

BGS 7, Naked caryopsis 1, *nud1*

Stock number: BGS 7  
Locus name: Naked caryopsis 1  
Locus symbol: *nud1*

Previous nomenclature and gene symbolization:

Naked caryopsis = *k* (16).  
Naked caryopsis = *s* (23).  
Naked caryopsis = *n* (8, 11).  
Hulless = *h* (12).

Inheritance:

Monofactorial recessive (8, 16, 21).  
Located in chromosome 7HL (4, 13, 14, 16, 22); near the centromere (4, 13); about 9.6 cM proximal from the *lks2* (short awn 2) locus (17); about 10.5 cM proximal from the *dsp1* (dense spike 1) locus (17, 18); in bin 7H-07 about 13.1 cM distal from RFLP marker MWG808 (2); co-segregating with AFLP markers KT3 and KT7 and SCAR marker sKT7 (9); about 0.06 cM distal from SCAR marker sTK3 and the same distance proximal from sTK9 (19); *nud1.a* is associated with SNP markers 1\_1437 and 2\_0685 (both at position 126.28 cM) in 7H bin 07 of the Bowman backcross-derived line BW638 (3); *nud1.a* is associated with SNP markers 2\_0975 to 2\_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW220 (3).

Description:

The lemma and palea do not adhere to the caryopsis and the grain will thresh free of the hull at maturity. The naked caryopsis trait is expressed in all environments (18). The naked lines fail to produce a cementing substance present in covered lines (6). The *nud1.a* mutant depressed the expression by 10 to 20% of other traits such as plant height, seed weight (1, 10) and altered malt quality parameters (10). The *nud1.a* gene is often associated with the *dsp1.a* (dense spike 1) gene in Japanese cultivars (18). The Bowman backcross-derived line for *nud1.a*, BW638, was more sensitive to environmental stress than Bowman. Plants were 15% shorter when grown at Dundee, Scotland, but almost equal to Bowman at other locations. The kernel weights of BW638 varied from 25% lower to almost equal, and grain yields ranged from 50 to 85% of those recorded for Bowman (5). Allele *IV* of the marker sKT7 near the *nud1* locus was the only one found in naked barley cultivars (20). The geographic distribution of haplotypes with the allele *IV* suggests migration of naked types was toward eastern Asia (20).

Origin of mutant:

In an unknown cultivar, but its origin was monophyletic probably in southwestern Iran (20), widespread in cultivated barley in Asia.

Mutational events:

*nud1.a* (GSHO 115) in Himalaya (CIho 1312) (23); *nud1.b* (Mut 4129) in Haisa, *nud1.c* (Mut 3041/62) in Ackermann's Donaria (PI 161974) (15).

Mutant used for description and seed stocks:

*nud1.a* (GSHO 115) in Himalaya, *nud1.a* from Sermo (CIho 7776) in Betzes (PI 129430)\*7 (CIho 16559, GP 37), *nud1.a* from Sermo in Compana (CIho 5438)\*7 (CIho 16185, GP 41), *nud1.a* from Sermo in Decap (CIho 3351)\*7 (CIho 16563, GP 45) (7); *nud1.a* from Stamm (PI 194555) in Betzes\*7 (CIho 16566, GP 48), *nud1.a* from Stamm in Compana\*7 (CIho 16183, GP 50), *nud1.a* from Stamm\*7 in Freja (CIho 7130)\*7 (CIho 16568, GP 52) (7); *nud1.a* from a Chinese introduction in Bowman (PI 483237)\*8 (GSHO 1847, BW638, NGB 20751); *nud1.a* with *cur2.b* (curly 2) from Choshiro-hen (UL006, GSHO 274) in Bowman\*5 (GSHO 1991); *nud1.a* with

*cur2.b* from Choshiro-hen in Bowman \*6 (BW220, NGB 22047).

References:

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Prepared:

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Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:51-52.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:195-196.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:51-53.

BGS 13, Desynapsis 4, *des4*

Stock number: BGS 13  
Locus name: Desynapsis 4  
Locus symbol: *des4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7H (1); *des4.af* is associated with SNP markers 1\_0772 to 2\_0790 (positions 71.81 to 73.96 cM) in 7H bin 05 and markers 2\_0311 to 2\_1448 (positions 126.28 to 134.43 cM) in 7H bin 08 of Bowman backcross-derived line BW240 (1); *des4.d* is associated with SNP markers 1\_838 to 2\_1201 (positions 49.53 to 134.43 cM) in 7H bins 04 to 08 of Bowman backcross-derived line BW241 (1), likely in 7H bin 08.

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is  $d = 3.3 \pm 2.2$  with a range from 7 ring bivalents ( $d = 0$ ) to 3 rod bivalents plus 8 univalents ( $d = 11$ ). Many of the univalents split longitudinally during anaphase I, and lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore tetrads contained an average of 1.0 micronuclei per tetrad and the micronuclei range 0 to 10. Ovule fertility was about 18% (3). Plants of the Bowman backcross-derived line for *des4.af*, BW240, were similar to Bowman except grain yields were 25 to 50% lower. Kernels were about 10% lighter than those of Bowman in most trials (2).

Origin of mutant:

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

Mutational events:

*des4.d* (GSHO 595), *des4.h* in Betzes (5, 6); *des4.z*, *des4.aa*, *des4.ab*, *des4.ac*, *des4.ad*, *des4.ae*, *des4.af*, *des4.ag* in Klages (Clho 15487) (4, 7); all the Klages mutants may be identical because they were isolated from the same field (4).

Mutant used for description and seed stocks:

*des4.d* GSHO 595) in Betzes; *des4.d* in Bowman (PI 483237)\*5 (BW241, NGB 22068; *des4.af* in Bowman\*7 (BW240, NGB 22067); *des4.h* in Bowman\*2 (BW242, NGB 22069).

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. 1973. Desynaptic mutants in Betzes barley. M.S. Thesis. Univ. of Arizona, Tucson.
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5. Ramage, R.T., and J.M. Hernandez-Soriano. 1971. Desynaptic genes in Betzes barley. *Barley Genet. Newsl.* 1:38.
6. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.
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Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:127.

Revised:

R.T. Ramage and J.F. Scheuring. 1976. Barley Genet. Newsl. 6:116.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:58.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:71-72.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:54-55.

BGS 14, Desynapsis 5, *des5*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 7HL (4); *des5.e* is associated with SNP markers 2\_0139 to 2\_1363 (positions 194.97 to 198.70 cM) in 7H bin12 and with SNP markers 1\_1198 to 2\_1275 (positions 73.70 to 104.73) of the Bowman backcross-derived line BW243 (1), most likely in 7H bin 12.

Description:

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

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (4, 5).

Mutational events:

*des5.e* (GSHO 596), *des5.f*, *des5.g* in Betzes (PI 129430) (4, 5).

Mutant used for description and seed stocks:

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

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.* 3:128.

Revised:

- J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:59.  
J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:73.  
J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:56.

