Barley Genetics Newsletter
Volume 49
2019 – 2020

Editorial Committee: J. Franckowiak, U. Lundqvist, P. Bregitzer

Udda's Street at the Lantmännen Plant Breeding
Photo courtesy of Bo Gertsson, Udda Lundqvist väg 11, Svalöv

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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 Victoria Carollo Blake (victoria.blake@montana.edu).

Acknowledgements

Publication of the BGN has been 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 possible by the time and expertise of Udda Lundqvist and Jerry Franckowiak. Special thanks to the USDA-ARS GrainGenes team.

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, 49, 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.

Descriptions of Barley Genetic Stocks for 2019

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In this volume of the Barley Genetics Newsletter, 106 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) www.ars.usda.gov.PacWest/Aberdeen

(2) www.ars-grin.gov:7000/npgs/descriptors/barley-genetics (GRIN)

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

(4) http://nordic-baltic-genebanks.org

(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.‡
25	Xnt1	X_a, xan-h, clo-b	7HS	Xantha seedling 1	49: 60	1606
38	smn1	smn	3H/5H	Seminudoides 1	49: 62	1602
68	Pvc 1	P_c	2HL	Purple veined lemma 1	49: 64	132
126	sld1	dw1	3HL	Slender dwarf 1	49: 66	2488
172	lks5	lk5, ari-c	4HL	Short awn 5	49: 68	1297
199	nec37	nec.r	4HS	Necrotic leaf spot 37	49: 71	
215	des6	des6	5HL	Desynapsis 6	49: 72	597
273	sdw10	sdw.g	6HS	Desynapsis 10	49: 74	2450
277	sdw21	sdw.ap	6H	Semidwarf 21	49: 75	49
306	var1	va	5HL	Variegated 1	49: 76	1278
334	raw6	r6	5HL	Smooth awn 6	49: 77	2437
338	lys1	lys	5HL	High lysine 1	49: 78	1784
344	var2	va2	5HL	Variegated 2	49: 80	2496
409	cer-o	cer-28	1HL	Eceriferum-o -/+ ++ ++	49: 81	436
429	cer-zk	cer-85	2H	Eceriferum-zk + + +/-	49: 82	458
430	cer-zl	cer-17		Eceriferum-zl - - ++	49: 84	459
440	cer-zw	cer-286	2H	Eceriferum-zw + + ++	49: 85	1530
444	cer-ya	cer-180	3HS	Eceriferum-ya ++ ++ -	49: 86	1534
447	cer-yd	cer-139	3HS	Eceriferum-yd - ++ ++	49: 87	1537
451	cer-yh	cer-116	3HS	Eceriferum-yh - ++ ++	49: 88	1541
472	abr1	abr	2HL	Accordion basal rachis internode 1	49: 89	1563
518	sdw1	denso, Hv20ox$_2$	3HL	Semidwarf 1	49: 91	2513
578	mat-b	mat-b	7HL	Praematurum-b	49: 95	1788
579	mat-c	Eam6, HvCEN	2H	Praematurum-c	49: 97	1789
586	bra-d	bra-d	1HL	Bracteatum-d	49:100	1696
634	pmr2	nec-50		Premature ripe 2	49:102	2421
676	clo-a	clo.117, fch16	2HS	Chlorina-a	49:103	
677	mtt7	mtt.h	2HS	Mottled leaf 7	49:105	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
724	lks6	lks.q	1H/5H/6H	Short awn 6	49:106	3674
755	sdw8	sdw.ab	5HL	Semidwarf 8	49:107	2442
756	sdw5	sdw.hf	1HL	Semidwarf 5	49:108	
757	sdw9	sdw.hg	1HL	Semidwarf 9	49:109	
758	sdw11	sdw.j	7HS	Semidwarf 11	49:110	2453
759	sdw12	sdw.l	2H	Semidwarf 12	49:111	2455
760	sdw13	sdw.m	3HS	Semidwarf 13	49:112	2456
761	sdw14	sdw.w	2H	Semidwarf 14	49:113	
762	sdw15	sdw.ab	7HS	Semidwarf 15	49:114	2440
763	sdw16	sdw.ac	7HL	Semidwarf 16	49:115	
764	sdw17	sdw.ad	2H	Semidwarf 17	49:116	
765	sdw18	sdw.ae	5HL	Semidwarf 18	49:117	
766	sdw19	sdw.ai	5H	Semidwarf 19	49:118	
767	sdw20	sdw.an	2HL	Semidwarf 20	49:119	2443
768	sdw22	sdw.aq	5HL/6H	Semidwarf 22	49:120	
769	sdw23	sdw.ar	5HL	Semidwarf 23	49:121	
770	sdw24	sdw.as	2HL/6H	Semidwarf 24	49:122	
771	sdw25	sdw.at	5H	Semidwarf 25	49:123	
772	sdw26	sdw.aw	2H	Semidwarf 26	49:124	2446
773	sdw27	sdw.ax	7H	Semidwarf 27	49:125	2447
774	sdw28	sdw.bc	7HL	Semidwarf 28	49:126	
775	sdw29	sdw.au		Semidwarf 29	49:127	2441
776	glo-g	glo.1	3H	Globosum-g	49:128	
777	glo-h	glo.2	7HS	Globosum-h	49:129	
778	glo-i	glo.h	7HS	Globosum-i	49:130	1756
779	gig3	gig.2	1H	Gigas 3	49:131	1749
780	lks9	lks.m	3H	Short awn 9	49:132	1782
781	lks7	lks.o	5HL	Short awn 7	49:133	
782	lks8	lks.p	1HL/7HS	Short awn 8	49:134	
783	ari-za	ari.49	5HS/5HL	Breviaristatum-za	49:135	
784	scl-c	scl.2	3HS	Scirpoides-c	49:136	
785	seg9	seg.l	6HL/7HS	Shrunken endosperm genetic 9	49:137	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
786	sex10	sex.m	2HL/7H	Shrunken endosperm xenia 10	49:138	
787	viv-d	viv.2	2HL	Viviparoides-d	49:140	
788	viv-e	viv.3	3HL/7H	Viviparoides-e	49:142	
789	viv-f	viv.8	4HS/5HS	Viviparoides-f	49:144	
790	wst8	wst.l	2HL/3H	White streak 8	49:145	
791	wst9	wst.m	5HL/7HS	White streak 9	49:146	1266
792	zeo4	zeo.e	1HL	Zeocriton 4	49:147	1609
793	smn2	smn.l	3H	Seminudoides 2	49:148	
794	Smn3	smn4	6HL	Seminudoides 3	49:149	
795	dsp12	dsp.au	3HL	Dense spike 12	49:151	
796	clo-c	clo.104	2H	Chlorina-c	49:152	
797	xan-l	xan.35	3H	Xantha-l	49:154	
798	clo-d	clo.113	1H/3HS	Chlorina-d	49:156	
799	fch18	fch.aa	2H	Chlorina seedling 18	49:157	1736
800	fch19	fch.ad	1HL	Chlorina seedling 19	49:158	
801	fch20	Fch.ae	2H	Chlorina seedling 20	49:159	
802	fch21	fch.af	1HL/3H	Chlorina seedling 21	49:160	
803	fch22	fch.ai	1H/3H	Chlorina seedling 22	49:161	
804	fch23	fch.al	4HL/7HL	Chlorina seedling 23	49:162	
805	srp1	srp.a	1HL/3HL	Serpentina 1	49:163	
806	glo-j	glo.j	3HL/7H	Globosum-j	49:164	
807	ajs1	lax. 228		Adjacent stigma 1	49:165	
808	cur6	eli.2,cur.j	5H/7HS	Curly 6	49:166	
809	cur7	cur.l	3HL/6H	Curly 7	49:167	
810	cur8	cur.m	4HL/5HS/	Curly 8	49:168	
811	des16	des.w	7H	Desynapsis 16	49:169	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
812	lin3	lax234, lin.e	5H/3H/5HL	Lesser internode number 3	49:170	
813	nec35	nec.n	3HL	Necrotic leaf spot 35	49:172	
814	nec36	nrc.q	1H/3H	Necrotic leaf spot 36	49:173	
815	nec38	nec.s	2HL/5HL	Necrotic leaf spot 38	49:174	
816	nec39	nec.u	5H/7HL	Necrotic leaf spot 39	49:175	
817	nec40	nec.39	2H/5HS	Necrotic leaf spot 40	49:176	
818	nec41	nec.42	5HL	Necrotic leaf spot 41	49:177	2319
819	nec42	nec.69	2HL/5HL	Necrotic leaf spot 42	49:178	
820	mac-a	mac.1	1HL/3HL	Maculosus-a	49:179	
821	mac-b	mac.4	3HL	Maculosus-b	49:180	
822	blf3	blf.3	4HL	Broad leaf 3	49:181	
823	Lax-p	Lax-58	1H/4HL/7H.	Laxatum-p	49:182	
824	lax-q	lax-86	33H/5H	Laxatum-q	49:184	
825	lax-of	Lax-312	3HS	Laxatum-of	49:185	
826	Lax-1a	lax.ag	3HL	Laxatum-la	49:186	1575
827	lax-1b	lax.ah	2HL	Laxatum-lb	49:187	
828	lax-1c	lax-.aj	3H/6H	Laxatum-lc	49:188	
829	lax-1d	lax.ak	3HL/6HL	Laxatum-ld	49:189	
830	Lax-le	Lax.al	7HS	Laxatum-le	49:190	2417
831	Wsa1	Ws	1HL	Weak spikelet attachment 1	49:191	

* 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.

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Descriptions of Barley Genetic Stocks Tables 2 and 3 (2019)

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In this section of the Barley Genetics Newsletter volume 49, 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 49 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, clo-b	7HL	Xantha seedling 1	49: 60	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	49: 62	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
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	49: 64	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	49: 66	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	49: 68	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	
199	nec37	nec.r	4HS	Necrotic leaf spot 37	49: 71	
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	5HL	Desynapsis 6	49: 72	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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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
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	mu12	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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
271	abo15	alb,,t	6HS	Albino seedling 15	26:251	
272	Rpt5	Pt_a	6HL	Reaction to *Pyrenophora teres* f. *teres* 5	43:120	
273	sdw10	sdw.g	6HS	Desynapsis 10	49: 74	2450
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	
277	sdw21	sdw.ap	6H	Semidwarf 21	49: 75	
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	49: 76	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	2HL	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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
334	raw6	r6	5HL	Smooth awn 6	49: 77	2437
335	msg49	msg,,jw	5HL	Male sterile genetic 49	45:122	2402
336	glo-b	glo-b	5HL	Globosum-b	48:125	1327
337	blf2	bb2, nlh	5HL	Broad leaf 2	41:137	1667
338	lys1	lys	5HL	High lysine 1	49: 78	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	49: 80	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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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
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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
407	cer-m	cer-15	1HL/ 3HL	Eceriferum-m +/++ + ++	41:161	434
408	cer-n	gs9,cer-20	2HL	Eceriferum-n - - ++ & - +/- ++	44:143	435
409	cer-o	cer-28	1HL	Eceriferum-o -/+ ++ ++	49: 81	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 ++ ++ +	48:125	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-85	2H	Eceriferum-zk + + +/-	49: 82	458
430	cer-zl	cer-17		Eceriferum-zl - - ++	49: 84	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-286	2H	Eceriferum-zw + + ++	49: 85	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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
444	cer-ya	cer-180	3HS	Eceriferum-ya ++ ++ -	49: 86	1534
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-139	3HS	Eceriferum-yd - ++ ++	49: 87	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-116	3HS	Eceriferum-yh - ++ ++	49: 88	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	49: 89	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:	
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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
518	sdw1	denso, Hv20ox$_2$	3HL	Semidwarf 1	49: 91	2513
519	mnd1	m	2HS	Many noded dwarf 1	48:156	253
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

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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
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	49: 95	1788
579	mat-c	Eam6, HvCEN	2H	Praematurum-c	49: 97	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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
586	bra-d	bra-d	1HL	Bracteatum-d	49:100	1696
587	abo3	a2, alb-za		Albino seedling 3	26:514	165
588	abo10	a_{t2}		Albino seedling 10	26:515	57
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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
621	Cal-c	Cal-c	5HL	Calcaroides-c	41:195	1567
622	cal-e	cal-23	5HS	Calcaroides-e	32:123	
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	49:102	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
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

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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	clo-a	clo.117. fch16	2HS	Chlorina-a	49:103	
677	mtt7	mtt.h	2HS	Mottled leaf 7	49:105	
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
697	Nec26			Necroticans 26	43:200	3631
698	nec27			Necroticans 27	43:201	3633
699	nec28			Necroticans 28	43:202	3635

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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	49:106	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; R47-23#1		Required for *Puccinia graminis* resistance 6	46:144	3700
736	rpr7	γ08-115; R3-18#3		Required for *Puccinia graminis* resistance 7	46:145	3701

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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-23	48:176	
747	ant24	ant-10		Anthocyanin-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	
755	sdw8	sdw.ab	5HL	Semidwarf 8	49:107	2442
756	sdw5	sdw.hf	1HL	Semidwarf 5	49:108	
757	sdw9	sdw.hg	1HL	Semidwarf 9	49:109	
758	sdw11	sdw.j	7HS	Semidwarf 11	49:110	2453
759	sdw12	sdw.l	2H	Semidwarf 12	49:111	2455
760	sdw13	sdw.m	3HS	Semidwarf 13	49:112	2456
761	sdw14	sdw.w	2H	Semidwarf 14	49:113	
762	sdw15	sdw.ab	7HS	Semidwarf 15	49:114	2440
763	sdw16	sdw.ac	7HL	Semidwarf 16	49:115	
764	sdw17	sdw.ad	2H	Semidwarf 17	49:116	
765	sdw18	sdw.ae	5HL	Semidwarf 18	49:117	
766	sdw19	sdw.ai	5H	Semidwarf 19	49:118	
767	sdw20	sdw.an	2HL	Semidwarf 20	49:119	2443
768	sdw22	sdw.aq	5HL/6H	Semidwarf 22	49:120	
769	sdw23	sdw.ar	5HL	Semidwarf 23	49:121	
770	sdw24	sdw.as	2HL/6H	Semidwarf 24	49:122	
771	sdw25	sdw.at	5H	Semidwarf 25	49:123	
772	sdw26	sdw.aw	2H	Semidwarf 26	49:124	2446
773	sdw27	sdw.ax	7H	Semidwarf 27	49:125	2447

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
774	sdw28	sdw.bc	7HL	Semidwarf 28	49:126	
775	sdw29	sdw.au		Semidwarf 29	49:127	2441
776	glo-g	glo.1	3H	Globosum-g	49:128	
777	glo-h	glo.2	7HS	Globosum-h	49:129	
778	glo-i	glo.h	7HS	Globosum-i	49:130	1756
779	gig3	gig.2	1H	Gigas 3	49:131	1749
780	lks9	lks.m	3H	Short awn 9	49:132	1782
781	lks7	lks.o	5HL	Short awn 7	49:133	
782	lks8	lks.p	1HL/ 7HS	Short awn 8	49:134	
783	ari-za	ari.49	5HS/ 5HL	Breviaristatum-za	49:135	
784	scl-c	scl.2	3HS	Scirpoides-c	49:136	
785	seg9	seg.l	6HL/ 7HS	Shrunken endosperm genetic 9	49:137	
786	sex10	sex.m	2HL/7H	Shrunken endosperm xenia 10	49:138	
787	viv-d	viv.2	2HL	Viviparoides-d	49:140	
788	viv-e	viv.3	3HL/7H	Viviparoides-e	49:142	
789		viv.8	4HS/ 5HS	Viviparoides-f	49:144	
790	wst8	wst.l	2HL/3H	White streak 8	49:145	
791	wst9	wst.m	5HL/ 7HS	White streak 9	49:146	1266
792	zeo4	zeo.e	1HL	Zeocriton 4	49:147	1609
793	smn2	smn.l	3H	Seminudoides 2	49:148	
794	Smn3	smn4	6HL	Seminudoides 3	49:149	
795	dsp12	dsp.au	3HL	Dense spike 12	49:151	
796	clo-c	clo.104	2H	Chlorina-b	49:152	
797	xan-l	xan.35	3H	Xantha-l	49:154	
798	clo-d	clo.113	1H/3HS	Chlorina-c	49:156	
799	fch18	fch.aa	2H	Chlorina seedling 18	49:157	1736
800	fch19	fch.ad	1HL	Chlorina seedling 19	49:158	
801	fch20	Fch.ae	2H	Chlorina seedling 20	49:159	
802	fch21	fch.af	1HL/3H	Chlorina seedling 21	49:160	
803	fch22	fch.ai	1H/3H	Chlorina seedling 22	49:161	
804	fch23	fch.al	4HL/ 7HL	Chlorina seedling 23	49:162	
805	srp1	srp.a	1HL/ 3HL	Serpentina 1	49:163	

BGS no.	Locus code*	Other codes	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
806	glo-j	glo.j	3HL/7H	Globosum-j	49:164	
807	ajs1	lax. 228		Adjacent stigma 1	49:165	
808	cur6	eli.2,cur.j	5H/7HS	Curly 6	49:166	
809	cur7	cur.l	3HL/6H	Curly 7	49:167	
810	cur8	cur.m	4HL/5HS/	Curly 8	49:168	
811	des16	des.w	7H	Desynapsis 16	49:169	
812	lin3	lax234, lin.e	5H/3H/5HL	Lesser internode number 3	49:170	
813	nec35	nec.n	3HL	Necrotic leaf spot 35	49:172	
814	nec36	nrc.q	1H/3H	Necrotic leaf spot 36	49:173	
815	nec38	nec.s	2HL/5HL	Necrotic leaf spot 38	49:174	
816	nec39	nec.u	5H/7HL	Necrotic leaf spot 39	49:175	
817	nec40	nec.39	2H/5HS	Necrotic leaf spot 40	49:176	
818	nec41	nec.42	5HL	Necrotic leaf spot 41	49:177	2319
819	nec42	nec.69	2HL/5HL	Necrotic leaf spot 42	49:178	
820	mac-a	mac.l	1HL/3HL	Maculosus-a	49:179	
821	mac-b	mac.4	3HL	Maculosus-b	49:180	
822	blf3	blf.3	4HL	Broad leaf 3	49:181	
823	Lax-p	Lax.58	1H/4HL/7H.	Laxatum-p	49:182	
824	lax-q	lax.86	33H/5H	Laxatum-q	49:184	
825	lax-of	lLax.312	3HS	Laxatum-of	49:185	
826	Lax-1a	lax.ag	3HL	Laxatum-la	49:186	1575
827	lax-1b	lax.ah	2HL	Laxatum-lb	49:187	
828	lax-1c	lax-.aj	3H/6H	Laxatum-lc	49:188	
829	lax-1d	lax.ak	3HL/6HL	Laxatum-ld	49:189	
830	Lax-le	Lax.al	7HS	Laxatum-le	49:190	2417
831	Wsa1	Ws	1HL	Weak spikelet attachment 1	49:191	

* 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	ACBV89B229
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
ajs1	lax-228	807		Adjacent sigma 1	49:166	Foma
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
ant3		594		Anthocyanin-deficient 3	29: 82	Bonus
ant4		595	4H	Anthocyanin-deficient 4	45:216	Foma

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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 23	48:176	Bonus
ant24	ant-10	747		Anthocyanin 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
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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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
ari-za	ari.49	783	5HS/ 5HL	Breviaristatum-za	49:135	Bonus
asp1		649		Aborted spike 1	43:172	Steptoe
blf1	bb	326	2HL	Broad leaf 1	46: 90	Bonus
blf2	bb2, nlh	337	5HL	Broad leaf 2	41:137	Hannchen
blf3	blf	822	4HL	Broad leaf 3	49:181	Bonus
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	49:100	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
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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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 + + ++	40:104	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 -/+ ++ ++	49: 81	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
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 ++ ++ -	49: 86	Bonus
cer-yb	cer-200	445	2HL	Eceriferum-yb ++ ++ -	41:171	Bonus
cer-yc	cer-135	446	6H/ 7HS	Eceriferum-yc - ++ ++	41:172	Bonus

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cer-yd	cer-139	447	3HS	Eceriferum-yd - ++ ++	49: 87	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 - ++ ++	49: 88	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
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 + + +/-	49: 82	Bonus
cer-zl	cer-17	430		Eceriferum-zl - - ++	49: 84	Bonus
cer-zn	cer-244	431	1H	Eceriferum-zn +/- ++ ++	40:112	Foma
cer-zo	cer-229	432	3HS	Eceriferum-zo - ++ ++	44:154	Foma

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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 + + ++	49: 85	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/5H	Curled leaf dwarf 1	40: 76	Hannchen
clo-a	clo.117, fch16	676	2HS	Chlorina-a	49:103	Bonus
clo-c	clo.104	796	2H	Chlorina-b	49:152	Tron
clo-d	clo.113	798	1H/ 3HS	Chlorina-c	49:156	Bonus
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
cur4	glo-d	460	2HL	Curly 4	45:172	Asahi 5
cur5	cu5	231	2HS	Curly 5	41:120	Glenn
cur6	eli2, cur.i	808	5HL/ 7HS	Curly 6	49:166	Foma
cur7	cur.l	809	3HL/ 6H	Curly 7	49:167	Morex
cur8	cur.m	810	4H/ 6HS	Curly 8	49:168	Morex

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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, HvDMC1	14	7HL	Desynapsis 5	48: 59	Betzes
des6		215	1HL	Desynapsis 6	49: 72	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
des16	des.w	811	7HL	Desynapsis 16	49:169	Freja
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.am	244	1HL	Dense spike 11	41:121	Akashinriki
dsp12	dsp.au	795	3HL	Dense spike 12	49:151	Bido
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
Eam6	Ea6, Ea, HvCEN	98	2HS	Early maturity 6	46: 57	Morex
eam7	HvCO7	252	6HS	Early maturity 7	45:118	California Mariout

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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
eog1	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
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

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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
fch18	fch.aa	799	2H	Chlorina seedling 18	49:157	ND13319-1
fch19	fch.ad	800	1HL	Chlorina seedling 19	49:158	Morex
fch20	fch.ae	801	2H	Chlorina seedling 20	49:159	Morex
fch21	fch.af	802	1HL/ 3HL	Chlorina seedling 21	49:160	Morex
fch22	fch.ai	803	1H/ 3HL	Chlorina seedling 22	49:161	Morex
fch23	fch.al	804	4H/ 7HL	Chlorina seedling 23	49:162	Morex
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
gig3	gig.2	779	1H	Gigas 3	49:131	Bonus
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
glo-g	glo-1	776	2H	Globosum-g	49:128	Bonus
glo-h	glo-2	777	7HS	Globosum-h	49:129	Bonus
glo-i	glo.h	778	7HS	Globosum-i	49:130	Bonus
glo-j	glo.i	806	3HL/ 7H	Globosum-j	49:164	Steptoe
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

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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
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:`5`	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-p	Lax.58	823	1H/4HL/7HL	Laxatum-p	49:182	Bonus
lax-q	lax.86	824	3HL/5HL	Laxatum-q	49:184	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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
lax-kf	lax-295	494		Laxatum-kf	47:163	Foma
Lax-la	Lax.ag	826	3HL	Laxatum-la	49:186	Volla
lax-lb	lax.ah	827	2HL	Laxatum-lb	49:187	Volla
lax-lc	lax.aj	828	3HL/ 6HL	Laxatum-lc	49:188	Volla
lax-ld	lax.ak	829	3HL/ 6HL	Laxatum-ld	49:189	Volla
Lax-le	Lax-al	830	7HS-	Laxatum-le	49:190	Steptoe
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
lax-of	lax.312	825	3HS	Laxatum-of	49:185	Foma
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
lin1	s, rin	99	2HS	Lesser internode number 1	41: 92	Natural occurrence
lin3	lax-234, lin.e	812	2H/3H /5HL	Lesser Internode number 3	49:170	Foma
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	49: 68	CIho 5641
lks6	lks.q	724	1H/5H /6H	Short awn 6	49:106	Morex
lks7	lks.o	781	5HL	Short awn 7	49:133	Donaria
lks8	lks.p	782	1HL/ 7HS	Short awn 8	49:134	Steptoe
ks9	lks.m	780	3H	Short awn 9	49:132	Donaria

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
lnt1	rnt	118	3HL	Low number of tillers 1	47: 74	Mitake
lys1	lys	338	5HL	High lysine 1	49: 78	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
mac-a	mac.1	820	1H/ 3HL	Maculosus-a	49:179	Bonus
mac-b	mac.4	821	3HL	Maculosus-n	49:180	Bonus
mat-b	mat-7	578	7HL	Praematurum-b	49: 95	Bonus
mat-c	Eam6, HvCEN	579	2H	Praematurum-c	49: 97	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
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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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
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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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
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	49:105	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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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
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
nec35	nec.n	813	3HL	Necrotic leaf spot 35	49:172	Bonus
nec36	nec.q	814	1H/3H	Necrotic leaf spot 36	49:173	Morex
nec37	nec.r	199	4HS	Necrotic leaf spot 37	49: 71	Morex

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
nec38	nec.s	815	3H/ 5HL	Necrotic leaf spot 38	49:174	Bonus
nec39	nec.u	816	5H/ 7HL	Necrotic leaf spot 39	49:175	Emir/*H. bulbosum*
nec40	nec.39	817	2H/ 5HS	Necrotic leaf spot 40	49:176	Kristina
nec41	nec.42	818	5HL	Necrotic leaf spot 41	49:177	Kristina
nec42	nec.69	819	2HL/ 5HL	Necrotic leaf spot 42	49:178	Kristina
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
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	49:102	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	48:185	Steptoe
Qsd2	SD2	753	3HL	Quantitative seed dormancy 2	48:187	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	49: 77	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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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
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

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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
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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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
sci-c	sci-2	784	3HS	Scirpoides-c	49:136	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	49: 91	M21
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	
sdw5	sdw.bf	756	5HL	Semidwarf 5	49:108	Hannchen
sdw6	sdw.f	240	1H/7H	Semidwarf 6	46: 77	Vada
sdw7	sdw.u	196	4HL	Semidwarf 7	43:103	Glenn
sdw8	sdw.ah	755	5HL	Semidwarf 8	49:107	Volla
sdw9	sdw.bg	757	1HL	Semidwarf 9	49:107	TR473
sdw10	sdw.g	273	6HS	Semidwarf 10	49: 74	Birgitta
sdw11	sdw.j	758	7HS	Semidwarf 11	49:110	Akashinriki
sdw12	sdw.l	759	2H	Semidwarf 12	49:111	Akashinriki
sdw13	sdw.m	760	3H	Semidwarf 13	49:112	Akashinriki
sdw14	sdw.w	761	2HL	Semidwarf 14	49:113	Julia
sdw15	sdw.ab	762	7HS	Semidwarf 15	49:114	Diamant
sdw16	sdw.ac	763	7HL	Semidwarf 16	49:115	Volla
sdw17	sdw.ad	764	2H	Semidwarf .17	49:116	Volla
sdw18	sdw.ae	765	5HL	Semidwarf 18	49:117	Volla
sdw19	sdw.ai	766	5H	Semidwarf 19	49:118	Volla
sdw20	sdw.an	767	2HL/ 7H	Semidwarf 20	49:119	Larker
sdw21	sdw.ap	277	6H	Semidwarf 21	49: 75	Harrington

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
sdw22	sdw.aq	768	5HL/ 6H	Semidwarf 22	49:120	Norbert
sdw23	sdw.ar	769	5HL	Semidwarf 23	49:121	Morex
sdw24	sdw.as	770	2H/6H	Semidwarf 24	49:122	Hazen
sdw25	sdw.at	771	5H	Semidwarf 25	49:123	Hazen
sdw26	sdw.aw	772	2H	Semidwarf 26	49:124	Morex
sdw27	sdw.ax	773	7H	Semidwarf 27	49:125	Birgitta
sdw28	sdw.bc	774	7HL	Semidwarf 28	49:126	Morex
sdw29	sdw.au	775		Semidwarf 29	49:127	Bomi Abed
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
seg9	seg.l	785	5HL/ 7HS	Shrunken endosperm genetic 9	49:137	Betzes
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
sex10	sex.m	786	2HL/ 7H	Shruken endosperm xenia 10	49:138	Washonupana
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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
sld1	dw-1	126	3HL	Slender dwarf 1	49: 66	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
sls1	sls1	227	1HS	Small lateral spikelet 1	48:111	Morex
smn1	smn	38	3H/ 5H	Seminudoides 1	49: 62	Haisa
smn2	smn-1	793	3H	Seminudoides 2	49:148	Bonus
smn3	smn.4	794	6HL	Seminudoides 3	49:149	Akashinriki
snb1	sb	26	7HS	Subnodal bract 1	48: 67	L50-200
srh1	S, l	321	5HL	Short rachilla hair 1	46: 86	Lion
srp1	srp.a	805	1H/ 3HL	Serpentina 1	49:163	Chikurin Ibaraki 1
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	49: 76	Montcalm
var2	va2	344	5HL	Variegated 2	49: 80	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
viv-d	viv-2	787	2HL/5 HL/7H	Viviparoides-d	49:140	Foma

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
viv-e	viv-3	788	3HL/ 7H	Viviparoides-e	49:142	Foma
viv-f	viv-8	789	4HS/ 5HL	Viviparoides-f	49:144	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
Wsa1	Ws	831	1HL	Weak spikelet attachment 1	49:191	Bowman
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
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
wst8	wst.l	790	2HL/ 3H/7H	White streak 8	49:145	
wst9	wst-m	791	5HS/ 7HS	White streak 9	49:146	MINN 139
wxs1	wxs	615	7H/ 2HL	Waxy spike 1	43:160	Steptoe
Xnt1	X_a, xan-h, clo-b	25	7HL	Xantha seedling 1	49: 62	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

Locus code*	Other codes	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
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:	Utah 41
Zeo1	Knd, Ert-r	82	2HL	Zeocriton 1	47: 63	Donaria
Zeo2	cly1.b, HvAP2	614	2HL	Zeocriton 2	47:177	36Ab51
Zeo3	Zeo2, cly1.c	184	4HL	Zeocriton 3	47: 95	Morex
Zeo4	Zeo.e	792	1HL	Zeocriton 4	49:147	Rubin

* 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 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 (8).
: Xantha-h = *xan-h* (12, 13, 15).
: Chlorina-125 = *Clo-125* (12, 13).
: Chlorina-b = *clo-b* (1).

Inheritance:

Monofactorial incomplete or semi-dominant (8, 13); allelic to recessive xantha-h (*xan-h*) mutants (5).

Located in chromosome 7HL (8); *Xnt1.a* is over 35.9 cM distal from the *lks2* (short awn 2) locus (8, 14); *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 (3); *Clo.125* was not associated with any 7H SNP markers in a presumed heterozygous plant of the Bowman backcross-derived line BW186 (3), in 7H bin 10.

Description:

Segregation is observed 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 (8). Color differences between normal and heterozygous plants were observed in the *Xnt1.a2* mutant only until just prior to heading (11). Mutants at the *Xnt1* locus must be maintained as heterozygous stocks (4, 8). 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 (5). 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 (5, 6, 7). The chlorophyll content of *xan-h* heterozygotes is reduced slightly (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in the cross Akashinriki (OUJ659, PI 467400) X linkage tester 191 (OUL094) (8); a sodium azide induced mutant in Bonus (NGB 14657, PI 189763) (9).

