-a	45:116	Foma
flo-b	flo-a	327	6HL	Extra floret-b	45:121	Foma
flo-c	flo-a	74	6HL	Extra floret-c	45: 97	Foma
fol-a		73	2HL	Angustifolium-a	43: 69	Proctor
Fol-b	Ang	548	1HS	Angustifolium-b	48:161	Mars
fst1	fs	301	5HL	Fragile stem 1	48:122	Kamairazu
fst2	fs2	208	1HL	Fragile stem 2	41:114	Oshichi
fst3	fs3	24	7HS	Fragile stem 3	41: 74	Kobinkatagi 4
fxp1		728		Fenoxaprop-p-ethyl reaction 1	43:223	Morex

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gig1	gig	463	2H	Gigas 1	44:164	Tochigi Golden Melon
gig2		612	4HL	Gigas 2	44:191	ND12463
glf1	gl, cer-zh	155	4HL	Glossy leaf 1 ++ ++ -	47: 81	Himalaya
glf3	gl3, cer-j	165	4HL	Glossy leaf 3 ++ ++ -	47: 86	Goseshikoku
glo-a		168	4H	Globosum-a	45:115	Proctor
glo-b		336	5HL	Globosum-b	48:125	Villa
glo-c		72	2H	Globosum-c	43: 68	Villa
glo-e		230	1HL	Globosum-e	45:117	Foma
glo-f	glo-e	342	5HL	Globosum-f	48:127	Damazy
gpa1	gp	59	2HL	Grandpa 1	45: 91	Lyallpur
gpc1	HvNAM-1	276	6HS	Grain protein content 1	48:120	Karl
gra-a	gran-a	131	7H	Granum-a	47: 79	Donaria
gsh1	gs1, cer-q	351	2HS	Glossy sheath 1 - - ++	46: 94	PI 195285
gsh2	gs2, cer-b	352	3HL	Glossy sheath 2 - - ++	47:125	Atlas
gsh3	gs3, cer-a	353	7HS	Glossy sheath 3 - - ++	41:143	Mars
gsh4	gs4, cer-x	354	6HL	Glossy sheath 4 - - ++	41:146	Gateway
gsh5	gs5, cer-s	355	2HL	Glossy sheath 5 + - ++	47:128	Jotun
gsh6	gs6, cer-c	356	2HS	Glossy sheath 6 - - ++	46:101	Betzes
gsh7	gs7	81	2H/ 5H	Glossy sheath 7 - - ++	48: 83	Akashinriki
gsh8	gs8, cer-u	413	2HS	Glossy sheath 8 + + ++	46:105	Akashinriki
Gth1	G	69	2HL	Toothed lemma 1	47: 59	Machine (Wexelsen)
hcm1	h	77	2HL	Short culm 1	26:115	Morex
Hln1	Hn	164	4HL	Hairs on lemma nerves 1	44: 99	Kogane-mugi
Hsh1	Hs	179	4HL	Hairy leaf sheath 1	44:107	Kimugi
ibl1	ibl1	716	7HL	Intense blue aleurone 1	48:174	Ethiopian 637
int-b	vrs2	320	5HL	Intermedium spike-b	47:118	Bonus
int-c	i, vrs5, HvTB1	178	4HS	Intermedium spike-c	47: 92	Gamma 4
int-f	int-20	543	2HS/ 3HL	Intermedium spike-f	44:178	Foma
int-h	int-42	544	5H	Intermedium spike-h	44:179	Kristina
int-i	int-39	545	2HS	Intermedium spike-i	41:181	Kristina

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int-k	int-47	546	7H	Intermedium spike-k	44:180	Kristina
int-m	int-85	547	5HL	Intermedium spike-m	44:181	Bonus
Kap1	K	152	4HS	Hooded lemma 1	26:179	Colsess
lab1		730	5HL	Labile 1	46:137	
lam1		651		Late maturity 1	43:174	Steptoe
lax-a	lax-8	474	5HL	Laxatum-a	46:113	Bonus
lax-b	lax-1	268	6HL	Laxatum-b	44:113	Bonus
lax-c	lax-21	475	6HL	Laxatum-c	47:137	Bonus
lax-d	lax-83	476		Laxatum-d	47:139	Bonus
Lax-f	Lax-61	477		Laxatum-f	48:151	Bonus
lax-g	lax-25	478		Laxatum-g	47:141	Bonus
lax-h	lax-26	479	3H	Laxatum-h	47:142	Bonus
lax-i	lax-50	480		Laxatum-i	47:144	Bonus
lax-j	lax-49	481	2H	Laxatum-j	47:145	Bonus
lax-k	lax-84	482	2H/3H	Laxatum-k	47:147	Bonus
lax-l	lax-60	483	1H	Laxatum-l	47:148	Bonus
lax-m	lax-67	484		Laxatum-m	47:149	Bonus
lax-n	lax-80	485	2H/4HL/5H	Laxatum-n	47:150	Bonus
lax-o	lax-79	486		Laxatum-o	47:152	Bonus
lax-df	lax-204	487		Laxatum-df	47:153	Foma
lax-ef	lax-225	488	2H	Laxatum-ef	47:154	Foma
lax-ff	lax-216	489		Laxatum-ff	47:156	Foma
lax-gf	lax-217	490		Laxatum-gf	47:157	Foma
lax-hf	lax-244	491	2H/3HL/5H	Laxatum-hf	47:158	Foma
lax-if	lax-246	492		Laxatum-if	47:160	Foma
Lax-jf	lax-253	493	4HS	Laxatum-jf	47:161	Foma
lax-kf	lax-295	494		Laxatum-kf	47:163	Foma
lax-lf	lax-274	495		Laxatum-lf	47:164	Foma
Lax-mf	Lax-302	496		Laxatum-mf	48:152	Foma
lax-nf	lax-322	497	2HL/4H	Laxatum-nf	47:166	Foma

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
lbi1	lb	308	5HL	Long basal rachis internode 1	43:125	Wisconsin Pedigree 38
lbi2	lb2	156	4HS	Long basal rachis internode 2	44: 92	Montcalm
lbi3	lb3	27	7HL	Long basal rachis internode 3	42: 79	Montcalm
lel1	lel	235	2H	Leafy lemma 1	46: 74	G7118
Lfb1	Lfb	343	5HL	Leafy bract 1	41:140	Montcalm
lfl1	lfl	275	6HL	Leafless 1	47:111	Golden Melon
Lga1	Log	549	7HS	Long glume awn 1	44:183	Guy Mayle
lgn2	lg2	169	4HS	Light green 2	42:264	Minn 75
lgn3	lg3, lg7	170	1HL	Light green 3	44:103	No 154
lgn4	lg4, lg1	171	4HL	Light green 4	44:105	Himalaya / Ingrescens
lig1	li, aur-a	60	2HL	Liguleless 1	45: 93	Muyoji
lit1	s, rin	99	2HS	Lesser internode number 1	41: 92	Natural occurrence
Lks1	Lk	75	2HL	Awnless 1	41: 84	*Hordeum inerme*
lks2	lk2	10	7HL	Short awn 2	45: 80	Honen 6
lks5	lk5	172	4HL	Short awn 5	47: 89	CIho 5641
lks6	lks.q	724	1H/ 5H/ 6H	Short awn 6	43:219	Morex
lnt1	rnt	118	3HL	Low number of tillers 1	47: 74	Mitake
lys1	lys	338	5HL	High lysine 1	26:286	Hiproly
lys3	sex3	339	5HL	High lysine 3	43:127	Bomi Abed
Lys4	Lys4d, sex5g	232	1HS	High lysine 4	48:113	Bomi Abed
lys6		269	6H	High lysine 6	44:114	Bomi Abed
lzd1	dw4	125	3H	Lazy dwarf 1	43: 87	Akashinriki
mat-b	mat-7	578	7HL	Praematurum-b	46:123	Bonus
mat-c	Eam6, HvCEN	579	2H	Praematurum-c	46:125	Bonus
mat-d	mat-14	580	4HL/ 6HL	Praematurum-d	45:208	Bonus
mat-e	mat-18	581		Praematurum-e	26:508	Bonus
mat-f	mat-23	582	1H	Praematurum-f	45:210	Bonus
mat-g	mat-30	583		Praematurum-g	26:510	Bonus
mat-h	mat-36	584	4HL	Praematurum-h	45:212	Bonus

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mat-i	mat-37	585	7HL	Praematurum-i	45:214	Bonus
min1	min	161	4HL	Semi-minute dwarf 1	44: 97	Taisho-mugi
min2	en-min	160		Enhancer of minute 1	26:186	Kaiyo Bozu
mnd1	m	519	2HS	Many noded dwarf 1	48:155	Mesa
mnd3	m3	618	4HS	Many noded dwarf 3	44:194	Montcalm
mnd4	m4	347	5HL	Many noded dwarf 4	44:122	Akashinriki
mnd5		632	7HL	Many noded dwarf 5	44:202	C2-95-199
mnd6	den-6	633	5HL	Many noded dwarf 6	44:203	Bonus
mnd7		726		Many noded dwarf 7	43:221	Steptoe
mov1	mo5	43	7HL	Multiovary 1	43: 59	Steptoe
mov2	mo	147	3HS	Multiovary 2	43: 91	Steptoe
mov3	mo-a	234	1H	Multiovary 3	32:102	Akashinriki
mov4	mo8	648		Multiovary 4	43:171	Steptoe
mov5	mov.o	723		Multiovary 5	43:218	Morex
msg1	ms, ms1	357	1HL	Male sterile genetic 1	45:126	CIho 5368
msg2	ms2	358	2HL	Male sterile genetic 2	45:128	Manchuria
msg3	ms3	359	1HL	Male sterile genetic 3	45:130	Gateway
msg4	ms4	360	1H	Male sterile genetic 4	45:132	Freja
msg5	ms5	361	3HS	Male sterile genetic 5	45:133	Carlsberg II
msg6	ms6	362	6HS	Male sterile genetic 6	45:135	Hanna
msg7	ms7	363	5HL	Male sterile genetic 7	45:137	Dekap
msg8	ms8	364	5HL	Male sterile genetic 8	45:139	Betzes
msg9	ms9	365	2HS	Male sterile genetic 9	45:141	Vantage
msg10	ms10	366	7HS	Male sterile genetic 10	48:128	Compana
msg11	ms11	367	5HS	Male sterile genetic 11	45:144	Gateway
msg13	ms13	368	3HL	Male sterile genetic 13	45:146	Haisa II
msg14	ms14	369	7HS	Male sterile genetic 14	45:147	Unitan
msg15	ms15	370		Male sterile genetic 15	45:149	Atlas /2* Kindred
msg16	ms16	371	5HS	Male sterile genetic 16	45:150	Betzes
msg17	ms17	372	5HL	Male sterile genetic 17	45:152	Compana
msg18	ms18	373	5HL	Male sterile genetic 18	45:153	Compana
msg19	ms19	374	5HS	Male sterile genetic 19	45:155	CIho 14393
msg20	msg,,ad	375	4H	Male sterile genetic 20	45:156	Hannchen
msg21	ms21	376	1HL	Male sterile genetic 21	45:157	Midwest Bulk

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
msg22	ms22	383	7H	Male sterile genetic 22	45:162	Glacier / Compana
msg23	ms23	384	5H	Male sterile genetic 23	45:163	Betzes
msg24	msg,,y	385	4HL	Male sterile genetic 24	48:132	Betzes
msg25	msg,,r	166	2HS	Male sterile genetic 25	45:113	Betzes
msg26	msg,,u	395	7HS	Male sterile genetic 26	45:166	Unitan
msg27	msg,,ae	464	2HS	Male sterile genetic 27	45:174	Firlbecks III
msg28	msg,,as	465	2HS	Male sterile genetic 28	45:175	York
msg29	msg,,a	466	5HL	Male sterile genetic 29	45:176	Ackermans MGZ
msg30	msg,,c	467	7HL	Male sterile genetic 30	45:177	Compana
msg31	msg,,d	468	1HL	Male sterile genetic 31	45:178	51Ab4834
msg32	msg,,w	469	7H	Male sterile genetic 32	45:179	Betzes
msg33	msg,,x	470	2HS	Male sterile genetic 33	45:180	Betzes
msg34	msg,,av	471	6HS/ 7HS	Male sterile genetic 34	45:181	Paragon
msg35	msg,,dr	498	2HL	Male sterile genetic 35	45:183	Karl
msg36	msg,,bk	499	6HS	Male sterile genetic 36	45:184	Betzes
msg37	msg,,hl	500	3HL	Male sterile genetic 37	45:186	Clermont
msg38	msg,,jl	501	3H	Male sterile genetic 38	45:187	Ingrid
msg39	msg,,dm	502	3H	Male sterile genetic 39	45:188	P11
msg40	msg,,ac	503	6HL	Male sterile genetic 40	45:190	Conquest
msg41	msg,,aj	504	6HS	Male sterile genetic 41	45:191	Betzes
msg42	msg,,db	505	3H	Male sterile genetic 42	45:193	Betzes
msg43	msg,,br	506	2HL	Male sterile genetic 43	45:194	Betzes
msg44	msg,,cx	507	5HL	Male sterile genetic 44	45:195	HA6-33-02
msg45	msg,,dp	508	5HL/ 7HS	Male sterile genetic 45	45:196	RPB439-71
msg46	msg,,ec	509	2H/ 6H	Male sterile genetic 46	45:197	Hector
msg47	msg,,ep	510	3HS/ 7HS	Male sterile genetic 47	45:198	Sel12384CO
msg48	msg,,jt	520	1H	Male sterile genetic 48	45:199	Simba
msg49	msg,,jw	335	5HL	Male sterile genetic 49	45:122	ND7369
msg50	msg,,hm	34	7HL	Male sterile genetic 50	45: 88	Berac
mss1	mss	84	5H	Midseason stripe 1	44: 75	Montcalm
mss2		39	7HS	Midseason stripe 2	44: 59	ND11258
mtt1	mt	521	1HS	Mottled leaf 1	41:179	Montcalm

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
mtt2	mt2	302	5HL	Mottled leaf 2	41:127	Montcalm
mtt4	mt,,e	78	2HL	Mottled leaf 4	41: 86	Victorie
mtt5	mt,,f	264	6HL	Mottled leaf 5	41:126	Akashinriki
mtt6		629	7HS	Mottled leaf 6	45:228	ND6809
mtt7	mtt.h	677	2HS	Mottled leaf 7	42:753	Morex
mtt8	Mut 1661	674		Mottled leaf 8	43:182	Bowman Rph3.c
mtt9	Mut 2721	675		Mottled leaf 9	44:207	Bowman Rph3.c
mul2	mlt2	251	6HL	Multiflorus 2	48:119	Montcalm
nar1		637	6HS	NADH nitrate reductase-deficient 1	35:194	Steptoe
nar2		638	5HL	NADH nitrate reductase-deficient 2	35:196	Steptoe
nar3		639	7HS	NADH nitrate reductase-deficient 3	35:197	Winer
nar4		640	2HL	NADH nitrate reductase-deficient 4	35:198	Steptoe
nar5		641	5HL	NADH.nitrate.reductase deficient 5-	35:199	Steptoe
nar6		642	2HL	NADH nitrate reductase-deficient 6	35:200	Steptoe
nar7		643	6HL	NADH nitrate reductase-deficient 7	35:201	Steptoe
nar8		644	6HS	NADH nitrate reductase-deficient 8	35:202	Steptoe
nec1	sp,,b	222	1HL	Necrotic leaf spot 1	43:108	Carlsberg II
nec2	nec2	261	6HS	Necrotic leaf spot 2	26:241	Carlsberg II
nec3	nec3	265	6HS	Necrotic leaf spot 3	43:116	Proctor
nec4	nec4	138	3H	Necrotic leaf spot 4	43: 88	Proctor
nec5	nec5	139	3H	Necrotic leaf spot 5	43: 89	Diamant
Nec6	Sp	611	7HS	Necrotic leaf spot 6	43:159	Awnless Atlas
nec7	nec-45	635	1H/6H/7H	Necroticans 7	43:166	Kristina
nec8	nec.w	671	5HL	Necrotic leaf spot 8	43:179	Bowman Rph3.c
nec9	Mut 3091	672	3HL	Necrotic leaf spot 9	43:181	Bowman Rph3.c

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
nec10	necS 1-1	681	3H	Necroticans 10	43:184	Steptoe
nec11		682	1H	Necroticans 11	43:185	Steptoe
nec12		683		Necroticans 12	43:186	Steptoe
nec13		684		Necroticans 13	43:187	Steptoe
nec14		685		Necroticans 14	43:188	Steptoe
nec15		686		Necroticans 15	43:189	Steptoe
nec16		687		Necroticans 16	43:190	Steptoe
nec17		688		Necroticans 17	43:191	Steptoe
nec18		689		Necroticans 18	43:192	Steptoe
nec19		690		Necroticans 19	43:193	Steptoe
nec20		691		Necroticans 20	43:194	Steptoe
nec21		692		Necroticans 21	43:195	Steptoe
Nec22		693		Necroticans 22	43:196	Steptoe
nec23		694		Necroticans 23	43:197	Steptoe
Nec24		695		Necroticans 24	43:198	Steptoe
nec25		696		Necroticans 25	43:199	Steptoe
Nec26		697		Necroticans 26	43:200	Steptoe
nec27		698		Necroticans 27	43:201	Steptoe
nec28		699		Necroticans 28	43:202	Morex
nec29		700		Necroticans 29	43:203	Morex
nec30		701		Necroticans 30	43:204	Morex
nec31		702		Necroticans 31	43:205	Morex
nec32		703		Necroticans 32	43:206	Morex
nec33		704		Necroticans 33	43:207	CIho 4196
nec34	nec.k	197	4HS	Necroticans 34	43:104	ND13917
nld1	nld	323	5HL	Narrow leafed dwarf 1	46: 88	Nagaoka
nld2		660	5H/ 6H/ 7H	Narrow leafed dwarf 2	43:176	Steptoe
nud1	n, nud	7	7HL	Naked caryopsis 1	44: 51	Himalaya
ops1	op-3	624	7HS	Opposite spikelets 1	45:226	Bonus
ops2	op-2	718	5HL	Opposite spikelets 2	43:213	Foma
ops3	op-1	719	5HS	Opposite spikelets 3	43:214	Bonus
ovl1		176	4H	Ovaryless 1	35:191	Kanto Bansei Gold
ovl2	ovl2	646		Ovaryless 2	43:169	Harrington
ovl3		725		Ovaryless 3	43:220	Harrington

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Pbg1	Pbg	740	7H	Pubescens on glume 1	47:182	
pmr1	pmr	40	7HS	Premature ripe 1	44: 60	Glenn
pmr2	nec-50	634		Premature ripe 2	32:135	Bonus
Pre2	Re2	76	2HL	Red lemma and pericarp 2	48: 77	Buckley 3277
Pub1	Pub	127	3HL	Pubescent leaf blade 1	44: 84	Multiple Dominant
Pvc1	P_c	68	2HL	Purple veined lemma 1	44: 67	Buckley 2223-6
Pyr1	Pyr.g	42	3HL	Pyramidatum 1	41: 78	Pokko / Hja80001
Qsd1	SD1	752	5HL	Quantitative seed dormancy 1	48:181	Steptoe
Qsd2	SD2	753	3HL	Quantitative seed dormancy 2	48:184	Chevron
Qsd3	qsd3	754	3HL	Quantitative seed dormancy 3	48:188	ND24260
raw1	r	312	5HL	Smooth awn 1	46: 84	Lion
raw2	r2	340	5HL	Smooth awn 2	46: 92	Lion
raw5	r,,e	257	6HL	Smooth awn 5	44:112	Akashinriki
raw6	r6	334	5HL	Smooth awn 6	26:282	Glenn
rcr1	γ08-122	737		Required for resistance to *Cochliobolus sativus* 1	45:249	Morex
rcr2	γ08-123	738		Required for resistance to *Cochliobolus sativus* 2	45:250	Morex
rcr3	γ08-124	739		Required for resistance to *Cochliobolus sativus* 3	45:251	Morex
rob1	o	254	6HS	Orange lemma 1	46: 78	CIho 5649
Rpc1		149	3H	Reaction to *Puccinia coronata* var. *hordei* 1	37:232	Hor 2596
Rpg1	T	511	7HS	Reaction to *Puccinia graminis* (wheat stem rust) 1	26:437	Chevron
Rpg2	T2	512	2HL	Reaction to *Puccinia graminis* (wheat stem rust) 2	48:153	Hietpas 5
Rpg3	Rpg3	748	5HL	Reaction to Puccinia graminis (wheat stem rust) 3	48:178	PI 382313
rpg4		319	5HL	Reaction to *Puccinia graminis* (wheat stem rust) 4	26:267	Q21861
rpg6	rpg6	750	6HS	Reaction to Puccinia graminis (wheat stem rust) 6	48:179	212Y1
Rpg7	Rpg7	751	3HL	Reaction to Puccinia graminis (wheat stem rust) 7	48:180	PI 681809
Rph1	Pa	70	2H	Reaction to *Puccinia hordei* 1	26:107	Oderbrucker

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rph2	Pa2	88	5HS	Reaction to *Puccinia hordei* 2	37:212	Peruvian
Rph3	Pa3	121	7HL	Reaction to *Puccinia hordei* 3	26:156	Estate
Rph4	Pa4	218	1HS	Reaction to *Puccinia hordei* 4	42:302	Gull
Rph5	Pa5	122	3HS	Reaction to *Puccinia hordei* 5	37:224	Magnif 102
Rph6	Pa6	575	3HS	Reaction to *Puccinia hordei* 6	26:501	Bolivia
Rph7	Pa7	136	3HS	Reaction to *Puccinia hordei* 7	37:228	Cebada Capa
Rph8	Pa8	576		Reaction to *Puccinia hordei* 8	26:502	Egypt 4
Rph9	Pa9, Pa12	32	5HL	Reaction to *Puccinia hordei* 9	37:201	HOR 2596
Rph10		137	3HL	Reaction to *Puccinia hordei* 10	26:174	Clipper C8
Rph11		267	6HL	Reaction to *Puccinia hordei* 11	26:247	Clipper C67
Rph12	Pa12, Pa9	333	5HL	Reaction to *Puccinia hordei* 12	26:281	Triumph
Rph13		590		Reaction to *Puccinia hordei* 13	28: 31	PI 531849
Rph14		591		Reaction to *Puccinia hordei* 14	28: 32	PI 584760
Rph15	Rph16	96	2HL	Reaction to *Puccinia hordei* 15	37:214	PI 355447
rpr1		707	4H	Required for *Puccinia graminis* resistance 1	42:757	Morex
rpr2	γ08-118	731	6H	Required for *Puccinia graminis* resistance 2	46:139	Morex
rpr3	γ08-112	732		Required for *Puccinia graminis* resistance 3	46:141	Morex
rpr4	γ08-114	733		Required for *Puccinia graminis* resistance 4	46:142	Morex
rpr5	γ08-117	734		Required for *Puccinia graminis* resistance 5	46:143	Morex
rpr6	γ08-119	735		Required for *Puccinia graminis* resistance 6	46:144	Morex
rpr7	γ08-115	736		Required for *Puccinia graminis* resistance 7	46:145	Morex
Rpt1	Pt	667	3HL	Reaction to *Pyrenophora teres* f. *teres* 1	43:177	Tifang
Rpt2	Rpt2c	237	1HS	Reaction to *Pyrenophora teres* f. *teres* 2	43:110	CIho 9819
Rpt3	QRptts2	711	2HS	Reaction to *Pyrenophora teres* f. *teres* 3	43:208	Tennessee Awnless D22-5
Rpt4	QRpt7	48	7HL	Reaction to *Pyrenophora teres* f. *maculata* 4	43: 61	Galleon

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rpt5	Rpt$_a$	272	6HL	Reaction to *Pyrenophora teres* f. *teres* 5	43:120	CIho 5791, CIho 9819
Rpt6		713	5HL	Reaction to *Pyrenophora teres* f. *maculata* 6	43:210	CIho 9819
Rpt7	Qrpts4	714	4HL	Reaction to *Pyrenophora teres* f. *teres* 7	43:211	Halcyon
Rpt8	QRpts4	198	4HS	Reaction to *Pyrenophora teres* f. *maculata* 8	43:105	Q21861
Rsg1	Grb	22	7H	Reaction to *Schizaphis graminum* 1	37:199	Omugi
Rsg2		577		Reaction to *Schizaphis graminum* 2	37:283	PI 426756
rsm1	sm	35	7HS	Reaction to BSMV 1	48: 71	Modjo 1
Rsp1	Sep	515		Reaction to *Septoria passerinii* 1	26:441	CIho 14300
Rsp2	Sep2	516		Reaction to *Septoria passerinii* 2	37:275	PI 70837
Rsp3	Sep3	517		Reaction to *Septoria passerinii* 3	37:276	CIho 10644
rtt1	rt	51	2HS	Rattail spike 1	47: 53	Goldfoil
Run1	Un	21	7HS	Reaction to *Ustilago nuda* 1	26: 67	Trebi
rvl1	rvl	226	1HL	Revoluted leaf 1	48:110	Hakata 2
Ryd2	Yd2	123	3HL	Reaction to BYDV 2	26:158	CIho 2376
Rym1	Ym	167	4HL	Reaction to BaYMV 1	32: 96	Mokusekko 3
Rym2	Ym2	20	7HL	Reaction to BaYMV 2	26: 66	Mihori Hadaka 3
rym3	ym3	345	5HS	Reaction to BaYMV 3	32:105	Chikurin Ibaraki
rym5	Ym	141	3HL	Reaction to BaYMV 5	32: 90	Mokusekko 3
sbk1	sk, cal-a	62	2HS	Subjacent hood 1	48: 75	Tayeh 13
sca1	sca	128	3HS	Short crooked awn 1	44: 85	Akashinriki
sci-a	sci-3	625	5H	Scirpoides-a	44:200	Bonus
sci-b	sci-4	239	1H/ 6H	Scirpoides-b	46: 76	Bonus
scl-a	scl-6	626	1HL	Scirpoides leaf-a	44:201	Foma
scl-b	scl-5	150	3HL/ 6HS	Scirpoides leaf-b	48: 90	Bonus
sdw1	denso, Hv20ox$_2$	518	3HL	Semidwarf 1	47:168	M21