BGS 30, Erectoides-m, *ert-m*

Stock number: BGS 30  
Locus name: Erectoides-m  
Locus symbol: *ert-m*

Previous nomenclature and gene symbolization:

Erectoides-34 = *ert-34* (3, 4).

Inheritance:

Monofactorial recessive (3, 4, 10).

Located in chromosome 7HS (6, 7, 8, 10); about 14.7 cM distal from the *cer-f* (*eceriferum-f*) locus (11, 12, 13); near the *ant1* (anthocyanin-less 1) locus (10); *ert-m.34* is associated with SNP markers 2\_1326 to 2\_1270 (positions 65.26 to 93.97 cM) in 7H bins 05 to 06 of the Bowman backcross-derived line BW316 (1).

Description:

Spikes have a compact appearance caused by a reduction in rachis internode length, with rachis internode length values from 2.0 to 2.8 mm. However, the rachis internodes within each spike are often variable in length, and the spike appears irregular similar to those of opposite spikelet mutants. Plants with an allele at the *ert-m* locus are often 10 to 15 cm shorter than parental cultivars, and some tillers of most plants have one or more extremely shortened upper internodes (10). Alleles at the *ert-m* locus respond positively to GA<sub>3</sub> treatments designed to increase rachis internode length (14). Some alleles at the *ert-m* locus lack normal anthocyanin pigmentation. The anthocyanin deficiency can not be separated from the *ert-m* allele and is apparently an allele at the *ant1* locus (9, 10). Plants of the Bowman backcross-derived line for *ert-m.34*, BW316, were slightly shorter than Bowman with an average rachis internode length of 3.8 vs. 4.5 mm. Kernels of BW316 varied in size from equal to 20% larger than those of Bowman, but test weight was 10% lower. Grain yields of BW316 averaged about 2/3 those of Bowman (2).

Origin of mutant:

A thermal neutron induced mutant in Bonus (PI 189763, NGB 14657) (4, 10).

Mutational events:

*ert-m.34* (NGB 112635, GSHO 487), *-m.35* (NGB 112636), *-m.40* (NGB 112640) with a *ant1* mutant, *-m.41* (NGB 112641), *-m.42* (NGB 112642), *-m.54* (NGB 112653), *-m.64* (NGB 112663) with a *ant1* mutant in Bonus (PI 189763, NGB 14657) (4); *ert-m.87* (NGB 112686) with a *ant1* mutant, *-m.107* (NGB 112706), *-m.115* (NGB 112714), *-m.130* (NGB 112729), *-m.144* (NGB 112743), *-m.168* (NGB 112768), *-m.169* (NGB 112769) in Bonus, *-m.314* (NGB 112829) in Foma (CIho 11333, NGB 14659) (10); *ert-m.328* (NGB 112843) in Foma (5); *ert-m.330* (NGB 112845), *-m.363* (NGB 112879), *-m.384* (NGB 112899), *-m.426* (NGB 112942) in Foma (10).

Mutant used for description and seed stocks:

*ert-m.34* (NGB 112635, GSHO 487) in Bonus; *ert-m.34* in Bowman (PI 483237)\*8 (GSHO 1843, BW316, NGB 22111).

References:

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

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:78-79.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:57-58.

BGS 39, Midseason stripe 2, *mss2*

Stock number: BGS 39  
Locus name: Midseason stripe 2  
Locus symbol: *mss2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7HS (3); based on linkage drag with the *Lga1* (Long glume awn 1) and *dsp1* (dense spike 1) loci (3, 4); *mss2.b* was associated with only one unmapped SNP marker in Bowman backcross-derived line BW594 (1); likely in 7H bin 05 based on association with the *Lga1* and *dsp1* (*ert-a*) loci.

Description:

A variable number of broad, white stripes develop in tillers during the joining stage. Leaves and spikes show white sectors that persist until maturity. Expression of *mss2* is temperature dependent with few or no stripes developing in cool environments and numerous white stripes in warm environments. When numerous stripes develop, spike length and plant vigor were much reduced (2). Plants of the Bowman backcross-derived line for *mss2.b*, BW594, had lower vigor than Bowman. Plants were 15% shorter and had narrower and shorter leaf blades. Kernels of BW594 were thinner and 10 to 20% lighter than those of Bowman. Grain yields of BW594 were 60 to 70% those of Bowman (2).

Origin of mutant:

A spontaneous mutant in breeding line ND11258 (Bowman\*2/ND7556) (2).

Mutational events:

*mss2.b* (GSHO 2409) in ND11258 (3).

Mutant used for description and seed stocks:

*mss2.b* (GSHO 2409) in ND11258; *mss2.b* in Bowman (PI 483237)\*7 (GSHO 2148, BW594, NGB 22160).

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. 2002. *Barley Genet. Newsl.* 32:79.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:59.

BGS 40, Premature ripe 1, *pmr1*

Stock number: BGS 40  
Locus name: Premature ripe 1  
Locus symbol: *pmr1*

Previous nomenclature and gene symbolization:

Premature ripe = *pmr* (4).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7HS (4); based on linkage drag with the *Lga1* (long glume awn 1) locus (3); near the centromere (6, 7); *pmr1.a* is associated with SNP markers 1\_1014 to 2\_0824 (positions 80.65 to 146.97 cM) in 7H bins 06 to 08 of the Bowman backcross-derived line BW645 (1).

Description:

The *pmr1* gene induces plants to start dying about two weeks after heading. Seedlings are slightly pale green in color and plants are shorter than normal sibs. The lighter shade of green persists until senescence of the plants begins. Premature dying of the plants caused rapid straw collapse and very thin grain (3). Plants of the Bowman backcross-derived line for *pmr1.a*, BW645, were slightly shorter and headed about three days later than Bowman plants. Kernels of BW645 were thin (2.96 vs. 3.82 mm in diameter) and weighed about half (29 vs. 59 mg) those of Bowman. Grain yields of BW645 ranged from almost none to 30% those of Bowman (3).

Origin of mutant:

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

Mutational events:

*pmr1.a* (DWS1069, GSHO 2429) in Glenn (CIho 15769) (5).

Mutant used for description and seed stocks:

*pmr1.a* (GSHO 2429) in Glenn, *pmr1.a* in Bowman (PI 483237)\*7 (GSHO 3434, BW645, NGB 22210).

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. Faue, A.C. 1987. Chemical mutagenesis as a breeding tool for barley. M.S. Thesis. North Dakota State Univ., Fargo.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
6. Kleinhofs, A. 1997. Integrating barley RFLP and classical marker maps. *Barley Genet. Newsl.* 27:105-112.
7. Kudrna, D., A. Kleinhofs, A. Kilian, and J. Soule. 1996. Integrating visual markers with the Steptoe x Morex RFLP map. Vol. 1. p. 343. *In* A.E. Slinkard, G.J. Scoles, and B.G. Rosnagel (eds.). *Barley Genetics VII. Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp.*, Saskatoon. Univ. Ext. Press, Univ. of Saskatchewan, Saskatoon, Canada.

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:80.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:60.