Mutational events:

Xnt1.a in the hybrid Akashinriki X linkage tester 191 (OUM215) (8, 13); *Xnt1.a2* in translocation stock T6-7d (10); *Xnt1.a3* in MC 20 (PI 357319) (10); 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) (5, 11, 12); *xan-h.30*, *-h.38*, *-h.56*, and *-57* in Bonus (6, 9, 12, 13). 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 (6).

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*) in Bonus; *Xnt1.125* in Bowman*8 (BW186, NGB 22018).

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BGS 38, Seminudoides 1, *smn1*

Stock number: BGS 38
Locus name: Seminudoides 1
Locus symbol: *smn1*

Previous nomenclature and gene symbolization:

Seminuoides = *smn* (5, 6).
Seminudoides-2 = *smn.2* (1, 4).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosomes 3H (1); *smn1.a* is associated with SNP markers 2_0607 to 1_0839 (positions 52.41 to 100.48 cM) in 3H bins 04 to 06 and with SNP markers 2_1324 to 2_0392 (positions 47.40 to 109.27 cM) in 5H bins 04 to 06 of the Bowman backcross-derived line BW871 (1); *smn1.2* is associated mainly with SNP markers 1_0672 to 2_0009 (positions 58.56 to 164.68 cM) in 3H bins 04 to 10 of Bowman backcross-derived line BW869 (1). Previously located in chromosome 7HS, based on linkage drag with the *ant1* (anthocyanin-less 1) locus (3).

Description:

The caryopsis of *smn1* plants is not completely covered because gaps develop between the margins of the lemma and palea. Adherence of the lemma and the palea to the pericarp is poor, but the grain does not thresh free from the hull at maturity. Tiller number and grain yield are often reduced; and leaf blades are narrow (6). Plants of the Bowman backcross-derived line for *smn1.a*, BW871, had kernels that were slightly shorter and thinner, and weighed 10 to 20% less, 47 vs. 56 mg, than Bowman kernels. Rachis internodes and awns were slightly longer. Test weight was 20% lower; and grain yields of BW871 varied from 1/3 to 3/4 of those for Bowman (2). Plants of the Bowman backcross-derived line for *smn1.2*, BW869, showed similar phenotypic deviations from Bowman, but the loss of vigor was greater. Plants were 20% shorter; kernels weighed nearly 20% less, 3.6 vs. 5.4 mg; and grain yields were 1/10 to 1/5 those for Bowman (2).

Origin of mutant:

An X-ray induced mutant in Haisa (PI 197617) (5, 6).

Mutational events:

smn1.a (Mut. 4128, GSHO 1602) in Haisa (PI 197617) (6); *smn1.2* (NGB 114697) in Bonus (NGB 14657, PI 189763) based on retained SNP markers and phenotype in the Bowman backcross-derived line, BW869 (1, 2, 4).

Mutant used for description and seed stocks:

smn1.a (GSHO 1602, Mut. 4128) in Haisa; *smn1.a* from Haisa in Bowman (PI 483237, NGB 22812)*5 (GSHO 3420, BW871, NGB20786); *smn1.2* from Bonus in Bowman*3 (BW869, NGB 20785).

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BGS 68, Purple veined lemma 1, *Pvc1*

Stock number:	BGS 68
Locus name:	Purple veined lemma 1
Locus symbol:	*Pvc1*

Previous nomenclature and gene symbolization:

Purple veined lemma = *C* (1).
Purple veined lemma = P_c (1, 6).
Purple veined lemma = P_e (1, 6).
Purple veined lemma = P_f (1, 6).

Inheritance:

Monofactorial dominant (4), but Buckley suggested that three pairs of genes controlled expression of purple pigmentation of lemma veins (1).

Located in chromosome 2HL (1, 5); *Pvc1.a* is about 22.2 cM distal from the *vrs1* (six-rowed spike 1) locus (1); no SNP markers polymorphisms compared to Bowman in the Bowman backcross-derived line for *Pvc1.a,* BW651, using BOPA markers (2); non-Bowman 50K SNP markers were retained in BW651 at 573.6 to 579.6 Mb, 69.88 cM (108.71 cM in Druka et al., 2011), 2H bin 08 (4).

Description:

Purple pigmentation of lemma veins is caused by the presence of anthocyanins. When *Pvc1.a* is expressed, purple pigmentation of the kernel is confined mainly to the lemma veins (1). The pigments are formed late during grain fill when the lemma is exposed to sunlight, and they tend to fade as the spike matures (3). The Bowman backcross-derived line for *Pvc1.a*, BW651, had slightly heavier kernel and showed a slight increase in grain yield compared to Bowman (3).

Origin of mutant:

Natural occurrence in some cultivars and in some *Hordeum vulgare* subsp. *spontaneum* accessions.

Mutational events:

Pvc1.a (GSHO 132) in Buckley 2223-6 (1); *Pvc1.a* in CIho 16125 and *pvc1.b* in CIho 16126 (GSHO 1779), near-isogenic lines with the purple and white veined lemma, respectively, selected from the F_{11} generation of the cross Deficiens (CIho 5419)/Chevron (CIho 1111), developed by G.A. Wiebe (https://npgsweb.ars-grin.gov/gringlobal/accessiondetail.aspx?id=1074638).

Mutant used for description and seed stocks:

Pvc1.a (GSHO 132) in Buckley 2223-6 and CIho 16125; *pvc1.b* in CIho 16126; *Pvc1.a* 22812)*7 (GSHO 1929, BW 651, NGB 22216).

References from R.I. Wolfe's Multiple Dominant Stock (GSHO 1565) in Bowman (PI 483237, NGB

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BGS 126, Slender dwarf 1, *sld1*

Stock number:	BGS 126
Locus name:	Slender dwarf 1
Locus symbol:	*sld1*

Previous nomenclature and gene symbolization:

Dwarf 1 = *dw1* (5).
Light green dwarf = *dw-1* (10).
Slender dwarf j = *sld.j* (1, 3).

Inheritance:

Monofactorial recessive (6, 11).

Located in chromosome 3HL (8, 10, 11); *sld1.a* is over 6.3 cM distal from the *uzu1* (uzu 1) locus (8, 10); *sld1.a* is about 20.5 cM distal from the *uzu1* locus (10); *sld1.a* is about 1.2 cM from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (9); *sld1.a* is associated with SNP markers 2_1402 to 2_0362 (positions 77.00 to 119.10 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW859 (1); *sld1.a* with *uzu1.a* is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman backcross-derived line BW860 (1); *sld1.c* is associated with SNP markers 2_1145 to 2_0093 (positions 65.96 to 127.91 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW861 (1); *sld1.j* is associated with SNP markers 3_0474 to 3_0170 (positions 74.51 to 120.83 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW856 (1); BW859 and BW860 have a common SNP patterns from 2_0017 to 2_0362 (positions 106.46 to 119.10 cM) (1, 3), in 3H bin 07.

Description:

Plant height is reduced to about 1/2 to 2/3 of normal, plant development is delayed, and plants are slightly yellow green in color (5, 10). Plants of the mutant *sld1.a* (*dw-a*, OUM148) headed 4 days later and were shorter, 81 vs. 122 cm, than their parent, Akashinriki (7). Kernel weights and kernels per spike of *sld1.a* plants were reduced; and grain yields were 30% lower (7). The distribution of leaf blades in *sld1* plants was altered because the peduncle is relatively long in proportion to the other internodes. Plants homozygous for the *sld1.c* allele were slightly weaker and shorter than *sld1.a* plants in their respective Bowman backcross-derived lines, BW861 and BW859 (3). Heading was delayed about 5 days in both BW859 and BW861. BW859 plants exhibited about 30% reduction in plant height, but had about three more kernels per spike. Kernel weights for BW859 were 5 to 15% lower than those of Bowman and grain yields ranged from 1/3 to 90% those of Bowman. Plants of BW861 showed a 40% reduction in plant height compared to Bowman, spikes had an average of two more kernels; kernel weights were 10 to 25% lower; and grain yield ranged from 10 to 75% those of Bowman (3). The allele symbol *sld1.j* is recommended for the mutant in Bowman backcross-derived line BW856 based on similar phenotypic characteristics and the position of the retained parental SNP markers (1, 3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (5).

Mutational events:

sld1.a (*dw-a*, OUM148, GSHO 2488) in Akashinriki (5, 8); *sld1.c* (862PK, GSHO 2489) in Plena (PI 321822) (3, 10); *sld1.j* (GSHO 2485, DWS1062, SA4114-2-4-2-1) in Glenn (CIho 15769) (1, 2).

Mutant used for description and seed stocks:

sld1.a in Akashinriki (GSHO 2488, OUM148); *sld1.j* (GSHO 2485) in Glenn; *sld1.a* in Bowman (PI 483237)*7 (GSHO 1970), in Bowman*8 (BW859, NGB 22296); *sld1.c* in

Bowman*7 (GSHO 1972, BW861, NGB 22298); *sld1.a* with *uzu1.a* (OUM148, GSHO 2489) from Akashinriki in Bowman*8 (GSHO 1971, BW860, NGB 22297); *sld1.j* in Bowman (PI 483237, NGB 22812)*6 (GSHO 2357); *sld1.j* in Bowman*7 (BW856, NGB 22293). .

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Prepared:

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Revised:

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:103-104.
J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:66-67.

BGS 172, Short awn 5, *lks5*

Stock number: BGS 172
Locus name: Short awn 5
Locus symbol: *lks5*

Previous nomenclature and gene symbolization:

Short awn 5 = *lk5* (7).
Breviaristatum-2 = *ari-2* (5, 6).
Breviaristatum-c = *ari-c.2* (6, 14, 15).
Short awn n = *lks.n* (2, 4, 13).

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 4HL (16); *lks5.f* is about 6.9 cM distal from the *Kap1* (Hooded lemma 1) locus (7, 9); *lks5.f* is near AFLP marker E4143-5 in subgroup 38 of the Proctor/Nudinka map (10); *lks5.f* is associated with SNP markers 1_0262 to 2_0072 (positions 76.26 to 95.92 cM) in 4H bin 06 of the Bowman backcross-derived line BW493 (2); *ari-c.2* is associated with SNP markers 2_0289 to 2_1322 (positions 69.62 to 112.64 cM) in 4H bins 05 to 08 of the Bowman backcross-derived line BW040 (2), in 4H bin 06; *lks5.p* was isolated in genetic stocks BW474 and BW475 from the *lel1* (leafy lemma 1) stock, G7118, *lks5.p* is associated with SNP markers 2_1122 to 1_1019 (positions 47.80 to 183.54) in 4H bins 05 to 13 of the Bowman backcross-derived line BW474 (2); *lks5.p* is associated with SNP markers 2_0422 to 2_0072 (positions 38.41 to 95.92 cM) in 4H bins 04 to 06 of the Bowman backcross-derived line BW475 (2); in 4H bin 06.

Description:

Awns on both central and lateral spikelets are reduced to 1/4 or less of normal length in six-rowed cultivars (7). Only the central spikelets exhibit reduced awn length in two-rowed cultivars (3, 6). The rachilla is often modified, and in extreme cases the rachilla may develop as a malformed additional floret (7). Awns are thin and brittle (6). Plants of the Bowman backcross-derived line for *lks5.f*, BW493, had awns that extended 3 to 4 cm beyond the tip of the spike, while those of Bowman were 12 to 13 cm beyond the tip. Kernels of BW493 were slightly shorter, narrower (3.4 vs. 3.9 mm), and lighter (4.6 vs. 5.5 mg). BW493 plants were slightly taller than Bowman and grain yields were slightly reduced (4). Presence of the mutant allele *lks5.p* is needed for expression of the leafy lemma 1 (*lel1.a*) gene (4, 10). Plants of the Bowman backcross-derived lines for *ari-c.2* (BW040) and *lks5.n* (*lks.n*, BW486) were phenotypically similar to BW493 plants; and donor parent SNP markers in the same region of chromosome 4H were retained in all three BW lines (2, 4).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (7).

Mutational events:

lks5.f (GSHO 1297) in CIho 5641 (7, 14); *lks5.g* (Kmut 218) in Asahi 5 (OUJ509) (13); *ari-c.2* (NGB 115847, GSHO 1651), *-c.59* (NGB 115913) in Bonus (NGB 14657, PI 189763), *-c.103* (NGB 115915) in Foma (NGB 14659, CIho 11333) (3); *ari-c.106* (NGB 115918) in Foma (5); *ari-c.109* (NGB 115921), *-c.110* (NGB 115922), *-c.111* (NGB 115923), *-c.112* (NGB 115924), *-c.120* (NGB 115932), *-c.139* (NGB 115949), *-c.157* (NGB 115967), *-c.159* (NGB 115969), *-c.179* (NGB 115989), *-c.180* (NGB 115990), *-c.199* (NGB 116008), *-c.201* (NGB 116010), *-c.203* (NGB 116012), *-c.204* (NGB 116013), *-c.206* (NGB 116014), *-c.210a* (NGB 116018), *-c.210b* (NGB 116019) *-c.229* (NGB 116039) in Foma, *-c.259* (NGB 116068), *-c.262* (NGB 116071), *-c.272* (NGB 116084), *-c.276* (NGB 116089), *-c.289* (NGB 116107), *-c.291* (NGB 116111) in Kristina

(NGB 14661, NGB 1500) (6); *ari-c.307* (NGB 116135) in Kristina (8); two possible additional alleles have been reported, *lks5.h* (*lk,,f*) in two-rowed Glacier (3); and a mutant in Morex (CIho 15773) (12); *lks5.r* in G7118 (leafy lemma, GSHO 1780) mutant stock (1, 3, 4, 11); *lks.n* (Mut 2263, GSHO 1783, DWS 1339) in Donaria (PI 161974) (2, 4, 13).

Mutant used for description and seed stocks:

lks5.f (GSHO 1297) in CIho 5641; *ari-c.2* (NGB 115847, GSHO 1651) in Bonus; *lks5.f* in Bowman (PI 483237, NGB 22812)*6 (GSHO 2014); *lks5.f* in Bowman*7 (BW493, NGB 20721); *ari-c.2* in Bowman*7 (GSHO 2013, BW040, NGB 20448); *lks5.r* from G7118 in Bowman*4 with *lel1.a* (BW474, NGB 20704); *lks5.r* from G7118 in Bowman*5 (BW475, NGB 20705); *lks5.n* from Donaria in Bowman*5 (GSHO 2281); *lks5.n* from Donaria in Bowman (BW486, NGB 20714).

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Revised:

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J.D. Franckowiak and U. Lundqvist. 2017. Barley Genet. Newsl. 47:89-90.
J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:68-70.

BGS 199, Necrotic leaf spot 37, *nec37*

Stock number:	BGS 199
Locus name:	Necrotic leaf spot 37
Locus symbol:	*nec37*

Previous nomenclature and gene symbolization:

Necroticans r = *nec.r* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 4HS (1); *nec37.r* is associated mainly with SNP markers 1_0132 to 2_1418 (positions 38.41 to 39.48 cM) in 4H bins 03 to 04 of the Bowman backcross-derived line BW624 (1).

Description:

Seedlings of the *nec37.r* mutant had whitish necrotic leaf spots and were very weak (2). Following crossing to Bowman, a mottled leaf mutant, *mtt7.h* (see BGS 677), and necrotic leaf spot mutant were isolated. Plants of the Bowman backcross-derived line for the necrotic leaf spot mutant, *nec37.r* (BW624), had necrotic spots on the first leaf and later necrotic blotches developed on older leaf blades. Plants had low vigor and were about half of normal height (2). The BW624 line retained from Morex the large lateral spikelet trait associated with the *Int-c.a* (Intermedium spike-c) gene. The locus name necrotic leaf spot 37, the locus symbol *nec37*, and the allele symbol *nec37.r* are recommended for this necrotic leaf spot mutant of Morex (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

nec37.r (MXM 56) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

nec37.r (MXM 56) in Morex; *nec37.r* in Bowman (PI 483237, NGB 22812)*4 (BW624, NGB 22190).

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. 2019. Barley Genet. Newsl. 49:71.

BGS 215, Desynapsis 6, *des6*

Stock number:	BGS 215
Locus name:	Desynapsis 6
Locus symbol:	*des6*

Previous nomenclature and gene symbolization:

Desynapsis ak = des.ak (1).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 5HL (1); *des6.i* is associated with SNP markers 2_0603 to 2_0772 (positions 199.4 to 205.07 cM) in 1H bins 14 to 15 and with SNP markers 2_0127 to 2_0988 (positions 189.08 to 247.08 cM) in 5H bins 10 to 13 of the Bowman backcross-derived line BW244 (1); *des6.o* is associated with SNP markers 2_0383 to 2_0772 (positions 192.78 to 205.07 cM) in 1H bins 13 to 15 and with SNP markers 2_0127 to 2_1355 (positions 189.10 to 234.98 cM) in 5H bins 10 to 12 of the Bowman backcross-derived line BW245 (1); *des6.ak* is associated with SNP markers 2_0127 to 2_0653 (positions 189.08 to 199.04 cM) in 5H bin 11 of the Bowman backcross-derived line BW227 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is 7.9 ± 2.1 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 3.3 micronuclei per quartet with a range of 0 to 12. Ovule fertility is about 16%, and about 22% of the selfed seeds are trisomics (3). Compared to Bowman plants of the Bowman backcross-derived line for *des6.i*, BW244, were slightly shorter. Kernels of BW244 were on average slightly lighter. Grain yields of BW244 were 1/5 to 1/4 those of Bowman (2). When grown under greenhouse conditions, BW244 and BW245 plants had 15 to 20% seed set (2). The *des.ak* mutant is likely an allele at the *des6* locus because the rough awn allele at the Smooth awn 1 (*Raw1*) locus was retained in BW227, BW244, and BW245 and the three lines had 15 to 20% seed set (2).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) isolated by R.T. Ramage (5, 6).

Mutational events:

des6.i (GSHO 597) in Betzes (PI 129430) (5, 6); *des6.m* in OAC 21 (CIho 1740), *des6.o* in Betzes (4, 6); *des6.ak* (GSHO 3322) in Steptoe (CIho 15229) (1, 2, 7).

Mutant used for description and seed stocks:

des6.i (GSHO 597) in Betzes; *des6.i* in Bowman (PI 483237, NGB 22812)*6 (BW244, NGB 22070); *des6.o* in Bowman*5 (BW245, NGB 22071); *des6.ak* from Steptoe in Bowman*6 (BW227, NGB 22054).

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.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:129.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:216.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:106-107.
J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:72-73.

BGS 273, Semidwarf 10, *sdw10*

Stock number: BGS 273
Locus name: Semidwarf 10
Locus symbol: *sdw10*

Previous nomenclature and gene symbolization:

Semidwarf g = *sdw.g* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 6HS (1); *sdw10.g* is associated with SNP markers 2_0262 to 2_1246 (positions 13.96 to 36.93 cM) in 6H bins 01 to 02 of the Bowman backcross-derived line BW807 (1).

Description:

The original mutant stock for *sdw10.g* was selected based on reduced plant height and loose hull attachment (2, 4). In the Bowman backcross-derived line for *sdw10.g*, BW807, plants averaged 15 to 20% shorter than Bowman and headed 2 to 3 days later. Kernels of BW807 weighed 10 to 15% more than those of Bowman, 61 vs. 55 mg. Grain yields of BW807 were 1/2 to 2/3 those of Bowman. Other morphological traits of BW807 were similar to those of Bowman (2). The locus name *sdw10* and the allele symbol *sdw10.g* are recommended for this Birgitta mutant because no other named semidwarf mutant is mapped in the short arm of chromosome 6H.

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 14667, NGB 1494) isolated by L.C. Lehmann (1, 4).

Mutational events:

sdw10.g (18:04:1, DWS1015, GSHO 2450) in Birgitta (NSGC 1870, NGB 14667, NGB 1494) (3, 4)

Mutant used for description and seed stocks:

sdw10.g (GSHO 2450) in Birgitta; *sdw10.g* in Bowman (PI 483237, NGB 22812)*3 (GSHO 2334); *sdw10.g* in Bowman*5 (BW807, NGB 22244).

References:

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4. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:74.

BGS 277, Semidwarf 21, *sdw21*

Stock number:	BGS 277
Locus name:	Semidwarf 21
Locus symbol:	*sdw21*

Previous nomenclature and gene symbolization:

Semidwarf ap = *sdw.ap* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 6H (1); *sdw21.ap* is associated mainly with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 04 to 07 of the Bowman backcross-derived line BW793 (1).

Description:

Plants with slightly reduced plant height were chosen during backcrossing to Bowman as likely to have the *sdw21.ap* gene. The plants of the Bowman backcross-derived line for *sdw21.ap*, BW793, were slightly shorter, about 4 cm, than Bowman plants; and peduncles were slightly shorter. Rachis internodes of BW793 plants averaged 5.2 mm while those of Bowman averaged 4.7 mm. Spikes had 1 to 2 fewer kernels. Kernels were shorter and weighed less than those of Bowman, 52 vs 57 mg. Grain yields of BW793 were 10 to 15% lower than those of Bowman (2). The response to gibberellic acid treatment was normal (3). The locus symbol *sdw21* and the allele symbol *sdw21.ap* are recommended for this Harrington mutant because no other named semidwarf mutant is mapped in the centromeric region of chromosome 6H (1, 2).

Origin of mutant:

A sodium azide induced mutant in Harrington isolated by S.E. Ullrich (1, 4).

Mutational events:

sdw21.ap (Wa14389-83, DWS 1265) in Harrington (3, 4).

Mutant used for description and seed stocks:

sdw21.ap (Wa14389-83) in Harrington; *sdw21.ap* in Bowman (PI 483237, NGB 22812)*3 (BW793, NGB 20770).

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Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:75.

BGS 306, Variegated 1, *var1*

Stock number:	BGS 306
Locus name:	Variegated 1
Locus symbol:	*var1*

Previous nomenclature and gene symbolization:

Variegated = *va* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5HL (5); *var1.a* is about 4.6 cM proximal from the *raw1* (smooth awn 1) locus (4. 5); *var1.a* is about 29.2 cM proximal from the *Rph9* (reaction to *Puccinia hordei* 9) locus in 5H bin 09 (1); *var1.a* is associated with SNP markers 1_0024 to 1_0477 (positions 165.44 to 173.49 cM) in chromosome 5H bin 10 of the Bowman backcross-derived line BW886 (2).

Description:

Narrow white stripes develop on young leaves, but they are not as well defined than those of *wst7* (white streak 7). White stripes are visible on the foliage and stems of older plants (4). When sown in plots, selections homozygous for the *var1.a* gene have a whitish cast until heading (3). Expression of the variegated trait is variable over environments and among individual plants and ranges from no effect to dying plants. Individual tillers with stripes often die before or shortly after heading. The Bowman backcross-derived line for *var1.a*, BW886, headed 1 to 2 days later than Bowman, was often slightly taller, and had 1 to 3 more kernel per spike. Kernels of BW886 slightly lighter; and its grain yields were 10 to 20% lower than those of Bowman (3).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (CIho 7149) (5).

Mutational events:

var1.a (Alb Acc 311, GSHO 1278) in Montcalm (CIho 7149) (5).

Mutant used for description and seed stocks:

var1.a (GSHO 1278) in Montcalm; *var1.a* in Bowman (PI 483237, NGB 22812)*7 (GSHO 2121, BW886, NGB 22319).

References:

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3. Franckowiak, J.D. (Unpublished).
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5. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:165.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:257.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:259.
J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:76.

BGS 334, Smooth awn 6, *raw6*

Stock number:	BGS 334
Locus name:	Smooth awn 6
Locus symbol:	*raw6*

Previous nomenclature and gene symbolization:

Smooth awn 6 = *r6* (4).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (4); *raw6.f* is near the *raw1* (smooth awn 1) locus based on linkage drag (4); *raw6.f* is associated with SNP markers 1_1456 to 2_1241 (positions 195.82 to 210.59 cM) in 5H bin 11 of the Bowman backcrossed-derived line BW665 (1).

Description:

The *raw6.f* plants have very fewer stigma hairs and seed set is greatly reduced (2, 3). In the Bowman backcross-derived line for *raw6.f*, BW665, which also contains the *raw1.a* gene. BW665 plants have very smooth awns and very few stigma hairs, and seed set is commonly less than 5%. Phenotypically, *raw6.f* plants closely resemble those produced by the *raw5.e* (smooth awn 5) gene. Recombination between the *raw6.f* and *raw1.a* genes is low because a recombinant was isolated only after several backcrosses to Bowman (3).

Origin of mutant:

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

Mutational events:

raw6.f (GSHO 2437) in Glenn (CIho 15769) (2).

Mutant used for description and seed stocks:

raw6.f (GSHO 2437) in Glenn; *raw6.f* in Bowman (PI 483237, NGB 22812)*8 (GSHO 2134, BW665, NGB 22229).

References:

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:282.

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:77.

BGS 338, High lysine 1, *lys1*

Stock number: BGS 338
Locus name: High lysine 1
Locus symbol: *lys1*

Previous nomenclature and gene symbolization:

High lysine = *lys* (11).

Inheritance:

Monofactorial recessive (11).

Located in chromosome 5HL (7, 8); *lys1.j* is about 10.8 cM distal from the *srh1* (short rachilla hair 1) locus (5, 7, 8). Donor parent SNP markers were retained in chromosomes 1HL, 2HL, 3H, and 7HL in Bowman backcross-derived line for *lys1.j*, BW495, with larger ones in 3H and 7HL (2).

Description:

After the hard dough stage, kernels develop a depression in the center of the lemma which becomes progressively more distinct with maturity. The mature endosperm of the mutant appears to be harder than normal. The mutant expresses xenia, permitting classification of kernels from heterozygous plants as normal or shrunken with an expected 3:1 ratio (11). Mutant plants have a higher lysine content in the endosperm than normal sibs (5, 9, 11). Field establishment and growth of mutant plants is normal, but grain yield is low (1, 12). The *lys1.j* gene reduced grain size and hordein protein content (1, 4). Morphologically the Bowman backcross-derived line for *lys1.j*, BW495, did not differ from Bowman; thus, both molecular data and physical information suggest that BW495 does not contain the *lys1.j* mutant (3).

Origin of mutant:

Natural occurrence in Hiproly (CIho 3947), an accession from Ethiopia (9, 10).

Mutational events:

lys1.j in Hiproly (CIho 3947, GSHO 1784) (6, 7, 9).

Mutant used for description and seed stocks:

lys1.j in Hiproly (GSHO 1784); *lys1.j* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2115); *lys1.j* in Bowman*4 (BW495, NGB 20723).

References:

1. Balasaraswathi, R., B. Køie, and H. Doll. 1984. The concentration and yield of hordein and some lysine-rich proteins as influenced by the *lys* gene of Hiproly barley. Hereditas 100:225-231.
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6. Jensen, J., and H. Doll. 1979. Gene symbols for barley high-lysine mutants. Barley Genet. Newsl. 9:33-37.
7. Karlsson, K.-E. 1972. Linkage studies on a gene for high lysine content in Hiproly barley. Barley Genet. Newsl. 2:34-36.
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Int. Barley Genet. Symp., Garching, 1975. Verlag Karl Thiemig, München.
9. Munck, L. 1972. High lysine barley - a summary of present research development in Sweden. Barley Genet. Newsl. 2:54-59.
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12. Oram, R.N., and H. Doll. 1981 Yield improvement in high lysine barley. Aust. J. Agric. Res. 32:425-434.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:286.

Revised:

J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:78-79.

BGS 344, Variegated 2, *var2*

Stock number:	BGS 344
Locus name:	Variegated 2
Locus symbol:	*var2*

Previous nomenclature and gene symbolization:

Variegated = *va2* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3H or 7HL (1); *var2.b* is associated with SNP markers 2_0356 to 2_0995 (positions 72.36 to 90.67 cM) in 3H bins 05 to 06 and with SNP markers 2_0354 to 2_1223 (positions 171.87 to 198.70 cM) in 7H bins 10 to 12 of the Bowman backcross-derived line BW887 (1); previously *var2.b* was mapped in 5HL over 29.8 cM from the *srh1* (short rachilla hair 1) locus (3).

Description:

Vertical white streaks of variable width and number are observed in leaf blades. White streaks are observed as leaf blades of new tiller emerge. The streaks often persist until maturity and are similar to those associated with the *wst7* (white streak 7) mutant. Expression of *var2.b* is variable from plant to plant and can be poor in certain genetic and climatic environments (2). No consistent agronomic difference between BW887, the Bowman backcross-derived line for *var2.b*, and Bowman were observed, but the grain yields of BW887 were 10 to 20% lower (2).

Origin of mutant:

Probably an X-ray induced mutant in Montcalm (CIho 7149) (4). (The stock line was obtained from the R.F. Eslick collection of barley mutants held at Montana State University, USA.)

Mutational events:

var2.b (Mont. *var2,* GSHO 2496) in Montcalm (CIho 7149) (3).

Mutant used for description and seed stocks:

var2.b (GSHO 2496) in Montcalm; *var2.b* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2362); *var2.b* in Bowman*4 (BW887, NGB 22320).

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. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.
4. Walker, G.W., K. Kasha, and R.A. Miller. 1958. Recombination studies in barley. Proc. Genet. Soc. Can. 3:41-43.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:104.

Revised:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:80.

BGS 409, Eceriferum-o, *cer-o*

Stock number:	BGS 409
Locus name:	Eceriferum-o
Locus symbol:	*cer-o*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 1HL (1); *cer-o.28* is associated with SNP markers 2_0229 to 1_0006 (positions 106.61 to 110.10 cM) in 1H bin 10 of the Bowman backcross-derived line BW119 (1), in 1H bin 10.

Description:

Surface wax coating on the spike appears absent or reduced (wax code -/+ ++ ++) (4). All *cer-o* mutants have pointed lateral spikelets and exhibit semi-sterility (50 to 75% seed set) (3). Mutant segregates in the Bowman backcross-derived progenies were about 3/4 of normal height and had spikes with about 20% fewer fertile rachis nodes (2). Plants of Bowman backcross-derived line for *cer-o.28*, BW119, headed about two days later than Bowman and were about 15% shorter. Kernel weights were 10-15% lower; and grain yields were about half those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) (1, 3).

Mutational events:

cer-o.28 (NGB 110912, GSHO 436) in Bonus (NGB 14657, PI 189763) (4, 5); *cer-o.687* (NGB 111575)*, -o.787* (NGB 11675) in Bonus (6); *cer-o.251* (NGB 111138) in Foma (NGB 14659, CIho 11333), *-o.1144* (NGB 112032) in Kristina (NGB 14661, NGB 1500) (7).

Mutant used for description and seed stocks:

cer-o.28 (NGB 110912, GSHO 436) in Bonus; *cer-o.28* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2193); *cer-o.28* in Bowman*7 (BW119, NGB 20525).

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. 1962. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. Hereditas 48:342-362.
5. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
6. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
7. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.

Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:127.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:359.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:106.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:81.

BGS 429, Eceriferum-zk, *cer-zk*

Stock number: BGS 429
Locus name: Eceriferum-zk
Locus symbol: *cer-zk*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive *(9).*
Located in chromosome 2HL (1); *cer-zk.85* is associated with SNP markers 2_0667 to 2_0528 (positions 117.73 to 118.78 cM) in 2H bin 08 of the Bowman backcross-derived line BW167 (1).