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
sdw2	sdw-b	133	3HL	Semidwarf 2	45:108	Mg2170
sdw3	gai	663	2HS	Semidwarf 3	46:134	Hv287
sdw4		45	7HL	Semidwarf 4	46: 51	
sdw6	sdw.f	240	1H/ 7H	Semidwarf 6	46: 77	Vada
sdw7	sdw.u	196	4HL	Semidwarf 7	43:103	Glenn
seg1	se1	377	7HL	Shrunken endosperm genetic 1	45:158	Betzes
seg2	se2	378	7HS	Shrunken endosperm genetic 2	26:326	Betzes
seg3	se3	379	3H	Shrunken endosperm genetic 3	45:160	Compana
Seg4	se4	380	7HL	Shrunken endosperm genetic 4	37:267	Compana
seg5	se5	381	7HS	Shrunken endosperm genetic 5	26:329	Sermo / 7*Glacier
seg6	se6	396	3HL	Shrunken endosperm genetic 6	44:138	Ingrid
seg7	se7	397		Shrunken endosperm genetic 7	37:269	Ingrid
seg8	seg8	455	7H	Shrunken endosperm genetic 8	48:149	60Ab1810-53
sex1	se6f, lys5	382	6HL	Shrunken endosperm xenia 1	48:130	Compana
sex6	ssIIa	31	7HS	Shrunken endosperm xenia 6	45: 86	K6827
sex7	sex.i	628	5HL	Shrunken endosperm xenia 7	32:129	I90-374
sex8	sex.j	143	3HS	Shrunken endosperm xenia 8	43: 90	I89-633-1
sex9	sex.1	195	4HL	Shrunken endosperm xenia 9	43:102	Alf
sgh1	sh1	163	4HL	Spring growth habit 1	26:188	Iwate Mensury C
Sgh2	Sh2	309	5HL	Spring growth habit 2	26:259	Indian Barley
Sgh3	Sh3	213	1HL	Spring growth habit 3	26:212	Tammi / Hayakiso 2
sid1	nls	180	4HL	Single internode dwarf 1	43: 97	Akashinriki
Sil1	Sil	228	1H	Subcrown internode length 1	48:112	NE 62203
sld1	dw-1	126	3HL	Slender dwarf 1	41:103	Akashinriki
sld2		83	2HS	Slender dwarf 2	44: 74	Akashinriki
sld3	ant-567	186	4HS	Slender dwarf 3	48: 97	Manker
sld4	sld.d	100	2HS	Slender dwarf 4	43: 72	Glacier
sld5	sld.h	144	3HS	Slender dwarf 5	44: 90	Indian Dwarf
sld6	sld.g	242	1H	Slender dwarf 6	48:117	Glenn
sld7	sld.f	194	4HL	Slender dwarf 7	43:101	Glenn
sld8	sld.i	49	7HS/ 4HL	Slender dwarf 8	43: 63	Wisconsin Pedigree 38

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
sls1	sls1	227	1HS	Small lateral spikelet 1	48:111	Morex
smn1	smn	38	3H/ 5H	Seminudoides 1	43: 58	Haisa
snb1	sb	26	7HS	Subnodal bract 1	48: 67	L50-200
srh1	S, l	321	5HL	Short rachilla hair 1	46: 86	Lion
stb1	stb	741		Stubble 1	47:183	
sun1	sun1	650		Sensitivity to *Ustilago nuda* 1	43:173	Steptoe
tfm1		190	1HL	Thick filament 1	48: 99	Volla
trd1	t, bra-c	202	1HL	Third outer glume 1	46: 65	Valki
trp1	tr	61	4HL	Triple awned lemma 1	41: 82	CIho 6630
tst1	tst1	647	6HL	Tip sterile 1	43:170	Steptoe
tst2		636	4HL	Tip sterile 2	43:167	Donaria
twk1	tw	743	7H	Tweaky spike 1	47:185	
ubs4	lks2, ari-d	11	7HL	Unbranched style 4	45: 84	Ao-Hadaka
ubs5		727		Unbranched style 5	43:222	Harrington
uzu1	uz, HvBRI1	102	3HL	Uzu 1 or semi brachytic 1	47: 70	Baitori
var1	va	306	5HL	Variegated 1	37:259	Montcalm
var2	va2	344	5HL	Variegated 2	32:104	Montcalm
var3	va3	303	5HL	Variegated 3	44:115	Montcalm
viv-a	viv-5	627	2H	Viviparoides-a	45:227	Foma
viv-b	viv-6	193	4HS	Viviparoides-b	43:100	Foma
viv-c	viv-1	720	5H	Viviparoides-c	43:215	Foma
vrs1	v	6	2HL	Six-rowed spike 1	37:192	Trebi
vrs1	lr	58	2HL	Six-rowed spike 1	26: 94	Nudihaxtoni
vrs1	V^d	66	2HL	Two-rowed spike 1	26:103	Svanhals
vrs1	V^t	67	2HL	Deficiens 1	47: 57	White Deficiens
vrs2	v2, int-b	314	5HL	Six-rowed spike 2	47:113	Svanhals
vrs3	v3, int-a	315	1HL	Six-rowed spike 3	47:115	Hadata 2
vrs4	v4, int-e, HvRA2	124	3HL	Six-rowed spike 4	47: 76	MFB 104
wax1	wx	16	7HS	Waxy endosperm 1	42: 65	Oderbrucker
wnd1	wnd	23	4HL	Winding dwarf 1	42: 74	Kogen-mugi
wst1	wst	107	3HL	White streak 1	41: 97	CIho 11767
wst2	wst2	304	5HL	White streak 2	46: 83	Manabe
wst4		56	2HL	White streak 4	44: 51	Kanyo 7

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
wst5	wst5	221	1HL	White streak 5	46: 73	Carlsberg II
wst6	wst,,j	129	3HL	White streak 6	41:105	Akashinriki
wst7	rb	79	2HL	White streak 7	47: 61	GS397
wxs1	wxs	615	7H/ 2HL	Waxy spike 1	43:160	Steptoe
Xnt1	X_a, xan-h	25	7HL	Xantha seedling 1	48: 65	Akashinriki
xnt2	x_b	513		Xantha seedling 2	26:440	Black Hulless
xnt3	x_c	105	3HS	Xantha seedling 3	26:139	Colsess
xnt4	x_{c2}	36	7HL	Xantha seedling 4	26: 85	Coast
xnt5	x_n	255	6HL	Xantha seedling 5	26:237	Nepal
xnt6	x_s	113	3HS	Xantha seedling 6	26:147	Smyrna
xnt7	xan,,g	233	1HL	Xantha seedling 7	26:231	Erbet
xnt8	xan,,h	140	3HS	Xantha seedling 8	26:177	Carlsberg II
xnt9	xan,,i	37	7HL	Xantha seedling 9	26: 86	Erbet
yhd1	yh	158	4HL	Yellow head 1	42:250	Kimugi
yhd2	yh2	592		Yellow head 2	45:215	Compana
ylf1	ylf1	652	7HS	Yellow leaf 1	43:175	Villa
Ynd1	Yn	183	4HS	Yellow node 1	44:109	Morex
yst1	yst	104	3HS	Yellow streak 1	42:178	Gateway
yst2		109	3HS	Yellow streak 2	44: 81	Kuromugi 148 / Mensury C
yst3	yst,,c	462	3HS	Yellow streak 3	44:163	Lion
yst4		85	2HL	Yellow streak 4	44: 76	Glenn
yst5	yst5	346	7HS	Yellow streak 5	43:130	Bowman / ant10.30
yvs1	y_x	63	2HS	Virescent seedling 1	26: 99	Minn 71-8
yvs2	y_c	3	7HS	Virescent seedling 2	26: 46	Coast
yhd2	yh2	592		Yellow head 2	45:215	Compana
ylf1	ylf1	652	7HS	Yellow leaf 1	43:175	Villa
zeb1	zb	120	3HL	Zebra stripe 1	43: 86	Mars
zeb2	zb2, fch10	461	4HL	Zebra stripe 2	43:152	Unknown cultivar
Zeb3	zb_c. zb3	223	1HL	Zebra stripe 3	48:105	Utah 41
Zeo1	Knd, Ert-r	82	2HL	Zeocriton 1	47: 63	Donaria
Zeo2	cly1.b, HvAP2	614	2HL	Zeocriton 2	47:177	36Ab51

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Zeo3	Zeo2, cly1.c	184	4HL	Zeocriton 3	47: 95	Morex

* The recommended locus symbols or codes are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

† Chromosome numbers and arm designations are based on the Triticeae system. Utilization of this system for naming of barley chromosomes was at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

BGS 2, Chlorina seedling 12, *fch12*

Stock number:	BGS 2
Locus name:	Chlorina seedling 12
Locus symbol:	*fch12*

Previous nomenclature and gene symbolization:

Chlorina seedling-c = f_c (5).

Chlorina seedling-fc = *clo-fc* (9).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HS (2, 6); *fch12.b* is about 3.6 cM distal from the *gsh3* (glossy sheath 3) locus (8); *fch12.b* is about 9.3 cM proximal from the *brh1* (brachytic 1) locus (10); *fch12.b* is in 7H bin 02 about 1.8 cM proximal from RFLP marker ABG320 and co-segregating with markers BCD130 and ABC327 (7); *fch12.b* is associated with SNP markers 2_0242 to 2_0495 (positions 6.89 to 32.35 cM) in 7H bins 01 to 03 of the Bowman backcross-derived line BW354 (1), in 7H bin 02 at about 14 Mb.

Description:

Seedling leaves are yellow with green tips, and new leaves show a yellow base and a green tip. As the plant develops, leaf color changes to pale green (5). Plants are vigorous, but anthesis is delayed by 6 to 10 days. Kernel weights of BW354 vary from similar to those of Bowman to 10% less. Grain production of BW354 is 1/2 to 2/3 of that of Bowman (3).

Origin of mutant:

A spontaneous mutant in Colsess (CIho 2792) (5).

Mutational events:

fch12.b (f_c) (Colsess V, GSHO 36) in Colsess (CIho 2792) (5); *fch12.l* (Trebi chlorina 453, GSHO 155), *fch12.m* (Trebi V, GSHO 158), *fch12.n* (Trebi IX, GSHO 18), *fch12.o* (Trebi XI, GSHO 163) in Trebi (PI 537442) (4); *clo-fc.110* in Bonus (NGB 14657, PI 189763) (9); *fch12.b* may be present in the brachytic chlorina stocks (GSHO 124 and GSHO 174) (11).

Mutant used for description and seed stocks:

fch12.b (GSHO 36) in Colsess; *fch12.b* in Bowman (PI 483237, NGB 22812)*7 (GSHO 1826); *fch12.b* in Bowman*8 (BW354, NGB 20593).

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BGS 14, Desynapsis 5, *des5*

Stock number: BGS 14
Locus name: Desynapsis 5
Locus symbol: *des5*

Previous nomenclature and gene symbolization:

Hordeum vulgare Disrupted Meiotic cDNA 1 = *HvDMC1* (1).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 5H (1, 2); *des5.e* is associated with SNP markers 2_0139 to 2_1363 (positions 194.97 to 198.70 cM) in 7H bin12 and with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73) in 5H bins 04 to 06 of the Bowman backcross-derived line BW243 (2); in the centromeric region of chromosome 5H (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is 11.1 ± 2.6 ranging from 7 ring bivalents (d = 0) to 14 univalents (d = 14). Many univalents split longitudinally during anaphase I. Lagging chromosomes, and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 4.5 micronuclei per quartet with a range of 0 to 18. Ovule fertility is about 7%. When crossed with non-allelic desynaptic lines, the F_1's frequently show a low degree of desynapsis (up to 3 rod bivalents per cell) (4). Under field conditions, plants of the Bowman backcross-derived line for *des5.e*, BW243, exhibited variable seed set with grain yields from 1/4 to 1/2 those of Bowman. Plant heights of BW243 ranged from 90% of Bowman to the same height and kernels weights ranged from 80% of those for Bowman to almost the same (3). *HvDMC1* RNA was observed in all tissues, but was higher in young 5 mm developing inflorescence and highest in 1 to 1.5 cm inflorescences corresponding to pre-meiosis and meiosis stages, respectively (1).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (5, 6).

Mutational events:

des5.e (GSHO 596), *des5.f*, *des5.g* in Betzes (PI 129430) (5, 6).

Mutant used for description and seed stocks:

des5.e (GSHO 596) in Betzes; *des5.e* in Bowman (PI 483237)*4 (BW243, NGB 22470).

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BGS 15, Non-blue aleurone xenia 1, *blx1*

Stock number:	BGS 15
Locus name:	Non-blue aleurone xenia 1
Locus symbol:	*blx1*

Previous nomenclature and gene symbolization:

Blue aleurone = *Bl* (1).

Complementary factors for blue vs. white aleurone = *Bl1* and *bl1* (4).

Complementary factors for blue vs. white aleurone = *Blx* and *blx* (11).

Hordeum vulgare Myb protein Colorless 1 ortholog 3 = *HvMpc1-H3* is the third *Blx* gene (*Blx1*) (9); the Bowman backcross-derived line with blue aleurone (BW063) retained donor parent SNP markers from 2_1359 to 2_0670 (27.52 to 117.80 cM) in 4H bins 02 to 08 (2).

Inheritance:

Monofactorial recessive (1, 4) when complementary dominant alleles are present at the *Blx2, Blx3, Blx4,* and *Blx5* loci (3).

Located in chromosome 4HL (1, 7, 8); *blx1.a* is over 13.6 cM distal from the *glf3* (glossy leaf 3) locus (10).

Description:

Blue aleurone color is due to anthocyanin pigments (6), which occur as lumps inside many aleurone granules in some or all aleurone cells (3). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (3, 4). Aleurone color is best observed in well-filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (5). *HvMpc1-H3* (*Blx1*) is apparently the co-regulator of anthocyanin pigments accumulation in the aleurone layer (9).

Origin of mutant:

Non-blue aleurone (*blx1.a*) is recessive allele that occurs in many cultivars, *blx1.a* is more frequently in two-rowed cultivars of Occidental origin, while the blue allele (*Blx1*) is more common in Oriental cultivars.

Mutational events:

blx1.a (GSHO 185) in Goldfoil (PI 5975) (7).

Mutant used for description and seed stocks:

blx1.a (GSHO 185) in Goldfoil; the dominant allele (*Blx1*) is present in Bowman (PI 483237, NGB 22812); the dominant allele (*Blx1*) is present in Bowman*6/ICARDA sel. Green (BW063, NGB20471).

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BGS 19, Non-blue aleurone xenia 2, *blx2*

Stock number:	BGS 19
Locus name:	Non-blue aleurone xenia 2
Locus symbol:	*blx2*

Previous nomenclature and gene symbolization:

Blue aleurone 1 = Bl_1, a second factor for blue aleurone (8).

Non-blue aleurone 2 = *bl2* (9).

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1, Blx3, Blx4,* and *Blx5* loci (2, 5, 8).

Located in chromosome 7HS (2, 5, 8); *blx2.b* is about 3.9 cM distal from the *msg10.ay* (male sterile genetic 10) gene (5); *blx2.b* is approximately 9.9 cM distal from the *nud1* (naked caryopsis 1) locus (8); *blx2.b* is approximately 12.1 cM from the *nud1* locus (5); *blx2.b* is about 29.9 cM from the *fch12.b* (chlorina seedling 12) gene (10); *blx2.b* is weakly linked to *blx5.e* (10).

Description:

Blue aleurone color is due to anthocyanin pigments (7), which occur as lumps inside many aleurone granules in some or all aleurone cells (2). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (2, 5, 12). Aleurone color is best observed in well-filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (6). Some heterozygous plants at the *Blx2* locus showed little or no male transmission of the dominant allele (4, 5, 11).

Origin of mutant:

Non-blue aleurone (*blx2.b*) is recessive allele that occurs more frequently in six-rowed cultivars of Oriental origin (5, 8).

Mutational events:

blx2.b in Nepal (PI 12709, GSHO 209) (5, 8).

Mutant used for description and seed stocks:

blx2.b (PI 12709, GSHO 209) in Nepal; the recessive allele, *blx2.b*, is present in Bowman (PI 483237, NGB 22812) in combination with the recessive allele (*ant1.b*, *rst1.b*) at the anthocyanin-less 1 locus (1, 3).

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BGS 25, Xantha seedling 1, *Xnt1*

Stock number:	BGS 25
Locus name:	Xantha seedling 1
Locus symbol:	*Xnt1*

Previous nomenclature and gene symbolization:

Xantha a = X_a (7).
Xantha-h = *xan-h* (11, 12, 14).
Chlorina-125 = *Clo-125* (11, 12).

Inheritance:

Monofactorial incomplete or semi-dominant (7, 12); allelic to recessive xantha-h (*xan-h*) mutants (4).

Located in chromosome 7HL (7); *Xnt1.a* is over 35.9 cM distal from the *lks2* (short awn 2) locus (7, 13); *Xnt1.a* is associated with SNP marker 2_0354 (position 171.87 cM) in 7H bin 10 of a presumed heterozygous plant of the Bowman backcross-derived line BW919 (2); *Clo.125* was not associated with any 7H SNP markers in a presumed heterozygous plant of the Bowman backcross-derived line BW186 (2), in 7H bin 10.

Description:

Segregation is observed in each generation for xantha, chlorina, and green seedlings, but only the last two classes survive to maturity. Chlorina plants are slightly yellow-green in color until near maturity. Crosses to chlorina plants produce chlorina and green F_1 plants in a 1:1 ratio. In the progeny of chlorina plants, xantha, chlorina, and green plants occur in a 1:2:1 ratio (7). Color differences between normal. and heterozygous plants were observed in the *Xnt1.a2* mutant only until just prior to heading (10). Mutants at the *Xnt1* locus must be maintained as heterozygous stocks (3, 7). The semi-dominant mutants at the *Xnt1* locus are defective in the 42 kDa protein subunit (42-kDa XANTHA-H) involved in insertion of Mg^{2+} into protoporphyrin IX (4). The heterozygous chlorina seedlings have 25-50% of Mg-chelatase activity of green seedlings. The semi-dominant *Xnt1* mutants are alleles at the *xan-h* locus, but the lethal recessive *xantha-h* mutants do not retain the defective protein in the 42-kDa subunit (4, 5, 6). The chlorophyll content of *xan-h* heterozygotes is reduced slightly (1).

Origin of mutant:

An ethyl methanesulfonate induced mutant in the cross Akashinriki (OUJ659, PI 467400) X linkage tester 191 (OUL094) (7); a sodium azide induced mutant in Bonus (NGB 14657, PI 189763) (8).

Mutational events:

Xnt1.a in the hybrid Akashinriki X linkage tester 191 (OUM215) (7, 12); *Xnt1.a2* in translocation stock T6-7d (10); *Xnt1.a3* in MC 20 (PI 357319) (9); semi-dominant mutants *Chlorina-125* (*Xnt1.125*) in Bonus (NGB 14657, PI 189763), *Chlorina-157* (*Xnt1.157*), *Chlorina-161* (*Xnt1.161*) in breeding line Ca710516 (Triumph/Goldspear) (4, 10, 11); *xan-h.30*, *-h.38*, *-h.56*, and *-57* in Bonus (5, 8, 11, 12). All *Xnt1* and *xan-h* mutant stocks are stored in the Biology Department, Lund University with Mats Hansson who is the coordinator for chlorophyll biosynthesis (5).

Mutant used for description and seed stocks:

Xnt1.a (GSHO 1606) in the hybrid Akashinriki X linkage tester 191; *Xnt1.a* in Bowman (PI 483237, NGB 22812)*7 (GSHO 1862, BW919, NGB 20790); *Xnt1.125* (*Clo-125*, NGB??) in Bonus; *Xnt1.125* in Bowman*8 (BW186, NGB 22018).

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Revised:
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BGS 26, Subnodal bract 1, *snb1*

Stock number: BGS 26
Locus name: Subnodal bract 1
Locus symbol: *snb1*

Previous nomenclature and gene symbolization:
Subnodal bract = *sb* (4, 5).

Inheritance:
Monofactorial recessive (4).
Located in chromosome 7HS (3, 5); *snb1.a* is near the centromere of chromosome 7H (3); *snb1.a* is about 36.3 cM proximal from the *brh1* (brachytic 1) locus (5).

Description:
A glume-like or stick-like bract arises immediately under the node-base (below and between the outer glumes) of the central spikelets. The bracts are present at only a few internodes on randomly arranged central spikelets. Expression of the subnodal bract trait is variable because not all spikes on homozygous *snb1.a* plants have the extra bract (5). The subnodal bract trait was not observed in progeny from crosses to Bowman; however, the Bowman backcross-derived line for *snb1.a* (BW872) contains donor parent markers for 7H in the critical region (1, 2).

Origin of mutant:
Natural occurrence in L50-220 (*Hordeum sativum* var. *ibericum*) from Russia (Alb Acc 67A, GSHO 1217) (5).

Mutational events:
snb1.a in L50-200 (GSHO 1217, Alb Acc 67A) (2, 5), a recessive allele at the *brh1* (brachytic 1) locus is present also in this stock (5).

Mutant used for description and seed stocks:
snb1.a (GSHO 1217) in L50-200; *snb1.a* is likely present in Bowman backcross line BW372 (Bowman*2/L50-200), but the trait was not observed (1, 2).

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Revised:
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:67.

BGS 33, Anthocyanin-less 1, *ant1*

Stock number:	BGS 33
Locus name:	Anthocyanin-less 1
Locus symbol:	*ant1*

Previous nomenclature and gene symbolization:

Purple pericarp = *P* (14, 16, 17).
Red pericarp = *Re* (13).
Green stem = *rs* (1).
Purple lemma (second gene) = *C* (17).
Exrubrum-a = *rub-a* (6).
Hordeum vulgare Myb protein Colorless 1 ortholog H1 = *HvMpc1-H1* (13, 15).
Purple seed coat color = *Psc* (18).

Inheritance:

Monofactorial recessive (1, 9). The first of two dominant complementary genes *Pre1* and *Pre2* (Red and lemma and pericarp 1 and 2) that control purple or red pigmentation of the lemma, palea, and pericarp (2, 12, 14, 17, 19, 20).

Located in chromosome 7HS (1, 8); *ant1.b* is near the centromere (4); *ant1* mutants are near the *ert-m* (erectoides-m) locus (10, 19); *ant1.b* is about 15.0 cM distal from the *nud1* (naked caryopsis 1) locus (1); *Rst1.a* is associated with SNP markers 2_0074 to 2_0113 (positions 71.81 to 75.21 cM) in 7H bin 05 of the Bowman backcross-derived line BW762 (3); *ant1.1* is associated with SNP markers 1_0838 to 2_0103 (positions 49.53 to 139.86 cM) in 7H bins 04 to 08 of the Bowman backcross-derived line BW013 (3); the *Ant1* locus is close to the erectoides-m (*ert-m*) locus in a 4.7 cM interval flanked by SNP markers 3_0576 and 1_0721 (18); a locus controlling anthocyanin pigment is in 7HS (18, 20), in 7H bin 05.

Description:

When grown under favorable light conditions, red pigmentation of the stem does not develop (1). As plants approached maturity, anthocyanin pigments are not observed in the stem, auricles, awns, or lemma veins of induced *ant1* mutants (1, 6, 10). However, moderate to strong pigmentation of these plant parts is observed in plants homozygous for the normal allele *Rst1.a* at this locus (1, 19). The *ant1.b* allele, which occurs frequently in cultivars of Manchurian origin and is present in Bowman (PI 483237, NGB 22812), reduces considerably the red pigmentation of stem, auricles, awns, and lemma veins. Expression of alleles at the *Ant1* locus is easier to observe at the stem base of seedlings (5, 19). Sequencing of HvERECTA in barley *ert-m* (erectoides-m) mutants identified full gene deletions in both *ert-m.40* and *ert-m.64*, which additionally cau NGBsed anthocyanin deficiency. Analyses of *ert-m* and *ant1* single and double deletion mutants suggested that *Ant1* encodes a R2R3 myeloblastosis (*MYB*) transcription factor (8, 13, 19).The *ant1.b* variant is a leaky mutant that can synthesize small amounts of anthocyanin (19). The relative anthocyanin content of the leaf sheath extracts from Bowman (*ant1.b*) as measured by OD_{530} (anthocyanin content measured spectrophotometrically at 530 nm) was less than half that of Bowman backcross-derived lines with the normal allele, *Ant1.a* (*HvMpc1*) (13). The combination of dominant alleles at the *Ant1* and the *Pre2* (Red lemma and pericarp 2) loci produces reddish to purple grain color (13, 18, 20).

Origin of mutant:

Natural occurrence in some cultivars, frequently in those of Oriental origin (1, 13, 17, 18); an alpha ray induced mutant in Bonus (NGB 14657, PI 189763) (9).

Mutational events:

ant1.b (*rst1.b*) in Manchurian introductions (5, 13); *ant1.1* (NGB 114552), *ant1.2* (NGB 114553), *ant1.4* (NGB 114555) in Bonus (NGB 14657, PI 189763) (9); *ant1.56* in Bonus (9); *ert-m.40* (NGB 112640) and *ert -m.64* (NGB 112663) with *ant1* mutant in Bonus (NGB 14657, PI 189763) (7, 11, 13); *ant1.b* or an unnamed variant in hulless Chinese landraces (18).

Mutant used for description and seed stocks:

ant1.1 (NGB 114552, GSHO 1620) in Bonus; *ant1.1* from Bonus in Bowman (PI 483237, NGB 22812)*3 (BW013, NGB 20421); *Ant1.a* (*Rst1.a*) in Goldfoil (PI 5975, GSHO 185) (1, 3); *ant1.b* from six-rowed Manchurian type cultivars is in Bowman (5); *Ant1.a* from Mut. 4128 of Haisa (PI 197617) in Bowman*6 (GSHO 1834); *Ant1.a* from Mut. 4128 in Bowman*7 (BW762, NGB 22230); *Ant1.a* with *Pre2.b* in Bowman*9 (GSHO 1926, BW648, NGB 22213).

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Prepared:
T.E. Haus. 1975. Barley Gent. Newsl. 5:96 as BGS 15, Red stem, *Rs.*

Revised:
J.D. Franckowiak. 1997. Barley Gent. Newsl. 26:82.
J.D. Franckowiak. 2012. Barley Gent. Newsl. 42:89-90.
J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:49-50.
J.D. Franckowiak and U. Lundqvist. 2018. Barley Genet. Newsl. 48:68-70.

BGS 35, Reaction to barley stripe mosaic virus 1, *rsm1*

Stock number:	BGS 35
Locus name:	Reaction to barley stripe mosaic virus 1 (BSMV)
Locus symbol:	*rsm1*

Previous nomenclature and gene symbolization:

Resistance to barley stripe mosaic virus = *sm* (2).
Resistance to barley stripe mosaic virus 3 = *sm3* (5).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 7HS (1, 4); *rsm1.a* is over 24.3 cM distal from the *nud1* (naked caryopsis 1) locus (4); *rsm1.a* is over 28.2 cM from the *lks2* (short awn 2) locus (4); *rsm1.a* co-segregated with RFLP marker ABC455 (1).

Description:

Reaction to BSMV is estimated as the frequency or percentage of plants infected following inoculation of barley seedlings with a specific strain of BSMV. Highly resistant cultivars produce few or no infected plants 7 to 14 days after inoculation (3). Most or all seedlings of highly susceptible cultivars produce broad mosaic stripes within 7 days after inoculation (3). Several genes control reaction to BSMV and show additive inheritance patterns (2, 5). The study of progeny from crosses between resistant and moderately susceptible cultivars indicated that one recessive factor controls the frequency of infected plants following inoculation with strain CV42 (1, 4). The presence of virus in protoplasts after inoculation with BSMV strains is associated with susceptibility to these virus strains (6).