BGS 56, White streak 4, *wst4*

Stock number: BGS 56  
Locus name: White streak 4  
Locus symbol: *wst4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HL (3, 4, 5), about 6.5 cM distal from the *eog1* (elongated outer glume 1) locus (4); *wst4.d* is associated with SNP markers 1\_0084 to 2\_1258 (positions 76.05 to 114.96 cM) in 2H bins 06 to 08 of the Bowman backcross-derived line BW913 (1), likely in 2H bin 07.

Description:

Mutants grown at low temperatures exhibit numerous, wide, chlorotic (white) streaks on developing leaves. If temperatures are continuously low, plants appear highly chlorotic. As temperature rises, the white streaks gradually disappear. Exposure to 3°C for two weeks after sowing is sufficient to induce distinct streaks in the first and second leaves (4). Compared to Bowman, plants of the Bowman backcross-derived line for *wst4.d*, BW913, were morphologically similar, but they headed about four days later. Kernels of BW913 weighed 5 to 10% less than those of Bowman, but grain yields were equal to or slightly higher (2).

Origin of mutant:

A spontaneous mutant in Kanyo 7 (OUK651) (4).

Mutational events:

*wst4.d* (OUL068, GSHO 568) in Kanyo 7 (4).

Mutant used for description and seed stocks:

*wst4.d* (GSHO 568, OUL068) in Kanyo 7; *wst4.d* in Bowman (PI 483237)\*4 (GSHO 1905); *wst4.d* in Bowman\*7 (BW913, NGB 22344).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:116.

Revised:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:91.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:61.

BGS 59, Grandpa 1, *gpa1*

Stock number: BGS 59  
Locus name: Grandpa 1  
Locus symbol: *gpa1*

Previous nomenclature and gene symbolization:

Grandpa = *gp* (3).  
Grandpa 2 = *gp2* (7, 8).

Inheritance:

Monofactorial recessive (3).  
Located in chromosome 2HL (6, 7); about 24.5 cM distal from the *lig1* (liguleless 1) locus (5); *gpa1.a* is associated with SNP markers 2\_0069 to 10085 (positions 179.99 to 247.86 cM) in 2H bins 11 to 14 of the Bowman backcross-derived line BW397 (1).

Description:

Seedlings display a pattern of transverse of alternating white and green bands on the first, second, and occasionally the third foliage leaves. Plants have a slightly pale green color prior to heading. Grandpa plants are sensitive to flooding and produce an albino flag leaf, peduncle, and spike (5). Plants are viable in the field, but kernels are thin and yields are low (6). Compared to Bowman, plants of the Bowman backcross-derived line for *gpa1.b*, BW397, were very sensitive to stressed environments. BW397 plants headed 4 to 10 days later than Bowman and were 50 to 75% as tall. Kernels were thin, 3.18 vs. 3.86 mm, and weighed 50 to 80% of Bowman kernels. Grain yields of BW397 were 10 to 30% of those for Bowman (2).

Origin of mutant:

A spontaneous mutant in Lyallpur (NSL 40271) isolated by GA Wiebe (4).

Mutational events:

*gpa1.a* (CIho 6854, GSHO 519) in Lyallpur (NSL 40271) (4); *gpa1.b* (*gp2*) (GSHO 1379) in Montcalm (CIho 7149) (5, 7, 8).

Mutant used for description and seed stocks:

*gpa1.b* (GSHO 1379) in Montcalm; *gpa1.b* in Bowman (PI 483237)\*7 (GSHO 1934, BW397, NGB 22147).

References:

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:119.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl.10:107.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:95.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:62-63.

BGS 65, Early maturity 1, *Eam1*

Stock number: BGS 65  
Locus name: Early maturity 1  
Locus symbol: *Eam1*

Previous nomenclature and gene symbolization:

Early maturity = *Ea* (8).  
Early maturity 1 = *Ea1* (7).  
Photoperiod response gene H1 = *Ppd-H1* (11).

Inheritance:

Monofactorial dominant (9, 13).  
Located in chromosome 2HS (1, 8, 13); weakly linked to the *vrs1* (six-rowed spike 1) locus (1, 15, 19); the *Ppd-H1* (*Eam1*) locus is in the 6 cM interval between the RFLP loci XMWG858 and XpsrB9, 1 cM proximal to XM WG858 (11, 12); specific sequence tagged site (STS) markers were developed for the *Eam1* gene of Igri (3); in bin 2H-04 near RFLP marker MWG858 (13); in Azumamugi 6 cM proximal from marker ABG602 (15), *Eam1.c* is associated with SNP markers 1\_0216 to 2\_1338 (positions 47.48 to 66.78 cM) in 2H bins 04 to 06 of the Bowman backcross-derived line BW280 (4); *Eam1.d* is associated with SNP markers 12\_1386 to 2\_1261 (position 50.56 cM) in 2H bin 05 of the Bowman backcross-derived line BW281 (4); *Eam1.f* is associated with SNP markers 1\_0216 to 2\_1015 (positions 47.48 to 48.68 cM) in 2H bin 04 of the Bowman backcross-derived line BW282 (4), likely in 2H bin 05.

Description:

This gene controls the strong response of some cultivars to long photoperiods. The *Eam1* gene is described as a simply inherited dominant and the main factor for early maturity (1, 7, 8, 14). Under long-day condition, a near-isogenic line with *Eam1* is reported to be 7 to 8 days earlier than the *eam1* line 'ea1' (16). The early maturity gene is weakly linked to the *vrs1* (six-rowed spike 1) locus (1, 13, 19). In North Dakota, USA, progenies from crosses of Bowman to *Hordeum vulgare* subsp. *spontaneum*, California Coast and North African accessions, facultative winter barleys, far northern spring barleys (from Finland and Alaska), and winter barleys, extremely early segregates were found (6). The *Eam1* locus in barley is homoeologous to the *Ppd1*, *Ppd2*, and *Ppd3* loci in wheat, which control strong photoperiod response (11, 12). The reduced photoperiod responsiveness of the *ppd-H1* (*eam1.a*) mutant is explained by altered circadian expression of the photoperiod pathway gene CONSTANS (CO) (10, 19) and reduced expression of its downstream target, FLOWERING LOCUS T (*HvFT1*), a key regulator of flowering (2, 18). The CCT (CO, CO-like, and TOC1) domain mutation was a G-to-T change and produced a Gly-to-Trp change in the CCT domain of the barley pseudo-response regulator (PRR) gene (18). The DNA code sequence of the dominant alleles was variable among accessions while the recessive allele was not (18). Alleles at the *Eam1* locus interact with flowering time control mutants at the *eam7* (17) and *eam10* (2), but not *eam8* (5), loci to induce earlier heading under both short and long days.

Origin of mutant:

The strong photoperiod response to short nights occurs naturally in many barley cultivars and its wild relative, *Hordeum vulgare* subsp. *spontaneum*.