Description:
Surface wax coating on the spike, leaf sheath, and stem is greatly reduced, and surface wax on the leaf blade is greatly reduced or absent (wax code + + +/-) (9). In the Bowman backcross-derived line for *cer-zk.85*, BW167, the reduction in surface wax on the leaf sheath and stem was not observed (wax code + ++ +/-) (2). Besides differences in surface wax accumulation and 1 to 2 days later in heading, BW167 did not differ from Bowman in agronomic traits (2).

Origin of mutant:
A neutron induced mutant in Bonus (NGB 14657, PI 189763) (9).

Mutational events:
cer-zk.85 (NGB 110969, GSHO 458)*, -zk.117* (NGB 111002) in Bonus (NGB 14657, PI 189763) (3, 9); *cer-zk.91* (NGB 110975) in Bonus (3); *cer-zk.157* (NGB 111043) in Bonus, *-zk.593* (NGB 111481)*, -zk.611* (NGB 111499)*, -zk.612* (NGB 111500) in Foma (NGB 14659, CIho 11333) (4); *cer-zk.952* (NGB 111840) in Bonus (5); *cer-zk.872* (NGB 111760) in Bonus, *-zk.1214* (NGB 112102)*, -zk.1218* (NGB 112106) in Kristina (NGB 14661, NGB 1500) (6); *cer-zk.165* (NGB 111051) in Bonus, *-zk.614* (NGB 111502) in Foma, *-zk.749* (NGB 111637) *, -zk.1396* (NGB 112284) in Bonus (7); *cer-zk.1716* (NGB 112529)*, -zk.1720* (NGB 112533) in Bonus (8).

Mutant used for description and seed stocks:
cer-zk.85 (NGB 110969, GSHO 458) in Bonus; *cer-zk.85* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2199); *cer-zk.85* in Bowman*6 (BW167, NGB 21999).

References:

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5. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
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7. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:147.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:381.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:146-147.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:82-83.

BGS 430, Eceriferum-zl, *cer-zl*

Stock number:	BGS 430
Locus name:	Eceriferum-zl
Locus symbol:	*cer-zl*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5H (1); *cer-zl.17* is associated with SNP markers 1_0974 to 1_1350 (positions 41.99 to 160.74) in 5H bins 02 to 09 of the Bowman backcross-derived line BW168 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears absent (wax code - - ++). Low seed set and poor plant vigor occurred in the original mutant plants (3). The Bowman backcross-derived line for *cer-zl.17*, BW168, also had poor vigor and appeared quiet susceptible to environmental stress (2). Compared to Bowman, BW168 plants headed 2 to 13 days later; and plant height ranged from 2/3 to nearly equal. Leaf blades were frequently shorter; and rachis internodes were slightly shorter. Kernels of BW168 were thinner, 3.5 vs. 3.9 mm, and weighed less, 42 vs. 58 mg. Grain yields of BW168 ranged from less than 10 to nearly 50% of those for Bowman (2).

Origin of mutant:

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

Mutational events:

cer-zl.17 (NGB 110901, GSHO 459) in Bonus (NGB 14657, PI 189763) (3, 4); *cer-zl.269* (NGB 111157) in Foma (NGB 14659, CIho 11333) (3, 6); *cer-zl.1027* (NGB 111915) in Carlsberg II (NGB 5085, CIho 10114) (5).

Mutant used for description and seed stocks:

cer-zl.17 (NGB 110901, GSHO 459) in Bonus; *cer-zl.17* in Bowman (PI 483237, NGB 22812) (GSHO 2200); *cer-zl.17* in Bowman)*5 (BW168, NGB 22000).

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. Lundqvist, U., and D. von Wettstein. 1962. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. Hereditas 48:342-362.
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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:148.

Revised:

U. Lundqvist. 1997. Barley Genet. Newsl. 26:382.

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:84.

BGS 440, Eceriferum-zw, *cer-zw*

Stock number:	BGS 440
Locus name:	Eceriferum-zw
Locus symbol:	*cer-zw*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located likely in chromosome 2H (1); *cer-zw.286* is associated with a large group of SNP markers 2_1338 to 1_1533 (positions 74.97 to 141.56 cM) in 2H bins 07 to 10 and with small groups of donor parent markers in other chromosomes of the Bowman backcross-derived line BW178 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears reduced (wax code + + ++), and the leaf sheath and stem have alternating, broad horizontal bands of waxless and wax covered zones (zebra-like stripes) (4). The Bowman backcross-derived line for *cer-zw.286*, BW178, headed 2 to 4 days later than Bowman and had 2 to 4 more fertile spikelets per spike. BW178 plants were 10 to 15% shorter than Bowman plants; and kernels were smaller and lighter, 51 vs. 58 mg. BW178 and Bowman had similar grain yields and test weights, but BW178 was more susceptible to lodging (2). Some of developmental differences could be caused by the presence of the late heading allele at the *Eam6* (Early maturity 6) locus retained from Foma in BW178 (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (3).

Mutational events:

cer-zw.286 (NGB 111173, GSHO 1530) in Foma (NGB 14659, CIho 11333) (4).

Mutant used for description and seed stocks:

cer-zw.286 (NGB 11173, GSHO 1530) in Foma; *cer-zw.286* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2208); *cer-zw.286* in Bowman*3 (BW178, NGB 22010).

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. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.

Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:158.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:392.

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:85.

BGS 444, Eceriferum-ya, *cer-ya*

Stock number: BGS 444
Locus name: Eceriferum-ya
Locus symbol: *cer-ya*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4HS (1); *cer-ya.180* is associated with SNP markers between 3_0150 to 2_1359 (positions ≈26.0 to 27.52 cM) in 4H bin 02 of the Bowman backcross-derived line BW132 (1).

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (4). In the Bowman backcross-derived line for *cer-ya.180*, BW132, leaf blades have a light green color that persists from the seedling stage until maturity. BW132 plants headed 13 to 15 days later than Bowman plants. BW132 had more kernels per spike, 26 vs. 22, but small and lighter kernels, 48 vs. 59 mg. The grain yields for BW132 were 1/2 to 2/3 those of Bowman (2).

Origin of mutant:

A propane disulfonic acid diethyl ester induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

cer-ya.180 (NGB 111066, GSHO 1534) in Bonus (NGB 14657, PI 189763) (4).

Mutant used for description and seed stock:

cer-ya.180 (NGB 111066, GSHO 1534) in Bonus; *cer-ya.180* in Bowman (PI 483237, NGB 22812)*3 (GSHO 1534); *cer-ya.180* in Bowman*7 (BW132, NGB 20538).

References:

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:162.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:396.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:86.

BGS 447, Eceriferum-yd, *cer-yd*

Stock number:	BGS 447
Locus name:	Eceriferum-yd
Locus symbol:	*cer-yd*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3HS (1); *cer-yd.139* is in 3HS based on linkage drag with the *btr1* (non-brittle rachis 1) locus (3); *cer-yd.139* is associated with SNP markers between 2_0778 to 2_0650 (positions 115.88 to 192.00 cM) in 3H bins 07 to 12 of the Bowman backcross-derived line BW135 (1).

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (5). The original *cer-yd.139* stock has narrow leaf blades, pointed lateral spikelets, and semi-sterility (5). In the Bowman backcross-derived line for *cer-yd.139* (BW135), surface wax coating appears reduced (wax code + ++ ++). BW135 has few stigma hairs, and very poor to slightly reduced seed set occurs in various environments. However, male fertility is normal. Lodicules appear pistiloid in plants grown in the greenhouse (2). Although *cer-yd.139* segregates showed normal vigor in F2 progenies, BW135 plots were not evaluated in field plots because seed production was low in the greenhouse increases for homozygous lines (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) (4).

Mutational events:

cer-yd.139 (NGB 111024, GSHO 1537) in Bonus (NGB 14657, PI 189763) (5).

Mutant used for description and seed stocks:

cer-yd.139 (NGB 111024, GSHO 1537) in Bonus; *cer-yd.139* in Bowman (PI 483237, NGB 22812)*4 (GSHO 1946); *cer-yd.139* in Bowman*5 (BW135, NGB 20541).

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:165.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:399.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:87.

BGS 451, Eceriferum-yh, *cer-yh*

Stock number:	BGS 451
Locus name:	Eceriferum-yh
Locus symbol:	*cer-yh*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3HS (1); *cer-yh.116* is associated with the *Btr1* (Brittle rachis 1) locus based on linkage drag (1); *cer-yh.116* is associated with SNP markers between 2_0931 to 2_0659 (positions 104.39 to 141.21 cM) in 1H bins 07 to 09 of the Bowman backcross-derived line BW139 (1).

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (5). Mutant plants are semi-sterile, heading is delayed, and lateral spikelets have a pointed apex (5). In the Bowman backcross-derived line for *cer-yh.116* (BW139), seed set is low because few hairs develop on the stigma. Although the anthers are malformed slightly, male fertility is good (2). Even though *cer-yh.116* segregates showed normal vigor in F2 progenies, the BW139 stock has not been evaluated in field plots because seed production was low in the greenhouse increases for homozygous lines (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4).

Mutational events:

cer-yh.116 (NGB 111001, GSHO 1541)*, -yh.654* (NGB 111542) in Bonus (NGB 14657, PI 189763) (5).

Mutant used for description and seed stocks:

cer-yh.116 (NGB 111001, GSHO 1541) in Bonus; *cer-yh.116* in Bowman (PI 483237, NGB 22812)*5 (GSHO 1947, BW139, NGB 20545).

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:169.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:403.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:88.

BGS 472, Accordion basal rachis internode 1, *abr1*

Stock number:	BGS 472
Locus name:	Accordion basal rachis internode 1
Locus symbol:	*abr1*

Previous nomenclature and gene symbolization:

Laxatum-3 = *lax-3* (3, 4, 5).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 2HL (7); *abr1.a* is about 7.4 cM proximal from the *fch15* (chlorina seedling 15) locus (7); *abr1.a* is about 6.3 cM proximal from the *Gth1* (Toothed lemma 1) locus (8); *abr1.a* is associated with SNP markers 2_0674 to 1_1533 (positions 85.71 to 141.56 cM) in 2H bins 07 to 10 of the Bowman backcross-derived line BW001 (1).

Description:

Rachis internodes in the upper part of the spike are about 12% longer than normal. Secondary and tertiary shoots may form at the accordion-like basal rachis nodes (4, 7). Manifestation of the extra shoots may be a day-length response and genotype dependent. Recombination with the *eog1.a* (elongated outer glume 1) allele has not been observed (7). Heading was delayed in the Bowman backcross-derived line for *abr1.a*, BW001, by 2 to 5 days (2). Over experiments, BW001 plants ranged from slightly shorter to slightly taller than Bowman. Plant heights for BW001 ranged from 10% shorter to slightly taller, and rachis internodes averaged 54 vs. 45 mm in length. The kernel of BW001 were lighter 53 vs. 6.1 mg; the test weight was lower; and yields ranged from 2/3 to almost equal to those of Bowman (2). Part of the differences between Bowman and BW001 might have been caused by the retention from the donor parent, Bonus, of the late heading allele at the *Eam6* (Early maturity 6, see BGS 98) locus (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4).

Mutational events:

abr1.a (*lax.3*, NGB 116337, GSHO 1563), *abr1.b* (*lax.12*, NGB 116346) in Bonus (NGB 14657, PI 189763); *abr1.c* (*lax.337*, NGB 116556) in Foma (NGB 14659, CIho 11333) (4, 6).

Mutant used for description and seed stocks:

abr1.a (GSHO 1563) in Bonus; *abr1.a* in Bowman (PI 483237, NGB 22812)*7 (GSHO 1887, BW001, NGB 20409).

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Prepared:

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Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:419.
J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49: 89-90.

BGS 518, Semidwarf 1, *sdw1*

Stock number:	BGS 518
Locus name:	Semidwarf 1
Locus symbol:	*sdw1*

Previous nomenclature and gene symbolization:

Denso dwarf = *denso* (8, 20).

Hordeum vulgare gibberellin 20-oxidase = *Hv20ox*$_2$ (11, 12, 23).

Semidwarf x = *sdw.x* (5, 7).

Inheritance:

Monofactorial recessive (8, 21); some F$_1$'s are intermediate in height (1, 14).

Located in chromosome 3HL (2, 15); *sdw1.d* is probably proximal from the *gsh2* (glossy sheath 2) locus and near RFLP marker PSR170 (15); *sdw1.d* is in bin 3H-11 (13); *sdw1.d* is near RFLP marker R1545 (24); *sdw.d1* is close to SNP marker 1_0867 (16); *sdw1.a* is associated with SNP markers 1_0044 to 2_0650 (positions about 190 to 192.00 cM) in 3H bin 12 of the Bowman backcross-derived line BW827 (5); *sdw1.d* is associated with SNP markers 2_0023 to 1_0821 (positions 169.94 to 190.87 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW828 (5); *sdw1.d* is near SNP marker 11_10867 (17); *sdw1.d* is near marker SCRI_RS_103215 (4); at about 113.42 cM or 634.6 Mb.

Description:

Plants homozygous for the *sdw1.a* gene ranged from 10 to 30 cm shorter than normal sibs, with expression partial dependent on environment (1, 20, 22). Spike length was variable, but fully as long as normal barley. The stock used for description of the *sdw1.a* gene, M21, has the short straw and long spike of the original 'Jotun Mutant' as well as a large culm diameter from its parent 'Vantage' (1, 22). The semidwarf mutants, 'Diamant' and ‘Abed Bomi Denso’, are alleles at the *sdw1* locus (8, 18). Alleles at the *sdw1* locus are associated with semi-prostrate juvenile growth (8, 20), delayed maturity (6, 8, 9, 20, 24), smaller grain size (8), and reduced malt quality (6, 9, 20). The *sdw1* mutants are GA sensitive (3, 25). They are very likely mutants in an orthologue of the rice *sd1* gene (25), which encodes a GA-oxidase that produces lower levels of GA and reduced levels of cause the dwarf phenotype (10, 19). A gibberellin 20-oxidase gene (*Hv20ox*$_2$) was identified as the candidate gene for *sdw1* (11, 12). The reduced expression of *Hv20ox*$_2$ increased the number of effective tillers and enhanced grain yield (12, 23). The reduction in *Hv20ox*$_2$ levels was 4-fold in the *sdw1.d* mutant and 60-fold in the *sdw1.a* mutant, which causes a reduced endogenous GAs concentration and delayed heading (12). Plants of the Bowman backcross-derived line for *sdw1.a*, BW827, were 15 to 30% shorter than Bowman and heading was delayed 1 to 3 days. Plants of the Bowman backcross-derived line for *sdw1.d*, BW828, were 10 to 20% shorter than Bowman, heading was delayed 1 to 3 days, and spikes had 1 to 2 more kernels in some trials. Kernels of BW827 and BW828 were up to 10% lighter than Bowman kernels in some trials. Grain yields of BW828 were similar to those of Bowman, while those of BW827 were about 85% of the Bowman yields (7). The QTL for *sdw1.d* co-located with QTL for yield, plant height, development score, hectoliter weight, and grain plumpness (12). When fall planted under short-day conditions, late heading caused by the *sdw1.d* gene was mitigated partially in a ‘Baronesse’/’Full Pint’ dihaploid population by the *Eam6.h* (Early maturity 6, *mat-c*, *esp2S*, *HvCEN*) gene (4) and by the f *Eam5.x* (Early maturity 5, *HvPhyC-e*) gene, which is present in both parents (7). Based on phenotype and retained SNP markers, the 392JK (GSHO 2463, *sdw1.x*) mutant in Julia (PI 339811) could be an allele at the *sdw1* locus (5, 7). However, grain yield for the Bowman backcross-derived line for *sdw1.x*, BW824, was about half that of Bowman (7).

Origin of mutant:

An X-ray induced mutant in the Norwegian cultivar Jotun (PI 467357) isolated as Jotun 22 by Knut Mikaelsen (1, 14).

Mutational events:

sdw1.a (66/86, GSHO 1414) in Jotun (PI 467357) (22); *sdw1.c* in Abed Denso (PI 361639) (8); *sdw1.d* (*denso*) (Diamant, NGB 9447, PI 330397, PI 467775) in Valticky (PI 268173) (8); *sdw1.e* (Risø no. 9265) in Abed Bomi (NGB 5096, PI 43371) (8, 10). Some cultivars demonstrated to have the *sdw1.a* and *sdw1.d* alleles are listed in Xu et al. (23). Note that the *denso* name was original assigned to the *sdw1.c* mutant (7), but *sdw1.d* mutant from Diamant is the only allele present in cultivars described as having the *denso* semidwarf (23); *sdw1.x* (GSHO 2463, 392JK) in Julia (PI 339811) (5, 7).

Mutant used for description and seed stocks:

sdw1.a in M21 (CIho 15481, GSHO 2513) from the cross Jotun Mutant/Kindred// Vantage (20); *sdw1.d* in Trumpf (Triumph, PI 548762, GSHO 2465) from Diamant (NGB 9447); *sdw1.a* from a Jotun derivative in Bowman (PI 483237, NGB 22812)*7 (GSHO 1978), *sdw1.a* in Bowman*8 (BW827, NGB 22264); *sdw1.d* from Trumpf in Bowman*4 (GSHO 1979), *sdw1.d* in Bowman*5 (BW828, NGB 22265); *sdw1.x* from Julia in Bowman*6 (GSHO 2345, BW824, NGB 22261).

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Prepared:

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Revised:

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BGS 578, Praematurum-b, *mat-b*

Stock number: BGS 578
Locus name: Praematurum-b
Locus symbol: *mat-b*

Previous nomenclature and gene symbolization:

Early 7 = *ea-b7* (3).
Early maturity-b = *ea-b* (11).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HL (9), *mat-b.7* is in a 5.74 cM interval between morex_contig_67392 and morex_contig_1561399 (positions 126.27 to132.01 cM) in 7H bin 13, but close to morex_contig_1561399 (9).

Description:

Early heading mutants at the *mat-b* locus show a rather drastic increase in earliness (heading 7 days earlier than the parents) under field cultivation in Sweden (3, 9). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (1, 2, 5). Early heading is also associated with decreased culm length, kernels per spike, and grain yield. Mutant plants are generally more productive in field trials than *mat-a* (*eam8*) mutants, but less resistant to lodging, partially caused by a modified culm structure. Compared with the original cultivars, they have one internode less per culm, a longer first internode, and a short basal rachis internode (3). At an early stage of development, *mat-b* mutants are characterized by pale green color when grown at 15 to 20°C, but they are bright green in color at lower temperatures (1, 2, 5). Earliness of the *mat-b* mutants was observed to be day length responsive averaging 9 days earlier than their mother cultivars under long days, but they failed to head under short days (9). Compared to the *mat-c.19* mutant, the *mat-b.7* mutant was similar in earliness, but the mutant effects on the plant height and kernels per spike were less pronounced (10).

Origin of mutant:

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

Mutational events:

mat-b.7 (NGB 110007, GSHO 1788), *-b.10* (trans) (NGB 110010), *-b.13* (NGB 110013) in Bonus (NGB 14657, PI 189763) (3); *mat-b.34* (NGB 110034), *-b.35* (NGB 110035), *-b.38* (NGB 110038), *-b.66* (NGB 110066) in Bonus, *-b.106* (NGB 110106), *-b.108* (NGB 110108), *-b.134* (NGB 110134), *-b.137* (NGB 110137), *-b.145* (NGB 110145), *-b.214* (NGB 110214), *-b.216* (NGB 110216), *-b.237* (NGB 110237), *-b.244* (NGB 110244), *-b.261* (NGB 110261), *-b.279* (NGB 110279), *-b.286* (NGB 110286), *-b.313* (NGB 110313), *-b.337* (NGB 110337), *-b.403* (NGB 110403) in Foma (NGB 14659, CIho 11333), *-b.852* (NGB 110852), *-b.853* (NGB 110853), *-b.855* (NGB 110855), *-b.859* (NGB 110859), *-b.861* (NGB 110861), *-b.867* (NGB 110867), *-b.869* (NGB 110869), *-b.870* (NGB 110870), *-b.871* (NGB 110871), *-b.904* (NGB 116859), *-b.920* (NGB 117451), *-b.922* (NGB 117453) in Bonus, *-b.963* (NGB 117954), *-b.977* (NGB 117508), *-b.980* (NGB 117511), *-b.986* (NGB 117517), *-b.991* (NGB 117522), *-b.992* (NGB 117523), *-b.1008* (NGB 117539) in Sv 79353, *-b.1082* (NGB 117613) in Sv Vg74233, *-b.1103* (NGB 117634) in Sv Semira (NGB 10716, NSL 206731), *-b.1110* (NGB 119558), *-b.1112* (NGB 119560), *-b.1116* (NGB 119564) in Sv Frida (NGB 1519) (6, 7, 8); *mat-b.1401* (NGB 110408) in Bonus (3, 8); *mat-b.1404* (NGB 110411), *-b.1405* (NGB 110412) in Bonus (8).

Mutant used for description and seed stocks:

mat-b.7 (NGB 110007, GSHO 1788) in Bonus; *mat-b.7* in Bowman (PI 483237, NGB 22812)*3 (GSHO 2282); *mat-b.7* in Bowman*7 (BW507, NGB 20735). The Bowman backcross-derived stocks developed for *mat-b.7* were found to have the *mat-c.19* mutant instead (9, 10).

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11. Søgaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. Carlsberg Res. Commun. 52:123-196.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:504-505.

Revised:

U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:123-124.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:95-96.

BGS 579, Praematurum-c, *mat-c*

Stock number:	BGS 579
Locus name:	Praematurum-c
Locus symbol:	*mat-c*

Revised locus symbol:

The *mat-c* mutants were demonstrated to be alleles at the early maturity 6 (*Eam6*) locus (1). However, continued use of the *mat-c* nomenclature as the locus and allele symbols is recommended because the large phenotypic differences occur between the early alleles at the *Eam6* locus (see BGS 098) and the *mat-c* mutants. The Bowman backcross-derived BW507 was originally reported to have a mutation at the *mat-b* locus (3), but subsequent studies determined that DNA sequence change was identical to that in *mat-c.19* and BW508 (1, 15).

Previous nomenclature and gene symbolization:

Early 16 = *ea-c16* (6).
Praematurum-c = *mat-c* (17).
Earliness per se 2S = *eps2S* (9)
Hordeum vulgare CENTRORADIALIS = *HvCEN* (1, 14, 15).
Early maturity 6 = *Ea6* (1, 16).

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 2H (3); *mat-c.19* is associated with SNP markers 1_0525 to 2_0781 (positions 46.10 to 135.19 cM) in 2H bins 05 to 09 of the Bowman backcross-derived line BW508 (3); the praematurum-c (*mat-c*) mutants mapped at 57.5 cM and were determined to be the structural gene *Hordeum vulgare* CENTRORADIALIS (*HvCEN*) (1, 14); the *mat-c.19* deletion is in a 0.27 cM segment of 2H near SNP markers 2_887, 2_0537, and 2_0390 (14), in 2H at 69.55 cM or about 519 Mb (4, 14, 15).

Description:

Early heading mutants at the *mat-c* locus show a rather drastic increase in earliness (heading 7 days earlier than the parents) under field cultivation in Sweden (6). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (2, 5, 8). Slightly later heading of some *mat-c* alleles was reported (8, 13). Early heading is also associated with decreased culm length, kernels per spike, and grain yield. Mutants have reduced culm length, caused by the reduction in internode number, and the length of the peduncle is increased. Spike length and spikelet number are markedly reduced (2, 6). The phenotypic effects of the *mat-c* mutants were greater in the Bowman genetic background than in Bonus (14, 15). The *mat-c* mutants are variant in the barley homolog of *Antirrhinum CENTORADIALIS* (*HvCEN*) (1).The *mat-c.19* deletion and seven additional *mat-c* mutants affect the barley ortholog of *Arabidopsis thaliana TERMINAL FLOWER 1* (*AtTFL1*) and *Antirrhinum majus CENTRORADIALIS* (*AmCEN*) gene (15). Not all mutant assigned to the *mat-c* allelic group have deletions or other structure change in the *HvCEN* gene (1, 14, 15). In comparison to Bowman, the Bowman backcross-derived line for *mat-c.19* (BW508) headed 5 to 8 days earlier, were 5 to 10% shorter, and 4 to 10 fewer fertile spikelets (4, 14, 15). Kernels were slightly larger and heavier, but grain yields of BW508 were only 15 to 35% of those for Bowman (4).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (6).

Mutational events:

mat-c.16 (NGB 110016) in Bonus (NGB 14657, PI 189763) (6); *mat-c.19* (NGB 110019, GSHO 1789), *-c.32* (NGB 110032), *-c.93* (NGB 110093), *-c.94* (NGB 110094) in Bonus, *-c.101* (NGB 110101), *-c.122* (NGB 110122), *-c.400* (NGB 110400) in Foma (NGB 14659, CIho 11333), *-c.745* (NGB 110745) in Kristina (NGB 14661, NGB 1500), *-c.758* (NGB 110758), *-c.760* (NGB 110760), *-c.770* (NGB 110770), *-c.865* (NGB 110865), *-c.881* (NGB 110881), *-c.907*116862), *-c.910* (NGB 117441), *-c.913* (NGB 117444, *-c.926* (NGB 117457), *-c.943* (NGB 117474) in Bonus, *-c.966* (NGB 117497) in Sv 79353, *-c.1091* (NGB 117622) in Sv Vg74233, *-c.1096* (NGB 117627) in Sv Frida (NGB 1519), *-c.1102* (NGB 117633) in Sv Semira (NGB 10716, NGB 10716, NSL 206731), *-c.1107* (NGB 119555), *-c.1108* (NGB 119556), *-c.1109* (NGB 119557), *-c.1111* (NGB 119559), *-c.1114* (NGB 119562), *-c.1115* (NGB 119563) in Sv Frida, *-c.1118* (NGB 119566), *-c.1120* (NGB 119568) in Sv Semira (11, 12, 13). The early variant (haplotype II) at the *Eam6* (*HvCEN*) locus is present in many domesticated winter barley accessions (1) and in many six-rowed spring barleys grown in North America (4). Bowman (PI 483237, NGB 22812) has the *Eam6.h* allele (haplotype I) at the *mat-c* or *Eam6* locus (1). The late allele (haplotype III) at the *HvCEN* locus is present in many European, spring barley cultivars (1). Detailed phenotyping and sequencing of the *HvCEN* locus revealed that available stocks for *mat-c.865* and *mat-c.910* are not maturity mutants and *mat-c.101*, *mat-c.758*, *mat-c.760*, *mat-c.881*, and *mat-c.926* are likely earliness mutants at other loci (14, 15).

Mutant used for description and seed stocks:

mat-c.19 (NGB 110019, GSHO 1789) in Bonus; *mat-c.19* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2283); *mat-c.19* in Bowman*6 (BW508, NGB 20736); *Eam6.h* (haplotype I) from Nordic (CIho 15216) is present in Bowman (1, 4).

References:

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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:506.
Revised:
U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:125-127.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:97-99.

BGS 586, Bracteatum-d, *bra-d*

Stock number:	BGS 586
Locus name:	Bracteatum-d
Locus symbol:	*bra-d*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 1HL (7); *bra-d.7* is about 4.1 cM from AFLP marker E3634-7 (7); *bra-d.7* is probably in 1H bin 14 based on the association with *trd1* (third outer glume 1) (4, 7); *bra-d.7* is associated with SNP markers 1_0041 to 2_0772 (positions 199.04 to 205.07 cM) in 1HL bin 14 of the Bowman backcross-derived line BW070 (1), in 1H bin 14.

Description:

The characteristic trait of this mutant is the presence of a bract (third outer glume) outside the two empty glumes of the central spikelet. The bract subtending the lowest spikelet is always the largest, embracing in some cases about one-half the spike. Bracts become progressively smaller toward the tip of the spike. Mutants have elongated basal rachis internodes (5, 6). Pozzi et al. (7) suggested that *bra-d.7* is allelic to *trd1* (third outer glume 1) or near the *trd1* locus. Allelism studies demonstrated that *bra-d.7* is not an allele at the *trd1* locus (5). Compared to Bowman backcross-derived lines with *trd1* mutants, the Bowman backcross-derived line for *bra-d.7*, BW070, had slightly shorter peduncles, 5 or more fertile rachis nodes per spike, and slightly shorter awns. Compared to Bowman, kernel weights for BW070 were 10 to 15% lower and grain yields were about one half (2).

Origin of mutant:

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

Mutational events:

bra-d.7 (NGB 114310, GSHO 1696) in Foma (NGB 14659, CIho 11333) (5).

Mutant used for description and seed stocks:

bra-d.7 (NGB 114310, GSHO 1696) in Foma; *bra-d.7* in Bowman (PI 483237, NGB 22812)*3 (GSHO 2185, BW070, NGB 20478).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:513.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:284.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:139-140.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:100-101.

BGS 634, Premature ripe 2, *pmr2*

Stock number:	BGS 634
Locus name:	Premature ripe 2
Locus symbol:	*pmr2*

Previous nomenclature and gene symbolization:

Necroticans 50 = *nec-50* (3, 4).
Necroticans 54 = *nec-54* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HS (1); *pmr2.b* is associated with SNP markers 1_0721 to 1_0153 (positions 82.82 to 101.23 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW646; *pmr2.c* is associated with SNP markers 2_1270 to 1_0531 (positions 93.97 to 116.68 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW647 (1).

Description:

The *pmr2.b* and *pmr2.c* plants appear normal until shortly before heading. Just prior to heading, tan to light brown blotches start to develop on the leaf blades. The blotches enlarge rapidly and coalesce, and the leaf blades gradually die (2, 4). Peduncle elongation was poor, and *pmr2* plants were shorter than normal sibs. Although leaf sheaths and spikes remained green, *pmr2* plants ripened prematurely and the straw collapsed easily (2). The Bowman backcross-derived lines for *pmr2.b* and *pmr2.c*, BW646 and BW647, respectively, were susceptible to environmental stress with slightly shorter plants and small kernels, about 51 mg vs. 60 mg for Bowman. BW646 and BW647 yielded 10 to 40% less grain than Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (NGB 14657, PI 189763) (4).

Mutational events:

pmr2.b (*nec-50*) (NGB 115311, GSHO 2421), *prm2.c* (*nec-54*) (NGB115316, GSHO 2422) in Bonus (NGB 14657, PI 189763) (4).

Mutant used for description and seed stocks:

pmr2.b (NGB 115311, GSHO 2421) in Bonus; *pmr2.b* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2313); *pmr2.b* in Bowman*7 (BW646, NGB 22211); *pmr2.c* in Bowman*6 (BW647, NGB 22212).

References:

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Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. Barley Genet. Newsl. 32:135.

Revised:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:102.

BGS 676, Chlorina-a, *clo-a*

Stock number:	BGS 676
Locus name:	Chlorina-a
Locus symbol:	*clo-a*

Previous nomenclature and gene symbolization:

Chlorina-117 = *clo-117* (4, 6).
Chlorina-a^{117} = clo-a^{117} (1).
Chlorina-117 = *clo.117* (2).
Chlorina seedling 16 = *fch16* (5).

Inheritance:

Monofactorial (3, 5).

Located likely in chromosome 2HS (2); *clo-a.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 (2).