Origin of mutant:

Natural occurrence in Modjo 1 (CIho 14048) and Moreval (PI 95258) (2, 5).

Mutational events:

rsm1.a in Modjo 1 (CIho 14048) (2, 4, 5).

Mutant used for description and seed stocks:

rsm1.a in Modjo 1; *rsm1.a* in Morex (CIho 15773, GSHO 2492) (1); *rsm1.a* is present in Bowman (PI 483237, NGB 22812).

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Prepared:

J.D. Franckowiak and M.C. Edwards. 1997. Barley Genet. Newsl. 26:84.

Revised:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:71.

BGS 52, Chlorina seedling 15, *fch15*

Stock number:	BGS 52
Locus name:	Chlorina seedling 15
Locus symbol:	*fch15*

Previous nomenclature and gene symbolization:

Orange seedling = *or* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HS (3); *fch15.x* is about 18.5 cM distal from the *fch1* (chlorina seedling 1) locus (2, 3); *fch15.x* is associated with SNP markers 2_1338 to 2_0699 (positions 74.97 to 126.33 cM) in 2H bins 06 to 09 of the Bowman backcross-derived line BW357 (1), likely in 2H bin 06.

Description:

The normal color of seedlings is altered to "apricot yellow" when *fch15.x* plants are grown in the field under low temperature. Plants respond better to higher temperatures and can be grown to maturity in suitable environments (3, 4). The yellow color of *fch15.x* plants is stable nearly to maturity (4).

Origin of mutant:

A spontaneous mutant in Trebi (PI 537442) (3).

Mutational events:

fch15.x (*or1.a*) (Trebi IV, GSHO 49) in Trebi (PI 537442) (3).

Mutant used for description and seed stocks:

fch15.x (GSHO 49) in Trebi, *fch15.x* in Bowman (PI 483237, NGB 22812)*2 (BW357, NGB20596).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:112.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:104.
J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:88.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:48.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:72.

BGS 55, Chlorina seedling 1, *fch1*

Stock number:	BGS 55
Locus name:	Chlorina seedling 1
Locus symbol:	*fch1*

Previous nomenclature and gene symbolization:

Chlorina seedling = *f* (6).
Light green = *lg* (5).
Light green 8 = *lg8* (4).
Light green 10 = *lg10* (4).

Inheritance:

Monofactorial recessive (3, 5, 6).

Located in chromosome 2HS (3, 10); *fch1.a* is in the centromeric region and about 4.0 cM distal from the *eog1* (elongated outer glume 1) locus (3, 7); *fch1.p* is associated with SNP markers 1_1493 to 2_0458 (positions 76.05 to 96.47 cM) in 2H bins 06 to 07 of the Bowman backcross-derived line BW351 (1).

Description:

Seedling and immature leaves are very pale yellow-green (chlorophyll deficient) (6). The leaves gradually change to a green color beginning with the leaf tip. Plants can be grown to maturity in the field, but they have a slightly yellow-green color and are stunted easily by stress. Plants of the Bowman backcross-derived line with *fch1.p* (BW351) headed about 10 days later than Bowman and were slightly shorter. Plants produced a few more kernels per spike, and rachis internodes were slightly shorter. Kernels were 10 to 15% lighter and they were slightly shorter and thinner. Grain yields of BW351 were 1/2 to 2/3 of those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Golden (Gull, NGB 1480, CIho 1145, GSHO 466) (6).

Mutational events:

fch1.a (GSHO 112) in Gull (NGB 1480, CIho 1145, GSHO 466) (6, 9); *fch1.p* (*lg*) (Minn 80, GSHO 548) (5, 9); *fch1.q* (*lg8*) (No 155, GSHO 8) (4, 8); and *fch1.r* (*lg10*) (No 157, GSHO 154) in Himalaya (CIho 1312) (4).

Mutant used for description and seed stocks:

fch1.p (GSHO 548) in Minn 84-7; *fch1.p* in Bowman (PI 483237, NGB 22812)*9 (GSHO 1886, BW351, NGB 20690).

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Prepared:
T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:115.

Revised:
T. Tsuchiya. 1980. Barley Genet. Newsl. 10:106.
J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:90.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:49-50.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:73-74.

BGS 62, Subjacent hood 1, *sbk1*

Stock number:	BGS 62
Locus name:	Subjacent hood 1
Locus symbol:	*sbk*

Previous nomenclature and gene symbolization:

Subjacent hood = *sk* (9).
Hooded awn 2 = *k2* (12).
Hoods = k_r (11).
Calcaroides-a = *cal-a* (4, 5).

Inheritance:

Monofactorial recessive (8, 9).

Located in chromosome 2HS (8, 9, 10); *cal-a.1* is distal from AFLP marker E3733-7 and RFLP marker CDO57 (7); *sbk1.b* is associated with SNP markers 1_0326 and 1_1059 (positions 16.91 and 17.96 cM) in 2H bin 02 of the Bowman backcross-derived line BW767; *sbk1.a* is associated with SNP markers 1_1059 to 2_0563 (positions 17.96 to 21.19 cM) in 2H bin 02 of the Bowman backcross-derived line BW766; *cal-a.1* is associated with SNP marker 1_0326 (position 16.91 cM) in 2H bin 02 of the Bowman backcross-derived line BW103 (2).

Description:

Unlike the *Kap1* (Hooded lemma 1) mutants, the lemma appendage or its modification is situated somewhat below the top of the lemma. Lemma modifications may include a central cup-like cavity or sac in some alleles and/or pronounced lemma wings in other alleles (1, 7). The modified lemma bears a short distal awn. Only a few florets of the spike have malformations in alleles (*cal-a.3*, *-a.6*, *-a.7*, and *-a.17*), and these alleles are associated with the formation of pronounced wings (7). There are no rudiments of a floral organ within the hood-like cavity (7, 8, 9). Leaf blade knots and leaf curling are present in some alleles (7). In the homozygous condition, the *sbk1.a* gene is epistatic to the *Kap1.a* (Hooded lemma 1) and to *Lks1.a* (Awnless 1) genes (8). Plants of the Bowman backcross-derived lines for *cal-a.1* (BW103), *sbk1.a* (BW766), and *sbk1.b* (BW767) were much less vigorous than Bowman, about 3/4 of normal height and 3 to 4 fewer fertile rachis nodes. The kernel of the BW766 and BW767 plants were about 1/2 of normal weight and grain yields were about 1/10 of normal. Plants of the BW103 line were more vigorous with kernel weights about 3/4 of those for Bowman and grain yield of about 1/2 of normal. The effects of the *sbk1* mutants on plant vigor were less pronounced in cooler environments (3).

Origin of mutant:

A spontaneous mutant identified as Tayeh 13 (OUC335, GSHO 267) (6); an X-ray induced mutant in Bonus (NGB 14657, PI 189763) (6).

Mutational events:

sbk1.a (OUC335, GSHO 267) in Tayeh 13 (8); *cal-a.1* (NGB 114280, 114281) in Bonus (NGB 14657, PI 189763) (5, 6); *cal-a.3* (NGB 114283), *-a.5* (NGB 114285) in Foma (NGB 14659, CIho 11333); *cal-a.6* (NGB 114286) in Bonus; *cal-a.7* (NGB 114287), *-a.8* (NGB 114288), *-a.11* (NGB 114291), *-a.12* (NGB 114292), *-a.13* (NGB 114293) in Foma; *cal-a.16* (NGB 114295), *-a.17* (NGB 114296), *-a.20* (NGB 114299), *-a.21* (NGB 114300) in Bonus (5, 6); *sbk1.b* (k_r) in Montcalm (CIho 7149) (11).

Mutant used for description and seed stocks:

sbk1.a (GSHO 267) in Tayeh 13; *sbk1.a* via R.I. Wolfe's Multiple Recessive Stock for chromosome 2 in Bowman (PI 483237, NGB 22812)*4 (BW766, NGB 22234); *sbk1.b* in Montcalm; *sbk1.b* from Montcalm in Bowman*7 (GSHO 1874, BW767, NGB 22235); *cal-*

a.1 (NGB 114280, NGB 114281, GSHO 286) in Bonus; *cal-a.1* from Bonus in Bowman*3 (GSHO 2186); *cal-a.1* in Bowman*6 (BW103, NGB 20509).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:122.

Revised:

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J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:51-52.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:75-76.

BGS 76, Red lemma and pericarp 2, *Pre2*

Stock number:	BGS 76
Locus name:	Red lemma and pericarp 2
Locus symbol:	*Pre2*

Previous nomenclature and gene symbolization:

Purple chaff color = *P* (1, 7).
Purple chaff color = P_1 (12).
Purple pericarp = *P* (3, 13, 17).
Purple lemma = *P* (2).
Red pericarp = *R* (2).
Red pericarp 2 = *Re2* (9, 14, 18).

Inheritance:

Purple or reddish pigmentation of the lemma and pericarp is controlled by one dominant gene (1, 3). Two dominant complementary genes (*Pre1* and *Pre2*) control purple or red pigmentation of the lemma, palea, and pericarp (2, 12, 19, 21). In some Chinese landraces and Bowman backcross-derived line BW648 (NGB 22213), the second gene required for expression of purple lemma and pericarp is probably a dominant allele at the Anthocyanin-less 1 (*Ant1*) locus (5, 15, 20).

Located in chromosome 2HL (2); *Pre2.a* is about 17.1 cM distal from the *vrs1* (six-rowed spike 1) locus (2, 3, 4, 9, 12, 13, 18); *Pre2.a* is over 11.2 cM proximal from the *ant2* (anthocyanin-less 2) locus (9, 10); *Pre2.a* is associated with SNP markers 1_0214 to 1_0876 (positions 150.96 to 161.08 cM) in 2H bins 10 to 11 of Bowman backcross-derived line BW648 (5); line BW648 also retained a donor parent segment in chromosome 7H overlapping the *Ant1* locus (5, 15); *Pre2.a* mapped in 2HL between the SSR markers Bmag125 and GBMS244 and was about 5.1 cM distal from the *vrs1* locus (11*)*, in 2H bin 10 at about 680 Mb.

Description:

Purple or red coloration of the hull (chaff) and pericarp develops during the soft dough stage of grain fill, and fades as the grain matures. Anthocyanin pigments in an acid cell solution produce the red to violet color observed in the pericarp and lemma (2). Bowman and the Bowman backcross-derived line for *Pre2.a*, BW648, were similar for all agronomic and morphological traits expect kernel color (6). The *Pre2.b* gene is up-regulated in the purple-grained line (BW648, NGB 22213) with coordinately co-expressed flavonoid biosynthesis structural genes (*Chs*, *Chi*, *F3h*, *Dfr*, and *Ans*) (16). Compared to Bowman, the anthocyanin content of BW648 showed a value over nine times higher (16). A similar increase was observed in another studies (21).

Origin of mutant:

Natural occurrence in a few cultivars and some *Hordeum vulgare* subsp. *spontaneum* accessions (2, 19, 20).

Mutational events:

Pre2.a in Buckley 3277 (NSL 32606, GSHO 234) (2).

Mutant used for description and seed stocks:

Pre2.a in Buckley 3277 (GSHO 234); *Pre2.b* and *Ant2* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1565) in Bowman (PI 483237, NGB 22812)*9 (GSHO 1926, BW648, NGB 22213).

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Revised:

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J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:53-54.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:77-79.

BGS 80, Anthocyanin-less 2, *ant2*

Stock number: BGS 80
Locus name: Anthocyanin-less 2
Locus symbol: *ant2*

Previous nomenclature and gene symbolization:

Purple straw = P_r or *Pr* (12, 15).
Anthocyanin-less = *ant-2* (3, 10).
Exrubrum = *rub* (6).
Colorless leaf tip 2 = clt_2 (7), c_2 (7).
Basic helix-loop-helix domain / Myelocytomatosis (bHLH / MYC) = *HvbHLH1 (13).*

Inheritance:

Monofactorial recessive (3, 12).

Located in chromosome 2HL (3, 12); *Ant2.c* (*Pr*) is about 15.1 cM distal from the *vrs1* (six-rowed spike 1) locus (5, 8, 12, 14, 16*); Ant2* (*Pr*) locus is about 5.5 cM from the *Pre2* (Purple lemma and pericarp 2) locus (8); *ant2.20* has no SNP markers in the Bowman backcross-derived line, BW019, that are deviant from those of Bowman (2); *ant2.h* is associated with SNP markers 1_0247 to 2_0182 (positions 150.96 to 185.53 cM) in 2H bins 10 to 12 in Bowman backcross-derived line BW020 (2); *ant2* from Saffron cosegregated with SNP markers 2_1007 and 2_1175 [position 98.82 cM (155.04 to 155.98 cM)] in 2H bin 10 (1); *Ant2.c* is between markers bmag140 and bmag125 in 2HL (13).

Description:

As plants approach maturity straw remains colorless instead of turning purple (10, 12). As plants approach maturity, anthocyanin pigments are not observed in any vegetative plant parts, including the stem, auricles, lemmas, and awns (3, 7, 10). The recommended symbol for the dominant allele is *Ant2.c* (formerly *Pr*) (10). Besides the lack of anthocyanin pigmentation of the stem bases, no other morphological differences were observed between Bowman and the Bowman backcross-derived lines for *ant2.20* (BW019) and *ant2.h* (BW020) (4). Resequencing the putative anthocyanin pathway gene *ant2* (*HvbHLH1*) identified a 16-bp deletion resulting in a premature stop codon upstream of the basic helix-loop-helix domain (1). The *Pre2* and *Ant2* loci were assumed as non-synonymous because the purple- and white-grained cultivars used for mapping *Pre2* did not have polymorphism for the *Ant2* diagnostic marker (11).

Origin of mutant:

Natural occurrence in few cultivars (9, 12), the first 3 or 4 alleles are likely natural occurrences the same locus.

Mutational events:

Ant2.c (*Pr*) in Nilsson-Ehle No. 2 is the wild type allele and colorless straw in Trebi (CIho 936) (12); *ant2.d* (*pr1.b*) in Alva (NGB 1507, NSGC1866), *ant2.e* (*pr1.c*) in Balder (NGB 14668, PI 195481), *ant2.f* (*pr1.d*) in Cambrinus (PI 321779), *ant2.g* (*pr1.e*) in Sultan (PI 339814) (9); *ant2.h* in Shyri from ICARDA in Mexico (2); *ant2.15* (NGB 114564)*, 2.20* (NGB 114569, GSHO 1632)*, 2.23* (NGB 114572)*, 2.25* (NGB 114575)*, 2.26* (NGB 114576)*, 2.27* (NGB 114278) in Foma (NGB 14659, CIho 11333) (10); *ant2.41* (NGB 114596) in Mari (NGB 14656, PI 428407) (9); *ant2.46* (NGB 111505) in Foma, *2.47* (NGB 111823)*, 2.48* (NGB 111782)*, 2.49* (NGB 111808)*, 2.50* (NGB 111811)*, 2.51* (NGB 111817)*, 2.54* (NGB 111872)*, 2.55* (NGB 111787) in Bonus (NGB 14657, PI 189763) (9); *2.112, 2.113, 2.114, 2.115, 2.116, 2.117, 2.118, 2.120, 2.121, 2.122, 2.130* in Nordal (NGB 13680, NGB 4704) (9); *ant2.h (pr1.f)* in Shyri (GSHO 2430) (4).

Mutant used for description and seed stocks:

Ant2.c (*Pr*) in Trebi (CIho 936); *ant2.20* (NGB 114569, GSHO 1632) in Foma; *ant2.h* (GSHO 2430) in Shyri; *ant2.h* from Shyri in Bowman (PI 483237, NGB 22812)*5 (GSHO 1919); *ant2.h* in Bowman*7 (BW020, NGB 20428); *ant2.20* (NGB 114569, GSHO 1632) from Foma in Bowman*2 (GSHO 1920); *ant2.20* in Bowman*6 (BW019, NGB 20427).

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Revised:

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BGS 81, Glossy sheath 7, *gsh7*

Stock number:	BGS 81
Locus name:	Glossy sheath 7
Locus symbol:	*gsh7*

Previous nomenclature and gene symbolization:

Glossy sheath 7 = *gs7* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosomes 1H, 2HL or 5H (1); based on segments of the donor parent chromosomes retained in the Bowman backcross-derived line for *gsh7.ae* (BW410), possible locations based on SNP markers included 1_0259 to 2_0229 (positions 70.78 to 106.61 cM) in 1H bins 07 to 10, markers 1_0916 to 2_0681 (positions 187.68 to 247.86 cM) in 2H bins 12 to 15, markers 1_0580 to 1_0955 (positions 54.27 to 69.76 cM) in 5H bins 03 to 04, and markers 2_0367 to 2_1445 (positions 116.66 to 134.85 cM) in 5H bins 07 to 08 (1).

Description:

The spike, leaf sheath and stem of mutant plants are glossy and bright green in color (wax code - - ++) (3). In early generation backcrosses to Bowman, the glossy sheath 7 segregates headed early and had poor vigor and small spikes. Also, spikes frequently abort after emasculation (2). Plants of the Bowman backcross-derived line for *gsh7.ae* (BW410) were 2/3 to 3/4 of normal height. Kernels are slightly longer and thinner than those of Bowman and kernel weights are about 2/3 of normal. Grain yields are less than 10% of normal (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (3).

Mutational events:

gsh7.ae (GSHO 1759) in Akashinriki (PI 467400, OUM022) (3).

Mutant used for description and seed stocks:

gsh7.ae (GSHO 1759) in Akashinriki; *gsh7.ae* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2269, BW410, NGB 20643).

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Prepared:

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Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:55.
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BGS 111, Dense spike 10, *dsp10*

Stock number: BGS 111
Locus name: Dense spike 10
Locus symbol: *dsp10*

Previous nomenclature and gene symbolization:

Dense spike c = l_c (6, 8).

Inheritance:

Monofactorial recessive (2, 8).

Located in chromosome 3HS (2, 5, 8); *dsp10.c* is about 1.3 cM distal from the *xnt3* (xantha seedling 3) locus (7, 8); *dsp10.c* is associated with SNP markers 2_0002 to 1_0628 (positions 82.03 to 135.80 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW278; *dsp10.ai* (previously *pyr.ai*) is associated with SNP markers 2_1109 to 2-1305 (positions 78.82 to 103.33 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW655; *dsp10.aj* (previously *dsp.aj*) is associated with SNP markers 2_0794 to 1_0747 (positions 39.80 to 144.30 cM) in 3H bins 04 to 09 of the Bowman backcross-derived line BW258 (1); the region of 3H with common SNP markers retained all three stocks is from 2_002 to 1_0224 (positions 82.03 to 85.26) (1, 3), in 3H bin 05 near the centromere at about 185 Mb.

Description:

Although rachis internode length or spike density is not a highly stable character, plants with relatively dense spikes can be selected from crosses to Club Mariout. Rachis internode length values of 2.8 to 3.4 mm, 2.9 to 3.6 mm, and 2.6 to 2.8 mm were recorded for Club Mariout in one experiment (8). Plants in Bowman backcross-derived lines for *dsp10* locus (BW258, BW278, and BW655) had average rachis internode lengths of 3.3 mm compared to 4.6 mm for Bowman. The plants were 5 to 15% shorter than Bowman plants and spikes averaged 2 to 3 more kernels. Kernel weights and grain yields of the Bowman lines with *dsp10* were similar to values for Bowman (3).

Origin of mutant:

Natural occurrence in Club Mariout (CIho 261, PI 9877) (2, 8) and other cultivars (9).

Mutational events:

dsp10.c in Club Mariout (CIho 261, PI 9877, GSHO 71) (2, 8).

Mutant used for description and seed stocks:

dsp10.c in Club Mariout (GSHO 71, CIho 261, PI 9877); *dsp10.c* in Bowman (PI 483237)*3 (GSHO 1956); *dsp10.c* in Bowman*6 (BW278, NGB 20562); *dsp10.ai* from a 6-rowed line mutated in Sweden (18:08:04, GSHO 2433) (4) in Bowman*6 (GSHO 2241); *dsp10.ai* in Bowman*7 (BW655, NGB 22220); *dsp10.aj* from a 6-rowed line mutated in Sweden (18:08:04, GSHO 1720) (4) in Bowman*5 (GSHO 2242); *dsp10.aj* in Bowman*6 (BW258, NGB 22083).

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Revised:
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BGS 117, Chlorina seedling 2, *fch2*

Stock number:	BGS 117
Locus name:	Chlorina seedling 2
Locus symbol:	*fch2*

Previous nomenclature and gene symbolization:

Chlorina seedling 2 = *f2* (13).
Light green 5 = *lg5* (12).
Chlorina seedling f2 = *clo-f2* (8).
Hordeum vulgare chlorophyllide α oxygenase = *HvCAO* (16).

Inheritance:

Monofactorial recessive (3, 4, 13).

Located in chromosome 3HL (11, 13, 14, 15); *fch2.c* is about 7.7 cM distal from the *cur2* (curly 2) locus (17); *fch2.c* is associated with SNP markers 1_0702 to 1_0694 (positions 239.73 to 248.51 cM) in 3H bin 15 in Bowman backcross-derived line BW358 (1); an *fch2* mutant is in the 682.2 to 684.5 Mb region of 3HL (16).

Description:

The *fch2.c* seedlings have a pale yellow-green color, which persists until near maturity under greenhouse or field conditions. Development of homozygous plants is delayed, but the stunted plants survive to produce seed (3). A complete absence or greatly reduced levels of chlorophyll *b* were found in mutant plants (3, 4, 8). The respiratory and photosynthetic rates of detached leaves, and intact plants are not significantly different from those of normal plants. However, the growth rate of mutant plants decreases after the endosperm is depleted (4). Plants of the Bowman backcross-derived line for *fch2.c*, BW358, showed a drastic response to environmental stress during the growing season. The heading date for BW358 plants was about 13 days later than Bowman. Plant height varied from near normal to 20% reduction. Average kernel weights were reduced up to 40%. Grain yields of BW358 were 1/3 to 1/2 those of Bowman (2). An absence of chlorophyll *b*-binding proteins in the photosynthetic membranes is found in *fch2* mutants (6, 7). Alleles at the *fch2* locus were shown to have DNA sequence changes in the gene encoding chlorophyllide a oxygenase or interfere with regulators of enzyme production (8). The enzyme converts chlorophyllide a to chlorophyllide b and it is essential for Chl b biosynthesis (8).

Origin of mutant:

A spontaneous mutant in progeny from the cross Moister (CIho 2799) X California Coast (CIho 6115) (3).

Mutational events:

fch2.c (28-3398 Chlorina, GSHO 107) in Moister/California Coast (3, 11); *fch2.y* (*lg5*, GSHO 294) in CIho 6151 (12); *clo-f2.2800*, *-f2.2807*, *-f2.3613* in Donaria (PI 209784), *-f2.101, -f2.102, -f2.103, -f2.105, -f2.107, -f2.108, -f2.109* in Tron, *-f2.122, -f2.123, -f2.133* in Bonus (NGB 14657, PI 189763) (9, 10). Additional mutants, presumably at the *fch2* locus, were reported and mapped (16). All the *clo-f* mutant stocks are stored in the Biology Department, Lund University with Mats Hansson who is the coordinator for chlorophyll biosynthesis (5).

Mutant used for description and seed stocks:

fch2.c (28-3398, GSHO 107) in Moister/California Coast; *fch2.c* in Bowman (PI 483237)*7 (GSHO 1993, BW358, NGB 20597).

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Revised:

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J.D. Franckowiak and U. Lundqvist. 2016. Barley Genet. Newsl. 46:63-64.
J.D. Franckowiak and U. Lundqvist. 2018. Barley Genet. Newsl. 48:86-87.

BGS 146, Calcaroides-d, *cal-d*

Stock number:	BGS 146
Locus name:	Calcaroides-d
Locus symbol:	*cal-d*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 3H (7); *cal-d.4* is near the centromere and near molecular marker CDO684 (7); *cal-d.4* is associated with SNP markers 1_0672 to 2_1502 (positions 58.56 to 100.48 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW106 (2).

Description:

At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, *cal-d* mutants bear a well-organized ectopic structure, the sac (1, 4). Only the allele *cal-d.22* does not produce pronounced lemma wings. The *cal-d* mutants bear a short distal awn (7). In contrast to the *Kap1* (Hooded lemma 1) phenotype, the sac does not develop into an epiphyllous flower. The *cal-d* alleles are associated with leaf curling also (7). The awn malformation of *cal-d* mutants is associated with developmental activation of the phytomeric triad separating the lemma from awn (4). Plants of the Bowman backcross-derived line for *cal-d.4* (BW106) were about 3/4 of normal height and headed one day later than Bowman. Awns were 1/2 and peduncles were 2/3 of normal length, and leaf blades were slightly narrower. Kernels of BW106 were thin and weighted about 1/3 less than those of Bowman. Test weights were low, and grain yields were less than 1/2 of normal (3).

Origin of mutant:

An X-ray induced mutant in Foma (NGB 14659, CIho 11333) (6, 7).

Mutational events:

cal-d.4 (NGB 114284, GSHO 1698) in Foma (NGB 14659, CIho 11333) (6); *cal-d.14* (NGB 119381) in Kristina (NGB 14661, NGB 1500), *-d.18* (NGB 114297), *-d.22* (NGB 114302) in Bonus (NGB 14657, PI 189763) (6).

Mutant used for description and seed stocks:

cal-d.4 (NGB 114284, GSHO 1698) in Foma; *cal-d.4* in Bowman (PI 483237, NGB 22812)*6 (GSHO 1875); *cal-d.4* in Bowman*7 (BW106, NGB 20512).

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Revised:
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BGS 150, Scirpoides leaf-b, *scl-b*

Stock number: BGS 150
Locus name: Scirpoides leaf-b
Locus symbol: *scl-b*

Previous nomenclature and gene symbolization:

Scirpoides leaf-5 = *scl-5* (3).

Inheritance:

Monofactorial recessive (2).

Probably located in chromosomes 3HL or 6HS (1); *scl-b.5* is associated with SNP markers 2_0130 to 1_1172 (positions 151.97 to 190.87 cM) in 3H bins 09 to 12 and with SNP markers 1_0061 to 1_1205 (positions 70.15 to 82.43 cM) in 6H bins 05 and 06 of the Bowman backcross-derived line BW777 (1).

Description:

Leaf blades of *scl-b.5* plants are folded inward and are narrow compared to those of normal sibs. Folding of the leaf blade persists until maturity (2, 3). Plants of Bowman backcross-derived line for *scl-b.5* (BW777) were 15% shorter than Bowman, kernels were narrower and 15% lighter, and grain yields were about 25% lower (2). Plants of BW777 have inward folded leaf blades that are less than 2/3 as wide as those of Bowman (2). When grown in the greenhouse *scl-b.5* plants had very narrow leaf blades that showed more inward folding than mutants at the *scl-a* (scirpoides leaf-a) locus. Also, the awns of spikes were often trapped by the collar of the flag leaf during spike emergence (2). A new locus symbol is recommended based on the morphological differences compared to *scl-a* mutants and the lack of SNP markers retained in chromosome 1HL (1, 2).