Mutational events:

A single dominant gene controls early maturity based on a cross to Lion (*Eam1.b*) (PI 32767, GSHO 27) (8); *Eam1.e* (GSHO 1569) was isolated from the Australian cultivar Prior (PI 221325) (9, 16); *eam1.a* is the normal allele in Manchurian six-rowed cultivars (7, 16); *eam1.a* is the allele present likely in many two-rowed cultivars from Europe origin (16).

Mutant used for description and seed stocks:

*Eam1.c* in Estate (PI 57700, GSHO 1316); *Eam1.c* from Estate in Bowman (PI 483237)\*7 (GSHO 1871); *Eam1.c* from Estate in Bowman\*8 (BW280, NGB 20564); *Eam1.d* from KT1031 (a winter barley from Bulgaria, GSHO 1568) in Bowman\*9 (GSHO 1872, BW281, NGB 20565); *Eam1.e* from Prior in Betzes\*7 (Erbet, CIho 13826) (4); *Eam1.f* from *Hordeum vulgare* subsp. *spontaneum* in Bowman\*8 (GSHO 1873, BW282, NGB 20466).

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Prepared:

J.D. Franckowiak and L.W. Gallagher. 1997. *Barley Genet. Newsl.* 26:101-102.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:64-66.

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).

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, 4); about 22.2 cM distal from the *vrs1* (six-rowed spike 1) locus (1); the Bowman backcross-derived line for *Pvc1.a*, BW651, did not retain any SNP markers polymorphisms compared to Bowman (2).

Description:

Purple pigment is produced by the presence of anthocyanins. When *Pvc1* 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).

Mutant used for description and seed stocks:

*Pvc1.a* (GSHO 132) in Buckley 2223-6; *Pvc1.a* from R.I. Wolfe's Multiple Dominant Stock (GSHO 1565) in Bowman (PI 483237)\*7 (GSHO 1929, BW 651, NGB 22216).

References:

1. Buckley, G.F.H. 1930. Inheritance in barley with special reference to the color of caryopsis and lemma. *Sci. Agric.* 10:460-492.
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Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:108.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:105.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:67.

BGS 69, Toothed lemma 1, *Gth1*

Stock number: BGS 69  
Locus name: Toothed lemma 1  
Locus symbol: *Gth1*

Previous nomenclature and gene symbolization:

Toothed lemma = G (4, 7).

Inheritance:

Monofactorial dominant (5, 6).

Located in chromosome 2HL (4, 7); about 15.4 cM proximal from the *vrs1* (six-rowed spike 1) locus (2, 4, 7); *gth1.b* is associated with SNP markers 2\_0528 to 1\_0823 (positions 118.78 to 133.59 cM) in 2H bins 08 to 09 of the Bowman backcross-derived line BW413 (1).

Description:

Large teeth or barbs are present on the upper part of lateral lemma nerves. The barbs are easiest to see on green spikelets. This trait may be difficult to study because Ubisch (6) reported three sizes of teeth, including one that could be seen only with magnification. According to Ubisch (6), one gene pair controls the presence and absence of large teeth and one or two other genes are responsible for less developed teeth. Segregation for only one pair of factors is reported by Wexelsen (7) and in subsequent studies. Besides barbs on the lateral lemma veins and slight heavier kernels, no other agronomic or morphological differs between the Bowman backcross-derived line for *gth1.b*, BW413, and Bowman (3).

Origin of mutant:

*Gth1.a* appears to be the normal allele; the recessive allele *gth1.b* is present in most two-rowed barley cultivars of Occidental origin.

Mutational events:

*Gth1.a* (GSHO 309) in Machine (Clho 4982) (7).

Mutant used for description and seed stocks:

*Gth1.a* (GSHO 309) in Machine; *Gth1.a* is present in Bowman (PI 483237); *gth1.b* from ND11894 (Gitane//ND4642/Robust/3/Bearpaw/4/TR218/ ND7015/3/ Norbert//ND4856/M38) in Bowman\*4 (GSHO 1897); *gth1.b* in Bowman\*6 (BW413, NGB 20646).

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7. Wexelsen, H. 1934. Quantitative inheritance and linkage in barley. *Hereditas* 18:307-348.

Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:109.

Revised:

T.E. Haus. 1978. Barley Genet. Newsl. 8:161.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:106.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:68-69.

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

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

Previous nomenclature and gene symbolization:

Purple chaff color = *P* (1, 7).  
Purple chaff color = *P<sub>1</sub>* (10).  
Purple pericarp = *P* (3, 11, 13).  
Purple lemma = *P* (2).  
Red pericarp = *R* (2).  
Red pericarp 2 = *Re2* (12).

Inheritance:

Two dominant complementary genes (*Pre1* and *Pre2*) control purple or red pigmentation of the lemma, palea, and pericarp (2, 10, 14). Located in chromosome 2HL (2); about 17.1 cM distal from the *vrs1* (six-rowed spike 1) locus (2, 11, 14); over 11.2 cM proximal from the *ant2* (anthocyanin-less 2) locus (4, 8, 9); *Pre2.a* is associated with SNP markers 1-0214 to 1\_0876 (positions 150.96 to 161.08 cM) in 2H bins 10 to 11 of Bowman backcross-derived line BW648 (5).

Description:

Purple or red coloration of the hull (chaff) and pericarp develops during the soft dough stage of grain fill, and fades as the grain matures. Anthocyanin pigments in an acid cell solution produce the red to violet color observed in the pericarp and lemma (2). Bowman and the Bowman backcross-derived line for *Pre2.a*, BW648, were similar for all agronomic and morphological traits except kernel color (6).

Origin of mutant:

Natural occurrence in a few cultivars and some *Hordeum vulgare* subsp *spontaneum* accessions (2, 14).

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

J.D. Franckowiak. 1997. Barley Genetics Newsl. 26:113-114.

Revised:

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:70-71.

BGS 80, Anthocyanin-less 2, *ant2*

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

Previous nomenclature and gene symbolization:

Non-purple straw = *p<sub>r</sub>* or *pr* (8).  
Anthocyanin-less = *ant-2* (2, 6).  
Exrubrum = *rub* (4).  
Colorless leaf tip 2 = *clt<sub>2</sub>* (5), *c<sub>2</sub>* (5).

Inheritance:

Monofactorial recessive (2, 8).  
Located in chromosome 2HL (2, 8), about 15.1 cM distal from the *vrs1* (six-rowed spike 1) locus (8, 9, 10); *ant2.20* is not associated with any heterogeneous SNP markers in BW019 (1); *ant2.h* is associated with SNP markers 1\_0214 to 2\_0182 (positions 150.96 to 185.53 cM) in 2H bins 10 to 12 of the Bowman backcross-derived line BW020 (1); most likely in 2H bin 11.

Description:

Anthocyanin pigments are not observed in any vegetative plant parts, including the stem, auricles, lemma, and awn (2, 5, 6). The straw does not develop a purple pigmentation as it approaches maturity (8). The recommended symbol for the dominant allele is *Ant2.c* (formerly *Pr*). Other consistent deviations from the Bowman phenotype were not observed in the Bowman backcross-derived lines BW019 (*ant2.20*) and BW020 (*ant2.h*) (3).