Description:

Seedling and immature leaves of the *clo-a.117* mutant are pale yellow-green (chlorophyll deficient) in color and gradually become darker. Mutant plants have a slight yellow green color prior to heading (3, 4). Mutants at the chlorina-a locus (*clo-a.117*, *clo-a.126*, and *clo-a.134*) lack or have only trace amounts of the light-harvesting chlorophyll a/b-binding proteins of Photosystems I and II (Lhca1, Lhca4, Lhcb1 and Lhcb3) (1). Leaf blades of the Bowman backcross-derived line for *clo-a.117* (BW185) were slightly wider than Bowman leaf blades. Spikes of BW185 plants had slightly few kernels than those of Bowman in some trials. The BW185 plants were 10 to 20% shorter than Bowman plants and showed about a four-day delay in anthesis. Kernel weights and grain yields were about normal (3). The locus symbol *clo-a* and the allele symbol *clo-a.117* were previously recommended for this Bonus mutant (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (4, 7).

Mutational events:

clo-a.117 (NGB 22623) in Bonus (NGB 14657, PI 189763) (1, 3, 4, 5); *clo-a.126*, *clo-a.134* in Bonus (1, 4, 6). The chlorina (*clo)* mutant stocks isolated in Scandinavia are stored in the Biology Department, Lund University with Mats Hansson who is the coordinator for chlorophyll biosynthesis (6, 7).

Mutant used for description and seed stocks:

clo-a.117 (NGB 22623) in Bonus; *clo-a.117* in Bowman (PI 483237, NGB 22812)*5 (BW185, NGB 22017).

References:

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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.
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:103-104.

BGS 677, Mottled leaf 7, *mtt7*

Stock number:	BGS 677
Locus name:	Mottled leaf 7
Locus symbol:	*mtt7*

Previous nomenclature and gene symbolization:

Mottled seedling h = *mtt.h* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HS (1); *mtt7.h* is associated with SNP markers 1_0326 to 2_0107 (positions 16.91 to 33.96 cM) in 2HS bins 02 and 03 of the Bowman backcross-derived line BW595 (1), in 2H bin 02 or 03.

Description:

Seedlings of the Bowman backcross-derived line for *mtt7.h*, BW595, are weak and leaf blades have vertical chlorotic to necrotic streaks where chlorophyll development is poor. BW595 plants are very weak, but they can be grown to maturity under greenhouse conditions. BW595 plants had few tillers and short spikes and were 1/2 to 2/3 of normal height (2). The locus symbol *mtt7* and the allele symbol *mtt7.h* are suggested for this Morex mutant because no other mottled mutant has a similar phenotype or is located in chromosome 2HS (1, 2). A second mutant, *nec37.r* (necrotic leaf spot 37), was isolated from the same original mutant plant, see BGS 199.

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) (2, 3).

Mutational events:

mtt7.h (MXM56) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

mtt7.h (MXM56) in Morex; *mtt7.h* in Bowman (PI 483237, NGB 22812)*5 (BW595, NGB 22161).

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. 2010. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:753.

Revised:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:105.

BGS 724, Short awn 6, *lks6*

Stock number:	BGS 724
Locus name:	Short awn 6
Locus symbol:	*lks6*

Previous nomenclature and gene symbolization:

Short awn q = *lks.q* (2).

Inheritance:

Monofactorial recessive (2, 3).

Located most likely in chromosomes 1H, 5H, or 6H (1); *lks6.q* is associated with large groups of SNP markers in 1H [2_1134 to 2_1361 (positions 64.79 to 82.35 cM) in 1H bins 06 to 08], 5H [1_0621 to 2_1344 (positions 56.40 to 98.42 cM) in 5H bins 03 to 06], and 6H [1_0799 to 1_0239 (positions 50.33 to 180.69 cM) in 6H bins 04 to 11] of the Bowman backcross-derived line BW489 (1).

Description:

Awns of *lks6.q* plants are about one half normal length compared to the control. Otherwise the plants appear fairly normal (3). Under greenhouse conditions plants of the Bowman backcross-derived line for *lks6.q*, BW489, had reduced plant vigor; slightly reduced seed set; and awns that were about 1/3 normal length (2). Based on phenotypic expression and the parental chromosome segments retained in BW489, the locus symbol *lks6* and the allele symbol *lks6.q* are suggested for this Morex mutant because it is unlikely to be allelic at previously described short awn (*lks*) loci or the breviaristatum (*ari*) loci (1, 2). The necrotic leaf spot mutant *nec36.q* is also present in the original mutant stock FN329 (GSHO 3674), see BGS 814.

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by A. Kleinhofs (3).

Mutational events:

lks6.q (FN329, GSHO 3674) in Morex (CIho 15773) (3).

Mutant used for description and seed stocks:

lks6.q (FN329, GSHO 3674) in Morex; *lks6.q* in Bowman (PI 483237, NGB 22812)*3 (BW489, NGB 20717).

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. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:219.

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:106.

BGS 755, Semidwarf 8, *sdw8*

Stock number:	BGS 755
Locus name:	Semidwarf 8
Locus symbol:	*sdw8*

Previous nomenclature and gene symbolization:

Semidwarf ah = *sdw.ah* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 5HL (1); *sdw8.ah* is associated with SNP markers 2_0097 to 1_0477 (positions 154.37 to 173.49 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW786 (1); the position in 5HL is at approximately 563.8 Mb (94.05 cM) (2).

Description:

Plants with the *sdw8.ah* gene selected during backcrossing to Bowman had reduced plant height and a slightly elongated basal rachis internode. In the Bowman backcross-derived line for *sdw8.ah*, BW786, plants averaged 15 to 20% shorter than Bowman with about half of this difference due to shorter peduncles. The leaf blades of BW786 plants were about 25% shorter, awns were slightly shorter, and spikes had 1 to 3 fewer kernels. Kernels of BW786 weighed 10 to 15% less than those of Bowman, but grain yields of BW786 were equal to or slightly higher compared to those of Bowman (2). No response to gibberellic acid was observed (3). The locus name semidwarf 8, the locus symbol *sdw8*, and the allele symbol *sdw8.ah* are suggested for this mutant because no other named semidwarf variant is located in this region of chromosome 5H. The *sdw8.ah* mutant is present in some high yielding lines selected from crosses to BW786 (2).

Origin of mutant:

An induced mutant in Volla (PI 280423) obtained from H.P.K. Gaul (3, 4).

Mutational events:

sdw8.ah (GSHO 2442, 7063, DWS1208) in Volla (PI 280423) (3, 4).

Mutant used for description and seed stocks:

sdw8.ah (GSHO 2442) in Volla; *sdw8.ah* in Bowman (PI 483237, NGB 22812)*7 (GSHO 2139, BW786, NGB 20763).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:107.

BGS 756, Semidwarf 5, *sdw5*

Stock number: BGS 756
Locus name: Semidwarf 5
Locus symbol: *sdw5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 5HL (1); *sdw5.bf* was mapped as a QTL in a two-rowed spring barley line from North Dakota, ND24388, and having bPb-5516 at 115.39 cM as the peak DArT marker (3); alignment of associated haplotype profiles using the 50k chip SNP marker system (1) placed the *sdw5* locus at approximately 553.19 Mb (82.31 cM), and 2 to 3 cM distal from the *srh1* (short rachilla hair 1) locus (2).

Description:

Plants with the *sdw5.bf* QTL are slightly shorter than normal sibs (2, 3), but the reduction in plant height is often not recognized visually. A greater effect on plant height was observed when the *sdw5.bf* QTL is present in combination with other semi-dwarfing genes such as *sdw1.d* (semidwarf 1 or denso, see BGS 518), *sdw4.ba* (semidwarf 4, BGS 045), or *ert-k.32* (erectoides-k or Pallas, BGS 562) (3). A specific 50k haplotype, which is associated with presence of *sdw9.bg*, has been observed in Northern European two-rowed spring barley landraces (2). The recommended locus symbol for this plant height QTL in 5HL is *sdw5*; and the recommended allele symbol is *sdw5.bf*.

Origin of mutant:

A spontaneous variant present in Hannchen (PI 10585) from Sweden and Betzes (PI 129430) from Germany (3).

Mutational events:

sdw5.bf is present based on SNP marker haplotype in Hannchen (PI 10585), Betzes (PI 129430), Norbert (PI 452125), and Bowman (PI 483237) (3).

Mutant used for description and seed stocks:

sdw5.bf in Betzes (PI 129430); *sdw5.bf* in Bowman (PI 483237, NGB 22812).

References:

1. Bayer, M.M., P. Rapazote-Flores, M. Ganel, P.E. Hedley, M. Macaulay, j. Pileske, L. Ramsay, J. Russell, P.D. Shaw, W. Thomas, and R. Waugh. 2017. Development and Evaluation of a barley 50k iSelect SNP array. Front. Plant Sci. 8:1792.
2. Franckowiak, J.D., and K.P. Smith. (Unpublished).
3. Lawson, W.R., and J.D. Franckowiak. (Unpublished).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:108.

BGS 757, Semidwarf 9, *sdw9*

Stock number:	BGS 757
Locus name:	Semidwarf 9
Locus symbol:	*sdw9*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 1HL (1); *sdw9.bg* was mapped as a QTL in a two-rowed spring barley line from North Dakota, ND24388, and having bPb-26569 at 142.85 cM as the peak DArT marker (3); alignment of associated haplotype profiles using the 50k chip SNP marker system (1) placed the *sdw9* locus at approximately 538.0 Mb (131.46 cM), and approximately 1 cM proximal from the *Blp1* (Black lemma and pericarp 1) locus (2).

Description:

Plants with the *sdw9.bg* QTL are slightly shorter than normal sibs (2, 3), but the reduction in plant height is often not recognized visually. A greater effect on plant height was observed when the *sdw9.bg* QTL is present in combination with other semi-dwarfing genes such as *sdw1.d* (semidwarf 1 or denso, see BGS 518), *sdw4.ba* (semidwarf 4, BGS 045), or *ert-k.32* (erectoides-k or Pallas, BGS 562) (3). A specific 50k haplotype associated with presence of *sdw9.bg* is present in some two-rowed spring barley cultivars from Canada and North Dakota (2). The recommended locus symbol for this plant height QTL in 1HL is *sdw9*; and the recommended allele symbol is *sdw9.bg*.

Origin of mutant:

A spontaneous variant present in TR473 (S75285/WM751-2) from Saskatchewan, Canada and ND23164 (PI 643371) from North Dakota (3).

Mutational events:

sdw9.bg is present based on SNP marker haplotype in ND23164 (PI 643371), ND Genesis (PI 677345), ACC Synergy (5), and ACC Goldman (4) (2).

Mutant used for description and seed stocks:

sdw9.bg in ND23164 (PI 643371); *sdw9.bg* in ND Genesis (PI 677345).

References:

1. Bayer, M.M., P. Rapazote-Flores, M. Ganel, P.E. Hedley, M. Macaulay, j. Pileske, L. Ramsay, J. Russell, P.D. Shaw, W. Thomas, and R. Waugh. 2017. Development and Evaluation of a barley 50k iSelect SNP array. Front. Plant Sci. 8:1792.
2. Franckowiak, J.D., and K.P. Smith. (Unpublished).
3. Lawson, W.R., and J.D. Franckowiak. (Unpublished).
4. Legge, W.G., J.R. Tucker, T.G. Fetch Jr, S. Haber, J.G. Menzies, A. Tekauz, T.K. Turkington, and M.E. Savard. 2014. AAC Synergy barley. Can. J. Plant Sci. 94:797-803.
5. Legge, W.G., A. Badea, J.R. Tucker, T.G. Fetch, M. Banik, S. Haber, J.G. Menzies, A. Tekauz, T.K. Turkington, R.A. Martin, T.M. Choo, B.A. Blackwell, and M.E. Savard. 2018. AAC Goldman barley. Can. J. Plant Sci. 98:1203-1211.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:109.

BGS 758, Semidwarf 11, *sdw11*

Stock number: BGS 758
Locus name: Semidwarf 11
Locus symbol: *sdw11*

Previous nomenclature and gene symbolization:
Semidwarf j = *sdw.j* (1).

Inheritance:
Monofactorial recessive (2, 3).
Located in chromosome 7HS (1); *sdw11.j* is associated with SNP markers 1_1014 to 2_0750 (positions 80.65 to 93.97 cM) in 7H bins 05 to 06 of the Bowman backcross-derived line BW810 (1).

Description:
Plants with the *sdw11.j* gene were selected during backcrossing to Bowman for reduced plant height and slightly malformed spikes. In the Bowman backcross-derived line for *sdw11.j*, BW810, plants were 10 to 15% shorter than Bowman. Grain yields of BW810 were about 25% lower than Bowman yields (2). A normal response to gibberellic acid was observed (3). The locus name semidwarf 11, the locus symbol *sdw11*, and the allele symbol *sdw11.j* are suggested for this Akashinriki mutant because no other named semidwarf variant is located in the short arm of chromosome 7H.

Origin of mutant:
A neutron induced mutant in Akashinriki (OUJ659, PI 467400) isolated by T. Konishi (1, 4).

Mutational events:
sdw11.j (GSHO 2453, OUM 073, DWS1030) in Akashinriki (OUJ659, PI 467400) (3, 4).

Mutant used for description and seed stocks:
sdw11.j (GSHO 2453) in Akashinriki; *sdw11.j* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2151); *sdw11.j* in Bowman*6 (BW810, NGB 22247).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Konishi, T. 1986. (Personal communications).

Prepared:
J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:110.

BGS 759, Semidwarf 12, *sdw12*

Stock number:	BGS 759
Locus name:	Semidwarf 12
Locus symbol:	*sdw12*

Previous nomenclature and gene symbolization:

Semidwarf l = *sdw.l* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 2H (1); *sdw12.l* is associated with SNP markers 1_0498 to 2_0528 (positions 81.43 to 118.78 cM) in 2H bins 06 to 08 of the Bowman backcross-derived line BW812 (1).

Description:

Plants with the *sdw12.l* gene were chosen during backcrossing to Bowman for reduced plant height and narrow leaf blades. In the Bowman backcross-derived line for *sdw12.l*, BW812, plants were about 20% shorter than Bowman plants, with nearly half of this difference due to shorter peduncles. The leaf blades of BW812 plants were slightly narrower and over 25% shorter; awns and rachis internodes were slightly longer; and spikes had 4 to 7 fewer kernels. Kernels of BW812 weighed 5 to 10% less than those of Bowman; test weight was reduced; and grain yields of BW812 were 50 to 75% lower (2). The response to gibberellic acid was normal (3). The locus symbol *sdw12* and the allele symbol *sdw12.l* are recommended for this Akashinriki mutant because no other named semidwarf mutant is mapped in the centromeric region of chromosome 2H.

Origin of mutant:

A neutron induced mutant in Akashinriki (OUJ659, PI 467400) isolated by T. Konishi (1, 4).

Mutational events:

sdw12.l (GSHO 2455, OUM 145, DWS1041) in Akashinriki (OUJ659, PI 467400) (3, 4).

Mutant used for description and seed stocks:

sdw12.l (GSHO 2455) in Akashinriki; *sdw12.l* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2338); *sdw12.l* in Bowman*6 (BW812, NGB 22249).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Konishi, T. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:111.

BGS 760, Semidwarf 13, *sdw13*

Stock number:	BGS 760
Locus name:	Semidwarf 13
Locus symbol:	*sdw13*

Previous nomenclature and gene symbolization:

Semidwarf m = *sdw.m* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 3H (1); *sdw13.m* is associated with SNP markers 1_0380 to 2_0115 (positions 78.82 to 126.83 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW813 (1).

Description:

Plants with the *sdw13.m* gene were selected during backcrossing to Bowman for reduced plant height. Plants of the Bowman backcross-derived line for *sdw13.m*, BW813, were about 20% shorter than Bowman plants; and peduncles were slightly shorter. Awns and rachis internodes of BW813 were slightly longer; and spikes had 1 to 3 fewer kernels. Kernels of BW813 weighed less than Bowman kernels, 51 vs. 58 mg. Grain yields of BW813 were 25 to 50% lower than Bowman yields (2). The response to gibberellic acid was normal (3). The locus symbol *sdw13* and the allele symbol *sdw13.m* are recommended for this Akashinriki mutant because no other named semidwarf mutant is mapped in the centromeric region of chromosome 3H (1, 2). The *sdw1* (semidwarf 1) locus is at 192 cM using position distances given in Druka et al. (1).

Origin of mutant:

A neutron induced mutant in Akashinriki (OUJ659, PI 467400) isolated by T. Konishi (1, 4).

Mutational events:

sdw13.m (GSHO 2456, OUM 155, DWS1044) in Akashinriki (OUJ659, PI 467400) (3, 4).

Mutant used for description and seed stocks:

sdw13.m (GSHO 2456) in Akashinriki; *sdw13.m* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2339, BW813, NGB 22250).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Konishi, T. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:112.

BGS 761, Semidwarf 14, *sdw14*

Stock number: BGS 761
Locus name: Semidwarf 14
Locus symbol: *sdw14*

Previous nomenclature and gene symbolization:
Semidwarf w = *sdw.w* (1).
Semidwarf y = *sdw.y* (1).

Inheritance:
Monofactorial recessive (2, 3).
Located in chromosome 2HL (1); *sdw14.w* is associated with SNP markers 2_0715 to 1_0072 (positions 213.08 to 239.78 cM) in 2H bins 13 to 15 of the Bowman backcross-derived line BW823; *sdw14.y* is associated with SNP markers 3_0823 to 3_1527 (positions 238.72 to 239.78 cM) in 2H bin 15 of the Bowman backcross-derived line BW825 (1).

Description:
Plants with the *sdw14.w* and *sdw14.y* genes were identified as semidwarf mutants during backcrossing to Bowman (4). Plants of the Bowman backcross-derived lines for *sdw14.w* and *sdw14.y*, BW823 and BW825, respectively, were about 3/4 the height of Bowman plants; and shorter peduncles accounted for about half the reduction in height. Heading date was 2 to 3 days later than that of Bowman. BW823 and BW825 plants had 2 to 3 fewer kernels per spike; rachis internodes were slightly shorter; and leaf blades were slightly narrower. Kernels of BW823 and BW825 were smaller than Bowman kernels and weighed less, 47 vs. 57 mg. Grain yields of BW823 and BW825 were 30 to 50% lower than Bowman yields (2). BW823 had a sensitive response to gibberellic acid (3). The locus symbol *sdw14* and the allele symbols *sdw14.w and sdw14.y* are recommended for these Julia mutants because no other named semidwarf mutant is mapped in the subteleomeric region of chromosome 2HL (1, 2).

Origin of mutant:
An N-methyl-N-nitrosourea mutant in Julia (PI 339811) isolated by I. Szarejko and M. Maluszynski (4).

Mutational events:
sdw14.w (392JK, DWS1155) in Julia (PI 339811), *sdw14.y* (GSHO 2464, 421JK, DWS1157) in Julia (2, 3). Allelism is based on retention of donor parent SNP markers in the same region of chromosome 2H in both BW823 (*sdw14.w*) and BW825 (*sdw14.y*, 421JK, GSHO 2464) (1, 2).

Mutant used for description and seed stocks:
sdw14.w (392JK) and *sdw14.y* (GSHO 2464, 421JK) in Julia; *sdw14.w* in Bowman (PI 483237, NGB 22812)*5 (BW823, NGB 22260); *sdw14.y* in Bowman*5 (GSHO 2346); *sdw14.y* in Bowman*7 (BW825, NGB 22262).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Szarejko, I. 1986. (Personal communications).

Prepared:
J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:113.

BGS 762, Semidwarf 15, *sdw15*

Stock number:	BGS 762
Locus name:	Semidwarf 15
Locus symbol:	*sdw15*

Previous nomenclature and gene symbolization:

Semidwarf ab = *sdw.ab* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 7HS (1); *sdw15.ab* is associated with SNP markers 1_0949 to 2_1437 (positions 0.0 to 20.56 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW780 (1).

Description:

During backcrossing to Bowman, plants with the *sdw15.ab* gene were selected based on reduced plant height and a slightly lighter green color. Plants of the Bowman backcross-derived line for *sdw15.ab*, BW780, were 25 to 30% shorter than Bowman plants; and peduncles were 2/3 normal length. Leaf blades of BW780 were narrower; spikes had 3 to 5 fewer kernels; and kernels were thinner and weighed less, 46 vs. 56 mg. Grain yields of BW780 were less than half those of Bowman; and the test weight was lower (2). The response to treatment with gibberellic acid was normal (3). The locus symbol *sdw15* and the allele symbol *sdw15.ab* are recommended for this Diamant mutant because no other named semidwarf mutant is mapped in the subterminal region of chromosome 7HS (1, 2).

Origin of mutant:

An induced mutant in a Diamant (NGB 9447, PI 467775) cross obtained from J. Lekeš (4).

Mutational events:

sdw15.ab (GSHO 2440, KM-1053-2004, DWS1173) in a Diamant (PI 467775, NGB 9447) cross (3, 4).

Mutant used for description and seed stocks:

sdw15.ab (GSHO 2440) in Diamant; *sdw15.ad* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2347); *sdw15.ab* in Bowman*6 (BW780, NGB 20757).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Lekeš, J. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:114.

BGS 763, Semidwarf 16, *sdw16*

Stock number:	BGS 763
Locus name:	Semidwarf 16
Locus symbol:	*sdw16*

Previous nomenclature and gene symbolization:

Semidwarf ac = *sdw.ac* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HL (1); *sdw16.ac* is associated with SNP markers 1_1512 to 2_0365 (positions 174.96 to 229.66 cM) in 7H bins 11 to 13 of the Bowman backcross-derived line BW781 (1).

Description:

During backcrossing to Bowman, segregates with reduced height were assumed to have the *sdw16.ac* gene. Plants of the Bowman backcross-derived line for *sdw16.ac*, BW781, were about 20% shorter than Bowman plants with about 70% of the height reduction due to shorter peduncles. BW781 spikes averaged about 4 fewer fertile spikelets. Kernel weights for BW781 averaged 51 mg while those for Bowman were 57 mg. Test weights for BW781 were low, and grain yields were about half those of Bowman (2). The response to gibberellic acid was normal (3). The locus symbol *sdw16* and the allele symbol *sdw16.ac* are recommended for this Volla mutant because only one other named semidwarf mutant is mapped near the subterminal region of chromosome 7HL. However, the Bowman backcross-derived line, BW831, for the semidwarf 4 mutant (*sdw4.ba*), see BGS 045, is phenotypically different from BW781 (1, 2).

Origin of mutant:

An induced mutant in Volla (PI 280423) obtained from H.P.K. Gaul (4).

Mutational events:

sdw16.ac (7004, DWS 1191) in Volla (PI 280423) (3, 4).

Mutant used for description and seed stocks:

sdw16.ac (7004) in Volla; *sdw16.ac* in Bowman (PI 483237, NGB 22812)*6 (BW781, NGB 20758).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:115.

BGS 764, Semidwarf 17, *sdw17*

Stock number: BGS 764
Locus name: Semidwarf 17
Locus symbol: *sdw17*

Previous nomenclature and gene symbolization:

Semidwarf ad = *sdw.ad* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 2H (1); *sdw17.ad* is associated primarily with SNP markers 1_0178 to 2_1096 (positions 66.78 to 90.54) and SNP markers 2_1166 to 1_0823 (positions 108.71 to 133.59 cM) in 2H bins 05 to 09 of the Bowman backcross-derived line BW782 (1).

Description:

Plants with the *sdw17.ad* gene were selected during backcrossing to Bowman for both reduced plant height and awn length. Plants of the Bowman backcross-derived line for *sdw17.ad*, BW782, were about 25% shorter than Bowman plants, 68 vs. 90 cm. Awns were about 3/4 normal length; rachis internodes were shorter, 39 vs. 47 mm; and peduncles were about 25% shorter. Leaf blades and kernels of BW782 were shorter. Kernels weighed less than those of Bowman, 51 vs 58 mg, but test weights were similar. Grain yields of BW782 were 15 to 20% lower than Bowman yields (2). The response to gibberellic acid treatment was normal (3). The locus name *sdw17* and the allele symbol *sdw17.ad* are recommended for this Volla mutant because the only named semidwarf mutant in the centromeric region of chromosome 2H, semidwarf 12 (*sdw12*, BGS 759) is phenotypically dissimilar (1, 2, 3).

Origin of mutant:

An induced mutant in Volla (PI 280423) isolated by H.P.K. Gaul (4).

Mutational events:

sdw17.ad (7015, DWS 1193) in Volla (PI 280423) (3, 4).

Mutant used for description and seed stocks:

sdw17.ad (7015) in Volla; *sdw17.ad* in Bowman (PI 483237, NGB 22812)*5 (BW782, NGB 20759).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:116.

BGS 765, Semidwarf 18, *sdw18*

Stock number: BGS 765
Locus name: Semidwarf 18
Locus symbol: *sdw18*

Previous nomenclature and gene symbolization:

Semidwarf ae = *sdw.ae* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 5HL (1); *sdw18.ae* is associated with SNP markers 1_1456 to 2_1077 (positions 195.82 to 223.57 cM) in 5H bins 11 to 12 of the Bowman backcross-derived line BW783 (1).

Description:

Plants with slightly reduced height were chosen during backcrossing to Bowman to represent the *sdw18.ae* mutant. Plants of the Bowman backcross-derived line for *sdw18.ae*, BW783, were 3 to 5 cm shorter than Bowman plants. Rachis internodes of BW783 were slightly longer. Kernel weights for BW783 ranged from equal to 15% less than Bowman kernels. Grain yields of BW783 ranged from equal to 20% less than Bowman yields (2). BW783 seedlings were not responsive to gibberellic acid treatment (3). The locus symbol *sdw18* and the allele symbol *sdw18.ae* are recommended for this Volla mutant because no other named semidwarf mutant is mapped near the middle of the long arm of chromosome 5H (1, 2).

Origin of mutant:

An induced mutant in Volla (PI 280423) obtained from H.P.K. Gaul (4).

Mutational events:

sdw18.ae (7044, DWS 1198) in Volla (PI 280423) (3, 4).

Mutant used for description and seed stocks:

sdw18.ae (7044) in Volla; *sdw18.ae* in Bowman (PI 483237, NGB 22812)*6 (BW783, NGB 20760).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:117.

BGS 766, Semidwarf 19, *sdw19*

Stock number:	BGS 766
Locus name:	Semidwarf 19
Locus symbol:	*sdw19*

Previous nomenclature and gene symbolization:

Semidwarf ai = *sdw.ai* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5H (1); *sdw19.ai* is associated with SNP markers 1_1198 to 2_0713 (positions 73.70 to 101.69 cM) in 5H bins 04 to 06 of the Bowman backcross-derived line BW787 (1).

Description:

During backcrossing to Bowman, plants with the *sdw19.ai* mutant were selected for reduced plant height and fewer kernels per spike. Plants of the Bowman backcross-derived line for *sdw19.ai*, BW787, were about 20% shorter than Bowman plants; and about half of the height difference was due to shorter peduncles. Leaf blades were shorter and narrower; spikes averaged 5 fewer kernels, 17 vs. 22; rachis internode were slightly shorter; and awns were slightly longer. Kernels of BW787 were thinner and weighed less than Bowman kernels, 49 vs 57 mg. Grain yields of BW787 averaged 2/3 of the Bowman yields (2). The response to gibberellic acid treatment was normal (3). The locus name semidwarf 19, the locus symbol *sdw19*, and the allele symbol *sdw19.ai* are recommended for this Volla mutant because no other named semidwarf plant height mutant is mapped in the centromeric region of chromosome 5H (1, 2).

Origin of mutant:

An induced mutant in Volla (PI 280423) obtained from H.P.K. Gaul (4).

Mutational events:

sdw19.ai (7177A, DWS 1229) in Volla (PI 280423) (3, 4).

Mutant used for description and seed stocks:

sdw19.ai (7177A) in Volla; *sdw19.ai* in Bowman (PI 483237, NGB 22812)*6 (BW787, NGB 20764).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:118.

BGS 767, Semidwarf 20, *sdw20*

Stock number:	BGS 767
Locus name:	Semidwarf 20
Locus symbol:	*sdw20*

Previous nomenclature and gene symbolization:

Semidwarf an = *sdw.an* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 2HL or 7H (1); *sdw20.an* is associated with SNP markers 1_0398 to 1_0398 (positions 161.08 to 206.17 cM) in 2H bins 11 to 13 and with SNP markers 1_0772 to 2_0824 (positions 71.81 to 146.97 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW792 (1).

Description:

Plants with reduced height were selected during backcrossing to Bowman as having the *sdw20.an* mutant. The plants of the Bowman backcross-derived line for *sdw20.an*, BW792, were about 10% shorter than Bowman plants, with most of the height reduction due to shorter peduncles. Spikes of BW792 had 2 to 3 more kernels than Bowman spikes. Kernels of BW792 weighed about 10% less than Bowman kernels; however, grain yields were equivalent (2). BW792 seedlings had a normal response to gibberellic acid treatment (3). The locus symbol *sdw20* and the allele symbol *sdw20.an* are recommended for this Larker mutant because no other named semidwarf mutant is mapped in the long arm of chromosome 2H or the centromeric region of chromosome 7H (1, 2).

Origin of mutant:

A sodium azide induced mutant in Larker (CIho 10648) isolated by S.E. Ullrich (1, 4).

Mutational events:

sdw20.an (GSHO 2443, WA14369-83, DWS 1262) in Larker (CIho 10648) (3, 4).

Mutant used for description and seed stocks:

sdw20.an (GSHO 2443) in Larker; *sdw20.an* in Bowman (PI 483237, NGB 22812)*3 (GSHO 2349); *sdw20.an* in Bowman*5 (BW792, NGB 20769).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator’s report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Ullrich, S.E. 1987. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:119.

BGS 768, Semidwarf 22, *sdw22*

Stock number:	BGS 768
Locus name:	Semidwarf 22
Locus symbol:	*sdw22*

Previous nomenclature and gene symbolization:

Semidwarf aq = *sdw.aq* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosomes 5HL or 6H (1); *sdw22.aq* is associated with SNP markers 2_805 to 1_1532 (positions 169.22 to 217.82 cM) in 5H bins 10 to 11 and with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW794 (1).

Description:

The original semidwarf mutant, *sdw22.aq*, had lower kernel weights and yielded 10% less than its parent Norbert (4). During backcrossing to Bowman, plants with reduced plant height and rough awns (the *Raw1* allele at the smooth awn 1 locus) were chosen as having the *sdw22.aq* mutant. Plants of the Bowman backcross-derived line for *sdw22.aq*, BW794, were 5 to 15% shorter than Bowman plants, with much of the difference caused by shorter peduncles. Both awns and rachis internodes of BW794 were slightly longer. Kernels of weights for BW794 averaged less than those of Bowman, 52 vs 58 mg. Grain yields of BW794 were 15 to 40% lower than Bowman yields (2). The response to gibberellic acid treatment was normal (3). The locus name *sdw22* and the allele symbol *sdw22.aq* are recommended for this Norbert mutant because no other named semidwarf mutant is mapped near the middle of the long arm of chromosome 5H or in the centromeric region of 6H (1, 2).

Origin of mutant:

A sodium azide induced mutant in Norbert (PI 452125) isolated by S.E. Ullrich (5).

Mutational events:

sdw22.aq (Wa14387-83, DWS 1264) in Norbert (PI 452125) (2, 4).