Origin of mutant:

The scirpoides leaf mutant was induced by UV-ray treatment of pollen grains of Bonus (NGB 14657, PI 189763) (3).

Mutational events:

scl-b.5 (NGB 117103) in Bonus (NGB 14657, PI 189763) (3).

Mutant used for description and seed stocks:

scl-b.5 (NGB 117103) in Bonus; *scl-b.5* in Bowman (PI 483237, NGB 22812)*3 (BW777, NGB 20754).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:60.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:90.

BGS 157, Brachytic 2, *brh2*

Stock number: BGS 157
Locus name: Brachytic 2
Locus symbol: *brh2*

Previous nomenclature and gene symbolization:

Brachytic 2 = *br2* (12).
Breviaristatum-l = *ari-l* (7, 8).
Hordeum vulgare U-box E3 ubiquitin ligase = *HvTUD1* (2).

Inheritance:

Monofactorial recessive (11).

Located in chromosome 4HL (11); *brh2.b* is about 1.5 cM proximal from the *glf3* (glossy leaf 3) locus (5, 11); *brh2.b* is over 22.8 cM proximal from the *Kap1* (Hooded lemma 1) locus (11); *brh2.b* is near AFLP marker E4140-7 in subgroup 38-40 of the Proctor/Nudinka map (10), *brh2.b* is about 15.9 cM distal from SSR marker Bmag0353 near the boundary between 4H bins 06 and 07 (3); *brh2.b* is associated with SNP markers 2_0012 to 1_1319 (positions 57.19 to 110.93 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW090 (4); *ari-l.3* is associated with SNP markers 2_1374 to 2_1332 (positions 41.13 to 112.64 cM) in 4H bins 04 to 08 of the Bowman backcross-derived line BW050 (4); *HvTUD1* is located at 550.51 Mb (59.89 cM) (2).

Description:

Plant height and vigor are reduced to about 2/3 normal; the awn is less than 1/4 normal length; the spike is semi-compact; and the leaf, kernel, glume and glume awn, rachilla, and coleoptile are shorter than in the original cultivar. Auricles are well developed and larger than those of the original cultivar (12). In the Bowman backcross-derived lines, the peduncle is about 1/2 normal length, kernel weights are slightly over 2/3 normal, yield is about 1/2 normal; however, rachis internode lengths are normal (3). The *ari-l.3* allele at the *brh2* locus is sensitive to gibberellic acid treatment (1). The Bowman backcross-derived for *brh2.b*, BW090, and *ari-l.3*, BW050, were morphologically similar to each other, shorter than Bowman, 65 vs. 90 cm. They also had short awns, 2.5 vs. 12 cm beyond the tip of the spike and small kernels. BW050 and BW090 have undulating leaf margins and more upright leaf blades than Bowman (2). Compared to Bowman, kernels were shorter, 7.5 vs. 9.8 mm, and thinner, 3.61 vs.3.83 mm, and weighed less, 40 vs. 56 mg. Grain yields for BW050 and BW090 were 1/2 to 2/3 of those produced by Bowman (6). The *brh2* and *ari-l* mutants responded to exogenously applied brassinolide, which suggests an apparent brassinosteroid deficient phenotype (2). The b*rh2* locus is orthologous to *TUD1* in rice (*Oryza sat*iva L.), which encodes a U-box E3 ubiquitin ligase (2).

Origin of mutant:

An X-ray induced mutant in Svanhals (NGB 1482, PI 5474) (12).

Mutational events:

brh2.b (Kmut 28, OUM283, GSHO 573) in Svanhals (NGB 1482, PI 5474) (11); *ari-l.3* (NGB 115848) in Bonus (NGB14657, PI 189763) (8); *ari-l.132* (NGB 115942) in Foma (NGB 14659, CIho 11333) (9); *ari-l.135* (NGB 115945), *-l.145* (NGB 115956), *-l.214* (NGB 116023), *-l.237* (NGB 116047) in Foma, *-l.257* (NGB 116066) in Kristina (NGB 14661, NGB 1500) (8).

Mutant used for description and seed stocks:

brh2.b (GSHO 573) in Svanhals; *ari-l.3* (GSHO 1660) in Bonus; *brh2.b* in Bowman (PI

483237)*7 (GSHO 2016, BW090, NGB 20496); *ari-l.3* in Bowman*7 (GSHO 2017, BW050, NGB 20458).

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:143.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:115.
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:184.
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J.D. Franckowiak and U. Lundqvist. 2017. Barley Genet. Newsl. 47:84-85.
J.D. Franckowiak and U. Lundqvist. 2018. Barley Genet. Newsl. 48:91-92.

BGS 173, Non-blue aleurone xenia 3, *blx3*

Stock number:	BGS 173
Locus name:	Non-blue aleurone xenia 3
Locus symbol:	*blx3*

Previous nomenclature and gene symbolization:

Non-blue aleurone 3 = *bl3* (1).
Complementary factors for blue vs white aleurone = *Bly* and *bly* (7).
Basic helix-loop-helix domain (bHLH) -coding gene = *HvMyc2* (6).
HvMpc1-H3.

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1, Blx2, Blx4,* and *Blx5* loci (1, 2).

Located in chromosome 4HL (1, 2); *blx3.c* is close to the *blx1* (non-blue aleurone xenia 1) locus (1, 2, 7); *blx3.c* is over 25.3 cM distal from the *Kap1* (Hooded lemma 1) locus (1, 5); *Blx3* (*HvMyc2*) mapped near SSR marker Bmac186 (6).

Description:

Blue aleurone color is due to anthocyanin pigments (4), which occur as lumps inside many aleurone granules in some or all aleurone cells (1). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (1, 2). Aleurone color is best observed in well filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (3). The *Blx3* (*HvMyc2*) gene is active only in the aleurone layer and shares 70.8% identity with Anthocyanin-less 2 (*HvAnt2*) (6).

Origin of mutant:

Natural occurrence in a line selected from Composite Cross V (CIho 6620) (7).

Mutational events:

blx3.c in line Blx (GSHO 2506) selected from Composite Cross V CIho 6620) (1).

Mutant used for description and seed stocks:

blx3.c in line Blx (GSHO 2506) selected from Composite Cross V; *blx3.c* in BW063 (NGB 20471)/Blx (BW064, NGB 20472).

References:

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Prepared:

R.A. Finch. 1978. Barley Genet. Newsl. 8:165.

Revised:

J.D. Franckowiak and R.A. Finch. 1997. Barley Genet. Newsl. 26:198.

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:93-94.

BGS 174, Non-blue (pink) aleurone xenia 4, *blx4*

Stock number:	BGS 174
Locus name:	Non-blue (pink) aleurone xenia 4
Locus symbol:	*blx4*

Previous nomenclature and gene symbolization:

Non-blue (pink) aleurone 4 = *bl4* (3).
Hordeum vulgare Cytochrome P450-coding = HvF3'5'H (8).
Hordeum vulgare Myb protein Colorless 1 ortholog H2 = HvMpc1-H2 (8, 9).

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1, Blx2, Blx3,* and *Blx5* loci (3).

Located in chromosome 4HL (3); *blx4.d* is very close to the *blx1* (non-blue aleurone xenia 1) locus (3); *blx4.d* is over 29.5 cM distal from the *Kap1* (Hooded lemma 1) locus (7); *Blx4* (*HvMpc2*) mapped between SSR loci XGBS0875-4H (3.4 cM distal) and XGBM1048-4H (3.4 cM proximal) (7).

Description:

Blue or pink aleurone color is due to pigments, known to be anthocyanin in the case of blue (6), which occur as lumps inside many aleurone granules in some or all aleurone cells (3). Variation in color expression from pink to an off-white is caused by environmental factors and modifying genes (3). The pink and red color aleurone colors are easier to observe in well filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (5). A brick red aleurone color results from the interaction of the *ibl1* (intense blue aleurone 1) gene with the *blx4.d* gene in homozygotes (2, 3). *HvMpc1-H2 (Blx4*) was expressed in different tissues, but its transcription was not detected in non-colored aleurone (8).

Origin of mutant:

Natural occurrence in a few Ethiopian and Nepalese lines (1, 2).

Mutational events:

blx4.d plus *ibl1.a* (intense blue aleurone 1) in Ethiopian 637 (GSHO 2508) (1); *blx4.d* only in Ab 6 (PI 548720, GSHO 2507), EP79, Grannenlose Zweizeilige (PI 548740) (3).

Mutant used for description and seed stocks:

blx4.d in Ab 6 (GSHO 2507); *blx4.d* in Ab6/BW063 (NGB 20471) (BW065, NGB 20473); *blx4.d* (blue aleurone 4) with Intense blue aleurone 1 *(ibl1)* and *nud1.a* (naked caryopsis 1) in BW063 (NGB 20471)/Ethiopian 637 (BW417, NGB20650) produces red aleurone color (2, 4).

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Prepared:
R.A. Finch. 1978. Barley Genet. Newsl. 8:166.
Revised:
J.D. Franckowiak and R.A. Finch. 1997. Barley Genet. Newsl. 26:199.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:95-96.

BGS 186, Slender dwarf 3, *sld3*

Stock number:	BGS 186
Locus name:	Slender dwarf 3
Locus symbol:	*sld3*

Previous nomenclature and gene symbolization:

Anthocyanin-free = *ant-567* (6).
Proanthocyanidin-free 17.567 = *ant17.567* (5).
Slender dwarf e = *sld.e* (4).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 4HS (3); *sld3.e* showed linkage drag with the *int-c* (intermedium spike-c) locus (3); *sld3.e* is associated with SNP markers 1_0208 to 2_0777 (positions 5.24 to 40.15 cM) in chromosome 4H bins 01 to 04 of the Bowman backcross-derived line BW863 (1).

Description:

The mutant gene *sld3.e* was isolated as a second mutant in the stock *ant17.567* (proanthocyanidin-free 17) (2). Plants show reduced vigor and are about 3/4 normal height. The number of spikelets per spike is about 3/4 that of normal sibs and kernels are slightly smaller. Rachis internodes can be slightly longer and grain yields are about 3/4 of normal. The Bowman backcross-derived line with *sld3.e* (BW863) did not show a reduction in anthocyanin pigmentation or a large reduction in kernel size (2). Plants of BW863 were about 10% shorter than Bowman and peduncles were about 20% shorter. Rachis nodes were slightly longer and kernels per spike can be reduced up to 20% in some environments. Kernels were slightly shorter and thinner than those of Bowman and seed weights were 10 to 15% less. Grain yields were slightly reduced compared to those of Bowman (2).

Origin of mutant:

A sodium azide induced mutant isolated with *ant.567* in Manker (CIho 15549) (6).

Mutational events:

sld3.e (*ant17.567*, DWS1050 GSHO 2480) in Manker (CIho 15549) (2).

Mutant used for description and seed stocks:

sld3.e (GSHO 2480) in Bowman/*ant17.567*; *sld3.e* in Bowman (PI 483237, NGB 22812)*7 (GSHO 1998, BW863, NGB 22300).

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Prepared:

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Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:243.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:63-64.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:97-98.

BGS 190, Thick filament 1, *tfm1*

Stock number:	BGS 190
Locus name:	Thick filament 1 (male sterile genetic)
Locus symbol:	*tfm1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1HL (1); *tfm1.a* is associated with SNP markers 2_0603 to 2_0915 (positions 199.04 to 202.94 cM) in 1H bin 14 of a heterozygous plant from the Bowman backcrossed-derived line BW877 (1).

Description:

The filaments supporting the anthers are much thicker than normal, having a stalk-like appearance and a light green color. Since the filaments do not elongate, the mutant plants are largely male-sterile. Pollen fertility is apparently normal because mutant segregates will set a few seeds. Besides very poor seed, *tfm1.a* plants in Bowman backcross-derived line BW877 appear normal (2).

Origin of mutant:

A spontaneous mutant in the Volla (PI 280423) induced mutant 7060 backcrossed twice to Bowman (PI 483237, NGB 22812) (2).

Mutational events:

tfm1.a from Volla 7060/2*Bowman (2).

Mutant used for description and seed stocks:

tfm1.a from Volla 7060/2*Bowman (PI 483237, NGB 22812); *tfm1.a* in Bowman*7 (BW877, NGB 22311).

References:

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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:67.

Revised:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:99.

BGS 191, Chlorina seedling 17, *fch17*

Stock number:	BGS 191
Locus name:	Chlorina seedling 17
Locus symbol:	*fch17*

Previous nomenclature and gene symbolization:

Very yellow 3 = vy3 (3).
Chlorina seedling vy = *fch.vy* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 1HL or 3HL (1); *fch17.vy* is associated with SNP markers 1_0830 to 2_0138 (positions 130.68 to 202.26 cM) in 1H bins 11 to 14 and SNP markers 2_0130 to 1_0343 (positions 151.97 to 255.13 cM) in 3H bins 09 to 16 of the Bowman backcrossed-derived line BW344 (1).

Description:

Seedlings are pale yellow with a slight mottled type streaking and vigor is poor. The second leaf blade is chlorina with the tip gradually turning. Mature plants are normal green and have apparently normal vigor (3). In the Bowman backcross-derived line for *fch17.vy* (BW344), heading date was delayed by about 9 days compared to Bowman, and grain yields were 50 to 70% of normal. Other morphological traits of BW344 plants were similar to those of Bowman (2). A new gene symbol is assigned to the *vy3* mutant because no other chlorina mutant with a similar phenotype, except *fch7*, is associated with either 1HL or 3HL (1, 2).

Origin of mutant:

A spontaneous mutant in Himalaya X Ingrescens (GSHO 681) probably isolated by Tak Tsuchiya (3).

Mutational events:

fch17.vy (E 37-517, NSL 30243, GSHO 1079) in Himalaya X Ingrescens (GSHO 681) (2, 3).

Mutant used for description and seed stocks:

fch17.vy (GSHO 1079) from Himalaya X Ingrescens; *fch17.vy* in Bowman (PI 483237, NGB 22812)*5 (BW344, NGB 22139).

References:

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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:68.

Revised:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:100.

BGS 200, Breviaristatum-z, *ari-z*

Stock number:	BGS 200
Locus name:	Breviaristatum-z
Locus symbol:	*ari-z*

Previous nomenclature and gene symbolization:

Breviaristatum-189 = *ari-189* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 4HS (1, 2); *ari-z.189* is associated with SNP markers 2_1228 to 2_1374 (positions 5.42 to 41.13 cM) in 4H bins 01 to 04 and a small segment from markers 2_0972 to 1_0015 (positions 156.09 to 160.38 cM) in 6H bin 10 of the Bowman backcross-derived line BW029 (1).

Description:

The *ari-z.189* mutant showed awn abortion on several apical spikelets (3). In the original stock for *ari-z.189*, the auricles were purple (4). In the Bowman backcross-derived line for *ari-z.189* (BW029), awns were about 3/4 normal length. Kernel sizes and shapes and grain yields for BW029 and Bowman were similar (2). A new locus symbol *ari-z* is suggested for mutant *ari.189* because none of the other named breviaristatum (*ari*) or short awn (*lks*) loci are associated with the terminal region of the short arm of chromosome 4H.

Origin of mutant:

A propyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (3, 4).

Mutational events:

ari-z.189 (NGB 115999) in Foma (NGB 14659, CIho 11333) (3, 4).

Mutant used for description and seed stocks:

ari-z.189 (NGB 115999) in Foma; *ari-z.189* in Bowman (PI 483237, NGB 22812)*4 (BW029, NGB 20437).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:101.

BGS 203, Black lemma and pericarp 1, *Blp1*

Stock number: BGS 203
Locus name: Black lemma and pericarp 1
Locus symbol: *Blp1*

Previous nomenclature and gene symbolization:

Black lemma and caryopsis = *B* (11).
Black pericarp = *Bk* (1).
Black lemma and pericarp = *B* (12).

Inheritance:

Monofactorial dominant (1, 8, 11).

Located in chromosome 1HL (5, 9); *Blp1.b* is about 16.0 cM proximal from the *trd1* (third outer glume 1) locus (5); *Blp1.b* is in 1H bin 13 about 8.8 cM proximal from RFLP marker ABC261 (2); *Blp1.b* is associated with SNP markers 2_0959 to 2_0603 (positions 173.49 to 199.04 cM) in 1H bins 13 to 15 of the Bowman backcross-derived line BW062 (3); *Blp1.g* is associated with SNP marker 2_0940 (about position 179 cM) in 1H bin 13 of the Bowman backcross-derived line BW060 (3); *Blp1.b* in BW062 was located between microsatellites *Xgbms0012* and *Xgbms0184* (10); *Blp1.b* is in a 1.66 Mb segment between markers HZSNP63 and HZSNP59 (6); *Blp1.b* mapped between two Insertion/deletion (Indel) markers MC_1570156 and MC_162350 at 538 Mb (7), in 1H bin 13.

Description:

Black pigmentation of the lemma and pericarp develops slightly before maturation of the spike. Pigmented organs may include all parts of the spike, awns, the upper portion of the stem, and upper leaves. The intensity of pigmentation associated with each of the dominant alleles at the *Blp1* locus is characteristic of that allele, and is relatively stable over environments (12). Black seed is produced by melanin-like pigment in the pericarp (1). Woodward (12) reported that the dominance ranking of alleles at the *Blp1* locus is related to the intensity of black pigmentation they confer, with the *Blp1.b* (*B*) allele conferring extreme black pigmentation. The *Blp1.mb* (B^{mb}) allele is associated with medium black and a reduced distribution pattern; and the *Blp1.g* (B^{g}) allele is associated with light black or gray coloration (12, 13). In the Bowman backcross-derived lines for the *Blp1* locus, BW060 and BW062, the expression of other morphological traits appeared similar to those of Bowman (4). The flavonoid pigments are not involved in development of the black lemma and pericarp trait (10).

Origin of mutant:

Natural occurrence in several cultivars (11, 12). Genotype-based clustering analyses showed that the black landraces of different geographical background may have evolved from a single origin (7).

Mutational events:

Blp1.b (*B*) in *Hordeum distichon* var. *nigrinudum* No 1 (NSL 3286, GSHO 988) (12); *Blp1.mb* (B^{mb}) in CIho 2970 (GSHO 226) (12); *Blp1.g* (B^{g}) in Blackhull (CIho 878, GSHO 199) and Black Smyrna (CIho 191, GSHO 222) (12). Since these are naturally occurring variants, the stock numbers are the same for both the mutant and the cultivar.

Mutant used for description and seed stocks:

Blp1.b in *Hordeum distichon* var *nigrinudum* No 1 (GSHO 988); *Blp1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 3450) in Bowman (PI 483237)*8 (GSHO 2054, BW062, NGB 20470); possibly *Blp1.g* from a Composite Cross in Bowman*5 (BW060, NGB 20468).

References:

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:148.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:209.
J.D. Franckowiak. 2007: Barley Genet. Newsl. 37:245-246.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:69-70.
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:67-68.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:102-103.

BGS 220, Chlorina seedling 3, *fch3*

Stock number:	BGS 220
Locus name:	Chlorina seedling 3
Locus symbol:	*fch3*

Previous nomenclature and gene symbolization:

Chlorina seedling 3 = *f3* (4).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 1HS (4, 5, 6, 7); *fch3.d* is near the tip of 1HS and associated with SNP markers 2_0479 to 3_0969 (at position 0.0 cM) in chromosome 1H bin 01 of the Bowman backcross-derived line BW359 (1).

Description:

Seedlings have bright yellow leaves, which gradually change color to light green as the plant grows. Plants are vigorous, but remain chlorina or light green until maturity. Plants expressing the *fch3.d* gene can be distinguished readily from normal plants at all stages of growth (4, 5). Heading of plants in the Bowman backcross-derived line for *fch3.d* (BW359) was delayed by 5 to 8 days, plants were about 3/4 of normal height, seeds were 10 to 20% lighter, and seed yields were less than 1/2 of normal (2).

Origin of mutant:

A spontaneous mutant in an unknown six-rowed cultivar (4).

Mutational events:

fch3.d (GSHO 851, Minn 89-4) in an unknown cultivar (3).

Mutant used for description and seed stocks:

fch3.d (GSHO 851) in an unknown cultivar; *fch3.d* in Bowman (PI 483237, NGB 22812)*6 (GSHO 2033); *fch3.d* in Bowman*7 (BW359, NGB20598).

References:

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Prepared:

A. Shahla and T. Tsuchiya. 1979. Barley Genet. Newsl. 9:132.

Revised:

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:218.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:71.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:104.

BGS 223, Zebra stripe 3, Z*eb3*

Stock number: BGS 223
Locus name: Zebra stripe 3
Locus symbol: *Zeb3*

Previous nomenclature and gene symbolization:

Zoned leaf c = zb_c (2, 4, 5, 6, 9).
Zebra stripe c = zb_c (6, 7).
Zoned leaf c2 = zb_c2 (2, 4, 5).
Zebra stripe c2 = zb_c2 (6).
Zebra stripe 3 = *zb3* (7).

Inheritance:

Monofactorial incomplete dominant (2, 8, 9).

Located in chromosome 1HL (2, 4); *Zeb3.c* is associated with SNP markers 1_0275 to 2_0997 (positions 63.72 to 89.01 cM) in 1H bin 08 of a heterozygous plant from the Bowman backcross-derived line BW932 (1).

Description:

Early leaves of homozygous plants have bright yellow bands across a light yellow background when grown under alternating temperatures, warm day and cool night (2). Later leaves have patches of bright yellow. Cool temperatures enhance the yellow banding while warm temperatures increase green pigments. Under very cold conditions, leaf blades become yellowish white and deteriorate. Heterozygotes have slightly pale green color compared to normal plants (2). The *Zeb3.c* gene must be maintained as a heterozygous stock because seed production on mutant plants is rare.

Origin of mutant:

A spontaneous mutant from the collection of genetic stocks maintained by Woodward (2, 5).

Mutational events:

Zeb3.c (Utah 41, Alb Acc 43, GSHO 1451) in an unknown cultivar (2, 3, 5).

Mutant used for description and seed stocks:

Zeb3.c (GSHO 1451) in an unknown cultivar; *Zeb3.c* in Bowman (PI 483237, NGB 22812)*3 (GSHO 2057); *Zeb3.c* in Bowman*7 (BW932, NGB 22361).

References:

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Prepared:

T. Tsuchiya and A. Shahla. 1984. Barley Genet. Newsl. 14:94 as BGS 223, Zoned leaf 3 or zebra striped leaf 3.

Revised:

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:221.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:72-73.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:105-106.

BGS 224, Erectoides-b, *ert-b*

Stock number: BGS 224
Locus name: Erectoides-b
Locus symbol: *ert-b*

Previous nomenclature and gene symbolization:

Erectoides-2 = *ert-2* (3, 5).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 1HL (9, 10, 11, 12, 13); *ert-b.2* is slightly distal from the *cer-e* (eceriferum-e) locus (6, 13, 14); *ert-b.2* is about 19.3 cM proximal from the *nec1* (necrotic leaf spot 1) locus (7); *ert-b.2* is associated with SNP markers 1_0259 to 1_0520 (positions 70.78 to 82.35 cM) in 1H bins 07 to 08 of the Bowman backcross-derived line BW304 (1), likely in 1H bin 08.

Description:

Spikes have a compact appearance caused by a reduction in rachis internode length, rachis internode length values from 1.9 to 2.3 mm. Culms are shorter than those of parental cultivars (12). GA_3 treatment of plants as the flag leaf emerges decreased spike density (15). Plants of the Bowman backcross-derived line for *ert-b.2* (BW304) had slightly shortened peduncles and were about 5/6 of normal height. Rachis internode lengths were 3.5 vs. 4.4 mm. Kernels were slightly shorter and wider and weights were about 10% higher. Grain yields were about 3/4 of normal (2).

Origin of mutant:

An X-ray induced mutant in Gull (NGB 1480, CIho 1145, GSHO 466) (3, 4, 5).

Mutational events:

ert-b.2 (NGB 112606, GSHO 470), *-b.4* (NGB 112607), *-b.5* (NGB 112608), *-b.9* (NGB 112611) in Gull (NGB 1480, CIho 1145, GSHO 466) (4); *ert-b.128* (NGB 112727), *-b.151* (NGB 112750) in Bonus (NGB 14657, PI 189763) (12); *ert-b.174* (NGB 112775) in Bonus, *-b.333* (NGB 112848) in Foma (NGB 14659, CIho 11333) (8); *ert-b.354* (NGB 112870), *-b.394* (NGB 112911) in Foma (12).

Mutant used for description and seed stocks:

ert-b.2 (NGB 112606, GSHO 470) in Gull; *ert-b.2* in Bowman (PI 483237, NGB 22812)*7 (GSHO 2049, BW304, NGB 20586).

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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:222.

Revised:
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:74-75.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:107-108.

BGS 225, Curled leaf dwarf 1, *clh1*

Stock number:	BGS 225
Locus name:	Curled leaf dwarf 1
Locus symbol:	*clh1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located likely in chromosome 7HL (1); *clh1.a* is associated donor parent SNP markers 1_1243 to 2_0365 (positions 167.56 to 229.66 cM) in 7H bins 10 to 13 in Bowman backcross-derived line BW182 (1), but a small group of donor parent SNP markers 1_1456 to 2_1177 (positions 195.82 to 203.85 cM) in 5H bin 11 are retained in BW182 (1). The *chl1.a* mutant was previously reported as located in chromosome 1H (3, 4), and *clh1.a* was linked by about 7.0 cM to the *msg1* (male sterile genetic 1) locus (4).

Description:

Leaf blades are erect, narrow and folded inward and appear thicker than normal. Plants show reduced vigor, fertility, and height (3/4 of normal) when grown in the greenhouse; further reduction in vigor, and fertility is observed when mutants are grown in the field. Spikes emerge poorly from the boot (2). Plants of the Bowman backcross-derived line for *clh1.a* (BW182) were 30 to 40% shorter than Bowman. Kernels were slightly thinner and were about 2/3 normal weight. BW182 plants produced very little grain (2).

Origin of mutant:

A neutron induced mutant in Hannchen (PI 10585) (4).

Mutational events:

clh1.a (GSHO 1212) in Hannchen (PI 10585) (4).

Mutant used for description and seed stocks:

clh1.a (GSHO 1212) in Hannchen; *clh1.a* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2051); *clh1.a* in Bowman*5 (BW182, NGB 22014).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:223.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:76.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:109.

BGS 226, Revoluted leaf 1, *rvl1*

Stock number:	BGS 226
Locus name:	Revoluted leaf 1
Locus symbol:	*rvl1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1HL (2, 4); *rvl1.a* is proximal from the *trd1* (third outer glume 1) locus, and distal from the *abo1* (albino seedling 1) locus (2); *rvl1.a* is associated with SNP markers 1_0764 to 1_1006 (positions 61.55 to 110.10 cM) in 1H bins 06 to 10 of the Bowman backcrossed-derived line BW763 (1); BW763 also retained smaller segments of donor parent SNP markers in chromosome arms 1HL, 4HL, 6HL, and 7HL (1).