Origin of mutant:

Natural occurrence in few cultivars (7, 8), the first 3 or 4 natural occurrences may be the same allele.

Mutational events:

*ant2.d* (*pr1.b*) in Alva (NSGC1866), *ant2.e* (*pr1.c*) in Balder (PI 195481), *ant2.f* (*pr1.d*) in Cambrinus (PI 321779), *ant2.g* (*pr1.e*) in Sultan (PI 339814) (5); *ant2.15* (NGB 114564), 2.20 (NGB 114569, GSHO 1632), 2.23 (NGB 114572), 2.25 (NGB 114575), 2.26 (NGB 114576), 2.27 (NGB 114276) in Foma (CIho 11333, NGB 14659) (6); *ant2.41* (NGB 114596) in Mari (CIho 11334, NGB 14656), 2.46 (NGB 111505) in Foma, 2.47 (NGB 111823), 2.48 (NGB 111782), 2.49 (NGB 111808), 2.50 (NGB 111811), 2.51 (NGB 111817), 2.54 (NGB 111872), 2.55 (NGB 111787) in Bonus (PI 189763, NGB 14657), 2.112, 2.113, 2.114, 2.115, 2.116, 2.117, 2.118, 2.120, 2.121, 2.122, 2.130 in Nordal (NGB 13680, NGB 4704) (7); *ant2.h* (*pr1.f*) in Shyri (GSHO 2430) (3).

Mutant used for description and seed stocks:

*ant2.20* in Foma (NGB 114569, GSHO 1632); *ant2.h* from Shyri in Bowman (PI 483237)\*5 (GSHO 1919); *ant2.h* in Bowman\*7 (BW020, NGB 20428); *ant2.20* in Bowman\*2 (GSHO 1920); *ant2.20* in Bowman\*6 (BW019, NGB 20427).

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Prepared:

T.E. Haus. 1975. *Barley Genet. Newsl.* 5:107 as BGS 53, Purple straw, *Pr.*

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:118.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:72-73.

BGS 83, Slender dwarf 2, *sld2*

Stock number: BGS 83  
Locus name: Slender dwarf 2  
Locus symbol: *sld2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HS (4); over 18.2 cM distal from the *eog1* (elongated outer glume 1) locus (4); *sld2.b* is associated with SNP markers 1\_1505 to 1\_0325 (positions 81.43 to 90.54 cM) in 2H bins 06 to 07 of the Bowman backcross-derived line BW862 (1).

Description:

Mutant plants have short and slender culms, narrow leaves, short and lax spikes, and thin kernels (4). When grown at Langdon, North Dakota, USA, semi-dwarf plants were difficult to identify in progenies from crosses between OUM142 and two-rowed spring barley. The frequency of semidwarf, late maturing plants is low because *sld2.b* is linked to an *Eam1* (early maturity 1) gene in the repulsion phase (3). Plant vigor and heading dates were highly variable across trial locations for the Bowman backcross-derived line for *sld2.b*, BW862. Plants headed 18 days later and were half as tall when grown near Dundee, Scotland, while plants were nearly normal at Aberdeen, Idaho. Grain yields for BW862 ranged from less than 10% to over 80% of the Bowman yields (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (4).

Mutational events:

*sld2.b* (OUM142, GSHO 2491) in Akashinriki (OUJ659, PI 467400) (4).

Mutant used for description and seed stocks:

*sld2.b* (GSHO 2491, OUM 142) in Akashinriki; *sld2.b* in Bowman (PI 483237)\*4 (GSHO 1876); *sld2.b* in Bowman\*7 (BW862, NGB 22299).

References:

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Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:121.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:74.

BGS 84, Midseason stripe 1, *mss1*

Stock number: BGS 84  
Locus name: Midseason stripe 1  
Locus symbol: *mss1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4), the deviation from 3:1 reported by Walker et al (3) may be caused by genotype-environment interactions.

Located in chromosome 5H (1); *mss1.a* is associated with SNP markers 1\_1048 to 2\_1344 (positions 46.35 to 98.421 cM) in 5H bins 02 to 06 of Bowman backcross-derived line BW593 (1); previously associated with chromosome 2H (3, 4), about 19.9 cM distal from the *vrs1* (six-rowed spike 1) locus (3).

Description:

Broad yellow to ivory vertical streaks develop in the leaves of some tillers prior to heading (3, 4). Affected tillers are weaker and often abort under moderate to severe heat or moisture stress. In some environments, the whole plant becomes a golden yellow prior to maturation (2). Compared to Bowman, plants of the Bowman backcross-derived line for *mss1.a*, BW593, were morphologically similar in 'good' environments. However, in some environments, tillering was reduced and premature dying of BW593 plants occurred. Kernel weights for BW593 varied from 75% to equal to those of Bowman. Grain yields of BW593 varied from 30 to 85% of those recorded for Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (Clho 7149) (4).

Mutational events:

*mss1.a* (Alb Acc 257, GSHO 1404) in Montcalm (Clho 7149) (3, 4).

Mutant used for description and seed stocks:

*mss1.a* (GSHO 1404) in Montcalm; *mss1.a* in Bowman (PI 483237)\*2 (GSHO 1918); *mss1.a* in Bowman\*6 (BW593, NGB 22159).

References:

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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:122.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:75.

BGS 85, Yellow streak 4, *yst4*

Stock number: BGS 85  
Locus name: Yellow streak 4  
Locus symbol: *yst4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HL (3); near the *vrs1* (six-rowed spike 1) locus (2), in 2H bin 07 near RFLP marker CDO537 (5). An incorrect seed lot was used for analysis of retained SNP markers in the Bowman backcross-derived line for *yst4.d*, BW927, by Druka et al. (1).

Description:

Plants have a yellow-green color with numerous, vertical yellow streaks in the leaves. The yellow-green color is retained until maturity, but the yellow streaks may be difficult to observe after heading. Plant vigor and height are reduced, heading is delayed, and seed yields are low (4). Plants of the Bowman backcross-derived line for *yst4.d*, BW927, headed 3 to 5 days later than Bowman and were on average much shorter, 62 vs. 91 cm. Kernels were smaller and lighter, 36 vs. 58 mg. Grain yields of BW927 were 1/3 to 1/2 of those for Bowman (4).

Origin of mutant:

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

Mutational events:

*yst4.d* (DWS1059, GSHO 2502) in Glenn (CIho 15769) (3).

Mutant used for description and seed stocks:

*yst4.d* in Glenn (GSHO 2502); *yst4.d* in Bowman (PI 483237)\*7 (GSHO 1922, BW927, NGB 22356B).

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. 1997. *Barley Genet. Newsl.* 26:123.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:210.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:76.