Mutant used for description and seed stocks:

sdw22.aq (Wa14387-83) in Norbert; *sdw22.aq* in Bowman (PI 483237, NGB 22812)*5 (BW794, NGB 20771).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Nedel, J.L., S.E. Ullrich, J.A. Clancy, and W.L. Pan. 1993. Barley semidwarf and standard isotype yield and malting quality response to nitrogen. Crop Sci. 33:258-263.
5. Ullrich, S.E. 1987. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:120.

BGS 769, Semidwarf 23, *sdw23*

Stock number: BGS 769
Locus name: Semidwarf 23
Locus symbol: *sdw23*

Previous nomenclature and gene symbolization:

Semidwarf ar = *sdw.ar* (1).

Inheritance:

Monofactorial recessive (1, 3).

Located likely in chromosome 5HL (1); *sdw23.ar* is associated with several small groups of SNP markers the largest being 2_1061 to 1_0869 (positions 169.22 to 217.82 cM) in 5H bin 13 and 2_1270 to 1_0869 (positions 169.22 to 264.33 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW795 (1).

Description:

The original semidwarf mutant, *sdw23.ar*, had a slightly lower average yield than its parent Morex (4). Plants with the *sdw23.ar* gene were selected for reduced plant height and slightly shorter awns during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *sdw23.ar*, BW795, were 10 to 15% shorter than Bowman plants. Kernels of BW795 weighed slightly less, 54 vs 58 mg; and grain yields were similar to those of Bowman (2). The response to gibberellic acid treatment was normal (3). The locus symbol *sdw23* and the allele symbol *sdw23.ar* are recommended for this Morex mutant because other named semidwarf mutants that mapped in the long arm of chromosome 5H were phenotypically different (1, 2).

Origin of mutant:

A sodium azide induced mutant in Morex (CIho 15773) isolated by S.E. Ullrich (5).

Mutational events:

sdw23.ar (Wa14351-83, DWS 1272) in Morex (CIho 15773) (1, 3).

Mutant used for description and seed stocks:

sdw23.ar (Wa14351-83) in Morex; *sdw23.ar* in Bowman (PI 483237, NGB 22812)*3 (BW795, NGB 20772).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Nedel, J.L., S.E. Ullrich, J.A. Clancy, and W.L. Pan. 1993. Barley semidwarf and standard isotype yield and malting quality response to nitrogen. Crop Sci. 33:258-263.
5. Ullrich, S.E. 1987. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:121.

BGS 770, Semidwarf 24, *sdw24*

Stock number:	BGS 770
Locus name:	Semidwarf 24
Locus symbol:	*sdw24*

Previous nomenclature and gene symbolization:

Semidwarf as = *sdw.as* (1).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosomes 2H or 6H (1); *sdw24.as* is associated with SNP markers 2_1304 to 1_0376 (positions 58.56 to 209.87 cM) in 2H bins 05 to 13 and with SNP markers 1_0462 to 1_0220 (positions 73.90 to 133.29 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW796 (1).

Description:

The original semidwarf mutant, *sdw24.as*, yielded 30% less than its parent Hazen did (4). During backcrossing to Bowman, plants with the *sdw24.as* gene were selected for reduced plant height. Plants of the Bowman backcross-derived line for *sdw24.as*, BW796, were 15 to 20% shorter than Bowman plants, but peduncles were only slightly shorter. BW796 plants headed 1 to 2 days earlier than Bowman. Awns and rachis internodes were slightly shorter. Kernels of BW796 were shorter, 8.3 vs. 9.4 mm, and weighed less, 59 vs 58 mg, than Bowman kernels. The test weight for BW796 was slightly higher than that for Bowman. Grain yields of BW796 varied from equal to 20% less than Bowman yields (2). The response to gibberellic acid treatment was normal (3). The locus symbol *sdw24* and the allele symbol *sdw24.as* are recommended for this Hazen mutant because no other named semidwarf mutant mapped to chromosome 2H or 6H headed slightly earlier and had relative short kernels (1, 2).

Origin of mutant:

A sodium azide induced mutant in Hazen (PI 483238) isolated by S.E. Ullrich (5).

Mutational events:

sdw24.as (Wa16235-85, DWS 1275) in Hazen (PI 483238) (3, 5).

Mutant used for description and seed stocks:

sdw24.as (Wa14351-83) in Hazen; *sdw24.as* in Bowman (PI 483237, NGB 22812)*3 (BW796, NGB 20773).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Nedel, J.L., S.E. Ullrich, J.A. Clancy, and W.L. Pan. 1993. Barley semidwarf and standard isotype yield and malting quality response to nitrogen. Crop Sci. 33:258-263.
5. Ullrich, S.E. 1987. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:122.

BGS 771, Semidwarf 25, *sdw25*

Stock number: BGS 771
Locus name: Semidwarf 25
Locus symbol: *sdw25*

Previous nomenclature and gene symbolization:

semidwarf at = *sdw.at* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located likely in chromosome 5H (1); *sdw25.at* is associated with SNP markers 2_0873 to 2_0236 (positions 40.91 to 124.50 cM) in 5H bins 02 to 07 and with SNP markers 2_1446 to 1_1277 (positions 136.36 to 144.55 cM) in 1H bin 11 of the Bowman backcross-derived line BW797 (1).

Description:

During backcrossing to Bowman, plants having the *sdw25.at* mutant were selected for reduced plant height and globe shaped kernels. Plants of the Bowman backcross-derived line for *sdw25.at*, BW797, were 15 to 20% shorter than Bowman plants; and peduncles averaged 7 cm shorter. BW797 plants were more susceptible to lodging and had lower test weights. Awns and rachis internodes of BW797 were slightly shorter. Leaf blades were nearly half the length of those for Bowman and slightly wider. Kernels of BW797 were globose shaped: 7.8 vs. 9.4 mm long and 4.1 vs. 3.9 mm wide. Kernels of BW797 weighed less than Bowman kernels, 51 vs. 57 mg. Grain yields of BW797 ranged from equal to 20% less than the yields of Bowman (2). The response to gibberellic acid treatment was normal (3). The locus symbol *sdw25* and the allele symbol *sdw25.at* are recommended for this Hazen mutant because it resembles globosum mutants and none of the vigorous globosum mutants is mapped in chromosome 5H. (1, 2).

Origin of mutant:

A sodium azide induced mutant in Hazen (PI 483238) isolated by S.E. Ullrich (4).

Mutational events:

sdw25.at (Wa16239-85, DWS 1276) in Hazen (PI 483238) (3, 4).

Mutant used for description and seed stocks:

sdw25.at (Wa16239-85) in Hazen; *sdw25.at* in Bowman (PI 483237, NGB 22812)*5 (BW797, NGB 20774).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Ullrich, S.E. 1987. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:123.

BGS 772, Semidwarf 26, *sdw26*

Stock number:	BGS 772
Locus name:	Semidwarf 26
Locus symbol:	*sdw26*

Previous nomenclature and gene symbolization:

Semidwarf aw = *sdw.aw* (1).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 2H (3, 5); *sdw26.aw* is associated with SNP markers 1_0837 to 1_0196 (positions 68.41 to 126.33 cM) in 2H bins 05 to 09 of the Bowman backcross-derived line BW800 (1).

Description:

Plants with the *sdw26.aw* gene were selected during backcrossing to Bowman for reduced plant height and globe shaped kernels. Plants of the Bowman backcross-derived line for *sdw26.aw*, BW800, were about 20% shorter than Bowman plants; and peduncles were slightly shorter. Rachis internodes of BW800 were shorter, 3.7 vs. 4.8 mm; and awns were 2 to 4 cm shorter. Kernels of BW800 were shorter, 7.9 vs. 9.3 mm, and weighed less, 50 vs. 56 mg, than Bowman kernels. The test weight was low. Grain yields of BW800 were about 20% lower than Bowman yields (2). The locus symbol *sdw26* and the allele symbol *sdw26.aw* are recommended for this Morex mutant because no other named semidwarf mutant with globosum kernels mapped in chromosome 2H (1, 2).

Origin of mutant:

An induced mutant in Morex (CIho 15773) isolated by R.T. Ramage (3, 5).

Mutational events:

sdw26.aw (GSHO 2446, dwf-mx, DWS 1369) in Morex (CIho 15773) (4, 5).

Mutant used for description and seed stocks:

sdw26.aw (GSHO 2446) in Morex; *sdw26.aw* in Bowman (PI 483237, NGB 22812)*3 (GSHO 1881); *sdw26.aw* in Bowman*7 (BW800, NGB 20777).

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. Franckowiak. J.D. 1995. Coordinator's report: Chromosome 2. Barley Genet. Newsl. 24:132-138.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Ramage, R.T. 1991. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:124.

BGS 773, Semidwarf 27, *sdw27*

Stock number:	BGS 773
Locus name:	Semidwarf 27
Locus symbol:	*sdw27*

Previous nomenclature and gene symbolization:

Semidwarf ax = *sdw.ax* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7H (1); *sdw27.ax* is associated with SNP markers 1_0050 to 2_1363 (positions 87.33 to 198.70 cM) in 7H bins 06 to 12 of the Bowman backcross-derived line BW801 (1).

Description:

Plants with the *sdw27.ax* gene were selected during backcrossing to Bowman for reduced plant height. Plants of the Bowman backcross-derived line for *sdw27.ax*, BW801, were 10 to 20% shorter than Bowman plants. BW801 headed 2 to 4 days earlier than Bowman in some nurseries. Kernel weights for BW801 averaged 10 to 15% less than Bowman kernels. Grain yields of BW801 averaged 10 to 15% lower than yields of Bowman (2). A normal response to gibberellic acid was observed (3). The locus symbol *sdw27* and the allele symbol *sdw27.ax* are recommended for this Birgitta mutant because BW801 appeared phenotypically distinct from other named semidwarf mutants that mapped in the centromeric region of chromosome 7H (1, 2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NGB 14667, NGB 1494, NSGC 1870) isolated by L.C. Lehmann (1, 4).

Mutational events:

sdw27.ax (GSHO 2447, 17:17:2, DWS 1009) in Birgitta (NGB 14667, NGB 1494, NSGC 1870) (3, 4).

Mutant used for description and seed stocks:

sdw27.ax (GSHO 2447) in Birgitta; *sdw27.ax* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2332, BW801, NGB 20778).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:125.

BGS 774, Semidwarf 28, *sdw28*

Stock number: BGS 774
Locus name: Semidwarf 28
Locus symbol: *sdw28*

Previous nomenclature and gene symbolization:

Semidwarf bc = *sdw.bc* (1).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HL (1); *sdw28.bc* is associated with SNP markers 1_1243 to 2_1104 (positions 167.56 to 183.90 cM) in 7H bins 10 to 11 of the Bowman backcross-derived line BW804 (1).

Description:

During backcrossing to Bowman, plants with much reduced plant height were selected as having the *sdw28.bc* mutant. Plants of the Bowman backcross-derived line for *sdw28.bc*, BW804, were about 30% shorter than Bowman plants; and peduncles were shorter, 26 vs. 38 cm. BW804 plants headed 11 days later than Bowman. Spikes had 4 fewer kernels. Awns of BW804 extended 6 cm beyond the last fertile spikelet while Bowman awns extended 11 cm (2). The locus symbol *sdw28* and the allele symbol *sdw28.bc* are recommended for this Morex mutant because only named semidwarf mutants mapped in the subterminal region of chromosome 7HL, *sdw4* and *sdw16*, are phenotypically different (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

sdw28.bc (MXM 82-2) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

sdw28.bc (MXM 82-2) in Morex; *sdw28.bc* in Bowman (PI 483237, NGB 22812)*5 (BW804, NGB 20781).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:126.

BGS 775, Semidwarf 29, *sdw29*

Stock number:	BGS 775
Locus name:	Semidwarf 29
Locus symbol:	*sdw29*

Previous nomenclature and gene symbolization:

Semidwarf au = *sdw.au* (2).

Inheritance:

Monofactorial recessive (3).

Location is unknown; no donor parent SNP markers were retained in the backcross-derived Bowman line, BW798 (2).

Description:

The *sdw29.au* mutant was isolated as a semidwarf plant in the backcross one progeny of a cross between the Risø 1508 (GSHO 1785) and Bowman. Risø 1508 is an induced mutant in Bomi Abed (NGB 5096, PI 43371) having the high lysine 3 (*lys3.a*) mutant, see BGS 339 (2). During backcrossing to Bowman, plants with the *sdw29.au* mutant were selected as having reduced plant height. Plants of the Bowman backcross-derived line for *sdw29.au*, BW798, were 20 to 30% shorter than Bowman plants; and peduncles averaged 10 cm shorter. Heading dates for BW798 varied from equal to Bowman to 6 or 7 days later. Awns were slightly longer; leaf blades were shorter and slightly narrower; and spikes had 1 to 3 fewer kernels. Kernels of BW798 were longer and thinner than Bowman kernels; and test weight was 10% lower. Kernel weights varied from equal to 20% less than Bowman kernel weights. Grain yields of BW798 averaged about 40% lower than yields of Bowman (3). The locus symbol *sdw29* and the allele symbol *sdw29.au* are recommended for this Bomi Abed mutant primarily because no other named semidwarf mutant has highly similar phenotypic characteristics (3).

Origin of mutant:

Probably a second induced mutant in the Bomi Abed (NGB 5096, PI 43371) mutant Risø 1508 (GSHO 1785) (1, 3).

Mutational events:

sdw29.au (GSHO 2441) in a Risø 1508 cross to Bowman (PI 483237, NGB 22812) (1, 2).

Mutant used for description and seed stocks:

sdw29.au (GSHO 2441) in Morex; *sdw29.au* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2350); *sdw29.au* in Bowman*6 (BW798, NGB 20775).

References:

1. Doll, H. 1973. Inheritance of a high-lysine character of a barley mutant. Hereditas 74:293-294.
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. Franckowiak, J.D. (Unpublished).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:127.

BGS 776, Globosum-g, *glo-g*

Stock number:	BGS 776
Locus name:	Globosum-g
Locus symbol:	*glo-g*

Previous nomenclature and gene symbolization:

Globosum-1 = *glo.1* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located likely in chromosome 2H (1); *glo-g.1* is associated with SNP markers 2_1187 to 2_0781 (positions 51.62 to 135.19 cM) in 2H bins 05 to 09 of the Bowman backcross-derived line BW388 (1).

Description:

Plants with the *glo-g.1* mutant were selected during backcrossing to Bowman for slightly plumper kernels and slightly shorter awns. Plants of the Bowman backcross-derived line for *glo-g.1*, BW388, headed 2 to 4 days later than Bowman and had more kernels per spike, 27 vs. 21. Leaf blades of BW388 were slightly wider and longer; kernel weights were slightly lower, 57 vs. 61 mg; and grain yields were equal or slightly higher (2). Some of these phenotypic differences are consistent with BW388 having the recessive or late allele at the *Eam6* (Early maturity 6) or *mat-c* (praematurum-c) locus (2). The retained donor parent segment of 2H in BW388 overlaps the *Eam6* locus (1). The locus name globosum-g, the locus symbol *glo-g*, and the allele symbol *glo-g.1* are suggested for this Bonus mutant because no other named globe shaped grain mutant mapped in this region of 2H (1, 2).

Origin of mutant:

A proton induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (3).

Mutational events:

glo-g.1 (NGB 115619) in Bonus (NGB 14657, PI 189763) (1, 3).

Mutant used for description and seed stocks:

glo-g.1 (NGB 115619) in Bonus; *glo-g.1* in Bowman (PI 483237, NGB 22812)* 5 (BW388, NGB 20626).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:128.

BGS 777, Globosum-h, *glo-h*

Stock number:	BGS 777
Locus name:	Globosum-h
Locus symbol:	*glo-h*

Previous nomenclature and gene symbolization:

Globosum-2 = *glo.2* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS (1); *glo-h.2* is associated mainly with SNP markers 2_1419 to 2_0307 (positions 0.0 to 9.55 cM) in 7H bin 01 of the Bowman backcross-derived line BW389 (1).

Description:

Plants with the *glo-h.2* mutant were selected mainly for slightly reduced awn length during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *glo-h.2*, BW389, headed about 2 days later than Bowman. Kernels were slightly longer; kernel weights were 10 to 20% less; and test weights were lower. The grain yield of BW389 was about 10% lower than the Bowman yield. BW389 and Bowman were similar for other morphological traits measured (2). The locus name globosum-h, the locus symbol *glo-h*, and the allele symbol *glo-h.2* are recommended for this Bonus mutant primarily because no other named mutant with globe shaped grain mapped in chromosome 7HS (1, 2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (3).

Mutational events:

glo-h.2 (NGB 115620) in Bonus (NGB 14657, PI 189763) (1, 3).

Mutant used for description and seed stocks:

glo-h.2 (NGB 115620) in Bonus; *glo-h.2* in Bowman (PI 483237, NGB 22812)*4 (BW389, NGB 20627).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:129.

BGS 778, Globosum-i, *glo-i*

Stock number:	BGS 778
Locus name:	Globosum-i
Locus symbol:	*glo-i*

Previous nomenclature and gene symbolization:

Globosum h = *glo.h* (1).

Inheritance:

Monofactorial recessive (2).

Located likely in chromosome 7HS (1); *glo-i.h* is associated with SNP markers 2_0495 to 1_0232 (positions 32.35 to 44.83 cM) in 7H bins 02 to 03 of the Bowman backcross-derived line BW390 (1).

Description:

Plants with the *glo-i.h* mutant were selected during backcrossing to Bowman for plump kernels. Plants of the Bowman backcross-derived line for *glo-i.h*, BW390, were phenotypically similar to Bowman plants. The only observed differences between BW390 and Bowman were slightly widerer kernels, a 5 to 10% reduction in kernel weights, and 10 to 20% lower grain yield (2). The locus symbol *glo-i* and the allele symbol *glo-i.h* are suggested for this Akashinriki mutant because no other named globe shaped grain mutant mapped in this region of 7HS (1, 2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) isolated by T. Konishi (3).

Mutational events:

glo-i.h (GSHO 1756, OUM158) in Akashinriki (OUJ659, PI 467400) (1, 3).

Mutant used for description and seed stocks:

glo-i.h (GSHO 1756) in Akashinriki; *glo-i.h* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2268); *glo-i.h* in Bowman*5 (BW390, NGB 20628).

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. Konishi, T. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:130.

BGS 779, Gigas 3, *gig3*

Stock number:	BGS 779
Locus name:	Gigas 3
Locus symbol:	*gig3*

Previous nomenclature and gene symbolization:

Gigas-2 = *gig.2* (1).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1H (1); *gig3.2* is associated with SNP markers 1_0744 to 2_1361 (positions 39.84 to 82.35 cM) in 1H bins 05 to 08 of the Bowman backcross-derived line BW377 (1).

Description:

During backcrossing to Bowman, larger, more robust plants were selected as having the *gig3.2* mutant. Plants of the Bowman backcross-derived line for *gig3.2*, BW377, were one day later and slightly tall than Bowman plants. Kernels of BW377 were slightly longer than Bowman kernels; their weights ranged from slightly heavier to over 20% heavier; and test weight was 15% lower. Grain yields of BW377 ranged from 25 to 40% lower than the yields of Bowman (2). The locus symbol *gig3* and the allele symbol *gig3.2* are recommended for this Bonus mutant primarily because no other named gigas mutant is mapped in chromosome 1H (1).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 3).

Mutational events:

gig3.2 (NGB 114156, GSHO 1749) in Bonus (NGB 14657, PI 189763) (1, 3); *gig3.1* (NGB 114155) in Bonus is likely an allele based on retention of the donor parent SNP markers in chromosome 1H and similar phenotypic characteristics (1, 2, 3).

Mutant used for description and seed stocks:

gig3.2 (NGB 114156, GSHO 1749) in Bonus; *gig3.2* in Bowman (PI 483237, NGB 22812)*5 (GSHO 3428); *gig3.2* in Bowman*6 (BW377, NGB 20616).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:131.

BGS 780, Short awn 9, *lks9*

Stock number: BGS 780
Locus name: Short awn 9
Locus symbol: *lks9*

Previous nomenclature and gene symbolization:

Short awn m = *lks.m* (1, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3H (1); *lks9.m* is associated with SNP markers 2_1101 to 2_0659 (positions 74.51 to 141.21 cM) in 3H bins 05 to 10 of the Bowman backcross-derived line BW485 (1).

Description:

During backcrossing to Bowman, plants with very short awns were selected as having the *lks9.m* mutant. Plants of the Bowman backcross-derived line for *lks9.m*, BW485, headed 2 to 3 days later than Bowman plants. Awns extended 1 to 3 cm beyond the last fertile spikelet of the spike. Kernels of BW485 were thinner than Bowman kernels, 3.0 vs. 3.9 mm; and weighed much less, 32 vs. 57 mg. Kernel weights for BW485 varied from equal to 20% less than Bowman kernels. Grain yields of BW485 averaged about 10% less Bowman yields (2). The response to gibberellic acid treatment was normal (3). The locus name short awn 9, the symbol *lks9*, and the allele symbol *lks9.m* are recommended for this Donaria mutant primarily because no other named short awned mutant has similar phenotypic characteristics (1).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) isolated by F. Scholz (1, 4).

Mutational events:

lks9.m (Mut. 2254, GSHO 1782, DWS 1338) in Donaria (PI 161974) (1, 2, 3, 4).

Mutant used for description and seed stocks:

lks9.m (GSHO 1782) in Donaria; *lks9.m* in Bowman (PI 483237, NGB 22812)*7 (GSHO 1928); *lks9.m* in Bowman*9 (BW485, NGB 20713).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L. s. l. I. Kulturpflanze 6:123-166.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:132.

BGS 781, Short awn 7, *lks7*

Stock number:	BGS 781
Locus name:	Short awn 7
Locus symbol:	*lks7*

Previous nomenclature and gene symbolization:

Short awn o = *lks.o* (1).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HL or 7HS (1); *lks7.o* is associated with SNP markers 1_0518 to 2_0327 (positions 154.37 to 159.80 cM) in 5H bin 09 and with SNP markers 1_0920 to 2_1528 (positions 40.61 to 60.52 cM) in 7H bins 03 to 05 of the Bowman backcross-derived line BW487 (1).

Description:

Plants with the *lks7.o* mutant were selected for short awns during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *lks7.o*, BW487, had awns that were about half the length of Bowman awns. Plants were slightly shorter than Bowman plants; and they had 1 to 2 fewer kernel per spike. Heading of BW487 varied from 1 to 3 days later than Bowman under long days to 6 or 7 days earlier under short days. Kernel weighs of BW487 varied from 15 to 40% less than Bowman kernels; kernels were thin, 3.1 vs. 3.8 mm; test weight was about 20% lower; and grain yields 1/4 to 1/3 of Bowman yields (2). The response to gibberellic acid treatment was normal (3). The locus symbol *lks7* and the allele symbol *lks7.o* are recommended for this Bido mutant primarily because no other named short awned mutant with similar phenotypic characteristics maps near the centromere in the long arm of chromosome 5H or in the short arm of chromosome 7H (1, 2).

Origin of mutant:

An induced mutant in Bido (PI 399485) obtained from H.P.K. Gaul (1, 4).

Mutational events:

lks7.o (10015, DWS1233) in Bido (PI 399485) (1, 2, 4).

Mutant used for description and seed stocks:

lks7.o (10015) in Bido; *lks7.o* in Bowman (PI 483237, NGB 22812)*8 (BW487, NGB 20715).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:133.

BGS 782, Short awn 8, *lks8*

Stock number:	BGS 782
Locus name:	Short awn 8
Locus symbol:	*lks8*

Previous nomenclature and gene symbolization:

Short awn p = *lks.p* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1HL or 7HS (1); *lks8.p* is associated with SNP markers 1_0686 to 1_0439 (positions 106.61 to 139.25 cM) in 1H bins 10 to 11 and with SNP markers 1_0965 to 1_0772 (positions 38.08 to 71.81 cM) in 7H bins 03 to 05 of the Bowman backcross-derived line BW488 (1).

Description:

The original *lks9.p* mutant in Steptoe developed hood-like malformation in the meristematic region between the lemma and its awn (3). As the stock was backcrossed to Bowman, the hood-like structure was gradually lost; however, awns are still about half normal length (2). Plants of the Bowman backcross-derived line for *lks8.p*, BW488, has awns that are slightly less than half the length of those for Bowman. Plants were 5 to 10% shorter than Bowman plants; and they had 2 to 7 fewer kernel per spike. Heading of BW488 averaged about 2 days later than Bowman. Kernels of BW488 were thinner and lighter, 45 vs. 57 mg; test weight was about 15% lower; and grain yields 1/5 to 1/3 of Bowman yields (2). The locus symbol *lks8* and the allele symbol *lks8.p* are recommended for this Steptoe mutant primarily because no other named short awned mutant with similar phenotypic characteristics maps in the long arm of chromosome 1H or in the short arm of chromosome 7H (1).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Steptoe (CIho 15229) isolated by S.E. Ullrich (1, 3).

Mutational events:

lks8.p (Steptoe cal) in Steptoe (CIho 15229) (1, 2, 3).

Mutant used for description and seed stocks:

lks8.p (Steptoe cal) in Steptoe; *lks8.p* in Bowman (PI 483237, NGB 22812)*7 (BW488, NGB 20716).

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. Ullrich, S.E. 1993. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:134.

BGS 783, Breviaristatum-za, *ari-za*

Stock number:	BGS 783
Locus name:	Breviaristatum-za
Locus symbol:	*ari-za*

Previous nomenclature and gene symbolization:

Breviaristatum-49 = *ari.49* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HS or 5HL (1); *ari-za.49* is associated with SNP markers 1_1198 to 2_0713 (positions 73.70 to 101.69 cM) in 5H bins 04 to 06 and with SNP markers 2_0676 to 1_0869 (positions 223.57 to 264.33 cM) in 5H bins 12 to 13 of the Bowman backcross-derived line BW036 (1).

Description:

Plants with the *ari-za.49* mutant were selected for short awns during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *ari-za.49*, BW036, were similar to Bowman except for slightly shorter awns (2). The locus name breviaristatum-za, the locus symbol *ari-za*, and the allele symbol *ari-za.49* are recommended for this Bonus mutant because no other named breviaristatum mutant mapped in chromosome 5H has similar phenotypic characteristics (1, 2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (3, 4).

Mutational events:

ari-za.49 (NGB 115902) in Bonus (NGB 14657, PI 189763) (3, 4).

Mutant used for description and seed stocks:

ari-za.49 (NGB 115902) in Bonus; *ari-za.49* in Bowman (PI 483237, NGB 22812)*3 (BW036, NGB 20444).

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. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:135.

BGS 784, Scirpoides-c, *sci-c*

Stock number:	BGS 784
Locus name:	Scirpoides-c
Locus symbol:	*sci-c*

Previous nomenclature and gene symbolization:

Scirpoides-2 = *sci-2* (1, 3).

Inheritance:

Monofactorial recessive (1, 3).

Located in chromosome 3HS (1); *sci-c.2* is associated with SNP marker 3_0571 (position 52.41 cM) in 3H bin 04 of the Bowman backcross-derived line BW770 (1).

Description:

The scirpoides phenotype is characterized by inward folded leaf blades and reduced plant vigor (3). Plants with the *sci-c.2* mutant were selected based on narrow, inward folded leaf blades during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *sci-c.2*, BW770, had inward folded leaf blades and a slight reduction in plant height. Kernels of BW770 were 10 to 15% lighter, 50 vs. 57 mg, than Bowman kernels; and grain yields averaged about 2/3rds the yields of Bowman (2). The locus name scirpoides-c, the locus symbol *sci-c*, and the allele symbol *sci-c.2* are recommended for this Bonus mutant because no other named folded leaf blade mutant mapped in chromosome 3H (1, 2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 3).

Mutational events:

sci-c.2 (NGB 117096) in Bonus (NGB 14657, PI 189763) (3).

Mutant used for description and seed stocks:

sci-c.2 (NGB 117096) in Bonus; *sci-c.2* in Bowman (PI 483237, NGB 22812)*5 (BW770, NGB 22238).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:136.

BGS 785, Shrunken endosperm genetic 9, *seg9*

Stock number:	BGS 785
Locus name:	Shrunken endosperm genetic 9
Locus symbol:	*seg9*

Previous nomenclature and gene symbolization:

Shrunken endosperm genetic l = *seg.l* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 6HL or 7HS (1); *seg9.l* is associated with SNP markers 1_0949 to 1_0748 (positions 180.69 to 199.22 cM) in 6H bins 11 to 12 and with SNP markers 1_0949 to 2_0710 (positions 0.0 to 4.74 cM) in 7H bin 01 of the Bowman backcross-derived line BW832 (1).

Description:

Mature kernels have a distinct depression on their dorsal side. During backcrossing to Bowman, seed lots with shrunken endosperms were selected as having the *seg9.l* mutant. Plants of the Bowman backcross-derived line for *seg9.l*, BW832, were about 15% shorter than Bowman; and awn length was nearly half that of Bowman awns (2). The locus name shrunken endosperm genetic 9, the locus symbol *seg9*, and the allele symbol *seg9.l* are suggested for this Betzes mutant because no other named shrunken endosperm genetic mutant with short awns is associated with chromosomes 6HL or 7HS (1, 2).

Origin of mutant:

The second mutant in the spontaneous mutant, *des10.p* (GSHO 601), from Betzes (PI 129430) isolated by R.T. Ramage (2, 3).

Mutational events:

seg9.l in (GSHO 601) Betzes (PI 129430) (2).

Mutant used for description and seed stocks:

seg9.l in (GSHO 601) Betzes; *seg9.l* in Bowman (PI 483237, NGB 22812)*6 (BW832, NGB 22269).

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. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. Barley Genet. Newsl. 2:65-68.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:137.

BGS 786, Shrunken endosperm xenia 10, *sex10*

Stock number:	BGS 786
Locus name:	Shrunken endosperm xenia 10
Locus symbol:	*sex10*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia m = *sex.m* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HL and 7H (1); *sex10.m* is associated with SNP markers 1_1533 to 1_1250 (positions 141.56 to 161.08 cM) in 2H bins 09 to 11 and with SNP markers 2_0249 to 2_0885 (positions 69.65 to 120.92 cM) in 7H bins 05 to 07 of the Bowman backcross-derived line BW843 (1).

Description:

The traits, waxy starch (*wax1.a*) from Waxy Oderbrucker (CIho 7563), and short-awned (*lks2.b*) and nude (*nud1.a*) from Sermo (CIho 7776) were added to Compana (PI 539111) by backcrossing to produce Washonupana (PI 608763) (2). Washonupana was treated with the mutagen diethylsulphate (DES) to generate shrunken endosperm mutant with a high fiber content named Prowashonupana (PI 596299) (2, 4). Plants with the *sex10.m* mutant were selected for shrunken endosperm during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *sex10.m*, BW843, were similar to Bowman except for kernel related traits (2). Kernels were slightly longer, 9.8 vs. 9.4 mm, and slightly thinner, 3.5 vs. 3.8 mm. Kernel weights for BW843 were lower, 41 vs. 58 mg; and test weight was 20% lower. Grain yields for BW843 were 40 to 60% lower than Bowman yields (3). The locus name shrunken endosperm xenia 10, the locus symbol *sex10*, and the allele symbol *sex10.m* are recommended for this mutant because BW843 differs in average kernel length, 9.8 vs. 13.3 mm, from BW846 (see BGS 31), the BW line for *sex6.h* (shrunken endosperm xenia 6) mutant, which was mapped in the same region of chromosome 7H (1, 3).