Description:

Tips of young leaf blades tend to roll into a tube through a counter-clockwise spiral, compared to flat surfaces of the control. Segregates can be scored from the three-leaf stage until near maturity (2). Plants of the Bowman backcross-derived line for *rvl1.a* (BW763) were 75 to 90% of normal height and peduncle length varied from slightly reduced to 2/3 of normal. Kernel weights of BW763 were slightly lower and grain yields approached normal (3).

Origin of mutant:

An X-ray induced mutant in Hakata 2 (OUJ807, PI 263407) (2).

Mutational events:

rvl1.a (Kmut 103, GSHO 608) in Hakata 2 (OUJ807, PI 263407) (2, 4).

Mutant used for description and seed stocks:

rvl1.a (GSHO 608) in Hakata 2; *rvl1.a* from Hakata 2 in Bowman (PI 483237, NGB 22812)*1 (GSHO 2319); *rvl1.a* in Bowman*5 (BW763, NGB 22231).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:224.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:77.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:110.

BGS 227, Small lateral spikelet 1, *sls1*

Stock number:	BGS 227
Locus name:	Small lateral spikelet 1
Locus symbol:	*sls1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 1HL (3); *sls1.a* is closely linked to the *msg1* (male sterile genetic 1) locus (3); *sls1.a* is associated with SNP markers 1_0933 to 3_0343 (positions 82.35 to 87.19 cM) in 1H bin 08 of the Bowman backcross-derived line BW867 (1), at about 314 Mb.

Description:

Sterile lateral spikelets become progressively smaller toward the tip of two-rowed spikes in plants, which express the *Vrs1.b* and *int-c.b* alleles at the six-rowed spike 1 and intermedium spike-c loci, respectively*.* The terminal rachis nodes generally have rudimentary lateral spikelets. Expression of the *sls1* is affected by genetic background, but express is often stronger in late tillers. The trait can be observed only in some two-rowed segregates from crosses between six- and two-rowed cultivars. No significant differences in agronomic traits were observed between Bowman backcross-derived line for *sls1.a* (BW867) and Bowman, but kernels tended to be wider and heavier and test weights are slightly higher (2).

Origin of mutant:

Natural occurrence in six-rowed cultivars derived from Manchurian introductions, but it can not be observed visually in barley cultivars with the six-rowed or deficiens spike traits (*vrs1.a* and *Vrs1.t*, respectively) (2).

Mutational events:

sls1.a in MSS005 [*msg1.ca* from CIho 5368 in Betzes (PI 129430)*11 (GSHO 1810)]; *sls1.a* in Morex (CIho 15773, GSHO 2492); molecular markers associated with the presence of the *sls1.a* allele occur frequently in six-rowed spring barleys of Manchurian origin (2).

Mutant used for description and seed stocks:

sls1.a in Morex (GSHO 2492); *sls1.a* from MSS005 in Bowman (PI 483237, NGB 22812)*8 (GSHO 2034, BW867, NGB 22304).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:225.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:78.

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:111.

BGS 228, Subcrown internode length 1, *Sil1*

Stock number:	BGS 228
Locus name:	Subcrown internode length 1
Locus symbol:	*Sil1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial incomplete dominant (1).

Located in chromosome 1H (4); *Sil1.a* is associated with the *sls1* (small lateral spikelet 1) locus based on linkage drag (4); *Sil1.a* is associated with SNP markers 1_0259 to 1_0890 (positions 70.78 to 110.10 cM) in chromosome 1H bins 08 to 09 in the centromeric region of the Bowman backcross-derived line BW852 (2).

Description:

Plants have relatively short subcrown internodes, 0.0 to 1.0 cm, when planted 9 cm deep in vermiculite. Planting depth and subcrown internode length determine the position of the crown in relation to the soil surface (1). Plants with a deeper crown placement show higher levels of winter survival (5). In generating the Bowman backcross-derived line for *Sil1.a* (BW852), the *Sil1* gene showed a dominant inheritance pattern. No other morphological effects for the *Sil1.a* gene were noted in Bowman backcross-derived line BW852 (3). When planted under cool fall conditions, short subcrown internodes are observed in many barley cultivars (3).

Origin of mutant:

Natural occurrence in NE 62203 (CIho 15542, GSHO 1604), a selection of unknown origin (1).

Mutational events:

Sil1.a in winter six-rowed barley NE 62203 (CIho 15542, GSHO 1604) (1).

Mutant used for description and seed stocks:

Sil1.a in NE 62203 (GSHO 1604); *Sil1.a* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2032); *Sil1.a* in Bowman*7 (BW852, NGB 22289).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:226.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:79.

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:112.

BGS 232, High lysine 4, *Lys4*

Stock number: BGS 232
Locus name: High lysine 4
Locus symbol: *Lys4*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia 5 = *sex5g* (8).
High lysine 4d = *Lys4d* (5).

Inheritance:

Monofactorial incomplete dominant (1, 5).

Located in chromosome 1HS (5, 6, 8); *Lys4.d* is over 35.1 cM distal from the *ert-b* (erectoides-b) locus (6); *Lys4.d* is associated with SNP markers 2_0373 to 1_0744 (positions 0.0 to 39.84 cM) in 1H bins 01 to 03 of the Bowman backcross-derived line BW497 (3).

Description:

At the hard dough stage, kernels homozygous for the *Lys4.d* gene develop a depression near the center of the lemma, which becomes progressively more distinct as the kernels mature. Grain produced by mutant plants has a 9% increase in lysine content (1, 2). Shrunken endosperm has a pleiotropic association with the high lysine gene *Lys4.d* (5). Kernels heterozygous at the *Lys4* locus may develop a slightly less distinct depression on the dorsal side (5). Maintenance of *Lys4.d* stocks may be difficult because outcrosses are not recognized easily. Plants of Bowman backcross-derived line for *Lsy4.d* (BW497) were slightly shorter, and kernel weights and grain yields were about 2/3 of normal (4).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bomi (PI 43371) (2).

Mutational events:

Lys4.d (Risø 8, GSHO 2475) in Bomi (PI 43371) (1, 2, 7).

Mutant used for description and seed stocks:

Lys4.d (GSHO 2475) in Bomi; *Lys4.d* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2035, BW497, NGB 20725).

References:

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Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:230.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:80-81.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:113-114.

BGS 241, Accordion rachis 3, *Acr3*

Stock number:	BGS 241
Locus name:	Accordion rachis 3
Locus symbol:	*Acr3*

Previous nomenclature and gene symbolization:

Lax spike = Lax (7, 8).
Accordion rachis = *acr* (6).
Accordion rachis c = *acr.c* (4).
Accordion rachis 1 = *acr1.a* (5).

Inheritance:

Monofactorial incomplete dominant for lax spike, the third factor required for expression of accordion rachis 1 (*acr1*) trait (3, 4).

Located in chromosome 1HL (3); *Acr3.a3* is associated with SNP markers 2_1357 to 2_0997 (positions 76.96 to 94.86 cM) in 1HL of the Bowman backcross-derived lines BW009 and BW439 (3), likely in 1H bin 08. Bowman backcross-derived lines BW007 with *Acr3.b3*, BW009 with *Acr3.a3*, BW438 with *Acr3.a*, and BW456 with *Acr3.am3* contain overlapping segments of variable length and SNP marker patterns in 1H from their donor parents (3).

Description:

Mutant plants have slightly elongated rachis internodes (1). The *Acr3* gene is in the third chromosomal region associated with expression of the accordion rachis trait in Bowman backcross-derived lines BW009 and BW439. The contribution of the 1HL region to characteristics of the accordion phenotype is unknown. Only the line BW438 (*Lax.an* or *Acr3.an*) has a 1HL donor chromosome segment in a line lacking both the 2H and 4HL segments identified as containing the *acr1* (see BGS 097) and *Acr2* (see BGS 189) genes, respectively. Plants of the Bowman derived line BW438 ranged from slightly shorter to slightly taller than Bowman and had slightly longer rachis internodes (4). Kernels of BW438 were slightly longer than those of Bowman, but weighed slightly less (5.3 vs. 6.0 mg). Grain yields of BW009 were about 2/3 that of Bowman (4).

Origin of mutant:

A naturally occurring deviant for lax spike from several sources (3, 4).

Mutational events:

Acr3.a3 in ACBV89B229 (GSHO 1617) and ACBV89B232 (GSHO 1573) (3, 9); *Acr3.b3* in Burma Girl (CIho 14831, GSHO 1071) (4, 9); *Acr2.am2* and *Acr3.an* in AB 1398 [GSHO 1115, likely CIho 14785 from G.A. Wiebe (1)]. *Acr3.c3* in T188 (GSHO 1480) from R.W. Woodward (2).

Mutant used for description and seed stocks:

Acr3.a3 in ACBV89B229 (GSHO 1617); *Acr3.b3* in Burma Girl (GSHO 1071); *Acr2.am2* and *Acr3.an* in AB 1398 (CIho 14785); *Acr3.an* from AB 1398 in Bowman*5 (BW438, NGB 20670); *Acr3.b3* from Burma Girl in Bowman *2 (GSHO 1898); *Acr3.b3* in Bowman*5 (BW007, NGB 20415); *Acr3.am3* from AB 1398 in Bowman*4 (BW456, NGB 20688); *Acr3.a3* plus *acr1.a* and *Acr2.a2* in Bowman*7 (BW009, NGB 20417 and BW439, NGB 20671); *Acr3.c3* in T188 (GSHO 1480); *Acr3.c3* from T188 in Bowman*6 (BW008, NGB 20416).

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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:85-86.

Revised:

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:105-106.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:115-116.

BGS 242, Slender dwarf 6, *sld6*

Stock number: BGS 242
Locus name: Slender dwarf 6
Locus symbol: *sld6*

Previous nomenclature and gene symbolization:

Slender dwarf g = *sld.g* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 1H (1); *sld6.g* is associated with SNP markers 1_0259 to 1_0552 (positions 70.78 to 88.33 cM) in chromosome 1H bins 07 to 08 and SNP markers 2_0226 to 2_0206 (positions 3.14 to 9.61 cM) in 5H bin 01 of the Bowman backcross-derived line BW854 (1).

Description:

Plants with the *sld6.g* mutant show reduced height, and leaf blades are much shorter and slightly narrower (2). Plants of the Bowman backcross-derived line for *sld6.g* (BW854) were 15 to 25% shorter than those of Bowman and spikes had about 4 fewer fertile rachis nodes. Spikes were semi-compact with rachis internodes about 25% shorter than those of Bowman. Kernels of BW854 were shorter and slightly thinner than those of Bowman. Kernel weights and grain yields were about 3/4 of normal (3). Based on the heterogeneous SNP marker positions in BW954, *sld6.g* is not an allele at any of the previously named slender dwarf loci (1, 3).

Origin of mutant:

A sodium azide induced mutant in Glenn (CIho 15769) (2).

Mutational events:

sld6.g (GSHO 2482) in Glenn (CIho 15769) (2, 3).

Mutant used for description and seed stocks:

sld6.g (GSHO 2482) in Glenn; *sld6.g* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2355); *sld6.g* in Bowman*7 (BW854, NGB 22291).

References:

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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:87.

Revised:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:117.

BGS 251, Multiflorus 2, *mul2*

Stock number:	BGS 251
Locus name:	Multiflorus 2
Locus symbol:	*mul2*

Previous nomenclature and gene symbolization:

Multiflorus 2 = *mlt2* (5).

The change to *mul2* was recommended by Robertson (4).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 6HL (3, 5); *mul2.b* is about 24.2 cM distal from the *rob1* (orange lemma 1) locus (3, 5); in the Bowman backcross-derived stock for *mul2.b* (BW607) only SNP markers associated with the *vrs1.a* allele were retained, 1_1100 to 2_0340 (positions 135.19 to 138.37 cM) in 2HL bin 09 (1).

Description:

Lateral spikelets may have supernumerary florets and occasionally nodal branches appear at random in the spike. The character shows variable expression in some crosses, and only a few spikes may be affected in some plants (5). The trait is expressed only as a malformed rachilla in some lateral spikelets of six-rowed plants in the Bowman backcross-derived line. The rachilla malformation is most pronounced near the middle of the spike and ranges from formation of a fertile spikelet to slight elongation of the rachilla (2). The lack of SNP markers from the donor parent in BW607 other than those associated with *vrs1.a* (six-rowed spike 1) allele suggests that the *mul2.b* is likely an unexpressed trait present in Bowman (2).

Origin of mutant:

A betatron induced mutant in Montcalm (CIho 7149) (5).

Mutational events:

mul2.b (Alb Acc 299, GBC326, GSHO 1394) in Montcalm (CIho 7149) (3, 5).

Mutant used for description and seed stocks:

mul2.b (GSHO 1394) in Montcalm (CIho 7149); *mul2.b* plus *vrs1.a* in Bowman (PI 483237, NGB 22812)*6 (GSHO 2089); *mul2.b* plus *vrs1.a* (six-rowed spike 1) in Bowman*7 (BW 607, NGB 22173). (A six-rowed phenotype is required for expression).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:154.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:232.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:118-119.

0BGS 276, Grain protein content 1, *gpc1*

Stock number:	BGS 276
Locus name:	Grain protein content 1
Locus symbol:	*gpc1*

Previous nomenclature and gene symbolization:

Hordeum vulgare NAC transcription factor = *HvNAM-1* (3).

Inheritance:

Monofactorial recessive (3, 12).

Located in chromosome 6HS (10, 12); *gpc1.c* is very close to HVM74 (an SSR marker positioned just above the endonuclease organizer region in 6HS) (10, 12); *gpc1.c* is in 0.7 cM interval encompassing the peak QTL for grain protein content (GPC) (3); *gpc1.c* is at 50.35 Mb (5).

Description:

The spring six-rowed barley Karl (CIho 15487) averaged over 2% lower in grain protein than its recurrent parent Traill (CIho 9538) (1, 14). Lines derived from complex crosses to Karl had 1 to 2% lower grain protein when grown under different nitrogen (N) fertilization levels (15). Presence of the *gpc1.c* allele was associated with a 1.3% reduction in grain protein (5, 12). Grain protein reduction associated with the *gpc1.c* allele were not observed in all environments (4). The *Gpc1* locus influences whole-plant N allocation and management (6). Following similar times for floral transition at the shoot apical meristem, as determined by the presence of double ridge, anthesis occurred on average 5 days earlier for the high-GPC near-isogenic line than for the low-GPC line (7, 9). A delayed in development was observed also after anthesis (8). Developmental differences in post-anthesis flag leaf and whole-plant senescence between low- and high-GPC lines persisted under both long and short days (11).

Origin of mutant:

Lower grain protein content is a spontaneous variant first reported in the cultivar Karl (CIho 15487) (1, 14). Variation in grain protein content values for Tibetan barleys was associated with the *Gpc1* (*HvNAM1*) locus (2, 13).

Mutational events:

The low grain protein content trait of Karl was likely obtained from Lousy (CIho 7147) (1); alleles that are associated with different grain protein levels are represented by *Gpc1.a* (Hap 2) in Chevron (PI 38061, CIho 1111); *gpc1.b* (Hap 7) in Lacey (PI 613603); *gpc1.c* (possibly Hap 1) Karl (CIho 15487) (5, 13); 10 haplotypes in the *HvNAM1* DNA sequence from Tibetan landraces and wild barley (13).

Mutant used for description and seed stocks:

The low grain protein content trait of Karl, *gpc1.c*, was likely inherited from Lousy (CIho 7147 (1); *Gpc1.a* in Chevron (PI 38061, CIho 1111) and Bowman (PI 483237, NGB 22812) (5, 15); *gpc1.b* in Lacey (PI 613603) and Rasmusson (PI 658495); *gpc1.c* in Karl (CIho 15487); *gpc1.c* in ND11231-01 (PI 643261) and Logan (PI 592784) (Weston); a recombinant between *gpc1.c* and *Rpt5.f* (Reaction to *Pyrenophora teres* 5 from CIho 5791) in ND Genesis (PI 677345).

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Prepared:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:120-121.

BGS 301, Fragile stem 1, *fst1*

Stock number:	BGS 301
Locus name:	Fragile stem 1
Locus symbol:	*fst1*

Previous nomenclature and gene symbolization:

Fragile stem = *fs* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5HL (5, 6); *fst1.a* is about 24.3 cM proximal from the *srh1* (short rachilla hair 1) locus (3, 4, 7); *fst1.a* is associated with SNP markers 2_0367 to 2_0850 (positions 116.66 to 157.13 cM) in 5H bins 07 to 09 of the Bowman backcross-derived line BW372 (1); *fst1.d* is associated with SNP markers 3_0314 to 2_0850 (positions ≈136 to 157.13 cM) in 5H bins 08 to 09 of the Bowman backcross-derived line BW373 (1).

Description:

Leaf blades and stems of mutant plants are easily broken when physical bent. This extraordinary fragility is exhibited even after maturity. Generally, stems are more flexible than in normal plants, and straw breakage prior to harvest is rare (6). In the Bowman backcross-derived line for *fst1.a* (BW372), nodding of the culms is frequent and forage yield is reduced. In Bowman backcross-derived line for *fst1.d* (BW373), culms are less fragile and nodding is much less (2). BW372 (*fst1.a*) plants were 10 to 15% shorter and yields were about 50% lower. Kernels of BW372 weight about 10% less than those of Bowman. BW373 (*fst1.d*) plants were similar to Bowman plants for all traits except for easily broken culms (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar and named Kamairazu, which means "sickle not needed to harvest" (6).

Mutational events:

fst1.a in Kamairazu (OUL008, GSHO 629) (6); *fst1.d* in a Western Plant Breeders selection (2).

Mutant used for description and seed stocks:

fst1.a in Kamairazu (GSHO 629, GSHO 858, OUL008); *fst1.a* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2100); *fst1.a* in Bowman*6 (BW372, NGB 20611); *fst1.d* in Bowman*7 (GSHO 2101, BW373, NGB 20612).

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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7. Yoshimi, R., and T. Konishi. 1995. Linkage analysis of several isozyme loci in barley. Barley Genet. Newsl. 24:35-37.

Prepared:
T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:160.

Revised:
J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:252.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:122-123.

BGS 329, Breviaristatum-h, *ari-h*

Stock number: BGS 329
Locus name: Breviaristatum-h
Locus symbol: *ari-h*

Previous nomenclature and gene symbolization:

Breviaristatum-127 = *ari-127* (4, 5).
Short awn 11 = *lk11* (6).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5HL (2); *ari-h.127* is very close to the *Raw1* (Rough awn 1) locus based on linkage drag (2). The SNP marker data for Bowman backcross-derived stock for *ari-h.127* (BW046, NGB20454) is incorrect as the heterogeneity pattern in 2H does not match that associated with other mutants in 2H induced in the cultivar Foma. Instead the pattern matches a mutant induced in Glenn, *cur5.h* (BGS 231) (3).

Description:

Awns are about 3/4 normal length, but plant height is normal (5). Phenotypic comparisons of BW046 with Bowman indicate the Bowman backcross-derived seed stock used for *ari-h.127* was incorrect (3).

Origin of mutant:

An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (5).

Mutational events:

ari-h.127 (NGB115939, GSHO 1656) in Foma (NGB 14659, CIho 11333) (5).

Mutant used for description and seed stocks:

ari-h.127 (NGB115939, GSHO 1656) in Foma; *ari-h.127* in Bowman (PI 483237)*6 (GSHO 2125) is a correct stock.

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:277.

Revised:

J.D. Franckowiak and U. Lundqvist. 2018. Barley Genet. Newsl. 48:124.

BGS 336, Globosum-b, *glo-b*

Stock number: BGS 336
Locus name: Globosum-b
Locus symbol: *glo-b*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HL (3, 4); *glo-b.1001* is over 31.9 cM proximal from the *ari-e* (breviaristatum-e) locus (7); *glo-b.1002* is associated with SNP markers 1_1198 to 2_1244 (positions 73.70 to 91.91 cM) in 5H bins 04 to 05 of the Bowman backcross-derived line BW393, and with SNP markers 2_0715 to 2_1453 (positions 213.08 to 245.71 cM) in 2H bins 13 to 15 of BW393 (1).,+,+66666--

Description:

Kernels are globe-shaped, plants are stunted (2/3 normal height), and 1000-kernel weights are low (3, 6). Plants in the Bowman backcross-derived line for *glo-b.1002* (BW393) have some brachytic traits (short culms, leaf blades, and awns) and slightly coiled leaf blades and awns (2). Plants of the Bowman backcross-derived line for *glo-b.1002* (BW393) were half as tall as Bowman and headed 1 to 3 days later. Peduncle lengths for BW393 were about 1/2 normal, awns were 40% shorter, rachis internodes were shorter, 30 vs. 44 mm, and leaf blades were shorter and wider. BW393 has fewer kernels per spike than Bowman, 19 vs. 23. Kernels of BW393 were shorter and lighter, 35 vs. 56 mg, test weight was about 20% lower, and grain yields were 50 to 80% lower (2).

Origin of mutant:

An X-ray induced mutant in Villa (PI 399506) (3, 4).

Mutational events:

glo-b.1001 (1345/72, GSHO 1327) in Villa (PI 399506), *glo-b.1002* (916/65, GSHO 1326) in Donaria (PI 161974) (3, 4, 7); *glo-b.1005* (859/74) in Villa (4, 7); *glo-b.1007* (1296/65) in Donaria (3, 5); *glo-b.1011* (1786/67) in Proctor (PI 280420) (6); *glo-b.1012* (1055/74) in Villa (7).

Mutant used for description and seed stocks:

glo-b.1002 (GSHO 1326) in Donaria; *glo-b.1002* in Bowman (PI 483237, NGB 22812)*7 (GSHO 2095, BW393, NGB 20631).

References:

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globe shaped grains. Barley Genet. Newsl. 18:54-58.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:284.

Revised:

J.D. Franckowiak and U. Lundqvist. 2018. Barley Genet. Newsl. 48:125-126.

BGS 342, Globosum-f, *glo-f*

Stock number:	BGS 342
Locus name:	Globosum-f
Locus symbol:	*glo-f*

Previous nomenclature and gene symbolization:

Globosum-e = *glo-e* (1).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 5HL (1).

Description:

The *glo-f.305* plants were much shorter than the mother cultivar and produced small kernels that were short and round or globe-shaped. Seedlings had short first leaves and coleoptiles; *glo-f.305* plants had a much shorter first leaf than *glo-f.307* plants. Spikes were shorter than normal, but awn length was not reduced (2).

Origin of mutant:

A N-methyl-N-nitrosurea induced mutant in Damazy (PI 467445) (2).

Mutational events:

glo-f.305 (D7305a, 4704) in Damazy (PI 467445); *glo-f.307* (D7307, 4979) in Damazy (1, 2).

Mutant used for description and seed stocks:

glo-f.305 (D7305a, 4704) in Damazy.

References:

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2. Sodkiewicz, T., and A.G. Gorney. 1982. Barley mutants with long-shaped and globe-shaped grains. Barley Genet. Newsl. 12:4-7.

Prepared:

G. Fischbeck and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:291.

Revised:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:127.

BGS 366, Male sterile genetic 10, *msg10*

Stock number:	BGS 366
Locus name:	Male sterile genetic 10
Locus symbol:	*msg10*

Previous nomenclature and gene symbolization:

Male sterile 3 = *ms3* (6).
Male sterile 10 = *ms10* (4).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 7HS (2, 5); *msg10.ay* is about 7.2 cM distal from the *nud1* (naked caryopsis 1) locus (3, 8); *msg10.ay* is about 14.1 cM from the *lks2* (short awn 2) locus (3); *msg10.ay* is about 2.0 cM from the *msg14* (male sterile genetic 14) locus (3); *msg10.ay* is about 3.9 cM from the *blx2* (non-blue aleurone 2) locus (9); *msg10.ay* is associated with SNP markers 1_0056 to 2_0485 (positions 51.93 to 84.97 cM) in 7H bins 04 to 07 in a homozygous male sterile plant from Bowman backcross-derived line BW546 (1).

Description:

Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (10).
Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (10).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (6).

Mutational events:

msg10.ay (MSS058, GSHO 1811) in Compana (PI 539111) (6, 7); *msg10.cj* (MSS059) in Manchuria (CIho 2330)*9 (4, 7).

Mutant used for description and seed stocks:

msg10.ay (GSHO 1811) in Compana; *msg10.ay* in Bowman (PI 483237, NGB 22812)*7 (GSHO 1835, BW546, NGB 23471).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:181-182.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:314.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:142-143.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:128-129.

BGS 382, Shrunken endosperm xenia 1, *sex1*

Stock number:	BGS 382
Locus name:	Shrunken endosperm xenia 1
Locus symbol:	*sex1*

Previous nomenclature and gene symbolization:

Shrunken endosperm 6 = *se6* (2, 7).
Shrunken endosperm 6 = *se6f* (7).
High lysine 5 = *lys5* (9, 10).

Inheritance:

Monofactorial recessive (2, 7, 9).

Located in chromosome 6HL (3, 9, 12); *sex1.a* is about 5.6 cM proximal from the *msg36* (male sterile genetic 36) locus (2, 4); *sex1.a* is associated with SNP markers 1_0244 to 1_1246 (positions 71.39 to 134.55 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW844 (1); *sex1.e* (*lys5.g*) is associated with SNP markers 2_1158 to 2_0746 (positions 88.73 to 125.86 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW845 (1); *sex1.k* is associated with SNP markers 1_0427 to 1_0040 (positions 56.54 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW841 (1); *sex1.a* is located in a 4.2 cM interval between the EST-derived markers GBM5012 and GBM1063 (11); at about 163 Mb.

Description:

After the hard dough stage, kernels develop a depression in the center of the lemma which becomes progressively more distinct with maturity. The 100-kernel weight of the mutant is about 75% of normal. The mature endosperm appears harder than normal endosperm. The mutant expresses xenia and kernels from heterozygous plants can be classified as normal or shrunken with an expected 3:1 ratio. Establishment and growth of mutant plants is normal (6, 8). Mutant plants have a higher lysine content in the endosperm than normal sibs (10, 14). Compared to Bowman, the Bowman backcross-derived lines for *sex1.e* (BW845) and *sex1.k* (BW841) exhibited a 10 to 20% reduction in kernel weights. Other characteristics were similar to those of Bowman (5).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (6, 7).

Mutational events:

sex1.a (GSHO 755) in Compana (PI 539111) (6, 12); *lys5.f* (Risø 13) in Bomi Abed (NGB 5096, PI 43371), *sex1.d* or *lys5.h* (Risø 86); *sex1.e* or *lys5.g* (Risø 29, GSHO 2474) in Carlsberg II (NGB 5085, CIho 10114) (10, 12); a variant, named *sex1.k*, observed in the progeny of a Bowman*4/Volla mutant 7175 retained in subsequent crosses to Bowman parental SNP markers in 6H and the *sex1* phenotype (5).