BGS 86, Chlorina seedling 13, *fch13*

Stock number: BGS 86  
Locus name: Chlorina seedling 13  
Locus symbol: *fch13*

Previous nomenclature and gene symbolization:

Chlorina seedling 13 = *f13* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosomes 5HL (1, 2); the plant tested from the Bowman backcross-derived line BW355 was heterozygous for *fch13.v* gene and retained heterozygous SNP markers only from 1\_0600 to 2\_0402 (positions 269.6 to 297.9 cM) in 5H bins 13 to 15 (1, 2). Although two small regions in 2HL and 5HL of BW355 were homozygous for SNP markers (1), collection of a leaf sample from a plant homozygous for *fch13.v* would have been very difficult (2).

Description:

The mutant is classified as white seedlings (devoid of chlorophyll and carotenoid pigments) and a heterozygous stock is maintained in the USDA-ARS Barley Genetic Stocks Collection. Mutant plants die at the seedling stage if planted in the field. When grown in the greenhouse, however, seedlings gradually develop a pale green color, leaves have a light green color at heading, and plants survive to maturity and produce plump seed (3). The Bowman backcross-derived line for *fch13.v*, BW355, failed to head in field trials, but maintenance as a homozygous line is possible when grown under greenhouse conditions (2).

Origin of mutant:

A spontaneous mutant in Nigrinudum (NSL 3286, GSHO 988) (3).

Mutational events:

*fch13.v* (Nigrinudum II, GSHO 16) in Nigrinudum (NSL 3286, GSHO 988) (3).

Mutant used for description and seed stocks:

*fch13.v* (GSHO 16) in Nigrinudum; *fch13.v* in Bowman (PI 483237)\*6 (BW355, NGB 20594).

References:

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Prepared:

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Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:77.

BGS 87, Chlorina seedling 14, *fch14*

Stock number: BGS 87  
Locus name: Chlorina seedling 14  
Locus symbol: *fch14*

Previous nomenclature and gene symbolization:

Chlorina seedling 14 = *f14* (3).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 2HL (3); probably between the *vrs1* (six-rowed spike 1) and the *ant2* (anthocyanin-less 2) loci (3), likely in 2H bin11 (4, 5); the Bowman backcross-derived line for *fch14.w*, BW356, did not retain any SNP markers polymorphisms compared to Bowman (1).

Description:

Seedlings have a pale yellow-green color. The leaves gradually become greener starting at the tip of the leaf blade, and mutant plants are indistinguishable in color from normal sibs at heading (3). When grown in the field, plants of the Bowman backcross-derived line for *fch14.w*, BW356, produced kernels having a 10% reduction in kernel weight (2). Grain yields of BW355 and Bowman were similar, but a delay of 14 days in heading was noted when BW355 was grown under short-day conditions at Warwick, Queensland, Australia (2).

Origin of mutant:

A spontaneous mutant in Shyri (GSHO 2430, Lignee 640//Kober/Teran 78) from Ecuador (3, 6).

Mutational events:

*fch14.w* (GSHO 1739) in Shyri (GSHO 2430) (3, 6).

Mutant used for description and seed stocks:

*fch14.w* in Shyri (GSHO 1739); *fch14.w* in Bowman (PI 483237)\*6 (GSHO 1911, BW356, NGB 20595).

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. 1997. *Barley Genet. Newsl.* 26:125.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:211.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:78.

BGS 89, Breviaristatum-g, *ari-g*

Stock number: BGS 89  
Locus name: Breviaristatum-g  
Locus symbol: *ari-g*

Previous nomenclature and gene symbolization:

Breviaristatum-18 = *ari-18* (4, 5).

Short awn 10 = *lk10* (7).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 2H (1, 3); the linkage drag association with the *Gth1* (toothed lemma 1) locus (1) may be caused by poor expression of the *Gth1.a* allele in the Bowman backcross-derived line (2, 3); *ari-g.24* is associated with SNP markers 1-0796 to 2\_0528 (positions 95.53 to 118.78 cM) in 2H bins 07 to 08 of a heterozygous plant from the Bowman backcross-derived line BW045 (1).

Description:

Plants with the *ari-g* mutation are semidwarf and very weak. Under greenhouse conditions, plants are 1/4 to 1/3 normal and stiff, spikes are short and small, and seed set is low. Leaf blades are very narrow and often involuted (5). When grown in the field at Fargo, North Dakota, USA, plant development is very slow, the upper portion of the sheath is white as new leaf blades emerge, and spikes are seldom produced. Thus, the Bowman backcross-derived line for *ari-g.24*, BW045, is maintained as a segregating stock (2).

Origin of mutant:

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

Mutational events:

*ari-g.18* (NGB 115865) in Bonus (PI 189763, NGB 14657) (5); *ari-g.24* (NGB 115872, GSHO 1655) in Bonus (6); *ari-g.134* (NGB 115944), *-g.138* (NGB 115948), *-g.142* (NGB 115952), *-g.158* (NGB 115968), *-g.221* (NGB 116030), *-g.234* (NGB 116044), *-g.246* (NGB 116056) in Foma (CIho 11333, NGB 14659), *-g.267* (NGB 116078) in Kristina (NGB 1500, NGB14661) (5); *ari-g.303* (NGB 116127) in Kristina (6).

Mutant used for description and seed stocks:

*ari-g.24* in Bonus (NGB 115872, GSHO 1655); *ari-g.24* in Bowman (PI 483237)\*7 (GSHO 2503); *ari-g.24* in Bowman\*8 (BW045, NGB 20453).

References:

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2. Franckowiak, J.D. (Unpublished).
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:128.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:79-80.

BGS 109, Yellow streak 2, *yst2*

Stock number: BGS 109  
Locus name: Yellow streak 2  
Locus symbol: *yst2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HS (3, 4, 5); about 0.9 cM distal from the *alm1* (albino lemma 1) locus (4); *yst2.b* is associated with SNP markers 2\_1402 to 1\_1911 (positions 76.82 to 98.41 cM) in 3H bins 05 to 06 of Bowman backcross-derived line BW925 (1); likely in 3H bin 05.

Description:

When grown at low temperatures, seedlings develop numerous wide yellow streaks in the seedling leaves. Exposure to 3°C for two weeks after sowing induces distinct streaks in the first and second leaves. As temperatures rise, newly developed leaves have only very fine yellow streaks (4). These streaks persist until the plant nears maturity. As plants of the original *yst2.b* stock develop, they have a yellow-green color, show delayed maturation, and have low seed yields (2). Compared to Bowman, plants of the Bowman backcross-derived line for *yst2.b*, BW925, were morphologically similar. Kernels of BW925 were similar in size and weight to those of Bowman when grown in non-stressed environments. Grain yields and test weights of BW925 were equal to or slightly lower than those of Bowman (2).

Origin of mutant:

A spontaneous mutant in the F<sub>5</sub> generation of the cross Kuromugi 148 (OUJ646)/Mensury C (OUJ732) (4).

Mutational events:

*yst2.b* (GSHO 570) in Kuromugi 148/Mensury C (OUJ073) (4).

Mutant used for description and seed stocks:

*yst2.b* (GSHO 570) in Kuromugi 148/Mensury C (OUJ073); *yst2.b* in Bowman (PI 483237)\*7 (GSHO 1952, BW925, NGB 22354).

References:

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

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:131.