Origin of mutant:

A diethylsulphate induced shrunken endosperm mutant in Washonupana (PI 608763) developed by R.F. Eslick (2, 4).

Mutational events:

sex10.m (Prowashonupana, PI 596299) in Washonupana (PI 608763) (2, 4).

Mutant used for description and seed stocks:

sex10.m in Prowashonupana; *sex10.m* from Prowashonupana in Bowman (PI 483237, NGB 22812)*5 (BW843, NGB 22280).

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. Eslick, R.F. 1981. Mutation and characterization of unusual genes associated with the seed. p. 864-867. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.) Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp., Edinburgh. Edinburgh Univ. Press, Edinburgh.

3. Franckowiak, J.D. (Unpublished).

4. Rendell, M., J. Vander Hoof, M. Venn, M. A. Shehan, E. Arndt, C.S. Rao, G. Gill, R.K. Newman, and C.W. Newman. 2005. Effect of a barley breakfast cereal on blood glucose and insulin response in normal and diabetic patients. Plant Foods Hum Nutr. 60:63-67.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:138-139.

BGS 787, Viviparoides-d, *viv-d*

Stock number:	BGS 787
Locus name:	Viviparoides-d
Locus symbol:	*viv-d*

Previous nomenclature and gene symbolization:

Viviparoides-2 = *viv.2* (2, 4, 5).

Inheritance:

Monofactorial recessive (2, 3, 5).

Located in chromosomes 2HL, 5HL, or 7H (2); *viv-d.2* is associated mainly with SNP markers 2_0590 to 1_0072 (positions 218.47 to 239.78 cM) in 2H bins 13 to 15, with SNP markers 1_0360 to 2_1355 (positions 199.04 to 234.98 cM) in 5H bins 11 to 12, and with SNP markers 2_0245 to 1_0169 (positions 13.19 to 142.65 cM) in 7H bins 01 to 08 of the Bowman backcross-derived line BW891 (2).

Description:

Tillers of *viv-d.2* plants may remain vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as the culm elongates. Occasionally a short, malformed spike is formed in a lateral position (1, 5). The development of the vegetative phytomers in the culm is normal, but the transition to reproductive phytomers is variable. Reproductive phytomers can fail to form or form abnormal spikes and spikelets, which may be viviparous. Some of the abnormalities in spike development were lost as viviparoides mutants were backcrossed to Bowman (3). Plants with the *viv-d.2* mutant were selected for short awns and delayed heading during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *viv-d.2*, BW891, headed 6 to 8 days later than Bowman plants. Plants were slightly shorter; and awn lengths varied from 1/3 to 2/3 that of Bowman awns. Kernels of BW891 were slightly thinner, 3.5 vs. 3.8 mm; kernel weights were lower, 48 vs. 56 mg; and test weight was 10% lower. Grain yields of BW891 averaged 2/3 to 3/4 of Bowman yields (3). The locus name viviparoides-d, the locus symbol *viv-d*, and the allele symbol *viv-d.2* are recommended for this Foma mutant because no other named viviparoides mutant has similar phenotypic characteristics or overlapping retained parental SNP markers (2, 3).

Origin of mutant:

A gamma-ray induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (1, 5).

Mutational events:

viv-d.2 (NGB 115361) in Foma (NGB 14659, CIho 11333) (2, 5).

Mutant used for description and seed stocks:

viv-d.2 (NGB 115361) in Foma; *viv-d.2* in Bowman (PI 483237, NGB 22812)*4 (BW891, NGB 22324).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. 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.

5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:140-141.

BGS 788, Viviparoides-e, *viv-e*

Stock number:	BGS 788
Locus name:	Viviparoides-e
Locus symbol:	*viv-e*

Previous nomenclature and gene symbolization:

Viviparoides-3 = *viv.3* (2, 5).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosomes 3HL or 7H (2); *viv-e.3* is associated mainly with SNP markers 2_0063 to 2_1438 (positions 133.92 to 151.97 cM) in 3H bins 08 to 09 and with SNP markers 2_0495 to 2_0385 (positions 32.35 to 152.29 cM) in 7H bins 02 to 09 of the Bowman backcross-derived line BW892 (2).

Description:

Tillers of *viv-e.3* plants can remain vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as the culm elongates. Occasionally a short, malformed spike is formed in a lateral position (1, 5). The development of the vegetative phytomers in the culm is normal, but the transition to reproductive phytomers of the spike is variable. Reproductive phytomers can fail to form or form abnormal spikes and spikelets, which may be viviparous. Some of the abnormalities in spike development were lost during the backcrossing of the viv-e.3 mutant to Bowman (3). Plants with the *viv-e.3* mutant were selected for short awns during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *viv-e.3*, BW892, were slightly shorter than Bowman plants; and they had awns that were 1/5 to 1/2 the length of Bowman awns. Kernels of BW892 were thin, 3.4 vs. 3.8 mm, weighed less, 48 vs. 56 mg, and had a seminudoides appearance. The grain yields of BW892 ranged from half to equal to Bowman yields; and the test weight was 10% lower (3). The locus symbol *viv-e* and the allele symbol *viv-e.3* are recommended for this Foma mutant because no other named viviparoides mutant has similar phenotypic characteristics and only *viv-d.2* (BGS 787) has an overlap in retained parental SNP markers (2, 3).

Origin of mutant:

A gamma-ray induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (1, 5).

Mutational events:

viv-e.3 (NGB 115362) in Foma (NGB 14659, CIho 11333) (2, 5).

Mutant used for description and seed stocks:

viv-e.3 (NGB 115362) in Foma; *viv-e.3* in Bowman (PI 483237, NGB 22812)*4 (BW892, NGB 22325).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. 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.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:142-143.

BGS 789, Viviparoides-f, *viv-f*

Stock number:	BGS 789
Locus name:	Viviparoides-f
Locus symbol:	*viv-f*

Previous nomenclature and gene symbolization:

Viviparoides-8 = *viv.8* (5). (The allele symbol and stock number in Druka et al. (2) are incorrect.)

Inheritance:

Monofactorial recessive (3, 5).

Located likely in chromosomes 4HS or 5HL (2); *viv-f.8* is associated mainly with SNP markers 2_0145 to 2_0411 (positions 2.58 to 52.11 cM) in 4H bins 01 to 05 and with SNP markers 2_0676 to 2_0132 (positions 223.57 to 298.99 cM) in 5H bins 12 to 15 of the Bowman backcross-derived line BW895 (2).

Description:

Tillers of *viv-f.8* plants can remain vegetative and fail to produce reproductive structures. The apex of some tillers remains vegetative as the culms elongate. The spikes that do develop are short and malformed (1, 5). The development of the vegetative phytomers in the culm is normal, but the transition to reproductive phytomers of the spike is variable. Reproductive phytomers can fail to form or form abnormal spikes and spikelets, which can be viviparous plantlets. Some of the abnormalities in spike development were lost during backcrossing of the *viv-f.8* mutant to Bowman (3). Segregates with the *viv-f.8* mutant were late heading and had short spikes. Plants of the Bowman backcross-derived line for *viv-f.8*, BW895, headed later than Bowman, exhibited reduced seed set, and had spike lengths of about 3/4 normal (3). The locus symbol *viv-f* and the allele symbol *viv-f.8* are recommended for this Foma mutant because no other named viviparoides mutant has similar phenotypic characteristics and only *viv-b.6* (BGS 193) has overlapping retained parental SNP markers (2, 3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (3, 4).

Mutational events:

viv-f.8 (NGB 115367) in Foma (NGB 14659, CIho 11333) (3, 4).

Mutant used for description and seed stocks:

viv-f.8 (NGB 115367) in Foma; *viv-f.8* in Bowman (PI 483237, NGB 22812)*2 (BW895, NGB 22328).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. 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.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:144.

BGS 790, White streak 8, *wst8*

Stock number: BGS 790
Locus name: White streak 8
Locus symbol: *wst8*

Previous nomenclature and gene symbolization:

White streak l = *wst.l* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 2HL, 3H, or 7H (1); *wst8.l* is associated mainly with SNP markers 2_1220 to 2_0561 (positions 190.87 to 247.80 cM) in 2H bins 12 to 16, with SNP markers 1_0863 to 1_0312 (positions 64.85 to 173.82 cM) in 3H bins 05 to 11, and with SNP markers 2_1528 to 2_0824 (positions 60.52 to 146.97 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW908 (1).

Description:

During backcrossing to Bowman, plants with vertical white stripes were classified as having *wst8.l* mutant. Plants of the Bowman backcross-derived line for *wst8.l*, BW908, were relatively weak and 10 to 20% shorter than Bowman. The white stripes persisted in adult plants; and a small number of albino seedlings were observed in lines homozygous for the *wst8.l* gene. BW908 plants headed late in some environment and had about 7 fewer fertile spikelets per spike. Kernel weights were 10 to 20% lower; the test weight was low; and grain yields were 1/4 to 1/2 the yields for Bowman (2). The locus name white streak 8, the locus symbol *wst8*, and the allele symbol *wst8.l* are recommended for this white streak mutant because plants are phenotypically different from *wst6.j* (BGS 129) plants, which is the only named white streak with retained parental SNP markers in an overlapping position (1, 2).

Origin of mutant:

A spontaneous mutant isolated from the progeny of six-rowed, spring barley selection C91-77-12 isolated by J.D. Franckowiak (1, 2).

Mutational events:

wst8.l (C91-77-12-1) from C91-7712 (1, 2).

Mutant used for description and seed stocks:

wst8.l (C91-77-12-1) from C91-7712; *wst8.l* in Bowman (PI 483237, NGB 22812)*3 (BW908, NGB 22339).

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).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:145.

BGS 791, White streak 9, *wst9*

Stock number:	BGS 791
Locus name:	White streak 9
Locus symbol:	*wst9*

Previous nomenclature and gene symbolization:

White streak m = *wst.m* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 5HL or 7HS (1); *wst9.m* is associated mainly with SNP markers 1_1507 to 2_1490 (positions 192.60 to 235.18 cM) in 5H bins 11 to 12 and with SNP markers 1_0023 to 1_1014 (positions 26.00 to 80.65 cM) in 7H bins 02 to 05 of the Bowman backcross-derived line BW909 (1).

Description:

A picture of *wst9.m* seedlings showing vertical white stripes on the leaf blades is in GSHO 1266 (https://npgsweb.ars-grin.gov/gringlobal/accessiondetail.aspx?id=1513962). Seedlings with *wst9.m* mutant were selected for white stripes during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *wst9.m*, BW909, were often later and taller than Bowman plants and had 1 to 2 more kernels per spike. Kernel weights averaged about 5% lower; and test weight was 10% lower. Grain yields of BW909 ranged from equal to 1/3 lower than Bowman yields (2). The locus symbol *wst9* and the allele symbol *wst9.m* are recommended for this white streak mutant because no other named white streak mutant has retained SNP markers a similar position in chromosomes 5H or 7H in (1, 2).

Origin of mutant:

A spontaneous mutant in a six-rowed, spring barley breeding line at the University of Minnesota, probably isolated by J.W. Lambert, and persevered by T. Tsuchiya (3).

Mutational events:

wst9.m (GSHO 1266, MINN 139) in a Minnesota breeding line (1, 3).

Mutant used for description and seed stocks:

wst9.m (GSHO 1266) in a Minnesota breeding line; *wst9.m* in Bowman (PI 483237, NGB 22812)*6 (BW909, NGB 22340).

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. Hang, A. 1995. List of genetic stocks in barley arranged in numerical order of BGS (Barley Genetic Stock) numbers. USDA-ARS National Small Grains Germplasm Research Facility, Aberdeen, ID 83210. (Notes from T. Tsuchiya on the collection of barley genetic stocks at Colorado State University).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:146.

BGS 792, Zeocriton 4, *Zeo4*

Stock number:	BGS 792
Locus name:	Zeocriton 4
Locus symbol:	*Zeo4*

Previous nomenclature and gene symbolization:

Zeocriton e = *Zeo.e* (1, 3).

Inheritance:

Monofactorial dominant (2).

Located in chromosomes 1HL (1); *Zeo4.e* is associated mainly with SNP markers 1_1484 to 2_11261_0869 (positions 76.28 to 110.10 cM) in 1H bins 08 to 10 of the Bowman backcross-derived line BW934 (1).

Description:

During backcrossing to Bowman, plants with reduced plant height and globe shaped kernels were selected as having the *Zeo4.e* mutant. Plants of the Bowman backcross-derived line for *Zeo4.e*, BW934, were about 20% shorter than Bowman, 71 vs. 92 cm; and peduncles were 30% shorter. Rachis internodes were shorter, 3.4 vs. 4.5 mm. Kernels were shorter, 8.2 v. 9.3 mm, and weighed less, 43 vs. 58 mg. The test weight and grain yields of BW934 were equivalent to those of Bowman (2). The response to gibberellic acid treatment was normal (3). The locus name Zeocriton 4, the locus symbol *Zeo4*, and the allele symbol *Zeo4.e* are recommended for this Rubin mutant because no other named zeocriton mutant has retained parental SNP markers in chromosome 1HL. The dense spike 11 (*dsp11*, BGS 224) locus is in the same region of 1H, but BW934 plants are shorter (1, 2).

Origin of mutant:

An X-ray induced mutant in Rubin (PI 599627) obtained from J. Lekeš (1, 4).

Mutational events:

Zeo4.e (GSHO 1609, HE902-1, DWS 1169) in Rubin (PI 599627) (3, 4).

Mutant used for description and seed stocks:

Zeo4.e (GSHO 1609) in Rubin; *Zeo4.e* in Bowman (PI 483237, NGB 22812)*5 (GSHO 2369); *Zeo4.e* in Bowman*7 (BW934, NGB 22363).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Lekeš, J. 1986. (personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:147.

BGS 793, Seminudoides 2, *smn2*

Stock number:	BGS 793
Locus name:	Seminudoides 2
Locus symbol:	*smn2*

Previous nomenclature and gene symbolization:

Seminudoides-1 = *smn.1* (1, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3H (1); *smn2.1* is associated mainly with SNP markers 2_1533 to 1_1172 (positions 67.01 to 190.87 cM) in 3H bins 05 to 12 of the Bowman backcross-derived line BW868 (1).

Description:

In plants with the *smn2.1* gene, the hull does not completely cover the tip of the caryopsis because a gap occurs between the lemma and palea. Adherence of the lemma and the palea to the pericarp is good. Leaf blades are narrow (2, 3). Plants with the *smn2.1* gene were selected during backcrossing to Bowman based on incomplete covering of the caryopsis by the hull. Plants of the Bowman backcross-derived line for *smn2.1*, BW868, headed 2 to 5 days later than Bowman and were slightly taller. Rachis internodes were slightly longer; and spikes had 1 to 4 more spikelets. BW868 plants were more susceptible to lodging. Kernels of BW868 were slightly longer, 10.3 vs. 9.5 mm, than Bowman kernels; and they weighed from 10% less to 10% more over trials. The test weight of BW868 was 15% lower; and grain yields were about half the Bowman yields (2). The SNP markers of BW868 from the donor parent are in the same region of chromosome 3H as those associated with the *smn1* (seminudoides 1) mutant (see BGN 38). Because the BW lines for *smn2.1* (BW868) and *smn1.a* (BW871) exhibited many phenotypic differences, the locus name seminudoides 2, the locus symbol *smn2*, and the allele symbol *smn2.1* are recommended for this seminudoides mutant (1, 2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 3).

Mutational events:

smn2.1 (NGB 114696) in Bonus (NGB 14657, PI 189763) (3); the mutant *smn.3* (NGB 114698) in Bonus is a possible allele based on the similar phenotypes of Bowman backcross-derived lines BW868 and BW870 (2); and the lack of any large group of parental SNP markers in BW870 (1).

Mutant used for description and seed stocks:

smn2.1 (NGB 114696) in Bonus; *smn2.1* in Bowman (PI 483237, NGB 22812)*5 (BW868, NGB 20784); *smn2.3* (tentative) in Bowman*4 (BW870, NGB 22305).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:148.

BGS 794, Seminudoides 3, *smn3*

Stock number:	BGS 794
Locus name:	Seminudoides 3
Locus symbol:	*smn3*

Previous nomenclature and gene symbolization:

Seminudoides-4 = *smn.4* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 6HL (1); a similar segment of 6HL was retained in several BW lines from different sources (1, 2); *smn3.4* (*smn.4*) is associated with SNP markers 2_0488 to 1_1111 (positions 119.40 to 209.69 cM) in 6H bins 08 to 14 of the Bowman backcross-derived line BW979 (1); *smn3.8* (*acr.8*) is associated with SNP markers 2_0746 to 2_0868 (positions 125.96 to 200.83 cM) in 6H bins 08 to 13 of the Bowman backcross-derived line BW006 (1); *smn3.b* is associated with SNP markers 2_0736 to 2_0036 (positions 73.90 to 169.88 cM) in 6H bins 06 to 11 of the Bowman backcross-derived line BW636 (1); *smn3.231* (*lax-c.231*, *sld.l*) is associated with SNP markers 2_0783 to 1_1534 (positions 146.43 to 180.69 cM) in 6H bins 09 to 11 of the Bowman backcross-derived line BW858 (1).

Description:

The seminudoides trait was observed as a second mutant phenotype while backcrossing several mutants into Bowman genetic background. Because several of the resulting BW lines retained parental SNP markers in the long arm of chromosome 6H, the seminudoides variants in these BW lines were likely related and they were tentatively assigned the locus symbol *smn3* (1, 2). During backcrossing to Bowman, plants with a presumed mutant at the *smn3* locus had incomplete covering of the caryopsis by the lemma and palea. The Bowman backcross-derived lines, BW006, BW636, BW858, and BW979 have possible *smn3* alleles, but the only consistent traits were short, thin kernels, reduced kernel weights, 37 to 43 mg, and very low test weights (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) isolated by T. Konishi (1, 4).

Mutational events:

smn3.4 with *dsp11.an* (OUM105) in Akashinriki (OUJ659, PI 467400) (3, 4); *smn3.8* with *acr.8* (NGB 115048) from Bonus (NGB 14657, PI 189763) (1, 2, 5); *smn3.231* with *lax.231* (NGB 116459, GSHO 2478) in Foma (NGB 14659, CIho 11333) (1, 2, 5); *smn3.b* with *nld2.b* (FN45, GSHO 3645) in Steptoe (CIho 15229) (1, 2, 3).

Mutant used for description and seed stocks:

smn3.4 (OUM105) in Akashinriki; *smn3.231* in *lax.231* (NGB 116459) in Foma; *smn3.4* from Akashinriki in Bowman (PI 483237, NGB 22812)*4 (BW979, NGB 22356); *snm3.8* (*acr.8*) from Bonus in Bowman*4 (BW006, NGB 20414); *smn3.231* (*lax.231*, *sld.l*) from Foma in Bowman*3 (GSHO 2359); *smn3.231* (*lax.231*, *sld.l*) from Foma in Bowman*6 (BW858, NGB 22295); *smn3.b* (*nld2.b*) from Steptoe in Bowman*6 (BW636, NGB 22202).

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. Kleinhofs, A. (Unpublished).

4. Konishi, T. 1975. Characteristics and inheritance of EMS-induced mutants in barley. Nogaku Kenkyu 55:53-56.
5. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:149-150.

BGS 795, Dense spike 12, *dsp12*

Stock number:	BGS 795
Locus name:	Dense spike 12
Locus symbol:	*dsp12*

Previous nomenclature and gene symbolization:

Dense spike au = *dsp.au* (1, 3).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 3HL (1); *dsp12.au* is mainly associated with SNP markers 1_0728 to 2_0659 (positions 96.85 to 141.21 cM) in 3H bins 06 to 09 of the Bowman backcross-derived line BW268 (1).

Description:

Plants with the *dsp12.au* gene were selected during backcrossing to Bowman for dense spikes or very short rachis internodes. Plants of the Bowman backcross-derived line for *dsp12.au*, BW268, had very short rachis internodes, 2.4 vs. 4.5 mm for Bowman (2). BW268 plants were 10 to 20% shorter, but peduncle lengths were similar. BW268 plants headed two days later than Bowman and had 2 to 3 more spikelets per spike. BW268 plants had lower lodging scores. Kernel weights for BW268 varied from 10% less to 10% more than for Bowman kernels. Test weight was slightly lower; and grain yields averaged 20% lower (2). The response to gibberellic acid treatment was normal (3). The locus name dense spike 12, the locus symbol *dsp12*, and the allele symbol *dsp12.au* are recommended for this Bido mutant because no other named dense spike or erectoides mutant mapped in 3HL is associated with similar phenotypic traits (1, 2).

Origin of mutant:

An induced mutant in Bido (PI 399485) obtained from H.P.K. Gaul (1, 4).

Mutational events:

dsp12.au (GSHO 2248, 10002, DWS 1231) in Bido (PI 399485) (3, 4).

Mutant used for description and seed stocks:

dsp12.au (GSHO 2248) in Bido; *dsp12.au* in Bowman (PI 483237, NGB 22812)*4 (GSHO 1728); *dsp14.au* in Bowman*5 (BW268, NGB 22093).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Gaul, H.P.K. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:151.

BGS 796, Chlorina-c, *clo-c*

Stock number:	BGS 796
Locus name:	Chlorina-c
Locus symbol:	*clo-c*

Previous nomenclature and gene symbolization:

Chlorina-104 = *clo-104* (6, 7).
Chlorina-104 = *clo.104* (1).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 2H (1); *clo-c.104* is associated with SNP markers 2_1285 to 2_0781 (positions 50.56 to 135.19 cM) in 2H bins 05 to 09 of the Bowman backcross-derived line BW183 (1).

Description:

The *clo-c.104* mutant is light and temperature sensitive and has reduced levels of chlorophyll b and high fluorescence values (5, 6, 7). The chloroplasts of *clo-c.104* have fewer thylakoids than wild type ones, and fewer appressed lamellae relative to non-appressed lamellae (5). When grown under restrictive conditions, the chlorophyll deficiency is primarily caused by the loss of light-harvesting complex II (LHCII) and LHCI-680, with the consequent loss of much of the chlorophyll b and the xanthophylls, neoxanthin, and lutein (5). Compared to wild type, the *clo-c.104* mutant had much less Mg-chelatase activity in lower segments of the leaf blade (2). During backcrossing to Bowman, the chlorina phenotype identified plants with the *clo-c.104* mutant. Plants of the Bowman backcross-derived line for *clo-c.104*, BW183, headed 5 to 19 days later than Bowman in various environments. Plants were often 20% shorter, but not always. BW183 plants had 2 to 5 more kernels per spike. Kernels of BW183 were lighter than those of Bowman, 51 vs. 59 mg; and test weight was about 10% lower. Grain yields averaged about half the Bowman yields (3). The locus name chlorina-c, the locus symbol *clo-c*, and the allele symbol *clo-c.104* are recommended because the only other named chlorina seedling mutant, *fch1* (see BGS 055), which maps in the centromeric region of chromosome 2H, is more vigorous (1, 3).

Origin of mutant:

A sodium azide induced mutant in Tron (NGB 9655) isolated by Diter von Wettstein (4, 5, 6).

Mutational events:

clo-c.104 (*clo-104*) in Tron (NGB 9655) (5, 6). The chlorina (*clo)* mutant stocks isolated in Scandinavia are stored in the Biology Department, Lund University with Mats Hansson who is the coordinator for chlorophyll biosynthesis (4, 7).

Mutant used for description and seed stocks:

clo-c.104 (*clo-104*) in Tron; *clo-c.104* in Bowman (PI 483237, NGB 22812)*7 (GSHO 3427); *clo-c.104* in Bowman*8 (BW183, NGB 22015).

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. Falbel, T.C., and A. Staehelin. 1994. Characterization of a family of chlorophyll-deficient wheat (*Triticum*) and barley (*Hordeum vulgare*) mutants with defects in the magnesium-insertion step of chlorophyll biosynthesis. Plant Physiol. 104:639-648.
3. Franckowiak, J.D. (Unpublished).
4. Lundqvist, U. (Unpublished).

5. Knoetzel, J., and D. Simpson. 1991. Expression and organisation of antenna proteins in the light- and temperature-sensitive barley mutant *chlorina-104*. Planta 185:111-123.
6. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). Carlsberg Res. Commun. 50:223-238.
7. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at Carlsberg Laboratory. Barley Genet. Newsl. 21:102-108.

Prepared:

U. Lundqvist, J.D. Franckowiak, and M. Hansson. 2019. Barley Genet. Newsl. 49:152-153.

BGS 797, Xantha-l, *xan-l*

Stock number:	BGS 797
Locus name:	Xantha-l
Locus symbol:	*xan-l*

Previous nomenclature and gene symbolization:

Xantha-l.35 = *xan-l*^{35} (1, 6, 11).

Chlorina-111 = *clo-111* (6, 8, 9).

Xantha-l chlorina-111 = *xan-l*$^{clo\text{-}111}$ (9).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HS (7); *xan-l.111* is associated with SNP markers 2_1197 to 1_0926 (positions 78.82 to 127.91 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW918 (2), likely near the centromere in 3HS bins 05 or 06.

Description:

Seedlings of the *xan-l.35* (*xantha-l*^{35}) mutant are non-viable and have a yellow to yellow green color, which is produced by carotenoid pigments (4, 7). The *xan-l.35* mutant is linked in repulsion to a recessive zygotic lethal in the mutant stock NGB 14829 (4). The *xan-l.35* mutant has a biochemical block between magnesium protoporphyrin monomethyl ester and protochlorophyllide (4) because of a mutation in the Mg-protoporphyrin monomethyl ester cyclase (7). Mg-protoporphyrin IX monomethyl ester accumulates in the double mutant, *xan-l.35* and *tig-d.12*, which is a phenocopy of the *xan-l.35* mutant fed with the chlorophyll biosynthetic precursor 5-aminolevulinate (11). In chloroplasts, formation of the isocyclic ring is catalyzed by the *xan-l* locus, which encodes a membrane-bound cyclase subunit, Mg-protoporphyrin IX monomethyl ester cyclase. The *xan-l.35* mutant has a leaky phenotype in which seedlings gradually become yellow-green, while the *xan-l.81* and *xan-l.82* mutants are non-leaky mutants that remain yellow (7, 10). The cloned gene was located in the short arm of chromosome 3H (7). The *chlorina-111* (*clo-111*) mutant was reported to be an allele at the *xan-l* locus (9) and is renamed *xan-l.111*. Analyses of *xan-l.111* seedlings showed slightly lower values for photosynthesis related pigments than wild type Bonus, except for chlorophyll-a (8). Seedlings of the *xan-l.111* mutant initially have a yellow color, but later they develop a chlorina phenotype, which is gradually lost as plants mature (3). Plants with the *xan-l.111* gene were selected as seedlings based on the xantha/chlorina phenotype during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *xan-l.111*, BW918, headed 6 to 12 days later than Bowman in various environments. BW918 plants were about 10% shorter and had about four kernels fewer per spike than Bowman. Kernels of BW918 weighed slightly less; and grain yields were 10 to 20% lower than Bowman yields (2).

Origin of mutant:

xan-l.35 is a sodium azide induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 5, 6).

Mutational events:

x*an-l.35* (NGB 14829) [a leaky mutant (7, 10)] in Bonus (NGB 14657, PI 189763) (1, 5, 6); non-leaky mutants *xan-l.81*, *xan-l.82* (NGB 14866) in the *tig-d.12* (*tigrina-d*^{12}) mutant (NGB 14922) of Bonus (7, 10); *xan-l.111* (*clo-111*), a sublethal mutant in Bonus (8, 9). The chlorina seedling (*clo)* and xantha (*xan*) mutant stocks isolated in Scandinavia are stored in the Biology Department, Lund University with Mats Hansson who is the coordinator for chlorophyll biosynthesis (4, 9).

Mutant used for description and seed stocks:

xan-l.35 and *xan-l.111* (*clo-111*) in Bonus; *xant-l.81* and *xant-l.82* in the *tig-d.12* (NGB 14922) mutant of Bonus; *xan-l.111* in Bowman (PI 483237, NGB 22812)*7 (BW918, NGB 20789).

References:

1. Boynton, J.E., and K.W. Henningsen. 1967. The physiology and chloroplast structure of mutants at loci controlling chlorophyll synthesis in barley. Studia Biophys. 5:85-88.
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. Franckowiak, J.D. (Unpublished).
4. Gough, S. 1972. Defective synthesis of porphyrins in barley plastids caused by mutation in nuclear genes. Biochim. Biophys. Acta 286:36-54.
5. Henningsen, K.W., J.E. Boynton, and D. von Wettstein. 1993. Mutants at *xantha* and *albina* Loci in Relation to Chloroplast Biogenesis in Barley (*Hordeum vulgare* L.) Biologiske Skrifter 42. The Royal Danish Academy of Sciences and Letters. Copenhagen, 1993.
6. Lundqvist, U. (Unpublished).
7. Rzeznicka, K., C.J. Walker, T. Westergren, C.G. Kannangara, D. von Wettstein, S. Merchant, S.P. Gough, and M. Hansson. 2005. *Xantha-l* encodes a membrane subunit of the aerobic Mg-protoporphyrin IX monomethyl ester cyclase involved in chlorophyll biosynthesis. Proc. Natl. Acad. Sci. U.S.A. 102:5886-5891.
8. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). Carlsberg Res. Commun. 50:223-238.
9. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at Carlsberg Laboratory. Barley Genet. Newsl. 21:102-108.
10. von Wettstein, D., S. Gough, and C.G. Kannangara. 1995. Chlorophyll biosynthesis. Plant Cell 7:1039-1057.
11. von Wettstein, D., A. Kahn, O.F. Nielsen, and S. Gough. 1974. Genetic regulation of chlorophyll synthesis analyzed with mutants in barley. Science 184:800-802.

Prepared:

M. Hansson, U. Lundqvist, and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:154-155.

BGS 798, Chlorina-d, clo-*d*

Stock number:	BGS 798
Locus name:	Chlorina-d
Locus symbol:	*clo-d*

Previous nomenclature and gene symbolization:

Chlorina-113 = *clo-113* (3, 4, 5).
Chlorina-113 = *clo.113* (1).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosomes 1H or 3HS (1); *clo-d.113* is associated mainly with SNP markers 1_0764 to 2_1126 (positions 61.55 to 110.10 cM) in 1H bins 06 to 10 and with SNP markers 2_0742 to 1_1002 (positions 29.05 to 68.06 cM) in 3H bins 03 to 05 of the Bowman backcross-derived line BW184 (1).

Description:

The *clo-d.113* mutant has a reduced level of β-carotene and low fluorescence values (4). The *clo-d.113* mutant has a partial loss of the α- and β-subunits of the chloroplast coupling factor (CF1) (4). Seedlings with the *clo-d.113* gene were selected during backcrossing to Bowman for a pale green phenotype. Plants of the Bowman backcross-derived line for *clo-d.113*, BW184, headed 2 to 8 days later than Bowman and were 5 to 15% shorter. Spikes had 1 to 2 more kernels; and kernel weights were frequently equal to Bowman kernel weights. Grain yields for BW184 were 20 to 40% lower than Bowman yields (2). The locus name chlorina-d, the locus symbol *clo-d*, and the allele symbol *clo-d.113* are recommended for this Bonus mutant because no other named chlorina mutant in chromosomes 1H or 3HS has similar phenotypic characteristics (1, 2).

Origin of mutant:

A sodium azide induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (3, 4, 5).