Mutant used for description and seed stocks:

sex1.a (GSHO 755) in Compana; *sex1.e* from Risø 29 in Bowman (PI 483237)*3 (GSHO 2071); *sex1.e* in Bowman*5 (BW845, NGB 22282); *sex1.a* in Bowman *7 (BW844, NGB 22281); *sex1.k* in Bowman*7 (BW841, NGB 22278).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

A.J. Jarvi and R.F. Eslick. 1971. Barley Genet. Newsl. 1:193.

Revised:

R.F. Eslick and E.A. Hockett. 1976. Barley Genet. Newsl. 6:140.
T. Tsuchiya. 1980. Barley Genet. Newsl. 10:129.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:330.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:130-131.

BGS 385, Male sterile genetic 24, *msg24*

Stock number:	BGS 385
Locus name:	Male sterile genetic 24
Locus symbol:	*msg24*

Previous nomenclature and gene symbolization:

Male sterile v = *msg,,v* (6, 7).

Male sterile 24 = *ms24* (3, 6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 4HL (6); *msg24.v* is about 11.2 cM proximal from the *blx1* (non-blue aleurone xenia 1) locus (9, 10); the plant of the Bowman backcross-derived line for *msg24.v* stock, BW559, evaluated for SNP markers did not have any deviant markers in 4H from those of Bowman (2).

Description:

Selfing - none (3, 6).

Outcrossing - complete female fertility (6).

Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (4).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (7).

Mutational events:

msg24.j (MSS078) in Betzes/Domen (CIho 13639) (7); *msg24.v* (MSS089, GSHO 2376) in Betzes (PI 129430 (7, 8); *msg24.ak* in Betzes (MSS302) (3, 7); *msg24.an* in Betzes (MSS305) (3, 8); *msg24.at* (MSS312) in OAC21 (CIho 1470), *msg24.bc* in Betzes (MSS317) (4, 8); *msg24.hg* (MSS460) in an unknown cultivar (1, 5).

Mutant used for description and seed stocks:

msg24.v (GSHO 2376) in Betzes; *msg24.v* in Bowman (PI 483237, NGB 22812)*7 (GSHO 2018, BW559, NGB 23427).

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Prepared:
E.A. Hockett. 1973. Barley Genet. Newsl. 3:123.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:333.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:164-165.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:132-133.

BGS 389, Desynapsis 10, *dsp10*

Stock number:	BGS 389
Locus name:	Desynapsis 10
Locus symbol:	*des10*

Previous nomenclature and gene symbolization:

Desynapsis p = *des,,p* (3, 5).

Hordeum vulgare MutL-Homolog 3 = *HvMlh3* (1).

Inheritance:

Monofactorial recessive (4, 6).

Located in chromosome 5HL (2); *des10.p* is associated with SNP markers 2_0127 to 2_0259 (positions 189.08 to 203.85 cM) in 5H bins 10 to 11 of the Bowman backcross-derived line BW230 (2); *des10.p* is between SNP markers 11_11273 (BOPA1_ABC11221-1-3-410 and 11_21203 (BOPA1_7167-466) in BAC contig (contig_38558) (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis was 2.0, ranging from 7 ring bivalents (d = 0) to 3 ring bivalents plus 2 rod bivalents plus 4 univalents (d = 6). Ovule fertility was 60 to 80% (5). Plants of the Bowman backcross-derived line for *des10.p*, BW230, were similar to Bowman except that reduced seed set decreased grain yields to about half that of Bowman (3). The *des10.p* phenotype is the result of a mutation in the mismatch repair gene encoding HvMutL-homolog 3 (*HvMlh3*) (1). Compared with wild-type, *des10* mutants exhibit reduced recombination and fewer chiasmata, resulting in the loss of obligate crossovers and leading to chromosome mis-segregation. Normal synapsis progression was disrupted in *des10* mutants, leading to occasional aberrant chromosome segregation at anaphase I, genetically unbalanced tetrads, and a subsequent semi-fertile phenotype (1).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (6).

Mutational events:

des10.p (GSHO 601) in Betzes (4, 6).

Mutant used for description and seed stocks:

des10.p in Betzes (GSHO 601); *des10.p* in Bowman*6 (BW230, NGB 22057).

References:

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Barley Genet. Newsl. 2:65-68.

Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1974. Barley Genet. Newsl. 4:138.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:337.
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:152.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:134-135.

BGS 400, Eceriferum-e, *cer-e*

Stock number:	BGS 400
Locus name:	Eceriferum-e
Locus symbol:	*cer-e*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 1HL (2, 14); *cer-e.8* is close to the centromere and near the *ert-b* (erectoides-b) locus (4, 14, 15); *cer-e.8* is associated with SNP markers 1_0764 to 1_1326 (positions 61.55 to 82.35 cM) in 1H bins 06 to 08 of the Bowman backcross-derived line BW109 (1), likely in 1H bin 08.

Description:

Surface wax coating on the spike appears absent or greatly reduced (wax code -/+ ++ ++) (5). A translocation is present in the allele *cer-e.18*, but it is not linked to the *cer-e* locus (5). The Bowman backcross-derived line for *cer-e.8* (BW109) has less wax on the spike and upper leaf sheath (wax code - + ++). Plants of BW109 had slightly longer awns and rachis internodes than Bowman. Kernels weights were slightly lower, but grain yields were equivalent (3).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (5).

Mutational events:

cer-e.8 (NGB 110892, GSHO 1518), *-e.18* (trans) (NGB 110902), *-e.34* (NGB 110918) in Bonus (NGB 14657, PI 189763) (5, 6); *cer-e.90* (NGB 110974), *-e.140* (NGB 111025) in Bonus, *-e.272* (NGB 111159), *-e.294* (NGB 111181), *-e.388* (NGB 111275), *-e.551* (NGB 111439), *-e.560* (NGB 111448), *-e.586* (NGB 111474), *-e.607* (NGB 111495) in Foma (NGB 14659, CIho 11333) (6); *cer-e.273* (NGB111160), *-e.277* (NGB 111164), *-e.296* (NGB 111183), *-e.317* (NGB 111204), *-e.321* (NGB 111208), *-e.473* (NGB 111361), *-e.480* (NGB 111369) in Foma (6, 13); *cer-e.663* (NGB 111551), *-e.692* (NGB 111580), *-e.716* (NGB 111604), *-e.717* (NGB 111605) in Bonus (6); *cer-e.161* (NGB 111047) in Bonus, *-e.577* (NGB 111465) in Foma, *-e.790* (NGB111678) in Bonus, *-e.1089* (NGB111977), *-e.1106* (NGB111994) in Kristina (NGB 14661, NGB 1500) (7); *cer-e.908* (NGB 111796), *-e.962* (NGB 111850) in Bonus, *-e.1162* (NGB 111050) in Kristina (8); *cer-e.1335* (NGB 112223) in Bonus (9); *cer-e.1366* (NGB 112254), *-e.1404* (NGB 112292), *-e.1425* (NGB 112313), *-e.1426* (NGB 112314) in Bonus (10); *cer-e.1403* (NGB 112291), *-e.1709* (NGB 112522), *-e.1715* (NGB 112528) in Bonus (11); *cer-e.1519* (NGB 112532) in Nordal (NGB 13680, NGB 4704), *-e.1760* (NGB 112575) in Bonus, *-e.1873* (NGB 117421), *-e.1878* (NGB 117426), *-e.1880* (NGB 117428), *-e.1884* (NGB 117432) in Sv 79353 (12).

Mutant used for description and seed stocks.

cer-e.8 (NGB 110892, GSHO 1518) in Bonus; *cer-e.8* via Wolfe's Recessive Marker Stock 5.2 in Bowman (PI 483237, NGB 22812)*7 (GSHO 2048, BW109, NGB 20515).

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9. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.
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11. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
12. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.
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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:118.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:347.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:102-103.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:136-137.

BGS 401, Eceriferum-f, *cer-f*

Stock number: BGS 401
Locus name: Eceriferum-f
Locus symbol: *cer-f*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 1H (1); *cer-f.9* is associated with SNP markers 1_0764 to 2_1126 (positions 61.51 to 110.10) in 1H bins 06 to 10 of the Bowman backcrossed-derived line BW110 (1). Previously *cer-f.9* was located in chromosome 7H (8); *cer-f.9* is near the centromere and about 4.5 cM proximal from the *ert-d* (erectoides-d) locus (8, 9, 10); *cer-f.9* is about 6.3 cM distal from the *nud1* (naked caryopsis 1) locus (9, 10).

Description:

In the original stock surface wax coating on the spike, leaf sheath, and stem is reduced (wax code + + ++) (3). Reduced surface wax coating was apparent only on the spike (wax code + ++ ++) in the Bowman backcross-derived line for *cer-f.9* (BW110). Plants of BW110 were slightly taller than Bowman. Kernel weights varied from slightly lower to slightly more; grain yields were slightly less (2). Allelism tests need to be conducted to confirm that BW110 has the *cer-f.9* mutant.

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

cer-f.9 (NGB 110893, GSHO 427) in Bonus (NGB 14657, PI 189763) (3, 4); *cer-f.230* (NGB 111117) in Foma (CIho 11333) (4, 7); *cer-f.1002* (NGB 111890) in Carlsberg II (CIho 10114) (4); *cer-f.763* (NGB 111651) in Bonus (5); *cer-f.1423* (NGB 112311) in Bonus (6).

Mutant used for description and seed stocks:

cer-f.9 (GSHO 427, NGB 110893) in Bonus; *cer-f.9* in Bowman (PI 483237, NGB 22812)*6 (GSHO 1846); *cer-f.9* in Bowman*7 (BW110, NGB 20516).

References:

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Prepared:
U. Lundqvist. 1975. Barley Genet. Newsl. 5:119.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:348.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:104-105.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:138-139.

BGS 422, Eceriferum-zd, *cer-zd*

Stock number:	BGS 422
Locus name:	Eceriferum-zd
Locus symbol:	*cer-zd*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (8).

Located in chromosome 3HL (2, 9); *cer-zd.67* is about 9.4 cM proximal from the uzu1 (uzu 1) locus (10, 11, 12, 13); *cer-zd.67* is about 4.6 cM distal from the breakpoint in the ert-c.1 (erectoides-c) line (10, 11, 12, 13); *cer-zd.67* is associated with SNP markers 1_0672 to 1_0281 (positions 58.56 to 98.41) in 3H bins 04 to 06 of the Bowman backcross-derived line BW160 (1), likely in 3H bin 05. The BW160 line for cer-zd.67 had only three crosses to Bowman; thus, probably unassociated DNA segments with donor parent markers were retained in chromosomes 1H, 3HL, 5HS, 5HL, and 7H (1, 3).

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (8). Concerning the chemical epicuticular wax composition, the amount of wax cm^{-2} is reduced and is accompanied by a decrease of the size and morphological complexity of the wax bodies. The bodies are smaller, simpler, and less dense. The wax class distribution is the same as in the mother cultivar (14). Plants of the Bowman backcross-derived line for *cer-zd.67* (BW160) were 10 to 15% shorter than Bowman and headed about 2 days later. Kernels of BW160 were slightly thinner and 10 to 15% lighter. Grain yields were about 2/3 of normal (3).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (8).

Mutational events:

cer-zd.67 (NGB 110951, GSHO 451) in Bonus (NGB 14657, PI 189763) (4, 8); *cer-zd.592* (NGB 111480) in Foma (NGB 14659, CIho 11333), *-zd.665* (NGB 111553), *-zd.668* (NGB 111556) in Bonus (4); *cer-zd.946* (NGB 111834) in Bonus (5); *cer-zd.1351* (NGB 112239) in Bonus (6); *cer-zd.1356* (NGB 112244) in Bonus (7).

Mutant used for description and seed stocks:

cer-zd.67 (GSHO 451, NGB 110951) in Bonus; *cer-zd.67* in Bowman (PI 483237, NGB 22812)*2 (GSHO 1962); *cer-zd.67* in Bowman*3 (BW160, NGB 21992).

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Barley Genet. Newsl. 12:169-172.
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Prepared:

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Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:373.
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BGS 425, Eceriferum-zg, *cer-zg*

Stock number:	BGS 425
Locus name:	Eceriferum-zg
Locus symbol:	*cer-zg*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4HL (7); *cer-zg.214* is about 7.0 cM distal from the *lks5* (short awn 5, *ari-c*) locus (1, 2, 3, 8); *cer-zg.214* is about 14.0 cM distal from the *lbi2* (long basal rachis internode 2) locus (8).

Description:

Surface wax coating on the leaf blade is reduced, but only on the three upper leaf blades (wax code ++ ++ +) (6). Identification of the mutant phenotype was difficult in progeny from crosses to Bowman; thus the Bowman backcross-derived line for *cer-zg.214* (BW163) likely does not contain this mutant depending on environmental situations.

Origin of mutant:

An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (6).

Mutational events:

cer-zg.214 (NGB 111105, GSHO 454) in Foma (NGB 14659, CIho 11333) (4, 6); *cer-zg.1195* (NGB 112083) in Kristina (NGB 14661) (5).

Mutant used for description and seed stocks:

cer-zg.214 (NGB 111105, GSHO 454) in Foma; *cer-zg.214* in Bowman (PI 483237, NGB 22812)*2 (BW163, NGB 21995).

References:

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:143.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:377.

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:142-143.

BGS 433, Eceriferum-zp, *cer-zp*

Stock number: BGS 433
Locus name: Eceriferum-zp
Locus symbol: *cer-zp*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5HL (7); *cer-zp.313* is about 7.5 cM distal from the *ert-g* (erectoides-g) locus (8, 9, 10); *cer-zp.313* is about 8.9 cM proximal from the *cer-t* (eceriferum-t) locus (9, 10); *cer-zp.313* is associated with SNP markers between 1_1198 to 2_0850 (positions 73.70 to 157.13 cM) in 5H bins 04 to 09 of the Bowman backcross-derived line BW171 (1), likely in 5H bin 09.

Description.

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -). Plant vigor is reduced, leaf blades are narrow and rolled inward, and they are maculated with dark and light green zones (6). Expression of the maculated trait is less pronounced in the Bowman backcross-derived line for *cer-zp.313* (BW171), and the plant vigor is better. Plants of the Bowman backcross-derived line for *cer-zp.313* (BW171) were 5 to 10% shorter and had 2 to 3 fewer kernels per spike. Kernels of BW171 were 5 to 10% lighter, and grain yields were about 75% of those for Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (6).

Mutational events:

cer-zp.313 (NGB 111200, GSHO 463), *-zp.382* (NGB 111269), *-zp.397* (NGB111274), *-zp.404* (111292) in Foma (NGB 14659, CIho 11333) (3, 6); *cer-zp.1205* (NGB 112093) in Kristina (NGB 14661, NGB 1500) (4); *cer-zp.1795* (NGB 117343), *-zp.1796* (NGB 117344) in Bonus (NGB 14657, PI 189763) (5).

Mutant used for descriptions and seed stocks:

cer-zp.313 (NGB 111200, GSHO 463) in Bonus; *cer-zp.313* in Bowman (PI 483237, NGB 22812)*7 (GSHO 2114, BW171, NGB 22003).

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:151.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:385.

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:144-145.

BGS 434, Eceriferum-zq, *cer-zq*

Stock number: BGS 434
Locus name: Eceriferum-zq
Locus symbol: *cer-zq*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (7).

Location is unknown. The one donor parent SNP marker retained in the Bowman backcross-derived line for *cer-zq.248* (BW172) was not mapped (1).

Description:

Surface wax coating on the leaf blades appears absent, but only on the three upper leaf blades (wax code ++ ++ -) (7). Plants of the original stock remain as a vegetative tuft for a long time before heading (7). Plants of the Bowman backcross-derived line for *cer-zq.248* (BW172) had thin, short culms, about 70% of normal. Comparing BW172 plants to Bowman plants, awns were 2/3 normal, leaf blades were shorter and narrower, and spikes had few kernels, 16 vs. 22. BW172 plants headed about 3 days later and were very susceptible to lodging at maturity. Kernels of BW172 were thinner, 3.6 vs. 3.9 mm, and about 25% lighter. Average grain yield was less than 50% of that for Bowman (2).

Origin of mutant:

A diethyl sulfate induced mutant in Foma (NGB 14659, CIho 11333) (7).

Mutational events:

cer-zq.248 (NGB 111135, GSHO 1524) in Foma (NGB 14659, CIho 11333) (3, 7); *cer-zq.761* (NGB 111649) in Bonus (NGB 14657, PI 189763) (4); *cer-zq.1343* (NGB 111231) in Bonus (3); *cer-zq.1378* (NGB 112266) in Bonus (6).

Mutant used for description and seed stocks:

cer-zq.248 (GSHO 1524, NGB 111135) in Foma; *cer-zq.248* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2202); *cer-zq.248* in Bowman*7 (BW172, NGB 22004).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:152.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:386.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:146-147.

3BGS 454, Non-blue aleurone xenia 5, *blx5*

Stock number: BGS 454
Locus name: Non-blue aleurone xenia 5
Locus symbol: *blx5*

Previous nomenclature and gene symbolization:

Non-blue aleurone 5 = *bl5* (1).

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1, Blx2, Blx3,* and *Blx4* loci (1).

Located in chromosome 7HL (1, 5); *Blx5* is associated with a red stem trait controlled by the dominant allele at the *ant5* (anthocyanin-less 5) locus (1); *blx5.e* is weakly linked to the *blx2* (non-blue aleurone xenia 2) locus, but not to the *fch12* (chlorina seedling 12) locus (5).

Description:

Blue aleurone color is due to anthocyanin pigments (4), which occur as lumps inside many aleurone granules in some or all aleurone cells (1). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (1, 2). Aleurone color is best observed in well filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (3). Treatment of cut kernels with a 10% HCl solution was used to determine presence of anthocyanin in the aleurone layer (5).

Origin of mutant:

Natural occurrence in BGM 122 (GSHO 2509) (1).

Mutational events:

blx5.e in BGM 122 (GSHO 2509) (1).

Mutant used for description and seed stocks:

blx5.e in BGM 122 (GSHO 2509).

References:

1. Finch, R. A., and E. Simpson. 1978. New colours and complementary colour genes in barley. Z. Pflanzenzücht. 81:40-53.
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Prepared:

R.A. Finch. 1978. Barley Genet. Newsl. 8:167.

Revised:

J.D. Franckowiak and R.A. Finch. 1997. Barley Genet. Newsl. 26:404
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:148.

BGS 455, Shrunken endosperm genetic 8, *seg8*

Stock number: BGS 455
Locus name: Shrunken endosperm genetic 8
Locus symbol: *seg8*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 7H (7); *seg8.k* in a 4.6 cM interval flanked by markers GBM1516 and Bmag341 (9); *seg8.k* is associated with SNP markers 1_0772 to 1_0169 (positions 71.81 to 142.56 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW840 (1), likely in 7H bin 07 at about 88 Mb.

Description:

Seed size is reduced and maturity is delayed. Seed weights of 24, 23, and 27% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (8). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg8.k* plants can be used to establish stands under field conditions (7). Endosperms of *seg8.k* plants developed as two-filled lateral lobes with no central endosperm lobe, resulting in a distinct dorsal crease (2). This is evidence that the endosperm is divided into three lobes as explained by the phytomeric triad model (4). Kernels of the Bowman backcross-derived line for *seg8.k*, BW840, were very thin 3.0 vs. 3.8 mm in width and weighed much less, 1.7 vs. 5.6 mg, compared to those of Bowman. BW840 plants were similar to Bowman morphologically, but their grain yield was about 1/20 that of Bowman (3). The *seg8.k* mutant has defective endosperm development, reduced starch synthesis, and elevated monosaccharide concentrations, which resulted in higher early seed development-specific (ESD) β-amylase mRNA levels and enzyme activities in seg8.k compared to wild type (5).

Origin of mutant:

A spontaneous mutant in 60Ab1810-53 (CIho 15686) (8).

Mutational events:

seg8.k (GSHO 2469) in 60Ab1810-53 (CIho 15686) (7, 8).

Mutant used for description and seed stocks:

seg8.k (GSHO 2469) in 60Ab1810-53; *seg8.k* in Bowman (PI 483237)*3 (GSHO 1854); *seg8.k* in Bowman*5 (BW840, NGB 22277).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D., B.P. Forster, U. Lundqvist, J. Lyon, I. Pitkethly, and W.T.B. Thomas. 2010. Developmental mutants as a guide to the barley phytomer. pp. 46-60. In: S. Ceccarelli and S. Grando (eds.), Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt. ICARDA, PO Box 5466, Aleppo, Syria.

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7. Ramage, R.T., and C.L. Crandall. 1981. Shrunken endosperm mutant *seg8*. Barley Genet. Newsl. 11:34.
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Prepared:
R.T. Ramage and C.L. Crandall. 1981. Barley Genet. Newsl. 11:103 as BGS 453.

Revised:
R.T. Ramage. 1983. Barley Genet. Newsl. 13:116 as BGS 453.
T. Tsuchiya. 1983. Barley Genet. Newsl. 13:117. BGS number changed to BGS 455.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:405.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:272.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:150-151.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:170-171.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:149-150.

BGS 477, Laxatum-f, *Lax-f*

Stock number:	BGS 477
Locus name:	Laxatum-f
Locus symbol:	*Lax-f*

Previous nomenclature and gene symbolization:

Laxatum-61 = *Lax-61* (3, 4).

Inheritance:

Monofactorial dominant (5).

Location is unknown.

Description:

Rachis internodes of *Lax-f.61* were about 14% longer than those of Bonus; and the mutants had lower kernel weights (4).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

Lax-f.7 (NGB 116341), *-f.61* (NGB 116395) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6, 7).

Mutant used for description and seed stocks:

Lax-f.7 (NGB 116341) and *Lax-f.61* (NGB 116395) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).
7. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:60.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:140.

U. Lundqvist. 2018. Barley Genet. Newsl. 48:151.

BGS 496, Laxatum-mf, *Lax-mf*

Stock number:	BGS 496
Locus name:	Laxatum-mf
Locus symbol:	*Lax-mf*

Previous nomenclature and gene symbolization:

Laxatum-302 = *Lax-302* (3, 4).

Inheritance:

Monofactorial dominant (5), but partially sterile F1 plants indicated that a translocation was present in *Lax-mf.302* (5).

Location is unknown.

Description:

Rachis internodes of *Lax-mf.302* were about 15% longer than those of Foma (4). Plants had few tillers and matured late. Compared to Foma, spikes were short and kernels weighed less (4, 5).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

Lax-mf.300 (NGB 116524), *-mf.301* (NGB 116525), *-mf.302* (NGB 116526) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6,).

Mutant used for description and seed stocks:

Lax-mf.302 (NGB 116526) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:79.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:165.
U. Lundqvist. 2018. Barley Genet. Newsl. 48:152.

BGS 512, Reaction to *Puccinia graminis* 2, *Rpg2*

Stock number:	BGS 512
Locus name:	Reaction to *Puccinia graminis* 2 (wheat stem rust)
Locus symbol:	*Rpg2*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia graminis tritici* = *T2* (5).

Resistance to *Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn = *Rpg2b* (4).

Inheritance:

Monofactorial dominant (6, 9); incomplete dominant to race QCC (3).

Located in chromosome 2HL (1, 2); *Rpg2.b* is in a 2 cM region proximal from the *Eam6* (Early maturity 6 or Praematurum-c) locus and is near the centromere (1, 2).

Description:

Moderate resistance to some races of *Puccinia graminis* f. sp. *tritici* is conferred by the *Rpg2.b* gene. Percent stem and leaf sheath infection and lesion size in adult plants are reduced compared with susceptible plants under field conditions (6, 9, 11). Patterson (6) used linkage data to demonstrate that the *Rpg2* locus differs from the *Rpg1* locus. Hietpas 5 exhibits a moderate-to-high level of adult plant resistance (APR) to races QCCJB and MCCFC and a mostly susceptible seedling phenotype (1). Seedling tests with wheat and rye stem rust isolates were ineffective in rapidly detecting resistance conferred by Hietpas 5 (12). Hietpas 5 had low adult plant reactions to African stem rust isolates TTKSK and PTKST (10).

Origin of mutant:

A spontaneous mutant in Oderbrucker (CIho 4666) isolated in Wisconsin, USA by Mr Hietpas and named Hietpas 5 (CIho 7124, GSHO 1584) (6, 9).

Mutational events:

Rpg2.b in Hietpas 5 (CIho 7124, GSHO 1584) (6). *Rpg2.b* is likely associated with the QTL Rpg-qtl-HH-Hie-2H.3 QTL, reported in wild barley by Sallam et al., (8) in chromosome 2H (2).

Mutant used for description and seed stocks:

Rpg2.b in Hietpas 5 (CIho 7124, GSHO 1584).

References:

1. Case, A., 2017. Genetics, sources, and mapping of stem rust resistance in barley. Ph.D. Dissertation, University of Minnesota, St. Paul, MN.
2. Case, A.J., S. Bhavani, G. Macharia, Z. Pretorius, V. Coetzee, F. Kloppers, P. Tyagi, G. Brown-Guedira, and B.J. Steffenson. 2018. Mapping adult plant stem rust resistance in barley accessions Hietpas-5 and GAW-79. Theor. Appl. Genet. 131:2245-2266.
3. Fox, S.L., and D.E. Harder. 1995. Resistance to stem rust in barley and inheritance of resistance to race QCC. Can J. Plant Sci. 75:781-788.
4. Franckowiak, J.D. 1991. BGS 512, Resistance to *Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn., *Rpg2b*. Barley Genet. Newsl. 20:116.
5. Miller, J.D., and J.W. Lambert. 1955. Variability and inheritance of reaction of barley to race 15B of stem rust. Agron. J. 47:373-377.
6. Patterson, F.L. 1951. Adult plant and seedling reactions of barley varieties and hybrids to 3 races of *Puccinia graminis tritici.* Ph.D. Thesis. Univ. of Wisconsin, Madison.
7. Patterson, F., R. Shands, and J. Dickson. 1957. Temperature and seasonal effects on seedling reactions of barley varieties to three races of *Puccinia graminis* f. sp. *tritici*. Phytopathology 47:395-402.

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Prepared:
J.D. Franckowiak. 1991. Barley Genet. Newsl. 20:116.

Revised:
J.D. Franckowiak and B.J. Steffenson. 1997. Barley Genet. Newsl. 26:439.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:153-154.

BGS 519, Many-noded dwarf 1, *mnd1*

Stock number:	BGS 519
Locus name:	Many-noded dwarf 1
Locus symbol:	*mnd1*

Previous nomenclature and gene symbolization:

Many noded dwarf = *m* (3, 5).

Inheritance:

Monofactorial recessive (3, 4, 5).

Located in chromosome 2HS (2, 6, 7); *mnd1.a* is over 12.0 cM from the *Pre2* (Red lemma and pericarp 2) locus (6); *mnd1.a* is associated with SNP markers 1_0638 to 1_0624 (positions 86.79 to 96.47 cM) in 2H bin 07 of the Bowman backcross-derived line BW518 (2).