Revised:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:144.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:81.

BGS 114, Curly 2, *cur2*

Stock number: BGS 114  
Locus name: Curly 2  
Locus symbol: *cur2*

Previous nomenclature and gene symbolization:

Deformed plant, Bikini (4, 6).

Curly 2 = *cu2* (8).

Inheritance:

Monofactorial recessive (8, 9).

Located in chromosome 3HL (7, 8, 12); over 36.8 cM distal from the *als1* (absent lower laterals 1) locus (5, 8, 9); about 7.7 cM proximal from the *fch2* (chlorina seedling 2) locus (13); *cur2.b* is associated with SNP markers 1\_1436 to 1\_0694 (positions 230.99 to 247.64 cM) in 3H bin 15 of the Bowman backcross-derived line BW220 (1); *cur2.g* is associated with SNP markers 2\_0952 to 1\_1516 (positions 230.5 to 249.45 cM) in 3H bins 15 to 16 of the Bowman backcross-derived line BW221 (1). The *nud1.a* (naked caryopsis 1) trait and the associated SNP molecular markers in chromosome 7H are retained in BW220 (1, 2).

Description:

The awn, lemma, and palea are extremely curly, the rachis is twisted slightly in most spikes, and the stem internodes are strongly curved. Leaf blades are short and severely twisted (5, 8). Roots are extremely curled compared to the straight or slightly coiled roots of normal sister plants (11). Plants of the Bowman backcross-derived lines for *cur2.b*, BW220, and *cur2.g*, BW221, were 1/3 to 1/2 of the Bowman height and produced very little grain in most environments. Kernel weights for BW221 were about 60% of those for the Bowman, while the weights for BW220 kernels were only about 40% (2).

Origin of mutant:

A spontaneous mutant in Choshiro (OUJ451, Clho 190266) (5, 9).

Mutational events:

*cur2.b* (Choshiro-hen, OUL006, GSHO 274) in Choshiro (OUJ451, Clho 190266) (5, 8); *cur2.c* (dwarf 2) in an unknown cultivar (10); *cur2.d* (deformed plant, Bikini 3) (NGB 115380) in Bonus (PI 189763, NGB 14657) (4, 6, 10); *cur2.g* (GSHO 1706) in Carina (PI 371632) (3).

Mutant used for description and seed stocks:

*cur2.b* (GSHO 274) in Choshiro; *cur2.b* in Bowman (PI 483237)\*5 (GSHO 1991); *cur2.b* in Bowman \*6 (BW220, NGB 22047); *cur2.g* in Bowman\*5 (GSHO 1992); *cur2.g* in Bowman\*7 (BW221, NGB 22048).

References:

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:136.

Revised:

J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:148.  
J.D. Franckowiak, and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:82-83.

BGS127, Pubescent leaf blade 1, *Pub1*

Stock number: BGS 127  
Locus name: Pubescent leaf blade 1  
Locus symbol: *Pub1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (4).

Located in chromosome 3HL (3); *Pub1.a* is associated with SNP markers 2\_0023 to 1\_1328 (positions 169.9 to 207.5 cM) in 3H bins 10 to 14 of Bowman backcross-derived line BW650 (1).

Description:

Both the upper and lower surface of the leaf blade have widely scattered, short (1 to 2 mm) hairs. The hairs tend to be aligned along the smaller leaf veins. The hairs are more difficult to observe on older leaves or plants grown in the field. Some accessions of *Hordeum vulgare* subsp. *spontaneum* have numerous short hairs on both surfaces of the leaf (2). Kernels of the Bowman backcross-derived line for *Pub1.a* (BW650) were up to 10% heavier than those of Bowman. Grain yields and test weights of BW650 were equal to or slightly greater than those of Bowman (2).

Origin of mutant:

Natural occurrence in Steptoe (Clho 15229) (3), and in many accessions of *Hordeum vulgare* subsp. *spontaneum* (2).

Mutational events:

*Pub1.a* in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1580) (4); *Pub1.a* in Steptoe (3).

Mutant used for description and seed stocks:

*Pub1.a* in Steptoe (GSHO 1576); *Pub1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)\*6 (GSHO 1976); *Pub1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman\*7 (BW 650, NGB 22215).

References:

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Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:163.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:84.

BGS 128, Short crooked awn 1, *sca1*

Stock number: BGS 128  
Locus name: Short crooked awn 1  
Locus symbol: *sca1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HS (4); about 1.4 cM distal from the *alm1* (albino lemma 1) locus (3, 4); *sca1.a* is associated with SNP markers 2\_0356 to 2\_0566 (positions 72.36 to 114.82 cM) in 3H bins 05 to 07 of Bowman backcross-derived line BW769 (1); likely in 3H bin 05.

Description:

In the original stock, awns are reduced to a length of only 2 cm and are curved outward at the tip (4). Awn tips may have a stigma-like appearance in the original stock. In the Bowman backcross-derived line, awns are short (less than 1/4 normal), but awn tips are not curved or stigma-like (2). Plant vigor was partially restored in the Bowman backcross-derived line for *sca1.a*, BW769, but the awns remained very short, 2 vs. 12 cm. BW769 plants were 5 to 10% shorter than Bowman plants and headed about two days later. Kernels of BW769 were thin (3.05 vs. 2.82 mm in diameter) and light (34 vs. 56 mg); and the grain yields of BW769 were 10 to 50% of those for Bowman at various field locations (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (4).

Mutational events:

*sca1.a* (OUM206, GSHO 2439) in Akashinriki (OUJ659, PI 467400) (3, 4).

Mutant used for description and seed stocks:

*sca1.a* in Akashinriki (GSHO 2439), *sca1.a* in Bowman (PI 483237)\*6 (GSHO 1951); *sca1.a* in Bowman\*8 (BW769, NGB 22237).

References:

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Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:164.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:85.

BGS 130, Early maturity 10, *eam10*

Stock number: BGS 130  
Locus name: Early maturity 10  
Locus symbol: *eam10*

Previous nomenclature and gene symbolization:

Early maturity sp = *ea<sub>sp</sub>* (10).

Inheritance:

Monofactorial recessive (10).

Located in chromosome 3HL (10); about  $2.0 \pm 5.8$  cM from the *Est1-Est4* (esterase 1, esterase 4) locus (10); about 5.8 cM distal from RFLP marker Xmwg546 (1); *eam10.m* is associated with SNP marker 1\_1516 (position 249.75 cM) in 3H bin 16 of Bowman backcross-derived line BW284 (4); at the position of SNP marker 2\_1500 [171.64 (252.98) cM] (2), in 3H bin 16.