Mutational events:

clo-d.113 (*clo.113*) in Bonus (NGB 14657, PI 189763) (3, 4). The chlorina (*clo)* mutant stocks isolated in Scandinavia are stored in the Biology Department, Lund University with Mats Hansson who is the coordinator for chlorophyll biosynthesis (3, 6).

Mutant used for description and seed stocks:

clo-d.113 (*clo.113*) in Bonus; *clo-d113* in Bowman (PI 483237, NGB 22812)*6 (BW184, NGB 22016).

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. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). Carlsberg Res. Commun. 50:223-238.
5. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at Carlsberg Laboratory. Barley Genet. Newsl. 21:102-108.

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:156.

BGS 799, Chlorina seedling 18, *fch18*

Stock number:	BGS 799
Locus name:	Chlorina seedling 18
Locus symbol:	*fch18*

Previous nomenclature and gene symbolization:

Chlorina seedling aa = *fch.aa* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HL (1); *fch18.aa* is associated with SNP markers 2_0590 to 2_0293 (positions 218.47 to 234.63 cM) in 2H bins 13 to 14 of the Bowman backcross-derived line BW336 (1).

Description:

Plants with the *fch18.aa* mutant are yellow green in color; and vertical yellow stripes are apparent in the leaf blades (2). During backcrossing to Bowman, seedlings with the chlorina phenotype were selected as having the *fch18.aa* mutant. Plants of the Bowman backcross-derived line for *fch18.aa*, BW336, headed 3 to 13 days later than Bowman and had 3 less to 3 more kernels per spike. Plants were often slightly shorter and had slightly shorter rachis internodes. Kernels for BW336 weighed 20 to 30% less than Bowman kernels; and test weight was 15% lower. Grain yields were 1/4 to 1/2 of Bowman yields (2). The locus name chlorina seedling 18, the locus symbol *fch18*, and the allele symbol *fch18.aa* are recommended for this ND13319 mutant because no other named chlorina mutant maps in the subterminal region of chromosome 2HL (1, 2).

Origin of mutant:

A spontaneous mutant in the progeny of the cross ND9147 (PI 643251)/ND10270 (PI 643257) isolated as ND13319-1 by J.D. Franckowiak (1, 2).

Mutational events:

fch18.aa (GSHO 1736, ND13319-1) in the progeny ND9147 (PI 643251)/ND10270 (PI 643257) (3, 4).

Mutant used for description and seed stocks:

fch18.aa (GSHO 1736) in ND9147/ND10270; *fch18.aa* in Bowman (PI 483237, NGB 22812)*6 (BW336, NGB 22131).

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).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:157.

BGS 800, Chlorina seedling 19, *fch19*

Stock number: BGS 800
Locus name: Chlorina seedling 19
Locus symbol: *fch19*

Previous nomenclature and gene symbolization:

Chlorina seedling ad = *fch.ad* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 7HS (1); *fch19.ad* is associated mainly with SNP markers 1_0050 to 2_1135 (positions 87.33 to 107.44 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW345 (1).

Description:

Seedlings of the *fch19.ad* mutant are yellow green with some paler patches. As leaf blades emerge, they are very pale yellow and gradually become greener. Under greenhouse conditions, plants develop slowly and are 3/4 normal height (2). Seedlings with the *fch19.ad* gene were selected for the pale green/mottled phenotype during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *fch21.ad*, BW345, were not viable in field plots (2). The locus name chlorina seedling 19, the locus symbol *fch19*, and the allele symbol *fch19.ad* are recommended for this Morex mutant because no other named chlorina seedling mutant maps in the centromeric region of the short arm of chromosome 7H (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

fch19.ad (MXM 81-1) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

fch19.ad ((MXM 81-1) in Morex; *fch19.ad* (in Bowman (PI 483237, NGB 22812)*5 (BW345, NGB 22140).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:158.

BGS 801, Chlorina seedling 20, *fch20*

Stock number:	BGS 801
Locus name:	Chlorina seedling 20
Locus symbol:	*fch20*

Previous nomenclature and gene symbolization:

Chlorina seedling ae = *fch.ae* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2H (1, 2); *fch20.ae* is associated with SNP markers 2_1005 to 1_1250 (positions 83.61 to 161.08 cM) in 2H bins 07 to 11 and with SNP markers 2_0873 to 2_1001 (positions 40.91 to 116.66 cM) in 5H bins 02 to 07 of the Bowman backcross-derived line BW346 (1); likely in 2H because *fch22.ae* could not be separated from the six-rowed spike (*vrs1.a*) trait from Morex during backcrossing (2).

Description:

Seedlings with the *fch20.ae* mutant are pale yellow green in color (2), similar to chlorophyll b deficient mutants at the *fch2* locus (3). Plants of the Bowman backcross-derived line for *fch22.ae*, BW346, remained yellow-green until maturity and had a six-rowed spike (*vrs1.a*) type. Plants headed 11 to 30 days later than Bowman and were 20 to 40% shorter. Rachis internodes of BW346 were shorter, 3.8 vs. 4.7 mm; and kernel weights were about 20% less than those typical of six-rowed spring barley (2). The locus name chlorina seedling 20, the locus symbol *fch20*, and the allele symbol *fch20.ae* are recommended for this Morex mutant because no other named chlorina seedling mutant located in 2HL has similar phenotypic characteristics (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 4).

Mutational events:

fch22.ae (MXM 110B) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

fch22.ae (MXM 110B) in Morex; *fch22.ae* in Bowman (PI 483237, NGB 22812)*5 (BW346, NGB 22141).

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. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). Carlsberg Res. Commun. 50:223-238.
4. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:159.

BGS 802, Chlorina seedling 21, *fch21*

Stock number:	BGS 802
Locus name:	Chlorina seedling 21
Locus symbol:	*fch21*

Previous nomenclature and gene symbolization:

Chlorina seedling af = *fch.af* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 1H, 3H, or 7HS (1); *fch21.af* is associated with SNP markers 1_0757 to 2_0798 (positions 37.21 to 82.35 cM) in 1H bins 04 to 08, with SNP markers 2_0742 to 2_0597 (positions 29.05 to 119.10 cM) in 3H bins 02 to 07, and with SNP markers 1_0965 to 2_0249 (positions 38.08 to 69.65) in 7H bins 03 to 05 of the Bowman backcross-derived line BW341 (1).

Description:

Seedlings with slightly pale green color were selected from the original M2 plant as having the *fch21.af* mutant. Plants with the *fch21.af* mutant were selected for a pale green seedling color during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *fch21.af*, BW341, were 15 to 20% taller than Bowman plants. Leaf blades were slightly wider; heading occurred from one day earlier to four days later; and kernel weights were slightly lower. Over trials, grain yields varied from 20% less to 20% more than Bowman yields (2). The locus name chlorina seedling 21, the locus symbol *fch21*, and the allele symbol *fch21.af* are recommended for this Morex mutant because no other named chlorina seedling mutant in chromosomes 1H and 3H has retained overlapping parental SNP markers, except for the chlorina seedling 5 (*fch5.f*) mutant in 7H. The BW 361 stock for *fch5.f* (BGS 18) retained overlapping SNP markers in 7HS, but it is phenotypically very different (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

fch23.af (MXM 118A) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

fch23.af (MXM 118A) in Morex; *fch23.af* in Bowman (PI 483237, NGB 22812)*3 (BW341, NGB 22136).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:160.

BGS 803, Chlorina seedling 22, *fch22*

Stock number:	BGS 803
Locus name:	Chlorina seedling 22
Locus symbol:	*fch22*

Previous nomenclature and gene symbolization:

Chlorina seedling ai = *fch.ai* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 1H or 6HS (1); *fch22.ai* is associated with parental SNP markers in three genomic regions [markers 1_0873 to 2_1072 (positions 32.99 to 55.85 cM) in 1H bins 04 to 05 of chromosome 1HS, markers 2_0121 to 2_0550 (positions 112.25 to 130.68) in bins 10 to 11 of chromosome 1HL, and markers 1_0799 to 1_0939 (positions 50.33 to 53.56 cM] in bin 04 of chromosome 6HS) of Bowman backcross-derived line BW340 (1).

Description:

As seedlings of the *fch22.ai* mutant emerge, they have a yellow (xantha) appearance and then gradually become yellow green. Emerging leaf blades are pale yellow and gradually change to a greener color (2). Plants with the *fch22.ai* mutant were selected as having a pale green seedling color during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *fch22.ai*, BW340, responded to different environments with anthesis dates being 8 to 12 days later than Bowman. Plant height varied from equal to15% shorter than Bowman plants; leaf blades were slightly wider; and spike had 1 to 2 more kernels. Kernels of BW340 averaged 10% lighter; test weight was 10% lower; and grain yields varied from 40 to 60% lower. The locus name chlorina seedling 22, the locus symbol *fch22,* and the allele symbol *fch22.ai* are recommended for this Morex mutant because no other named chlorina seedling mutant with a similar phenotype has retained overlapping parental SNP markers in chromosome 1H (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

fch22.ai (MXM 274) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

fch22.ai (MXM 274) in Morex; *fch22.ai* in Bowman (PI 483237, NGB 22812)*3 (BW340, NGB 22135).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:161.

BGS 804, Chlorina seedling 23, *fch23*

Stock number:	BGS 804
Locus name:	Chlorina seedling 23
Locus symbol:	*fch23*

Previous nomenclature and gene symbolization:

Chlorina seedling al = *fch.al* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 4HL or 7H (1); *fch23.al* is associated mainly with SNP markers 2_0838 to 2_1111 (positions 140.93 to 150.34 cM) in 4H bin 10 and with SNP markers 2_0750 to 2_0824 (positions 93.97 to 146.97) in 7H bins 06 to 08 of the Bowman backcross-derived line BW347 (1).

Description:

As leaf blades of *fch23.al* seedlings emerge they are pale yellow, but they become yellow green as they mature. The *fch23.al* plants are late and tall (2). Plants of the Bowman backcross-derived line for *fch23al*, BW347, headed 17 to 21 days later than Bowman plants and were 10 to 15% taller with 2 to 6 more kernels per spike. Leaf blades were longer and wider. Kernels of BW347 were slightly shorter and thinner; kernel weights were 25% lower; and test weight was slightly lower. Grain yields for BW347 were 1/4 to 1/2 of those for Bowman (2). The locus name chlorina seedling 23, the locus symbol *fch23*, and the allele symbol *fch23.al* are recommended for this Morex mutant even though the *fch4* mutants (see BGS 017) map in an overlapping region of chromosome 7H and have similar phenotypes (1, 2). BW347 plants had small kernels and lower grain yields than those for BW337 and BW360 plants, the BW lines with the *fch4.g* mutant, see BGS 17 (2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

fch23.al (MXM 275) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

fch23.al (MXM 275) in Morex; *fch23.al* in Bowman (PI 483237, NGB 22812)*5 (BW347, NGB 22142).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:162.

BGS 805, Serpentina 1, *srp1*

Stock number:	BGS 805
Locus name:	Serpentina 1
Locus symbol:	*srp1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosomes 1H or 3HL (1); only two groups of parental SNP markers were retained in both Bowman backcross-derived lines with *srp1.a* mutant, BW213 and BW675 (1, 2); *srp1.a* is associated with SNP markers 1_0814 to 2_0921 (positions 53.79 to 155.95 cM) in 1H bins 05 to 12 and with SNP markers 2_0115 to 1_1503 (positions 126.83 to 173.82 cM) in 3H bins 08 to 11 of Bowman backcross-derived lines BW213 and BW875 (1).

Description:

As seedlings of the *srp1.a* mutant emerge, they grow along the ground and later plants grow along the ground, which resembles a snake crawling. Plants grown in pots above the ground grew in the direction of gravity (3, 4). Gibberellin activities were greatly reduced in the *srp1.a* mutant throughout the growth period including leaf blades, culms, and spikes (4). The locus name serpentina 1, and the locus symbol *srp1*, and the allele symbol *srp1.a* are recommended for this serpentina or lazy mutant (1, 2). The parental SNP markers retained in BW213 and BW875 do not overlap the 3HL position identified for the prostrate tiller mutant (5), tentatively *srp2.b*.

Origin of mutant:

A gamma-ray induced mutant in Chikurin Ibaraki 1 (OUJ069, CIho 7370) isolated by A. Yamashita (3, 4).

Mutational events:

srp1.a (OUX042) in Chikurin Ibaraki 1 (OUJ069, CIho 7370) (1, 2).

Mutant used for description and seed stocks:

srp1.a (OUX042) in Chikurin Ibaraki 1; *srp1.a* in Bowman (PI 483237, NGB 22812)*2 (BW213, NGB 22040); *srp1.a* in Bowman*2 (BW875, NGB 22309).

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. Suge, H., H. Takahashi, Y. Kakizaki, and A. Yamashita. 1989. Barley mutant *serpentina* showing abnormal response to gravity. Biol. Sci. Space 3:363-364.
4. Türkan, İ., and H. Suge. 1991. Survey of endogenous gibberellins in a barley mutant showing abnormal response to gravity. Jap. J. Genet. 66:41-48.
5. Zhou, Y., G. Zhou, S. Broughton, S. Westcott, X. Zhang, Y. Xu, L. Xu, C. Li, and W. Zhang. 2018. Towards the identification of a gene for prostrate tillers in barley (*Hordeum vulgare* L.). PLoS ONE 13(2):e0192263.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:163.

BGS 806, Globosum-j, *glo-j*

Stock number:	BGS 806
Locus name:	Globosum-j
Locus symbol:	*glo-j*

Previous nomenclature and gene symbolization:

Globosum i = *glo.i* (1).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 3HL or 5HL (1); *glo-j.i* is associated mainly with SNP markers 1_1391 to 2_1381 (positions 100.48 to 157.14 cM) in 3H bins 06 to 10 and with SNP markers 1_0622 to 1_0477 (positions 158.46 to 173.44) in 5H bins 09 to 10 of the Bowman backcross-derived line BW391 (1).

Description:

Plants with the *glo-j.i* gene were very short and had small, globe shaped kernels. Plants of the Bowman backcross-derived line for *glo-j.i*, BW391, had low vigor and were nearly half as tall as Bowman. The roots of BW391 were coiled; and plants lodged easily. Heading was delayed by about 9 days; kernel weights were 20 to 50% less; and plants produced little grain under field conditions (2). The locus name globosum-j, the locus symbol *glo.j*, and the allele symbol *glo-j.i* are recommended for this Steptoe mutant because no other named globosum mutant has extremely low vigor; and no other named globosum locus maps in the same region of chromosomes 3H or 5H (1, 2).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) isolated by A. Kleinhofs (1, 3).

Mutational events:

glo-j.i (FN54) in Steptoe (CIho 15229) (1, 3).

Mutant used for description and seed stocks:

glo-j.i (FN54) in Steptoe; *glo-j.i* in Bowman (PI 483237, NGB 22812)*5 (BW391, NGB 20629).

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. Kleinhofs, A. (Unpublished).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:164.

BGS 807, Adjacent stigma 1, *ajs1*

Stock number:	BGS 807
Locus name:	Adjacent stigma 1
Locus symbol:	*ajs1*

Previous nomenclature and gene symbolization:

Laxatum-228 = *lax.228* (3, 4).

Inheritance:

Monofactorial recessive (2).

Location is unknown; *ajs1.228* is not located in chromosomes 1H, 4H, or 7H based on retained donor parent SNP markers in Bowman backcross-derived line BW432 (1).

Description:

The *ajs1.228* (*lax-228*) mutant was initially identified as having a laxatum phenotype with rachis internodes about 20% longer than those of Foma. Plant height was reduced and kernel weights were lower, 39 vs. 51 mg (4). The *ajs1.228* mutant showed partial dominance for the long rachis internode trait (4). During emasculation, styles of the *ajs1.228* ovary were observed to nearly touch each other (2). Plants of the Bowman backcross-derived line for *ajs1.228*, BW432, were 10 to 20% shorter than Bowman plants. Rachis internodes were slightly longer; heading was delayed by 1 to 2 days; and kernels were lighter, 51 vs. 57 mg. Grain yields for BW432 were 10 to 20% less than Bowman yields (2). Based on the unusual position of the style and stigma, the locus name adjacent stigma 1, the locus symbol *ajs1*, and the allele symbol *ajs1.228* are recommended for this Foma mutant (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (3, 5).

Mutational events:

ajs1.228 (lax.228, NGB 116458) in Foma (NGB 14659, CIho 11333) (1, 4, 5).

Mutant used for description and seed stocks:

ajs1.228 (lax.228, NGB 16458) in Foma; *ajs1.228* in Bowman (PI 483237, NGB 22812)*2 (BW432, NGB 20664).

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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
4. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
5. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:165.

BGS 808, Curly 6, *cur6*

Stock number: BGS 808
Locus name: Curly 6
Locus symbol: *cur6*

Previous nomenclature and gene symbolization:
Eligulum-2 = *eli.2* (3, 4).
Curly j = *cur.j* (1, 2).

Inheritance:
Monofactorial recessive (2).
Located in chromosomes 5H or 7HS (1); *cur6.j* (*eli.2*) is associated mainly with SNP markers 1_1198 to 2_0713 (positions 73.70 to 101.69 cM) in 5H bins 04 to 07 and with SNP markers 2_1419 to 2_1437 (positions 0.0 to 20.56 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW217 (1).

Description:
The *cur6.j* mutant is the second mutant isolated from the eligulum-2 (NBG 115389) mutant stock, which contains the *eli-a.2* (eligulum-a) mutant, see BGS 623 (1, 2, 4). Plants with the *cur6.j* mutant were selected based on a slight coiling or twisting of leaf blades and awns (2). Plants of the Bowman backcross-derived line for *cur6.j*, BW217, were 10 to 15% shorter than Bowman plants, but peduncles were slightly longer. Awns of BW217 were slightly coiled and 30 to 50% shorter than Bowman awns. Heading of BW217 plants occurred 2 to 5 days later; rachis internodes were longer, 5.3 vs. 4.7 mm; and spikes had 2 to 6 more kernels. Kernels were thinner and weighed less, 53 vs. 60 mg. Grain yields of BW217 were 40 to 60% less than Bowman yields (2). The locus name curly 6, the locus symbol *cur6,* and the allele symbol *cur6.j* are recommended for this Foma mutant because no other named curly mutant has this combination of phenotypic traits (2).

Origin of mutant:
An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (3, 4).

Mutational events:
cur6.j (NGB 115389) in Foma (NGB 14659, CIho 11333) (1, 4).

Mutant used for description and seed stocks:
cur6.j (NGB 115389) in Foma; *cur6.j* in Bowman (PI 483237, NGB 22812)*4 (BW217, NGB 22044).

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. 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. Lundqvist, U. (Unpublished).

Prepared:
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:166.

BGS 809, Curly 7, *cur7*

Stock number:	BGS 809
Locus name:	Curly 7
Locus symbol:	*cur7*

Previous nomenclature and gene symbolization:

Curly I = *cur.l* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 3HL, 6H, or 7H (1); *cur7.l* is associated mainly with SNP markers 2_1120 to 2_0612 (positions 98.91 to 198.3 cM) in 3H bins 06 to 13, with SNP markers 2_1246 to 2_0379 (positions 36.93 to 163.56 cM) in 6H bins 02 to 10, and with SNP markers 2_0750 to 1_0531 (positions 93.97 to 116.68) in 7H bins 06 to 07 of the Bowman backcross-derived line BW215 (1).

Description:

The original *cur7.l* mutant exhibited light and dark green vertical stripes as seedlings and slightly coiled or twisted awns (2). During backcrossing to Bowman, plants with fewer tillers were selected (2). Plants of the Bowman backcross-derived line for *cur7.l*, BW215, showed over a 50% reduction in tillering and lodged much easier than Bowman. Moderate coiling of the flag leaf was observed. Kernels of BW215 were slightly longer, 10.4 vs. 9.5 mm, and a little lighter, 56 vs. 59 mg, than Bowman kernels. Grain yields of BW215 were 60 to to 70% lower than Bowman yields (2). The locus name curly 7, the locus symbol *cur7*, and the allele symbol *cur7.l* are recommended for this Morex mutant that exhibits reduced tillering in the Bowman genetic backgroundmutant (1, 2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

cur7.l (MXM 20) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

cur7.l (MXM 20) in Morex; *cur7.l* in Bowman (PI 483237, NGB 22812)*3 (BW215, NGB 22042).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:167.

BGS 810, Curly 8, *cur8*

Stock number: BGS 810
Locus name: Curly 8
Locus symbol: *cur8*

Previous nomenclature and gene symbolization:

Curly m = *cur.m* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 4H, 5HS, or 7H (1); *cur8.m* is associated with SNP markers 1_0113 to 1_0010 (positions 26.58 to 94.76 cM) in 4H bins 02 to 06, with SNP markers 2_0894 to 1_0688 (positions 3.14 to 52.12 cM) in 5H bins 01 to 03, and with SNP markers 1_0050 to 2_0824 (positions 87.33 to 146.97 cM) in 7H bins 06 to 08 of the Bowman backcross-derived line BW216 (1).

Description:

The mutant plant that eventually became the *cur8.m* mutant line had slightly chlorina seedlings (2). During backcrossing to Bowman, seedlings with long, slightly coiled primary or first leaf were selected (2). Plants of the Bowman backcross-derived line for *cur8.m*, BW216, were 5 to 10% shorter than Bowman plants. Heading occurred about one day later than Bowman. Compared to Bowman, kernels of BW216 were slightly thinner, 3.5 vs. 3.9 mm; kernel weights were lower, 48 vs. 59 mg; and test weight was 10% lower. Grain yields of BW216 were 20 to 40% lower than Bowman yields (2). The locus name curly 8, the locus symbol *cur8*, and the allele symbol *cur8.m* are recommended for this Morex mutant because it has a unique set of morphological traits (2).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by J.D. Franckowiak (2, 3).

Mutational events:

cur8.m (MXM 163) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:

cur8.m (MXM 163) in Morex; *cur8.m* in Bowman (PI 483237, NGB 22812)*4 (BW216, NGB 22043).

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. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. Theor. Appl. Genet. 113:847-855.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:168.

BGS 811, Desynapsis 16, *des16*

Stock number: BGS 811
Locus name: Desynapsis 16
Locus symbol: *des16*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 7H (1); *des16.w* is associated with SNP markers 1_0772 to 2_1448 (positions 71.81 to 134.43 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW233 (1). The *des16.w* mutant was previously reported to be an allele at the *des12* locus (3, 4), which is located in chromosome 3H, see BGS 391.

Description:

In field trials, the Bowman backcross-derived line for *des16.w*, BW233, had very low seed set and grain yields were 10% of Bowman yields. Under greenhouse conditions, BW233 had less than 10% selfed seed set (2). The *des16.w* mutant was previously reported to be an allele at the *des12* locus (3, 4), but no parental SNP markers were retained in chromosome 3H of the Bowman backcross-derived line for *des16.w*, BW233 (1). The locus name desynapsis 16, the locus symbol *des16*, and the allele symbol *des16.w* are recommended for this desynapsis mutant in Freja. The desynapsis mutants *des1* (see BGS 12) and *des4* (see BGS 13), which map in the same region of chromosome 7H (1), were previously recorded as non-allelic (4). Also, alleles at these two loci had higher levels selfed seed set in their Bowman backcross-derived lines, BW229 (*des1.v*) and BW240 (*des4.af*) (2). The allele for red stem trait (*Rst1.a*) at the anthocyanin-less 1 (*ant1*) locus (see BGS 33) is retained from the donor parent in BW233 (2).

Origin of mutant:

A spontaneous mutant in Freja (PI 190482) isolated by R.F. Eslick (3, 5).

Mutational events:

des16.w in Freja (PI 190482) (1, 3, 5).

Mutant used for description and seed stocks:

des16.w in Freja; *des16.w* in Bowman (PI 483237)*6 (BW233, NGB 22060).

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. Hernandez-Soriano, J.M., and R.T. Ramage. 1973. Coordinator's report: Desynaptic genes. Barley Genet. Newsl. 3:91.
4. Hernandez-Soriano, J.M., and R.T. Ramage. 1974. BGS 391, Normal vs. desynapsis 12, *des12*. Barley Genet. Newsl. 4:140.
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. Barley Genet. Newsl. 2:65-68.

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:169.

BGS 812, Lesser internode number 3, *lin3*

Stock number:	BGS 812
Locus name:	Lesser internode number 3
Locus symbol:	*lin3*

Previous nomenclature and gene symbolization:

Laxatum-234 = *lax.234* (4, 5).
Low rachis internode number e = *lin.e* (1).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 2H, 3H, and 5HL (1); *lin3.e* is associated mainly with SNP markers 2_1338 to 2_1399 (positions 74.97 to 103.73 cM) in 2H bins 06 to 08, with markers 1_0672 to 2_1277 (positions 58.56 to 173.82 cM) in 3H bins 04 to 11, and with markers 1_1090 to 2_1452 (positions 203.85 to 244.39 cM) in 5H bins 11 to 12 of the Bowman backcross-derived line BW484 (1).

Description:

Plants with the *lin3.e* (*lax-234*) mutant have long rachis internodes, early heading, short spikes, and low kernel weights (4). Plants with the *lin3.e* gene were selected for fewer kernels per spike during backcrossing to Bowman (2). Plants of the Bowman backcross-derived line for *lin3.e*, BW484, were variable in height, 15% shorter to slightly taller than Bowman plants. Leaf blades were slightly wider; rachis internodes were slightly longer; heading occurred 3 to 7 days later; and kernels per spike averaged 5 fewer, 16 vs. 21. Compared to Bowman the kernels of BW484 were thinner; kernel weights were lower, 47 vs. 57 mg; and test weight was 20% less. Grain yields of BBW484 varied from 20% to 70% less than Bowman yields (2). BW484 seedlings were more responsive to gibberellic acid treatment than Bowman seedlings (3). The locus name lesser internode number 3, the locus symbol *lin3*, and the allele symbol *lin3.e* are recommended for this Foma mutant because it has a unique combination of morphological traits (2). Delayed heading of BW484 might in part due to present of late allele from Foma at the *Eam6* (Early maturity 6) locus in chromosome 2H (1, 2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (4, 5).

Mutational events:

lin3.e (*lax.234*, NGB 116462, DWS 1314) in Foma (NGB 14659, CIho 11333) (1, 2).

Mutant used for description and seed stocks:

lin3.e (*lax.234*, NGB 116462) in Foma; *lin3.e* in Bowman (PI 483237, NGB 22812)*4 (BW484, NGB 20172).

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. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:170-171.

BGS 813, Necrotic leaf spot 35, *nec35*

Stock number:	BGS 813
Locus name:	Necrotic leaf spot 35
Locus symbol:	*nec35*

Previous nomenclature and gene symbolization:

Necroticans n = *nec.n* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HL (1); *nec35.n* is associated mainly with SNP markers 2_1381 to 1_1172 (positions 157.14 to 190.87 cM) in 3H bins 10 to 12 of the Bowman backcross-derived line BW612 (1).

Description:

The *nec35.n* mutant is a second morphological mutant in the NGB 114280 stock, which has the *cal-a.1* mutant at the subjacent hood 1 or calcaroides-a locus, see BGS 62 (2). Seedlings and plants with the *nec35.n* gene had irregularly shaped and colored necrotic blotches on the leaf blades (2). Plants with the *nec35.n* gene were selected for irregularly shaped necrotic blotches during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *nec35.n*, BW612, were 10 to 15% shorter than Bowman plants and lodged easily. Rachis internodes were shorter, 4.0 vs. 4.7 mm. Kernels were slightly shorter and thinner and weighed less, 50 vs. 58 mg, and test weight was 5 to 10% lower. Grain yields of BW612 average 50 to 60% of those for Bowman (2). The locus name necrotic leaf spot 35, the locus symbol *nec35*, and the allele symbol *nec35.n* are recommended for this Bonus mutant because the necrotic leaf spot phenotype appears unique, and the mutant has a possible chromosome location (1, 2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) isolated by Åke Gustafsson (3, 4).

Mutational events:

nec35.n (NGB 114280, GSHO 286, *cal-a.1*) in Bonus (NGB 14657, PI 189763) (1, 2, 4).

Mutant used for description and seed stocks:

nec35.n (NGB 114280, GSHO 286) in Bonus; *nec35.n* in Bowman (PI 483237, NGB 22812)*2 (GSHO 2315); *nec35.n* in Bowman*5 (BW612, NGB 22178).

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. 1993. Coordinator's report: Ear morphology genes. Barley Genet. Newsl. 22:137-139.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:172.

BGS 814, Necrotic leaf spot 36, *nec36*

Stock number:	BGS 814
Locus name:	Necrotic leaf spot 36
Locus symbol:	nec36

Previous nomenclature and gene symbolization:

Necroticans q = *nec.q* (1, 2).

Inheritance:

Monofactorial recessive (2, 3).

Located likely in chromosomes 1H or 3H (1); *nec36.q* is associated in Bowman backcross-derived line BW610 with several small groups of parental SNP markers and two larger groups of parental SNP markers: one in chromosome 1H bins 07 to 08 [1_0259 to 1_1359 (positions 70.78 to 82.35 cM)] and the other in chromosome 3H bins 05 to 07 [2_1145 to 2_0597 (positions 65.96 to 119.10 cM)] (1).

Description:

The *nec36.q* plants have numerous small necrotic flecks on the leaf blades that persist to maturity (2). The Bowman backcross-derived line for *nec36.q*, BW610, was similar to Bowman except for the necrotic flecks (2). Based on phenotypic expression and chromosome segments retained in its Bowman backcross-derived line, BW610, the locus name necrotic leaf spot 36, the locus symbol *nec36*, and the allele symbol *nec36.q* are recommended for this necrotic leaf spot mutant in Morex (1, 2). The short awn mutant *lks6.q* is also present in the original mutant stock FN329 (GSHO 3674), see BGS 724.

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) isolated by A. Kleinhofs (3).

Mutational events:

nec36.q (FN329, GSHO 3674) in Morex (CIho 15773) (3).

Mutant used for description and seed stocks:

nec36.q (FN329, GSHO 3674) in Morex; *nec36.q* in Bowman (PI 483237, NGB 22812)*2 (BW610, NGB 22176).

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. Kleinhofs, A. (Unpublished).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:173.

BGS 815, Necrotic leaf spot 38, *nec38*

Stock number:	BGS 815
Locus name:	Necrotic leaf spot 38
Locus symbol:	*nec38*

Previous nomenclature and gene symbolization:

Necroticans s = *nec.s* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HL (1); *nec38.s* is associated with SNP markers 2_0130 to 2_1495 (positions 151.97 to 160.37 cM) in 3H bins 09 to 10 of the Bowman backcross-derived line BW623 (1).

Description:

The *nec38.s* mutant was identified as a second morphological mutant in the NGB 115896 stock (2). The other mutant is the *ari-d.44* allele located at the unbranched style 4 or breviaristatum-a locus, see BGS 11. Plants with the *nec38.s* mutant had scattered, irregularly shaped necrotic blotches on the leaf blades (2). Plants with necrotic botches were selected during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *nec38.s*, BW623, were similar to Bowman in greenhouse nurseries. They were not compared to Bowman in field nurseries (2). The locus name necrotic leaf spot 38, the locus symbol *nec38*, and the allele symbol *nec38.s* are recommended for this Bonus mutant because it is associated with a small chromosome segment from the donor parent (1, 2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 3).