Description:

When grown in the field, plants are about 1/2 normal height with numerous tillers. Each tiller has 12 to 20 small leaves and a spike of 1/2 normal size or less. Additional tillers with 4 to 7 leaves may develop at the uppermost tiller nodes, but these secondary and tertiary culm branches develop late and have very small spikes (3). When grown in the greenhouse, plants are taller and later than normal sibs and each tiller may have 15 to 20 nodes. The rate of primordium initiation is normal, but their expansion into leaves is much more rapid (1).

Origin of mutant:

A spontaneous mutant (CIho 2328) in Mesa (CIho 1313) (3).

Mutational events:

mnd1.a (GSHO 253, CIho 2328) in Mesa (CIho 1313) (3).

Mutant used for description and seed stocks:

mnd1.a (GSHO 253, CIho 2328) in Mesa; *mnd1.a* in CIho 6794 and CIho 6871 (tester stocks developed by M. Martini); *mnd1.a* from R.I. Wolfe's Multiple Recessive Marker Stock for chromosome 2 in Bowman (PI 483237)*9 (GSHO 2038, BW518, NGB 20746).

References:

1. Cooper, J.P. (Unpublished).
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Harlan, H.V., and M.N. Pope. 1922. Many-noded dwarf barley. J. Hered. 13:269-273.
4. Hor, K.S. 1922. A new variety of barley with striking characteristics. Science 55:378.
5. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
6. LeBaron, F.C. 1959. An inheritance and linkage study of 19 factor pairs in barley. M.S. Thesis, Utah State Univ. Pp. 56.
7. Wolfe, R.I. (Personal communications placing *mnd1.a* in a multiple recessive marker stock for chromosome 2H.)

Prepared:

J.P. Cooper and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:446.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:154.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:155.

BGS 533, Eceriferum-yt, *cer-yt*

Stock number:	BGS 533
Locus name:	Eceriferum-yt
Locus symbol:	*cer-yt*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 1HL or 5HL (1); *cer-yt.938* is associated with SNP markers 1_0516 to 2_1126 (positions 96.74 to 110.10 cM) in 1H bins 09 to 10 and markers 1_0622 to 1_1273 (positions 158.46 to 171.34 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW151 (1).

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (4). In the Bowman backcross-derived line for *cer-yt.758* (BW151), culm nodes appear visually to lack surface wax coating. Most other morphological traits of plants of the line BW151 were similar to those of Bowman, except for kernel weights were 10 to15% lower. Grain yields varied from equal to 50% lower (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

cer-yt.758 (NGB 111646), *-yt.938* (NGB 111826, GSHO 1553), *-yt.1333* (NGB 112221) in Bonus (NGB 14657, PI 189763) (4); *cer-yt.1127* (NGB 112015), *-yt.1304* (NGB 112192) in Kristina (NGB 14661, NGB 1500), *-yt.1427* (NGB 112315), *-yt.1458* (NGB112346), *-yt.1493* (NGB 112381), *-yt.1766* (NGB 112581), *-yt.1822* (NGB 117370) in Bonus (5); *cer-yt.1379* (NGB 112267) in Bonus (6).

Mutant used for description and seed stocks:

cer-yt.938 in Bonus (GSHO 1553, NGB 111826); *cer-yt.938* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2223); *cer-yt.938* in Bowman*7 (BW151, NGB 21963).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
5. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
6. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:460.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:126.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:156.

BGS 534, Eceriferum-yu, *cer-yu*

Stock number:	BGS 534
Locus name:	Eceriferum-yu
Locus symbol:	*cer-yu*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located probably in chromosome 1H (1); *cer-yu.159* is associated in centromeric region with SNP markers between 1_0275 to 2_1126 (positions 63.72 to 110.10 cM) in 1H bins 06 to 10 of the Bowman backcross-derived line BW152 (1), but small donor parent segments are also retained in 3HL (SNP markers 2_0523 to 1_0754 at positions 173.82 to 190.87) and in 4HL (SNP markers 2_0765 to 2_0384 at positions127.80 to 133.98) of the Bowman backcross-derived line BW152 (1).

Description:

Surface wax coating on the leaf blade appears absent only on upper leaves (wax code ++ ++ -) (3). Mutant plants have slightly coiled awns. The Bowman backcross-derived line for *cer-yu.159* (BS152) is weak in the field and has short leaves, but these traits were not as obvious in greenhouse grown plants. The peduncles of BW152 were about 2/3 of normal length, and rachis internodes were slightly shorter. Kernels of BW152 were slightly shorter and thinner, and their weights were about 1/4 lower. Grain yields of BW152 were less than half those of Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

cer-yu.158 (NGB 111044), *-yu.159* (NGB 111045, GSHO 1554), *-yu.174* (NGB 111060), *-yu.992* (NGB 111880), *-yu.1799* (NGB117347) in Bonus (NGB 14657, PI 189763), *-yu.1168* (NGB 112056), *-yu.1170* (NGB 112058) in Kristina (NGB 14661, NGB 1500) (4).

Mutant used for description and seed stocks:

cer-yu.159 (NGB 111045, GSHO 1554) in Bonus; *cer-yu.159* in Bowman (PI 483237, NGB 22812)*3 (GSHO 2224); *cer-yu.159* in Bowman*4 (BW152, NGB 21984).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:461.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:127.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:157.

BGS 535, Eceriferum-yx, *cer-yx*

Stock number: BGS 535
Locus name: Eceriferum-yx
Locus symbol: *cer-yx*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosomes 1HL, 3HL, or 5H (1); *cer-yx.421* is associated with SNP markers from 1_1198 to 2_0392 (positions 73.70 to 109.27 cM) and from 1_0783 to 1_1441 (positions 208.43 to 231.75 cM) in 5H bins 04 to 06 and 11 to 12, respectively, markers from 1_1241 to 2_0659 (positions 108.07 to 141.21 cM) in 3H bins 07 to 09, and markers from 2_0121 to 2_0921 (positions 112.25 to 155.95 cM) in 1H bins 10 to 12 of the Bowman backcross-derived line BW153 (1).

Description:

Surface wax coating on the spike, the leaf sheath, and stem appears reduced (wax code + + ++) (4). Plants of the Bowman backcross-derived line for *cer-yx.421* (BW153) were slightly shorter than Bowman plants, and kernels were 10 to 15% lighter. Grain yields were similar (2).

Origin of mutant:

A neutron induced mutant in Foma (NGB 14659, CIho 11333) (3).

Mutational events:

cer-yx.421 (NGB 111309, GSHO 1555) in Foma (NGB 14659, CIho 11333), *-yx.1226* (NGB 112114) in Kristina (NGB 14661, NGB 1500) (4); *cer-yx.1092* (NGB 111980), *-yx.1094* (NGB 111082) in Kristina (5).

Mutant used for description and seed stocks:

cer-yx.421 (NGB 111309, GSHO 1555) in Foma; *cer-yx.421* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2225); *cer-yx.421* in Bowman*3 (BW153, NGB 21985).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
5. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:462.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:128.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:158.

BGS 536, Eceriferum-yy, *Cer-yy*

Stock number:	BGS 536
Locus name:	Eceriferum-yy
Locus symbol:	*Cer-yy*

Previous nomenclature and gene symbolization:

Glaucous head = *ge* (11).
Glossy spike 1 = *Gle1* (10).

Inheritance:

Monofactorial dominant (6, 9).

Located in chromosome 1HS (10); *Gle1.a* is about 4.2 cM distal from the *Hor2* (Hordein 2, *HorB*) locus (3, 10); *Cer-yy.849* is in associated with SNP markers 1_0654 to 1_0419 (positions 0.00 to 6.37 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW154 (1); *Gle1.a* is in associated with SNP markers 1_0654 to 2_1226 (positions 0.0 to 13.50 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW383 (1), likely in 1H bin 01.

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (7). Concerning the chemical epicuticular wax composition, the *Cer-yy* mutant in Bonus determines waxes lacking β-hydroxy-β-diketones and having relatively increased proportions of primary alcohols. The distribution of the lipid classes is similar to that of wild type plants (9). Other morphological changes were not observed in Bowman backcross-derived lines BW154 and BW383 with *Cer-yy.849* and *Gle1.a*, respectively (2). Based on identical patterns of SNP markers retained in BW154 and BW383, *Cer-yy.849* and *Gle1.a* originated from the same source (1, 2).

Origin of mutant:

A dominant *Gle1* or *Cer-yy* gene is present in many *Hordeum vulgare* subsp. *spontaneum* accessions and in a few *Hordeum vulgare* subsp. *vulgare* cultivars (2); an ethyl methanesulfonate induced mutant in Bonus (NGB 14657, PI 189763) (4).

Mutational events:

Gle1.a in Cristal (PI 338354) (5, 6, 10, 12); *Cer-yy.437* (NGB 111325) in Foma (NGB 14659, CIho 11333), *-yy.649* (NGB 111537), *-yy.650* (NGB 111538), *yy.849* (NGB 111737, GSHO 1556), *-yy.898* (NGB 111786), *-yy.919* (NGB 111807), *-yy.920* (NGB 111808), *-yy.923* (NGB 111811), *-yy.929* (NGB 111817), *-yy.935* (NGB 111823), *-yy.941* (NGB 111829), *-yy.966* (NGB 111854), *-yy.968* (NGB 111856), *-yy.975* (NGB 111863), *-yy.982* (NGB 111870), *-yy.983* (NGB 111871), *-yy.984* (NGB 111872) in Bonus (NGB 14657, PI 189763) (7); *Cer-yy.974* (NGB 111862), *-yy.1717* (NGB 112513) in Bonus (8).

Mutant used for description and seed stocks:

Cer-yy.849 (NGB 111737, GSHO 1556) in Bonus; *Gle1.a* in Estate (CIho 3410, GSHO 1316); *Cer-yy.849* in Bowman (PI 483237, NGB 22812)*6 (GSHO 2029, BW154, NGB 21986); *Gle1.a* from Estate in Bowman*7 (GSHO 2030, BW383, NGB 20622).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Jensen, J. 1987. Coordinator's report: Chromosome 5. Barley Genet. Newsl. 17:111-113.

4. Lundqvist, U. (Unpublished).
5. Lundqvist, U. 1991. Coordinator's report: *Eceriferum* genes. Barley Genet. Newsl. 20:84.
6. Lundqvist, U. 1992. Coordinator's report: *Eceriferum genes.* Barley Genet. Newsl. 21:99-101.
7. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
8. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.
9. Lundqvist, U., and P. von Wettstein-Knowles. 1982. Dominant mutations at *Cer-yy* change barley spike wax into leaf blade wax. Carlsberg Res. Commun. 47:29-43.
10. Netsvetaev, V.P., and A.A. Sozinov. 1982. Linkage studies of genes *Gle1* and *HrdF* in barley chromosome 5. Barley Genet. Newsl. 12:13-18.
11. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.
12. Wettstein-Knowles, P. von. 1991. New alleles of *Cer-yy* and *cer-b.* Barley Genet. Newsl. 20:66-68.

Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:463.

Revised:
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:129-130.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:159-160.

BGS 548, Angustifolium-b, *Fol-b*

Stock number:	BGS 548
Locus name:	Angustifolium-b
Locus symbol:	*Fol-b*

Previous nomenclature and gene symbolization:

Angustifolia = *Ang* (4).

Inheritance:

Monofactorial incomplete dominant (3).

Location in chromosome 1H based on trisomic analysis (3); *Fol-b.2* is associated with on SNP markers 2_0502 to 2_1226 (positions 3.18 to 13.50 cM) in 1H bins 01 to 02 of a heterozygous plant from the Bowman backcross-derived line BW371 (1).

Description:

Homozygous plants are very weak with short thread-like leaves and often die at the 3 to 4 leaf stage. Heterozygotes have narrow leaves, small spikes and kernels, but vigor is good and fertility is normal (3). Heterozygous plants of the Bowman backcross-derived stock for *Fol-b.2* (BW371) are about 3/4 of normal height, heading is delayed a few days, and grain yields are low. The rachis internodes of heterozygotes are slightly elongated, awns are slightly shorter, and kernels per spike are 2 to 4 fewer. Heterozygotes of the BW371 stock have thin kernels that are about 1/2 of normal weight. The *Fol-b.2* gene needs to be maintained in a heterozygous stock (2).

Origin of mutant:

A spontaneous mutant in an unknown six-rowed cultivar (3), possibly Mars (CIho 7015) based on retained SNP molecular markers (1, 2).

Mutational events:

Fol-b.2 (GSHO 17) in an unknown cultivar (4).

Mutant used for description and seed stocks:

Fol-b.2 (GSHO 17) in an unknown cultivar; *Fol-b.2* in Bowman (PI 483237, NGB 22812)*1 (GSHO 2265); *Fol-b.2* in Bowman*6 (BW371, NGB 20610).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Tsuchiya, T., and R.L. Haines. 1975. Trisomic analysis of nine mutant genes in barley. Barley Genet. Newsl. 5:67-69.
4. Tsuchiya, T., S.D. Tanksley, and R. Ward. 1976. Trisomic analysis of three mutant genes in barley. Barley Genet. Newsl. 6:95.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:474.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:131.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:161.

BGS 560, Erectoides-f, *ert-f*

Stock number: BGS 560
Locus name: Erectoides-f
Locus symbol: *ert-f*

Previous nomenclature and gene symbolization:
Erectoides-18 = *ert-18* (3).

Inheritance:
Monofactorial recessive, but some partial dominance is expressed (3, 6).
Located in chromosome 1H (1), *ert-f.18* is association with SNP markers 2_0617 to 2_1361 (positions 50.96 to 82.35 cM) in 1H bins 05 to 08 of the Bowman backcross-derived line BW308 (1).

Description:
Spikes are semicompact with average rachis internode length values from 2.2 to 2.6 mm. Culm length is about 5/6 of normal (6). Sterile lateral spikelets of *ert-f* plants are larger than those of normal sibs, but apices are rounded. Plants of the Bowman backcross-derived line for *ert-f.18* (BW308) had an average rachis internode length of 3.4 vs. 4.4 mm for Bowman. Kernels of BW308 were slightly wider and shorter than those of Bowman, and grain yields were slightly lower (2).

Origin of mutant:
An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:
ert-f.18 (NGB 112620, GSHO 478) in Bonus (NGB 14657, PI 189763) (4); *ert-f.86* (NGB 112685)*, -f.145* (NGB 112744) in Bonus (5).

Mutant used for description and seed stocks:
ert-f.18 (GSHO 478, NGB 112620) in Bonus; *ert-f.18* in Bowman (PI 483237, NGB 22812)*6 (GSHO 2004, BW308, NGB 22104).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hagberg, A. 1958. Cytogenetik einger Gerstenmutanten. Züchter 28:32-36.
4. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
5. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
6. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:486.

Revised:
J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:133.
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:162.

BGS 563, Erectoides-l, *ert-l*

Stock number: BGS 563
Locus name: Erectoides-l
Locus symbol: *ert-l*

Previous nomenclature and gene symbolization:
Erectoides-12 = *ert-12* (3).
Inheritance:
Monofactorial recessive (3).
Located likely in chromosomes 5HL (1); *ert-l.12* is associated with SNP markers from 1_1198 to 1_1355 (positions 73.70 to 133.74 cM) in 5H bins 04 to 08 and with SNP markers in a small region from 2_0379 to 2_1271 (positions 163.56 to 169.88 cM) in 6H bin 10 of the Bowman backcross-derived line BW315 (1).
Description:
Spikes were slightly denser with rachis internode length values from 2.7 to 3.0 mm. Plant height was about 7/8 of normal (6). In the Bowman backcross-derived line for *ert-l.12* (BW315), plants were about 10% shorter and rachis internodes were shorter, 3.8 vs. 4.6 mm. Kernel weights for BW315 were about 10% lower, and grain yields appeared slightly lower than those for Bowman (2).
Origin of mutant:
An X-ray induced mutant in Maja Abed (NGB 8815, PI 184884) (3).
Mutational events:
ert-l.12 (NGB 112613, GSHO 486) in Maja Abed (NGB 8815, PI 184884) (3); *ert-l.45* (NGB 112645)*, -l.72* (NGB 112671) in Bonus (NGB 14657, PI 189763) (4); *ert-l.114* (NGB 112713)*, -l.155* (NGB 112754)*, -l.156* (NGB 112755)*, -l.162* (NGB 112762) in Bonus, *-l.304* (NGB 112821). *-l.324* (NGB 112839)*, -l.371* (NGB 112887) in Foma (NGB 14659, CIho 11333) (5); *ert-l.450* (NGB 112965) in Foma (6).
Mutant used for description and seed stocks:
ert-l.12 (NGB 112613, GSHO 486) in Maja Abed; *ert-l.12* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2254); *ert-l.12* in Bowman*5 (BW315, NGB 22110).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
4. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
5. Lundqvist, U. (Unpublished).
6. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:489.
Revised:
U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:163.

BGS 564, Erectoides-p, *ert-p*

Stock number: BGS 564
Locus name: Erectoides-p
Locus symbol: *ert-p*

Previous nomenclature and gene symbolization:

Erectoides-44 = *ert-44* (3).

Inheritance:

Monofactorial recessive (3).

Located likely in chromosomes 5HL (1); *ert-p.44* is associated with SNP markers from 2_1480 to 2_1390 (positions 137.96 to ≈173.0 cM) in 5H bins 08 to 10 and with SNP markers in small regions from 2_1370 to 1_1486 (positions 199.54 to 202.70 cM) in 2H bin 13 and from 2_0607 to 1_0863 (positions 52.41 to 64.85 cM) in 3H bins 04 to 05 of the Bowman backcross-derived line BW320 (1).

Description:

Spikes were semicompact with an estimated rachis internode length of 2.7 mm, and the culm length was 5/6 of normal (5). Plants of the Bowman backcross-derived line for *ert-p.44* (BW320) had shorter rachis internodes, 3.8 vs 4.6 mm, and were 10% shorter. Kernels of BW320 were slightly shorter and wider, however grain yields did not differ from those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3, 5).

Mutational events:

ert-p.44 (NGB 112644, GSHO 490) in Bonus (NGB 14657, PI 189763) (3); *ert-p.116* (NGB 112715), *-p.117* (NGB 112716) in Bonus, *-p.301* (NGB 112818), *-p.370* (NGB 112886), *-p.501* (NGB 113017) in Foma (NGB 14659, CIho 11333) (4).

Mutant used for description and seed stocks:

ert-p.44 (NGB 112644, GSHO 490) in Bonus; *ert-p.44* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2255); *ert-p.44* in Bowman*6 (BW320, NGB 22115).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
4. Lundqvist, U. (Unpublished).
5. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:490.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:164.

BGS 565, Erectoides-s, *ert-s*

Stock number:	BGS 565
Locus name:	Erectoides-s
Locus symbol:	*ert-s*

Previous nomenclature and gene symbolization:

Erectoides-50 = *ert-50* (3).

Inheritance:

Monofactorial recessive (3).

Located likely in chromosomes 7H (1); *ert-s.50* is associated with SNP markers from 2_0249 to 1_1521 (positions 69.65 to 174.96 cM) in 7H bins 05 to 10 and with SNP markers in small regions from 2_0715 to 2_0994 (positions 213.08 to 233.44 cM) in 2H bins 13 to 14 and from 1_1411 to 1_0283 (positions ≈249.0 to 25.13 cM) in 3H bins 15 to 16 of the Bowman backcross-derived line BW323 (1).

Description:

The rachis internode length of *ert-s.50* spikes was reduced slightly to about 3.0 mm, and culm length was about 5/6 of normal (4). The *ert-s.50* mutant was a very late segregate from the F_2 progeny of the cross to Bowman. However, the Bowman backcross-derived line for *ert-s.50* (BW323) only headed slightly later and had slightly shorter awns (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

ert-s.50 (NGB 112649, GSHO 493) in Bonus (NGB 14657, PI 189763) (3, 4).

Mutant used for description and seed stocks:

ert-s.50 (NGB 112649, GSHO 493) in Bonus; *ert-s.50* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2256); *ert-s.50* in Bowman*3 (BW323, NGB 22118).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
4. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:491.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:165.

BGS 569, Erectoides-y, *ert-y*

Stock number:	BGS 569
Locus name:	Erectoides-y
Locus symbol:	*ert-y*

Previous nomenclature and gene symbolization:

Erectoides-69 = *ert-69* (2).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Plants of *ert-y.69* had slightly denser spikes than the parent with an average rachis internode length value of 2.8 mm. Culm length is about 5/6 of normal (2). The mutant phenotype was not observed in crosses to Bowman (1).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (2, 3).

Mutational events:

ert-y.69 (NGB 112668, GSHO 499) in Bonus (NGB 14657, PI 189763) (2).

Mutant used for description and seed stocks:

ert-y.69 (NGB 112668, GSHO 499) in Bonus; *ert-y.69* in Bowman (PI 483237, NGB 22812) (BW328, NGB 22123).

References:

1. Franckowiak, J.D. (Unpublished).
2. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
3. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:495.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:166.

BGS 570, Erectoides-z, *ert-z*

Stock number:	BGS 570
Locus name:	Erectoides-z
Locus symbol:	*ert-z*

Previous nomenclature and gene symbolization:

Erectoides-71 = *ert-71* (3).

Inheritance:

Monofactorial recessive (3).

Located likely in chromosome 5H (1); *ert-z.71* is associated with SNP markers from 2_1253 to 2_1341 (positions 65.06 to 98.42 cM) in 5H bins 04 to 06 of the Bowman backcross-derived line BW329 (1); also retained in BW329 were small groups of parental markers in 1HL from 2_1446 to 2_1373 (positions 136.36 to 141.35 cM) in 1H bin 11, and 7HL 1_1243 to 1_0861 (positions 167.56 to 183.90 cM) in 7H bins 10 to 11 (1).

Description:

Plants of the *ert-z.71* mutant had slightly denser spikes than their parent; with a rachis internode length value of 2.8 mm. Culm length was about 3/4 of normal (4). In the Bowman backcross-derived line for *ert-z.71* (BW329), variability in the rachis internode length observed and average internode lengths were 3.8 vs. 4.5 mm for Bowman. BW329 plants were 10 to 15% shorter and their spikes had about two fewer kernels. Kernels of BW329 were 10 to 15% shorter and slightly wider and weighed 10% less, 52 vs 58 mg. The leaf blades of BW329 were slightly wider, and awns were slightly shorter. Grain yields of BW329 were about 15% lower than those of Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

ert-z.71 (NGB 112670, GSHO 500) in Bonus (NGB 14657, PI 189763) (3).

Mutant used for description and seed stocks:

ert-z.71 (NGB 112670, GSHO 500) in Bonus; *ert-z.71* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2260); *ert-z.71* in Bowman*7 (BW329, NGB 22124).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:496.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:167.

BGS 596, Anthocyanin-deficient 5, *ant5*

Stock number:	BGS 596
Locus name:	Anthocyanin-deficient 5
Locus symbol:	*ant5*

Previous nomenclature and symbolization:

Green stem = *rs2* (2).

Exrubrum = *rub-a* (4).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosomes 7HL (2); *ant5.9* is possibly allelic to the *blx5.e* (non-blue aleurone 5) gene (2, 6); the Bowman backcross-derived line for *ant5.9* (BW025) retained donor parent SNP markers 1_1346 to 1_0429 (163.20 to 183.40 cM) in chromosome 2HL in bin 11 and 2_0298 to 1_0236 (203.85 to 276.77 cM) in chromosome 5HL bins 11 to 14 (1).

Description:

Just prior to maturity, the *ant5.9* mutation showed no anthocyanin pigmentation of culms, auricles, and awns and reduced anthocyanin pigmentation of lemmas (5).

The mutant plants do not synthesize anthocyanins in their vegetative parts under normal growing conditions (6, 7). The stem does not develop a purple pigmentation as plants approaches maturity (2). The Bowman backcross-derived line for *ant5.9* (BW025) was selected in F2 progenies based on the absence of basal stem pigmentation in greenhouse grown seedlings before heading (3). Plants of the Bowman backcross-derived line for *ant5.9* (BW025) were similar to those of Bowman except for anthocyanin pigmentation (3).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (5).

Mutational events:

ant5.9 (NGB 114558, GSHO 1643) in Bonus (NGB 14657, PI 189763) (8); *ant5.18* (NGB 114567) in Foma (NGB 14659, CIho 11333) (6); *ant5.24* (NGB 114573) in Foma (8); *blx5.e* (BGM 122) (6).

Mutant used for description and seed stock:

ant 5.9 (NGB 114558, GSHO 1643) in Bonus; *ant5.9* in Bowman (PI 483237, NGB 22812)*4 (BW025, NGB 20433).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

B. Jende-Strid. 1999. Barley Genet. Newsl. 29:84.

Revised:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:168-169.

BGS623, Eligulum-a, *eli-a*

Stock number:	BGS 623
Locus name:	Eligulum-a
Locus symbol:	*eli-a*

Previous nomenclature and gene symbolization:

Eligulum-a = *lig-a* (3).

Eligulum-3 = *eli-3* (5).

Inheritance:

Monofactorial recessive (3, 6).

Located in chromosome 2HS (6); *eli-a.17* mapped in 2HS 2.2 cM proximal of SNP marker 2_0964 at (position 17.85 cM) (6); *eli-a.18* mapped in 2HS 1.6 cM proximal of SNP 3_1284 (19.47 cM) (6); Bowman backcross-derived lines for *eli-a.3* (BW295), *eli-a.9* (BW296), and *eli-a.216* (BW293) retained donor parent markers in this region of 2HS (1).

Description:

Plants do not have ligules in the junction between the sheath and leaf blade, auricles are rudimentary and asymmetrically displaced. Plants are about 2/3 of normal height and have very wide leaves (4, 5). The peduncle is short and spike emergence from the sheath of the flag leaf is poor. Spikes have a compact arrangement of spikelets and are extremely compacted near the tip (2, 4). The culm breaks very easily between the upper and lower halves of the nodes. The Bowman backcross-derived lines have glume awns that are nearly twice as long as those of Bowman, but the lemma awns are about 2/3 of normal (2). The *eli-a.17* and *eli-a.18* mutants increased tillering of uniculm 2 (*cul2*) plants (6). ELI-A produce shorter plants with fewer tillers and disrupt the leaf blade-sheath boundary, producing liguleless leaves and reduced secondary cell wall development in stems and leaves. Presence of *ELI-A* transcripts at the preligule boundary, suggesting that *Eli-a* contributes to boundary formation between the blade and sheath (6).

Origin of mutant:

An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (3, 4).

Mutational events:

eli-a.2 (NGB 115389), *eli-a.3* (NGB 115390), *-a.7* (NGB 115392), *-a.9* (NGB 115393), -*a.10* (NGB 115394) in Foma (NGB 14659, CIho 11333) (5); *eli-a.11* (NGB 115395), -*a.14* (NGB 115397) in Kristina (NGB 14661, NGB 1500); *eli-a.15* (NGB 115398), *-a.16* (NGB 151399) in Bonus (NGB 14657, PI 189763) (5), *eli-a.216* (FN216, GSHO 3647) in Steptoe (CIho 15229) (2, 4); *eli-a.17* and *eli-a.18* are sodium azide induced mutants in a Bowman *cul2.b-rob1.a* backcross-derived line (BW206, NGB 22034) (6).