Mutational events:

nec38.s (NGB 115896, *ari-d.44*) in Bonus (NGB 14657, PI 189763) (1, 2).

Mutant used for description and seed stocks:

nec38.s (NGB 115896) in Bonus; *nec38.s* in Bowman (PI 483237, NGB 22812)*4 (BW623, NGB 22189).

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. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:174.

BGS 816, Necrotic leaf spot 39, *nec39*

Stock number:	BGS 816
Locus name:	Necrotic leaf spot 39
Locus symbol:	*nec39*

Previous nomenclature and gene symbolization:

Necroticans u = *nec.u* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 5H or 7H (1); *nec39.u* is associated mainly with SNP markers 1_1198 to 2_0549 (positions 73.70 to 166.96) in 5H bins 04 to 10 and with SNP markers 1_0576 to 2_0691 (positions 54.30 to 229.66) in 7H bins 04 to 13 of the Bowman backcross-derived line BW609 (1). If a terminal segment from *Hordeum bulbosum* is involved in expression of *nec39.u* mutant, it is likely that the long arm of chromosome 7H is involved.

Description:

Plants with the *nec39.u* mutant had many dark, irregularly shaped, necrotic blotches on the leaf blades (2). Seedlings of the Bowman backcross-derived line for *nec39.u*, BW609, had low vigor; and plants were about 3/4 normal height (2). The locus name necrotic leaf spot 39, the locus symbol *nec39*, and the allele symbol *nec39.u* are recommended for this necrotic leaf spot mutant (1, 2).

Origin of mutant:

An introgress line from a cross between Emir and *Hordeum bulbosum* isolated by R.A. Pickering (1, 3).

Mutational events:

nec39.u (181P150/1/1) in Emir/*H. bulbosum* (1, 2).

Mutant used for description and seed stocks:

nec39.u (181P150/1/1) in Emir/*H. bulbosum*; *nec39.u* in Bowman (PI 483237, NGB 22812)*2 (BW609, NGB 22175).

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. Pickering, R.A. 2000. (Personal communications).

Prepared:

J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:175.

BGS 817, Necroticans 40, *nec40*

Stock number:	BGS 817
Locus name:	Necroticans 40
Locus symbol:	*nec40*

Previous nomenclature and gene symbolization:

Necroticans-39 = *nec.39* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located likely in chromosomes 2HL or 7HS (1); *nec40.39* is associated with several small groups of parental SNP markers in Bowman backcross-derived line BW618 with largest ones being from SNP markers 2_0590 to 2_0293 (positions 218.47 to 234.63 cM) in 2H bins 13 to 14 and from SNP markers 1_0949 to 2_0245 (positions 0.0 to 13.19 cM) in 7H bin 01 (1).

Description:

Plants with the *nec40.39* mutant had low vigor and many dark, irregularly shaped, necrotic blotches on the leaf blades (2, 3). Plants with necrotic botches were selected during backcrossing to Bowman, but the severe blotching trait was lost (2). Plants of the Bowman backcross-derived line for *nec40.39*, BW618, were slightly shorter and had about five more kernels per spike. Kernels of BW618 weighed about 10% less than Bowman kernels; and grain yield was about 20% less (2). The locus name necroticans 40, the locus symbol *nec40*, and the allele symbol *nec40.39* are recommended for this necroticans mutant in Kristina (1, 2).

Origin of mutant:

A gamma-ray induced mutant in Kristina (NGB 14661, NGB 1500) isolated by U. Lundqvist (1, 3).

Mutational events:

nec40.39 (NGB 115299) in Kristina (NGB 14661, NGB 1500) (1, 2).

Mutant used for description and seed stocks:

nec40.39 (NGB 115299) in Kristina; *nec40.39* in Bowman (PI 483237, NGB 22812)*4 (BW618, NGB 22184).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:176.

BGS 818, Necroticans 41, *nec41*

Stock number:	BGS 818
Locus name:	Necroticans 41
Locus symbol:	*nec41*

Previous nomenclature and gene symbolization:

Necroticans-42 = *nec.42* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (1); *nec41.42* is associated mainly with SNP markers 2_0988 to 1_0310 (positions 247.08 to 286.68 cM) in 5H bins 13 to 15 of the Bowman backcross-derived line BW619 (1).

Description:

Plants with the *nec41.42* mutant developed scattered large, dark, necrotic blotches on the leaf blades (2, 3). Plants with large necrotic blotches were selected during backcrossing to Bowman. Plants of the Bowman backcross-derived line for *nec41.42*, BW619, had a few large necrotic leaf spots and were slightly shorter than Bowman plants. Compared to Bowman, heading occurred from one day earlier to four days later; and kernel weights were slightly lower, 55 vs 59 mg. Over trials, grain yields of BW619 varied from 20% less to 20% more than Bowman yields (2). The locus name necroticans 41, the locus symbol *nec41*, and the allele symbol *nec41.42* are recommended for this Kristina mutant because parental SNP markers in a specific region of the long arm of chromosome 5H are retained in BW619 (1, 2).

Origin of mutant:

A gamma-ray induced mutant in Kristina (NGB 14661, NGB 1500) isolated by U. Lundqvist (1, 3).

Mutational events:

nec41.42 (NGB 115302, GSHO 2419) in Kristina (NGB 14661, NGB 1500) (1, 2).

Mutant used for description and seed stocks:

nec41.42 (NGB 115302, GSHO 2419) in Kristina; *nec41.42* in Bowman (PI 483237, NGB 22812)*5 (BW619, NGB 22185).

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).
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Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:177.

BGS 819, Necroticans 42, *nec42*

Stock number:	BGS 819
Locus name:	Necroticans 42
Locus symbol:	*nec42*

Previous nomenclature and gene symbolization:

Necroticans-69 = *nec.69* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosomes 2HL or 5HL (1); *nec42.69* is associated with SNP markers 2_0590 to 1_0072 (positions 218.47 to 239.78 cM) in 2H bins 13 to 15 and with SNP markers 1_1473 to 2_0320 (positions 154.37 to 166.29 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW621 (1).

Description:

Plants with the *nec42.69* mutant developed numerous necrotic flecks on older leaf blades and were very weak (2, 3). Plants of the Bowman backcross-derived line for *nec42.69*, BW621, had numerous necrotic flecks on older leaf blades when grown in the greenhouse. BW621 plants were slightly shorter than Bowman plants, headed three days later, and had about two more kernels per spike. The locus name necroticans 42, the locus symbol *nec42*, and the allele symbol *nec42.69* are recommended for this necrotic fleck mutant in Kristina (1, 2).

Origin of mutant:

A gamma-ray induced mutant in Kristina (NGB 14661, NGB 1500) isolated by U. Lundqvist (1, 3).

Mutational events:

nec42.69 (NGB 115329) in Kristina (NGB 14661, NGB 1500) (1, 2).

Mutant used for description and seed stocks:

nec42.69 (NGB 115329) in Kristina; *nec42.69* in Bowman (PI 483237, NGB 22812)*3 (BW621, NGB 22187).

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).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:178.

BGS 820, Maculosus-a, *mac-a*

Stock number:	BGS 820
Locus name:	Maculosus-a
Locus symbol:	*mac-a*

Previous nomenclature and gene symbolization:

Maculosus-1 = *mac.1* (1, 3).

Inheritance:

Monofactorial recessive (1, 2).

Located likely in chromosomes 1H, 3HL, or 7HS (1); *mac-a.1* is associated mainly with three large groups of parental SNP markers in Bowman backcross-derived line BW501: SNP markers 2_1361 to 2_1126 (positions 53.70 to 110.10 cM) in 1H bins 05 to 10, SNP markers 2_0115 to 2_0659 (positions 126.83 to 141.21 cM) in 3H bins 08 to 09, and SNP markers 1_0838 to 2_0790 (positions 49.53 to 73.69 cM) in 7H bins 04 to 05 (1).

Description:

The *mac-a.1* mutant has widely scattered dark necrotic flecks on the leaf blades (3). Plants of the Bowman backcross-derived line for *mac-a.1*, BW501, had widely scattered necrotic flecks on older leaf blades. No other morphological differences between BW501 and Bowman were noted (2). The locus name maculosus-a, the locus symbol *mac-a*, and the allele symbol *mac-a.1* are recommended for this Bonus mutant because no other named mutant is assigned to the maculosus locus group of mutants (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 3).

Mutational events:

mac-a.1 (NGB 116696) in Bonus (NGB 14657, PI 189763) (1, 3).

Mutant used for description and seed stocks:

mac-a.1 (NGB 116696) in Bonus; *mac-a.1* in Bowman (PI 483237, NGB 22812)*3 (BW501, NGB20729).

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. 2005. The Swedish Collection of barley mutants held at the Nordic Genebank. Barley Genet. Newsl. 35:150-154.

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:179.

BGS 821, Maculosus-b, *mac-b*

Stock number: BGS 821
Locus name: Maculosus-b
Locus symbol: *mac-b*

Previous nomenclature and gene symbolization:
Maculosus-4 = *mac.4* (1, 3).
Maculosus-6 = *mac.6* (1, 3).

Inheritance:
Monofactorial recessive (1, 2).
Located in chromosome 3HL (1); *mac-b.4* is associated mainly with parental SNP markers 2_2_0659 to 1_1172 (positions 141.21 to 190.87 cM) in 3H bins 09 to 12 of Bowman backcross-derived line BW504 (1); *mac-b.6* is associated with SNP markers 2_0009 to 2_0525 (positions 164.68 to 173.82 cM) in 3H bins 10 to 11 of Bowman backcross-derived line BW505 (1).

Description:
The *mac-b.4* and *mac-b.6* mutants have widely scattered dark necrotic flecks on the leaf blades (3). Plants of the Bowman backcross-derived lines for *mac-b.4*, BW504, and *mac-b.6*, BW505, were selected as having widely scattered necrotic flecks on older leaf blades. Other morphological differences between BW504, BW596, and Bowman were not observed (2). The locus name maculosus-b, the locus symbol *mac-b*, and the allele symbols *mac-b.4* and *mac-b.6* are recommended for these Bonus mutants because the parental SNP markers retained in BW504 and BW505 do not overlap those retained by BW501, which has the *mac-a.1* mutant (1, 2).

Origin of mutant:
A neutron induced mutant and an ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 3).

Mutational events:
mac-b.4 (NGB 116699) and *mac-b.6* (NGB 116700) in Bonus (NGB 14657, PI 189763) (1, 3).

Mutant used for description and seed stocks:
mac-b.4 (NGB 116699) and *mac-b.6* (NGB 116700) in Bonus; *mac-b.4* in Bowman (PI 483237, NGB 22812)*4 (BW504, NGB20732); *mac-b.6* in Bowman*5 (BW505, NGB20733).

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. 2005. The Swedish Collection of barley mutants held at the Nordic Genebank. Barley Genet. Newsl. 35:150-154.

Prepared:
U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:180.

BGS 822, Broad leaf 3, *blf3*

Stock number:	BGS 822
Locus name:	Broad leaf 3
Locus symbol:	*blf3*

Previous nomenclature and gene symbolization:

Maculosus-3 = *mac.3* (4, 5).

Inheritance:

Monofactorial recessive (1, 2).

Located likely in chromosome 4HL (1); *blf3.3* is associated mainly with SNP markers 1_0262 to 2_1332 (positions 76.26 to 112.64 cM) in 4H bins 06 to 07 of Bowman backcross-derived line BW503 (1).

Description:

The NGB 116698 stock was identified originally as having a maculosus leaf spot mutant, *mac.3*, with widely scattered dark necrotic flecks on older leaf blades (3, 4). The NGB 116698 stock had very wide leaf blades also (2). During backcrossing to Bowman, the wide leaf or broad leaf blade trait was selected in segregating. The leaf blades of the Bowman backcross-derived line for *blf3.3*, BW503, are wider than Bowman leaf blades, 10 vs. 7 mm for the flag-1 leaf. BW503 plants headed one to four days later than Bowman and were slightly shorter. Kernels of BW503 were slightly longer and wider than Bowman kernels, but kernel weights were similar. The test weight was slightly lower; and grain yields were 70 to 80% of Bowman yields (2). The locus name broad leaf 3, the locus symbol *blf3*, and the allele symbol *blf3.3* are recommended for this Bonus mutant because the other named broad leaf mutant in barley, *blf1* (see BGS 326), is in the long arm of chromosome 5H (1, 2, 3).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (1, 4).

Mutational events:

blf3.3 (NGB 116698) in Bonus (NGB 14657, PI 189763) (1, 2).

Mutant used for description and seed stocks:

blf3.3 (NGB 116698) in Bonus; *blf3.3* in Bowman (PI 483237, NGB 22812)*5 (BW503, NGB 20731).

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. Jöst, M., G. Hensel, C. Kappel, A. Druka, A. Sicard, U. Hohmann, S. Beier, A. Himmelbach, R. Waugh, J. Kumlehn, N. Stein, and M. Lenhard. 2016. The INDETERMINATE DOMAIN protein BROAD LEAF1 limits barley leaf width by restricting lateral proliferation. Curr. Biol. 26:903-909.
4. Lundqvist, U. 2005. The Swedish Collection of barley mutants held at the Nordic Genebank. Barley Genet. Newsl. 35:150-154.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:181.

BGS 823, Laxatum-p, *lax-p*

Stock number: BGS 823
Locus name: Laxatum-p
Locus symbol: *Lax-p*

Previous nomenclature and gene symbolization:

Laxatum-58 = *Lax-58* (2, 5, 7).

Inheritance:

Monofactorial recessive (6); semi-dominant in Bowman backcross-derived lines (3). Located likely in chromosomes 1H, 4H, or 7H (1); *Lax-p.58* is associated with three large groups of parental SNP markers in Bowman backcross-derived line BW433: SNP markers 1_0814 to 2_1126 (positions 53.70 to 110.10 cM) in 1H bins 05 to 10, SNP markers 1_0113 to 1_1513 (positions 26.58 to 101.44 cM) in 4H bins 02 to 10, and SNP markers 2_1419 to 2_1229 (positions 0.0 to 176.37 cM) in 7H bins 01 to 010 (1).

Description:

Rachis internodes of *Lax-p.58* are about 20% longer than those of Bonus, the awns are slightly coiled, leaf blades were narrow, and kernel weights were low (5). The original stock for *Lax.58* (NGB 116392) might contain a second mutant because Larrson (6) observed small plants with low fertility in the cross to Bonus. Plants of the Bowman backcross-derived line for *Lax-p.58*, BW433, headed about five days later than Bowman and had rachis internodes that were longer, 6.4 vs. 4.7 mm. Compared to Bowman, BW433 plants were slightly taller and had four more to four fewer kernels per spike (3). Kernels were longer, 12.3 vs. 9.4 mm, and thinner, 3.6 vs. 3.8 mm; and kernel weights were slightly lower. The grain yields of BW433 were about 50% of Bowman yields (3). The locus name Laxatum-p, the locus symbol *Lax-p*, and the allele symbol *Lax-p.58* are recommended because no other named laxatum mutant of Bonus has the combination of very long rachis internodes, delayed heading, and long thin kernels (1, 3, 7).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (2, 5, 6, 7).

Mutational events:

Lax-p.58 (NGB 116392), DWS 1293) in Bonus (NGB 14657, PI 189763) (1, 5, 7).

Mutant used for description and seed stocks:

Lax-p.58 (NGB 116392) in Bonus; *Lax-p.58* in Bowman (PI 483237, NGB 22812)*2 (BW433, NGB20665).

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. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
3. Franckowiak, J.D. (Unpublished).
4. 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.
5. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
6. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
7. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:182-183.

BGS 824, Laxatum-q, *lax-q*

Stock number: BGS 824
Locus name: Laxatum-q
Locus symbol: *lax-q*

Previous nomenclature and gene symbolization:

Laxatum-86 = *lax-86* (1, 4, 5).

Inheritance:

Monofactorial recessive (6).

Located likely in chromosomes 3H or 5H (1); *lax-q.86* is associated mainly with SNP markers 2_1197 to 2_1277 (positions 78.82 to 173.82 cM) in 3H bins 05 to 11 and with SNP markers 2_0010 to 1_0477 (positions 28.11 to 173.49 cM) in 5H bins 01 to 10 of the Bowman backcross-derived line BW434 (1).

Description:

Compared to Bonus, rachis internodes of *lax-q.86* were about 20% longer. Plants were shorter with broad, light green leaf blades; and kernels were longer and thinner (5). Plants of the Bowman backcross-derived line for *lax-q.86*, BW434, had coiled awns, which were about 2/3 as long as Bowman awns (3). BW434 plants headed three to five days later than Bowman plants. They were shorter, 65 vs. 88 cm, and had longer rachis internodes, 4.9 vs. 4.5 mm. Kernels of BW434 were longer, 9.9 vs. 9.4 mm, and thinner, 3.4 vs. 3.8 mm, and weighed less, 49 vs. 59 mg. Grain yields of BW434 were 50 to 75% of Bowman yields (3). The locus name laxatum-q, the locus symbol *lax-q*, and the allele symbol *lax-q.86* are recommended for this Bonus mutant because no other named laxatum mutant in the Bonus group has a similar combination of traits (1, 3, 7).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) isolated by U. Lundqvist (5, 7).

Mutational events:

lax-q.86 (NGB 116419, DWS 1307) in Bonus (NGB 14657, PI 189763) (1, 5, 7).

Mutant used for description and seed stocks:

lax-q.86 (NGB 116419) in Bonus; *lax-q.86* in Bowman (PI 483237, NGB 22812)*2 (BW434, NGB20666).

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. 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.
5. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
6. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
7. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:184.

BGS 825, Laxatum-of, *lax-of*

Stock number:	BGS 825
Locus name:	Laxatum-of
Locus symbol:	*lax-of*

Previous nomenclature and gene symbolization:

Laxatum-312 = *lax-312* (1, 5, 6).

Inheritance:

Monofactorial recessive (1, 3).

Located in chromosome 3HS (1); *lax-of.312* is associated mainly with SNP markers 2_0797 to 2_0742 (positions 5.45 to 29.05.63 cM) in chromosome 3H bins 01 to 02 of the Bowman backcross-derived line BW436 (1).

Description:

Rachis internodes of *lax-of.312* were about 15% longer than Foma internodes; kernels weighed about 25% less; and spikes had irregular kernel placement (6, 7). Compared to Bowman, the Bowman backcross-derived line for *lax-pf.312*, BW436, had slightly longer rachis internodes, 5.1 vs. 4.7 mm; and plants were 15% shorter. Awns were slightly coiled and slightly shorter, 10 vs. 13 cm beyond the last kernel. BW436 plants headed 4 to 5 days later than Bowman plants. Kernels were slightly longer, 10.2 vs. 9.4 m) and weighed slightly less. Grain yields of BW436 were less than half the Bowman yields (3). BW436 had a sensitive response to gibberellic acid (4). The locus name laxatum-of, the locus symbol *lax-of*, and the allele symbol *lax-of.312* are recommended for this Foma mutant because no other named laxatum mutant has been mapped in the subterminal region of chromosome 3H (1, 3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) isolated by U. Lundqvist (6, 7).

Mutational events:

lax-of.312 (NGB 116535, DWS 1331) in Foma (NGB 14659, CIho 11333) (1, 6, 7).

Mutant used for description and seed stocks:

lax-of.312 (NGB 116535) in Foma; *lax-of.312* in Bowman (PI 483237, NGB 22812)*4 (BW436, NGB20668).

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. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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7. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2019. Barley Genet. Newsl. 49:185.

BGS 826, Laxatum-la, *Lax-la*

Stock number:	BGS 826
Locus name:	Laxatum-la
Locus symbol:	*Lax-la*

Previous nomenclature and gene symbolization:

Laxatum ag = *Lax.ag* (1).

Inheritance:

Monofactorial dominant (1, 2).

Located in chromosome 2HL (1); *Lax-la.ag* is associated with SNP markers 1_0551 to 1_0085 (positions 221.70 to 247.86 cM) in 2H bins 13 to 15 of the Bowman backcross-derived line BW450 (1).

Description:

In crosses to Bowman, plants with the *Lax-la.ag* mutant were selected based on the lax spike phenotype (2). Compared to Bowman, the Bowman backcross-derived line for *Lax-la.ag*, BW450, had longer rachis internodes, 5.6 vs. 4.5 mm. BW450 plants averaged about 10% shorter than Bowman plants; kernels were slightly longer, 10.9 vs. 9.5 mm; but kernel weights were similar. Grain yields of BW450 were 2/3rds the Bowman yields (2). Because the *Lax-la.ag* mutant was not compared with the laxatum mutants of Bonus or Foma, a separate group of locus symbols starting with *Lax-la* is proposed for laxatum mutants not originating as induced mutants of Bonus or Foma (2, 4). The locus name Laxatum-la, the locus symbol *Lax-la*, and the allele symbol *Lax-al.ag* are suggested for this Volla mutant (2, 4).

Origin of mutant:

An induced mutant in Volla (PI 280423) isolated by H.P.K. Gaul (3).

Mutational events:

Lax-la.ag (GSHO 1575, 7014, DWS 1192) in Volla (PI 280423) (2, 3).

Mutant used for description and seed stocks:

Lax-la.ag (GSHO 1575) in Volla; *Lax-la.ag* in Bowman (PI 483237, NGB 22812)*6 (GSHO 1923); *Lax-la.ag* in Bowman*7 (BW450, NGB 20682).

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. Gaul, H. 1986. (Personal communications).
4. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:186.

BGS 827, Laxatum-lb, *lax-lb*

Stock number: BGS 827
Locus name: Laxatum-lb
Locus symbol: *lax-lb*

Previous nomenclature and gene symbolization:
Laxatum ah = *lax.ah* (1).
Inheritance:
Monofactorial recessive (1, 2).
Located in chromosome 2HL (1); *lax-lb.ah* is associated mainly with SNP markers 1_0876 to 1_0551 (positions 161.08 to 221.70 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW451 (1).
Description:
Plants of the Volla mutant *lax-lb.ah* have elongated rachis internodes. The long rachis internode trait was selected for during backcrossing to Bowman (2). Compared to Bowman, plants of the Bowman backcross-derived line for *lax-lb.ah*, BW451, had longer rachis internodes, 5.6 vs. 4.6 mm, but they were 10% shorter in stature and lodged less. Leaf blades were slightly shorter and narrower; awns were slightly longer; and kernels were longer, 10.8 vs. 9.4 mm. Kernel weights for BW451 were slightly more, 61 vs. 58 mg. Grain yields of BW451 were highly variable, but never more than half the Bowman yields(2). The locus name laxatum-lb, the locus symbol *lax-lb*, and the allele symbol *lax-lb.ah* are recommended for this Volla mutant because the parental SNP markers retained in BW451 do not overlap those retained in BW450, the Bowman backcross-derived line for *Lax-la.ag* (1, 2, 4). The *lax-lb.ah* mutant was not evaluated in comparisons with the laxatum mutants of Bonus or Foma; thus, this locus is included in a new proposed group of locus symbols for laxatum mutants starting *Lax-la* (2, 4).
Origin of mutant:
An induced mutant in Volla (PI 280423) isolated by H.P.K. Gaul (3).
Mutational events:
lax-lb.ah (7100, DWS 1210) in Volla (PI 280423) (2, 3).
Mutant used for description and seed stocks:
lax-lb.ah (DWS 1210) in Volla; *lax-lb.ah* in Bowman (PI 483237, NGB 22812)*4 (BW451, NGB 20683).
References:
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2. Franckowiak, J.D. (Unpublished).
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4. Lundqvist, U. (Unpublished).
Prepared:
J.D. Franckowiak and U. Lundqvist. 2019. Barley Genet. Newsl. 49:187.

BGS 828, Laxatum-lc, *lax-lc*

Stock number: BGS 828
Locus name: Laxatum-lc
Locus symbol: *lax-lc*

Previous nomenclature and gene symbolization:

Laxatum aj = *lax.aj* (1).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosomes 3H or 6HL (1); *lax-lc.aj* is associated mainly with SNP markers 2_1533 to 2_0704 (positions 67.01 to 100.48 cM) in 3H bins 04 to 06 and with SNP markers 2_1339 to 1_0390 (positions 95.18 to 206.61 cM) in 6H bins 06 to 14 of the Bowman backcross-derived line BW453 (1).

Description:

The *lax-lc.aj* mutant plants were selected during backcrossing to Bowman for slightly longer rachis internodes (2). Compared to Bowman, rachis internodes of the Bowman backcross-derived line for *lax-lc.aj*, BW453, were slightly longer, 4.8 vs. 4.3 mm. Kernels of BW453 weighed slightly less, 53 vs. 59 mg; and grain yields were 20 to 40% lower than those of Bowman (2). The locus name laxatum-lc, the locus symbol *lax.lc*, and the allele symbol *lax-lc.aj* are recommended for this laxatum mutant of Volla because parental SNP markers were retained in different chromosomes than previously named mutants in this group (2).

Origin of mutant:

An induced mutant in Volla (PI 280423) isolated by H.P.K. Gaul (3).

Mutational events:

lax-lc.aj (7175, DWS 1227) in Volla (PI 280423) (2, 3).

Mutant used for description and seed stocks:

lax-lc.aj (DWS 1227) in Volla; *lax-lc.aj* in Bowman (PI 483237, NGB 22812)*4 (BW453, NGB 20685).

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 2019. Barley Genet. Newsl. 49:188.

BGS 829, Laxatum-ld, *lax-ld*

Stock number:	BGS 829
Locus name:	Laxatum-ld
Locus symbol:	*lax-ld*

Previous nomenclature and gene symbolization:

Laxatum ak = *lax.ak* (1).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosomes 3HL or 6HL (1); *lax-ld.ak* is associated mainly with SNP markers 2_1272 and 3_0921 (positions 223.38 and 229.99 cM) in 3H bins 14 to 15 and with SNP markers 2_0036 and 3_1495 (positions 169.88 and 180.69 cM) in 6H bin 11 of the Bowman backcross-derived line BW454 (1).

Description:

Plants with the *lax-ld.ak* mutant were selected in progeny from crosses to Bowman based on long rachis internodes (2). Compared to Bowman, rachis internodes of the Bowman backcross-derived line for *lax-ld.ak*, BW454, were longer, 5.5 vs. 4.6 mm; and spikes had a few more kernels. Kernels of BW454 were longer, 11.2 vs. 9.4 mm; and weighed about 10% less. Grain yields of BW454 were 50 to 70% of the Bowman yields (2). The locus name laxatum-ld, the locus symbol *lax.ld*, and the allele symbol *lax-ld.ak* are recommended for this laxatum mutant of Volla because BW454 plants are phenotypically different from other laxatum mutants previously associated with chromosome arms 3HL or 6HL (2, 4).

Origin of mutant:

An induced mutant in Volla (PI 280423) isolated by H.P.K. Gaul (3).

Mutational events:

lax-ld.ak (7176, DWS 1228) in Volla (PI 280423) (2, 3).

Mutant used for description and seed stocks:

lax-ld.ak (DWS 1228) in Volla; *lax-ld.ak* in Bowman (PI 483237, NGB 22812)*3 (BW454, NGB 20686).

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 2019. Barley Genet. Newsl. 49:189.

BGS 830, Laxatum-le, *Lax-le*

Stock number: BGS 830
Locus name: Laxatum-le
Locus symbol: *Lax-le*

Previous nomenclature and gene symbolization:
Laxatum al = *Lax.al* (1).
Inheritance:
Monofactorial dominant (1, 2).
Located in chromosome 7HS (1); *Lax-le.al* is associated with SNP markers 2_0790 to 3_0290 (positions 73.69 to 76.28 cM) in 7H bin 05 of the Bowman backcross-derived line BW455 (1).
Description:
Plants with the *Lax-le.al* mutant were selected in progeny of crosses to Bowman based on slightly longer rachis internodes (2). Compared to Bowman, rachis internodes of the Bowman backcross-derived line for *Lax-le.al*, BW455, were slightly longer; plants were slightly taller; and awns were slightly shorter. Plants headed about one day later and had 1 to 3 more kernels per spike. Kernels of BW455 were similar in size and shape to Bowman kernels, but weighed slightly more. Grain yields of BW455 were similar to Bowman yields (2). The locus name Laxatum-le, the locus symbol *Lax.le*, and the allele symbol *lax-le.al* are recommended for this laxatum variant from Steptoe because BW455 retained parental SNP markers in different chromosomes than previously named mutants in this group (1, 2, 4).
Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) isolated by A. Kleinhofs (3) or a natural variant in Steptoe (2).
Mutational events:
Lax-le.al (GSHO 1576, GSHO 2417, AZ68) in Steptoe (CIho 15229) (2, 3).
Mutant used for description and seed stocks:
Lax-le.al (GSHO 1576, GSHO 2417) in Steptoe; *Lax-le.al* in Bowman (PI 483237, NGB 22812)*4 (GSHO 2278); *Lax-le.al* in Bowman*5 (BW455, NGB 20687).
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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4. Lundqvist, U. (Unpublished).
Prepared:
J.D. Franckowiak 2019. Barley Genet. Newsl. 49:190.

BGS 831, Weak spikelet attachment 1, *Wsa1*

Stock number:	BGS 831
Locus name:	Weak spikelet attachment 1
Locus symbol:	*Wsa1*

Previous nomenclature and gene symbolization:

Weakly (attached) spikelet = *Ws* [(6) see 4].

Inheritance:

A dominant factor or possibly dominant complementary factors [(5, 6) see 4].

Located in chromosome 1HL [(5) see 4]; *Wsa1.a* is linked in repulsion to the *Blp1.b* (Black pericarp and lemma 1) allele [(5) see 4].

Description:

The normal threshing pattern for covered two-rowed barley cultivars is detachment of the spikelets from the rachis. When threshing process is fairly gentle the rachis often remains intact. In some naked two-rowed accessions, detachment of the spikelet from the rachis does not occur, instead the caryopsis is removed from the hulls (lemma and palea) during threshing. The lemmas and paleas remain attached to the rachis [(5, 6) see 4]. Based on the barley phytomer model for segments of the culm and rachis (1) and the phytomeric triad model of bud structure (3), detachment of the kernel from the rachis occurs above the glumes and below the lemma (2). This detachment likely happens at the first node of the bud that forms the spikelet (2). Zheng et al. (7) described this detachment position as disarticulation at the first rachilla node.

Origin of mutant:

Wsa1.a (brittle attachment) is the spontaneous variant present in covered, white two-rowed cultivars [(5, 6) see 1, 4]; *wsa1.b* (non -brittle attachment) is the normal variant found in naked, black two-rowed barley [(5, 6) see 4] and wild barley; the *wsa1.b* allele is present in the Ethiopia landrace Jet (CIho 2222) with the *Blp1.b* (Black lemma and pericarp 1) and *nud1.a* (naked caryopsis 1) genes (2).

Mutational events:

Wsa1.a in Bowman (PI 483237, NGB 22812) (2); *wsa1.b* in Jet (CIho 2222) (2, 6).

Mutant used for description and seed stocks:

Wsa1.a in Bowman (PI 483237, NGB 22812) and many covered two-rowed barleys; *wsa1.b* in the black naked accession Jet (CIho 2222).

References:

1. Forster, B.P., J.D. Franckowiak, U. Lundqvist, J. Lyon, I. Pitkethly, and W.T.B. Thomas. 2007. The barley phytomer. Ann. Bot. 100:725-733.
2. Franckowiak, J.D. (Unpublished).
3. 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, Aleppo, Syria.
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