Mutant used for description and seed stocks:

eli-a.3 (NGB 115390) in Foma; *eli-a.3* in Bowman (PI 483237, NGB 22812)*4 (BW295, NGB 20579); *eli-a.9* from Foma in Bowman*2 (BW296, NGB 20580); *eli-a.14* from Kristina in Bowman*3 (BW294, NGB 20578); *eli-a.216* from Steptoe in Bowman*3 (BW293, NGB20577).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:126.

Revised:

J.D. Franckowiak and A. Kleinhofs. 2005. Barley Genet. Newsl. 35:192.
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J.D. Franckowiak and U. Lundqvist. 2018. Barley Genet. Newsl. 48:170-171.

BGS 661, Double seed 1, *dub1*

Stock number:	BGS 661
Locus name:	Double seed 1
Locus symbol:	*dub1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (2); *dub1.1* is near AFLP marker E4038-4 in subgroups 66 to 67 of the Proctor/Nudinka map of chromosome 5H (2), *dub1.1* is slightly distal from the *mnd6* (many noded dwarf 6) locus (2), which is in 5H bin 10.

Description:

The modification of the top of spike is distinctive and occurs on all tillers. The tip of the spike is compacted and a few spikelets form two and three fertile florets adjacent to each other. The double spikelets have fused lemmas and paleas often enclose the part of two, and occasionally more, florets: six anthers and two ovaries (1). The tip of the spike appears phenotypically similar to those of *int-m* (intermedium spike-m) mutants (1).

Origin of mutant:

An X-ray and ferrisulfate induced mutant in Bonus (NGB 14657, PI 189763) (1).

Mutational events:

dub1.1 (NGB 114331), *dub1.2* (NGB 114332) in Bonus (NGB 14657, PI 189763) (1); *dub1.3* (NGB 114333), *dub1.7* (NGB 114337), *dub1.8* (NGB 114338), *dub1.9* (NGB 114339), *dub1.10* (NGB114340), *dub1.11* (NGB 114341), *dub1.12* (NGB 114342) in Foma (NGB 14659, CIho 11333) (1); *dub1.18a* (NGB 114345), *dub1.18b* (NGB 114347) in Kristina (NGB 14661, NGB 1500) (1); *dub1.19* (NGB 114348), *dub1.20* (NGB 114350) in Bonus (1).

Mutant used for description and seed stocks:

dub1.1 (NGB 114331) in Bonus (2).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:301.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:172.

BGS 676, Chlorina seedling 16, *fch16*

Stock number:	BGS 676
Locus name:	Chlorina seedling 16
Locus symbol:	*fch16*

Previous nomenclature and gene symbolization:

Chlorina seedling 117 = *clo.117* (3, 4).

Inheritance:

Monofactorial recessive (3, 4).

Located likely in chromosome 2HS (1); *fch16.117* is associated with SNP markers 2_1187 to 2_1338 (positions 51.52 to 74.97 cM) in 2H bins 05 to 06 and also with a few SNP markers 2_0119 to 1_0510 (positions 144.81 to 149.26) in 4HL bin 10 of the Bowman backcross-derived line BW185 (1).

Description:

Seedling and immature leaves are pale yellow-green (chlorophyll deficient) in color and gradually become darker. A slight yellow green color may be observed prior to heading (2, 3). Leaf blades of the Bowman backcross-derived line for *fch16.117* (BW185) were slightly wider than those of Bowman. The spikes of BW185 plants were observed to have slightly few kernels than those of Bowman in some trials. The BW185 plants were 10 to 20% shorter than Bowman and showed about a four day delay in anthesis. Kernel weights and grain yields were about normal (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (NGB 14657, PI 189763) (3, 5).

Mutational events:

fch16.117 (NGB 22623) in Bonus (NGB 14657, PI 189763) (3, 4, 5).

Mutant used for description and seed stocks:

fch16.117 (NGB 22623) in Bonus; *fch16.117* in Bowman (PI 483237, NGB 22812)*5 (BW185, NGB 22017).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:144.

Revised:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:173.

BGS 716, Intense blue aleurone 1, *ibl1*

Stock number:	BGS 716
Locus name:	Intense blue aleurone 1
Locus symbol:	*ibl1*

Previous nomenclature and gene symbolization:

Enhancer of blue aleurone = *en-Bl* (5).

Intense blue aleurone = *ibl* (2, 3).

Inheritance:

Monofactorial recessive (2, 4, 5).

Located in 7HL (5); *ibl1.a* (*en-Bl*) is about 30.1 cM from the *blx2.b* (non-blue aleurone 2) gene (5); *ibl1.a* is about 29.5 cM from the *msg10.ay* (male sterile genetic 10) gene (5); the presence of *ibl1.a* in BW417 and BW 418 is associated with parental SNP markers in 7HL (1); the dark purple coloration of kernels in the hulless accession Nierumuzha from China was associated with QTL in 7HL (7).

Description:

The *ibl1.a* variant was identified based on mature aleurone color. Two new colors, brick red and intense blue, were found in the Abyssinian lines, Ethiopian 637 and Ab 2231, respectively. Aleurone color expression is influenced by the environment in much the same way as that of normal blue, but they are reasonably distinct from normal blue and white aleurones in well grown material (2). The *ibl1.a* gene intensifies the red anthocyanin pigmentation of the stem base of seedlings and on the culms of maturing plants (4, 6). The leaf sheath anthocyanin content of the *ibl.a* variant [BW418 (NGB 20651)] having the dominant allele *Ant1.a* (*Rst1.a*) at the *Ant1* (Anthocyanin-less 1) or *HvMpc1* locus as measured by OD_{530} (anthocyanin content spectrophotometry at 530 nm) was about three times greater than that of Bowman backcross-derived lines with *Ant1.a*, but lacking *ibl1.a* (6).

Origin of mutant:

Natural occurrence in Ethiopian 637 (GSHO 2508) (2); present in Ubamer (PI 296470) (5); possibly present in the Chinese landrace Nierumuzha (7).

Mutational events:

ibl1.a in Ethiopian accessions Ethiopian 637 (GSHO 2508) and in Ab 2231 (2, 3).

Mutant used for description and seed stocks:

ibl1.a in Ethiopian 637; *ibl1.a* with *blx4.d* (blue aleurone 4) and *nud1.a* (naked caryopsis 1) in BW063 (NGB 20471)/Ethiopian 637 (BW417, NGB20650) produces red aleurone color; *ibl1.a* with *Blx1.a* (Blue aleurone 1) and *nud1.a* (naked caryopsis 1) in BW063 (NGB 20471)/Ethiopian 637 (BW418, NGB 20651) produces deep blue aleurone color.

References:

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Prepared:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:241.
Revised:
J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:136-137.
J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:174-175.

BGS 746, Anthocyanin-deficient 23, *ant23*

Stock number:	BGS 746
Locus name:	Anthocyanin-deficient 23
Locus symbol:	*ant23*

Previous nomenclature and gene symbolization:

Exrubrum = *rub-a* (4).

Anthocyanin-deficient 3 = *ant-3* (3, 6).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosomes 2HL or 5HL (1); *ant23.3* is associated with SNP markers 1_1346 to 2_1459 (163.20 to 202.70 cM) in chromosome 2HL in bins 11 to 13 and 2_0127 to 2_0731 (189.08 to 223.57 cM) in chromosome 5HL bins 10 to 12 of the Bowman backcross-derived line BW023 (1).

Description:

Just prior to physiological maturity, the *ant23.3* mutation showed no anthocyanin pigmentation of culms and auricles and reduced anthocyanin pigmentation of awns and lemmas (5). The Bowman backcross-derived line for *ant23.3* (BW023) was selected in F2 progenies grown in greenhouses based on the absence of basal stem pigmentation in seedlings before heading (2). The retention of SNP markers from Bonus in BW023 in the long arms of chromosomes 2H and 5H suggests that these chromosomal regions are associated with the lack of basal stem pigmentation (1, 2). SNP markers were retained in same two chromosomal regions in BW025, the Bowman backcross-derived line for *ant5.9*, anthocyanin-deficient 5 (1, 2).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (1, 3, 5).

Mutational events:

ant23.3 (NGB 114554) in Bonus (NGB 14657, PI 189763) (5, 6).

Mutant used for description and seed stocks:

ant23.3 (NGB 114554) in Bonus; *ant23.3* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2156); *ant23.3* in Bowman*3 (BW023, NGB 20431).

References:

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6. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. Barley Genet. Newsl. 14:76-79.

Prepared:

U. Lundqvist and J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:176.

BGS 747, Anthocyanin-deficient 24, *ant24*

Stock number:	BGS 747
Locus name:	Anthocyanin-deficient 24
Locus symbol:	*ant24*

Previous nomenclature and gene symbolization:
Exrubrum = *rub-a* (2).
Anthocyanin-deficient 10 = *ant-10* (1, 3).

Inheritance:
Monofactorial recessive (3, 4).
Location is unknown.

Description:
Just prior to maturity, the *ant24.10* mutation showed no anthocyanin pigmentation of culms and lemmas and reduced anthocyanin pigmentation of auricles and awns (3).

Origin of mutant:
An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (1, 3).

Mutational events:
ant24.10 (NGB114559) in Foma (NGB 14659, CIho 11333) (2, 3).

Mutant used for description and seed stocks:
ant24.10 (NGB114559) in Foma.

References:
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2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
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Prepared:
U. Lundqvist. 2018. Barley Genet. Newsl. 48:177.

BGS 748, Reaction to *Puccinia graminis* 3, *Rpg3*

Stock number:	BGS 748
Locus name:	Reaction to *Puccinia graminis* 3 (wheat stem rust)
Locus symbol:	*Rpg3*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (4, 5).

Located in chromosome 5HL (2); *Rpg3.c* is near the centromere (2); *Rpg3.c* was estimated to be between 74.2 and 85.5 cM (2).

Description:

PI 382313 showed moderate seedling resistance to six *Puccinia graminis* f. sp. *tritici* isolates and improved resistance in field evaluations (4, 5). PI 382313 exhibited a moderate-to-high level of adult plant resistance (APR) to races QCCJB and MCCFC, but had mostly susceptible seedling phenotypes (1, 2, 3). Seedling tests with wheat and rye stem rust isolates were ineffective in rapidly detecting resistance conferred by PI 382313 (7). PI 382313 exhibited lower seedling and adult plant reactions to reactions to African stem rust race TTKSK (6).

Origin of mutant:

A spontaneous variant in GAW-79 (PI 382313) (4, 5) collected from Ethiopia (3).

Mutational events:

Rpg3.c in GAW-79 (PI 382313) from Ethiopia (1, 2, 3).

Mutant used for description and seed stocks:

Rpg3.c in GAW-79 (PI 382313) from Ethiopia.

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Prepared:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:178.

BGS 750, Reaction to *Puccinia graminis* 6, *rpg6*

Stock number:	BGS 750
Locus name:	Reaction to *Puccinia graminis* 6 (wheat stem rust)
Locus symbol:	*rpg6*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 6HS (1, 2); *rpg6.h* is located in the terminal region of 6HS in experimental line 212Y1 as determined by GISH and the PCR-based markers (1, 2).

Description:

Seedling resistance (infection type = 120;) to several races of *Puccinia graminis* f. sp. *tritici* is conferred by the *rpg6.h* gene of 212Y1. It is resistant to stem rust races MCCF (avirulent on *Rpg1.a* and *rpg4.d*) and QCCJ (virulent on *Rpg1.a* and avirulent on *rpg4.d*) at the seedling stage in glasshouse tests (1). Seedling tests indicated that *rpg6.h* is not effective against the highly virulent African race TTKSK (1). The introgressed region from *H. bulbosum* in chromosome 6HS of barley is less than 40 cM, or approximately 29% of the chromosomal length of 6H (1).

Origin of mutant:

A spontaneous variant in *Hordeum bulbosum* identified in accession Cb2920 and transferred to a line from a backcross to *Hordeum vulgare* cultivar Golden Promise (PI 467829) (1, 2).

Mutational events:

rpg6.h from *Hordeum bulbosum* identified in a doubled haploid line 212Y1 selected from the progeny of the triploid hybrid *H. vulgare* ‘Golden Promise’ (2n = 2x = 14)/*H. bulbosum* Cb2920/4/Colch (2n = 4x = 28) crossed to Golden Promise (PI 467829) (2).

Mutant used for description and seed stocks:

Rpg6.h in 212Y1 (1).

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Prepared:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:179.

BGS 751, Reaction to *Puccinia graminis* 7, *Rpg7*

Stock number: BGS 751
Locus name: Reaction to *Puccinia graminis* 7 (wheat stem rust)
Locus symbol: *Rpg7*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Located in chromosome 3HL (1); *Rpg7.i* is near the telomeric region of 3HL (1) between 135 and 155 cM based on the POPSEQ consensus map or between 667 and 693 Mbp based on the barley physical map.

Description:

The *Rpg7.j* gene confers moderate seedling resistance, Infection Types (ITs) 0;1 to 23, to a wide spectrum of domestic and foreign races of the wheat stem rust pathogen *Puccinia graminis* f. sp. *tritici* (*Pgt*) and also to an isolate of rye stem rust pathogen *P. graminis* f. sp. *secalis* (*Pgs*) (2). Accessions WBDC094 (ICARDA number: 40035 and USDA National Small Grains Collection number PI 681809) from Karak, Jordan and WBDC238 (ICARDA number: 40037; PI 681943) from Amman, Jordan were resistant as seedlings to *Pgt* race HKHJC in a greenhouse evaluation (2). Additional molecular and genetic studies revealed this gene to be novel; thus, a new locus designation, *Rpg7*, and an allele designation, *Rpg7.i*, were recommended (1, 2).

Origin of mutant:

Natural occurrence in wild barley (*Hordeum vulgare* subsp. *spontaneum*) accessions from Jordan, accession WBDC094 (ICARDA number: 40035; USDA number: PI 681809) from Karak and accession WBDC238 (40037; PI 681943) from Amman (2).

Mutational events:

Rpg7.i in WBDC094 (ICARDA number: 40035; USDA number: PI 681809) from Karak, Jordan and WBDC238 (40037; PI 681943) from Amman, Jordan (1, 2).

Mutant used for description and seed stocks:

Rpg7.i in WBDC094 (ICARDA number: 40035; USDA number: PI 681809) and WBDC238 (ICARDA number: 40037; PI 681943).

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Prepared:E.

Henningsen and B.J. Steffenson. 2018. Barley Genet. Newsl. 48:180.

BGS 752, Quantitative seed dormancy 1, *Qsd1*

Stock number: BGS 752
Locus name: Quantitative seed dormancy 1
Locus symbol: *Qsd1*

Previous nomenclature and gene symbolization:
Seed dormancy 1 = SD1 (4).
Quantitative seed dormancy 1 = *Qsd1* (13).

Inheritance:

Monofactorial recessive for a long seed dormancy period in wild barley (13); previously identified as a QTL in cultivated barley for seed dormancy (1, 3, 4, 5, 7, 11, 13, 17). Located in chromosome 5HL (4, 17); *Qsd1.b* is in the centromeric region of 5HL (4); *Qsd1.b* is between RFLP markers Ale and ABC302 (4); *Qsd1.b* is near marker ABC302 (5); *qsd1.a* is located between 56.9 and 61.9 cM (10); the *qsd1* locus is located in a 9,467 bp region between markers EST5 and EST4F (14).

Description:

Seed dormancy in barley is described as the inability of a viable embryo to germinate under environmental conditions favorable to germination (4). Dormant grain may require a storage period prior to re-planting or malting while non-dormant grain can result in pre-harvest sprouting in the field which can reduce malting and feed quality (4, 17). Seed dormancy levels are high among wild barley accessions and show geographical differentiation among barley cultivars (15). The first of two quantitative seed dormancy loci (*Qsd1*) involved in maintenance of post-harvest grain dormancy was identified as a QTL contributed by Steptoe (CIho 15229) in the doubled haploid progeny of a Steptoe by Morex (CIho 15773) cross (4, 17). The *Qsd1.b* allele in Steptoe for dormancy has a partly epistatic interaction with alleles at *Qsd2* locus (4). The presence of the Steptoe allele at the *Qsd1* locus kept precocious germination to a minimum until the end of the seed development process (12). QTL in the *Qsd1* region were associated with different degrees of dormancy (7). The recessive *qsd1.a* allele from wild barley H602 (*Hordeum vulgare* subsp. *spontaneum*) encodes an alanine aminotransferase (AlaAT), which likely controls the metabolic flux associated with germination. Nineteen days after anthesis transcripts of the qsd1 RNA were present in the embryo, but not the endosperm (14). Variations in dormancy levels associated with the *qsd1* locus exist among cultivated barley accessions and likely arose after domestication (14). Sequence variations in the AlaAT gene are inherited as dominants and reduce the level of dormancy observed in domesticated barley (14). In North American malting barley cultivars [Harrington (two-rowed) and Morex (six-rowed)], alleles at the *Qsd1* locus are associated with little or no dormancy (1, 2, 3, 4, 6, 11, 17). The unexpected pattern of dormancy release observed in Triumph (PI 290195) by Prada et al. (11) might be closer to wild type than that of other cultivars. Higher lipoxygenase (LOX) content, which affects foam stability and beer flavor, was associated with more dormant alleles at the *Qsd1* locus (8). Low values for other malting quality was associated with the presence of a *Qsd1.b* allele for dormancy in Baronesse (PI 568246) (2).

Origin of mutant:

A wild type, *qsd1.a*, occurs as a recessive allele in wild barley (*Hordeum vulgare* subsp. *spontaneum*) accession H602 (8, 14); *Qsd1* variants have accumulated in cultivated barley to reduce dormancy levels (14).

Mutational events:

The allele, *qsd1.a*, is present in H602 and represents wild type (14); many *Qsd1* variants are present in cultivated barley (7, 13, 14); partially dormant alleles (mutants) in the *Qsd1.b* series are present in Steptoe (CIho 15229) (4, 16, 17), in Triumph (PI 290195) (9), in Stirling (PI 466919) (1, 3), in Flagship (6); Haruna Nijo has a non-dormant allele (4, 13, 14); Harrington, Morex (CIho 15773), Chevron (CIho 1111), and Stander (PI 564743) may have the same non-dormant allele at the *Qsd1* locus (9).

Mutant used for description and seed stocks:

qsd1.a in the wild barley accession H602; *Qsd1.b* variants in cultivars, both two- and six-rowed spring barley cultivars.

References:

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11. Prada, D., S.E. Ullrich, J.L. Molina-Cano, L. Cistué, J.A. Clancy, and I. Romagosa. 2004. Genetic control of dormancy in a Triumph/Morex cross in barley. Theor. Appl. Genet. 109:62-70.
12. Romagosa, I., F. Han, J.A. Clancy, and S.E. Ullrich. 1999. Individual locus effects on dormancy during seed development and after ripening in barley. Crop Sci. 39:74-79.
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Prepared:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:181-183.

BGS 753, Quantitative seed dormancy 2, *Qsd2*

Stock number: BGS 753
Locus name: Quantitative seed dormancy 2
Locus symbol: *Qsd2*

Previous nomenclature and gene symbolization:

Seed dormancy 2 = SD2 (6).
Quantitative seed dormancy 1 = *Qsd2* (18).

Inheritance:

Monofactorial recessive for rapid loss of dormancy in wild barley (14); previously identified as a dominant QTL in cultivated barley for seed dormancy (4, 5, 6, 9, 22, 23). Located in chromosome 5HL (6, 23); the *qsd2* locus is in terminal region of 5HL near RFLP marker MWG851 (5); *qsd2* is in a 0.8-cM interval between molecular markers MWG851D and MWG851B (4); the main QTL for dormancy is near RFLP markers ABC57 CDO506 (1, 11); the *Qsd2* locus is in the terminal region between 196.6 and 197.5 cM (15).

Description:

Malting and dormancy testing are conducted under conditions unfavorable for germination of barley. Wild barley (*Hordeum vulgare* subsp. *spontaneum*) is a winter annual for which germination must be prevented until soils is cool and moist. To break dormancy experimentally, kernels are placed, after imbibition for 24 to 48 hours, in near freezing temperatures for 3 to 5 days. Dormancy in wild barley is established by the recessive allele at the *Qsd1* locus, which encodes for an alanine aminotransferase (AlaAT) (19). Dormancy is maintained in wild barley until favorable conditions for seedling establishment exist by a recessive allele at the *Qsd2* locus, which encodes for *Mitogen-activated Protein Kinase Kinase 3* (*MKK3*) (14). Domestication resulted in a partial loss of dormancy; however, more dormancy is retained in cultivars grown as winter barley (19). The *Qsd2* locus is the second quantitative seed dormancy locus involved in maintenance of post-harvest grain dormancy (6, 23). Dominant QTL at the *Qsd2* locus in 5HL caused reduced seed germination following grain harvest (2, 4, 5, 6, 14, 15). Alleles in the terminal region of 5HL are associated with many malt quality parameters In the Harrington/TR306 DH progeny (3, 9, 13). In the Chebec (PI 606292)/Harrington DH progeny, extract and diastatic power levels were associated with alleles in 5HL (1) and also with α-amylase activity and free amino acids (11). The *Qsd2* allele of Baronesse was associated with higher yield and inferior malt quality in backcross-derived lines (20). Higher lipoxygenase (LOX) content, which affects foam stability and beer flavor, was associated with more dormant alleles at the *Qsd2* locus (10); however, it is possible that closely linked loci are involved in the dormancy/malt quality associations (5, 10). The *Qsd2* locus 5HL has been associated with rapid release of after-ripening dormancy in the non-dormant parent (16, 17) and preharvest sprouting (22, 24). The N260T substitution in *Mitogen-activated Protein Kinase Kinase 3* allele of wild barley decreases MKK3 kinase activity and increases dormancy (14). A large number of sequence variations in the *MKK3* were identified, but their relationships with dormancy levels were reported as variable (14).

Origin of mutant:

The rapid dormancy release allele at the *Qsd2* locus in wild barley H206 was named *Qsd2-OK* (*Qsd2.c*) (14); the slow dormancy release allele (from Azumamugi) of *MKK3* with the N260T was named *Qsd2.AK* (*Qsd2.d*), which likely arose in northeastern China and was established as a major allele in cultivars from southeastern China, Korea, and Japan (14); many other sequence variants in *MKK3* (*Qsd2*) are present in wild and cultivated barley accessions (14).

Mutational events:

Wild type alleles were considered recessives (14); the *Qsd2.c* series of allele symbols is suggested for the recessive variants present in *Hordeum vulgare* subsp. *spontaneum*; sequence changes in cultivars produce dominant variants (14), which were placed in the *Qsd2.d* group of alleles. Cultivars with strong dormancy alleles at the *Qsd2* locus: included Steptoe (CIho 15229) (6, 23), TR306 (3, 24), Chebec (1, 11), Stirling (2, 5), Baronesse (20); dormancy QTL were detected in Chevron (CIho 1111) and Morex (CIho 15773) (12); Harrington (1, 3, 5), Haruna Nijo (14, 15), Flagship (7), and AC Metcalfe (25, 26) have a non-dormant allele at the *Qsd2* loci.

Mutant used for description and seed stocks:

qsd1.c in the wild barley accession H602; a series of sequence variants (*qsd1.c* alleles) in wild barley accessions; *Qsd1.d* variants associated with a range of dormancy levels in barley cultivars.

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17. Romagosa, I., F. Han, J.A. Clancy, and S.E. Ullrich. 1999. Individual locus effects on dormancy during seed development and after ripening in barley. Crop Sci. 39:74-79.

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Prepared:

J.D. Franckowiak. 2018. Barley Genet. Newsl. 48:184-187.

BGS 754, Quantitative seed dormancy 3, *Qsd3*

Stock number:	BGS 754
Locus name:	Quantitative seed dormancy 3
Locus symbol:	*Qsd3*

Previous nomenclature and gene symbolization:

QTL in terminal region of 5HL = *qSDND* (Hickey 2012).

Inheritance:

Monofactorial dominant (4, 11). Located in chromosome 5HL (4, 11); *Qsd3* is likely near the *Qsd2* locus in the telomeric region of 5HL (4, 5, 11); the *Qsd3* locus may be positioned 1 to 3 cM proximal from *Qsd2* locus (2, 12).

Description:

Maintenance of seed dormancy in wild barley under conditions unfavorable for seedling establishment involves alleles at the *Qsd1* (7) and *Qsd2* (6) loci and a series of modifiers. One modifier in the terminal region 5HL is associated with variability in seed dormancy and malt quality parameters (1, 2, 11). The chromosome region above the MWG851D-MWG851B interval, the *Qsd2* position, might play a role in reducing barley seed dormancy during after-ripening (1). A QTL for seed dormancy was detected near the *Qsd2* locus in Morex (CIho 15773) (5), which was previously reported to lack seed dormancy (1, 3). QTL clusters for both seed dormancy and preharvest sprouting (PHS) in the terminal region of 5HL were assumed to be either a pleiotropic effect and/or closely linked genes (8, 9). If the QTL in the scssr09041A-scssr03907 interval is *Qsd2*, the QTL at E6104BANP-E6126_ANP is the QTL proximal to *Qsd2* (2). The dormant allele at the *Qsd3* locus is tentatively designated as *Qsd3.e* while the non-dormant allele is *Qsd3.f*. The PHS tolerance allele at 5HL the cultivar Baudin contributes to higher malt yield without significant impact on diastatic power, β-glucan content and wort viscosity (10, 12). Dormant DH lines were recovered from a cross between two non-dormant cultivars, Flagship and ND24260, with the main effect QTL in the terminal region of 5HL (4). The dormant allele (*Qsd3.e*) apparently present in ND24260 is not associated with a relatively non-dormancy allele at the *Qsd2* locus (4). The non-dormant allele at markers E6140BANP-E6126_ANP (*Qsd3.f*) is likely linked to a strong dormancy allele (*Qsd2.d*) in Baudin (2). Thus, Baudin and ND24260 have possible recombinants between alleles at the *Qsd2* and *Qsd3* loci.

Origin of mutant:

The dominant and more dormant allele (*Qsd3.e*) is frequently linked to a dormant allele at the *Qsd2* locus in non-malting cultivars, while the less dormant alleles (*Qsd3.f* and the *Qsd2.d* series) are present in many elite malting barley cultivars.

Mutational events:

The *Qsd3.f* (non-dormant) allele in Baudin linked to a strong dormancy allele (*Qsd2.d*) at the *Qsd2* locus (2); the *Qsd3.e* (more dormant) allele in ND24260 is linked to a non-dormant allele at the *Qsd2* locus (4); the *Qsd3.f* allele is linked with a non-dormant allele at the *Qsd2* locus in malting cultivars Harrington and Morex (CIho 15773) (5).

Mutant used for description and seed stocks:

Qsd3.e (dormant) in ND24260); *Qsd3.f* (non-dormant) in Baudin; *Qsd3.f* with non-dormant allele at *Qsd2* locus in Harrington and Morex.

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