Description:

In winter nurseries at Ciudad Obregón, Sonora, Mexico and Davis, California, USA, plants of Super Precoz 2H head about 11 days earlier than lines with the genes *eam7.g* or *eam8.k* for photoperiod insensitivity from Atsel and Sv Mari, respectively (10). The *eam10.m* gene appears to suppress expression of the *eam7.g* and *eam8.k* genes (10). Plants expressing *eam10.m* become chlorotic (yellow green) under photothermal stress. Zeaxanthin increased at the expense of chlorophyll and other pigments (9). The chlorotic appearance was similar to that observed in plants homozygous for other recessive genes for early maturity (*eam7*, *eam8*, and *eam9*) (3, 8, 9). Plants in the Bowman *eam10.m* line, BW284, headed one to three days earlier than Bowman under long days and about 12 days earlier under short days (7). BW284 plants were slightly shorter and had two to three fewer kernels per spike (7). Rate of stem elongation was accelerated in *eam10* mutants, but the timing of meristem development closely followed that of Bowman (2). The candidate gene underlying the *eam10* locus was reported to be *Hvlux1*, an ortholog of the Arabidopsis circadian gene LUX ARRHYTHMO. Of the sixteen polymorphic haplotypes of *HvLUX1* characterized in accessions, most were present in wild barley (*Hordeum vulgare* subsp. *spontaneum*) (2). Campoli et al. (2) also demonstrated that *eam10* caused circadian defects and interacts with the strong photoperiod response gene *Ppd-H1* (*Eam1*) to accelerate flowering under both long- and short-day conditions.

Origin of mutant:

Present in Super Precoz 2H (PI 527381) from Russia (9), but originating probably as an induced mutant in MC20 (5, 6, 9).

Mutational events:

*eam10.m* in Super Precoz 2H (PI 527381) plus a dominant maturity enhancer (6, 8, 9); *eam10.m* in Amber Nude (GSHO 2505) without the enhancer (6).

Mutant used for description and seed stocks:

*eam10.m* in Super Precoz 2H (GSHO 2504); *eam10.m* in Amber Nude (GSHO 2505); *eam10.m* from Super Precoz in Bowman (PI 483237)\*4 (GSHO 3421); *eam10.m* from Super Precoz in Bowman\*5 (BW284, NGB 20568); *eam10.m* from Amber Nude in Bowman\*3 (BW283, NGB 20567).

References:

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phylogeny, diversity, and interactions with the circadian clock and photoperiodic pathways. *New Phytologist* 199:1045-1059.

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Prepared:

L.W. Gallagher and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:166.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:226-227.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:86-87.

BGS 131, Granum-a, *gra-a*

Stock number: BGS 131  
Locus name: Granum-a  
Locus symbol: *gra-a*

Previous nomenclature and gene symbolization:

Granum-a = *gran-a* (3).

Inheritance:

Monofactorial recessive (3, 7).

Located in chromosome 7H (2); *gra-a.1* is associated with SNP markers 1\_0861 to 1\_0078 (positions 183.90 to 187.83 cM) in 7H bin 11 of the Bowman backcross-derived line BW398 (2); *gra-a.2* is associated with SNP markers 1\_0078 to 1\_0547 (position 187.83 to 231.00 cM) in 7H bins 11 to 13 of the Bowman backcross-derived line BW399 (2), likely in 7H bin 11. Previously the *gra-a.1* mutant was reported to be in chromosome 3HL (3, 7).

Description:

Plants have numerous, thin tillers with narrow leaves and short internodes (1/2 normal plant height). Spikes are less than half normal length and seeds are thin and small (3, 7). Spikes emerge from the sheath of the flag leaf prematurely, 4 to 7 days before anthesis (5). Compared to Bowman plants of Bowman, backcross-derived lines for *gra-a.1* (BW398) and *gra-a.2* (BW399) were about half of normal height and peduncles were about 1/3 normal length (4). Awns and rachis internodes of the BW398 spikes were slightly shorter than those of Bowman (1, 4). The tip of the spike has a fasciated appearance because spikelets are very close together (1, 4). The number of kernels per spike for BW398 and BW399 were often 4 to 7 less than the number for Bowman. Kernel weights were about 25% less (45 vs. 59 mg) than those of Bowman, but grain yields were almost normal (4). Combining the *gra-a.1* and *cul2.b* (uniculm 2) mutants produced short plants that occasionally produced two tillers (1).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (3, 7).

Mutational events:

*gra-a.1* (GSHO 1757) in Donaria (PI 161974) (3, 7); *gra-a.2* (GSHO 1758) from a Tokak (PI 178421) mutant in OR-SS-2 (5, 6, 8); *gra-a.3* (DWS1176) in HE2816 (likely from HE-MN-C 292) from Milan Váša (5, 6).

Mutant used for description and seed stocks:

*gra-a.1* (GSHO 1757) in Donaria; *gra-a.1* in Bowman (PI 483237)\*7 (GSHO 1980, BW398, NGB 20635); *gra-a.2* in Bowman\*7 (GSHO 1981, BW 399, NGB 20636).

References:

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:167.

Revised:

J.D. Franckowiak. 2012. Barley Genet. Newsl. 42: 216-217.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:88-89.

BGS 144, Slender dwarf 5, *sld5*

Stock number: BGS 144  
Locus name: Slender dwarf 5  
Locus symbol: *sld5*

Previous nomenclature and gene symbolization:

Indian Dwarf (1, 6).  
Slender dwarf-h = *sld.h* (4).

Inheritance:

Monofactorial recessive (1).  
Located in chromosome 3HS (2, 4); based on linkage drag with the *Btr1* (non-brittle rachis 1) locus (4); *sld5.h* is associated with SNP markers 1\_0565 to 2\_1381 (positions 29.05 to 157.14 cM) in 3H bins 03 to 10 of the Bowman backcross-derived line BW865 (2); likely in 3H bins 04 or 05.

Description:

Plants with the *sld5.h* gene show reduced vigor and have thin grain. Plants are about 2/3 normal height in the XV 2334-6R line and about 1/2 normal in Indian Dwarf accession (1, 4). Seedlings with the *sld5.h* gene are insensitive to treatment with gibberellic acid (1). The second factor for reduced height in Indian Dwarf may be the *Eam5.x* (early maturity 5, BGS 348) mutant (3). Compared to Bowman, plants of the Bowman backcross-derived line for *sld5.h*, BW865, were 20 to 30% shorter and headed 3 to 4 days later. Kernels of BW865 were smaller and weighed nearly 20% less (47 vs. 56 mg) than those of Bowman. Grain yields of BW865 were 1/3 to 1/2 of those for Bowman (3).

Origin of mutant:

A spontaneous mutant identified as Indian Dwarf (CIho 13994) (1).

Mutational events:

*sld5.h* (DWS1238, GSHO 2483) in XV2334-6R from Indian Dwarf (CIho 13994) (1, 5, 6); Apam Dwarf likely has an allele at the *sld5* locus (6).

Mutant used for description and seed stocks:

*sld5.h* (GSHO 2483) in XV2334-6R, *sld5.h* in Bowman (PI 483237)\*7 (GSHO 1940, BW865, NGB 22302).

References:

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Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:94.

Revised:

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:90-91.

BGS 151, Chlorina seedling 9, *fch9*

Stock number: BGS 151  
Locus name: Chlorina seedling 9  
Locus symbol: *fch9*

Previous nomenclature and gene symbolization:

Chlorina k =  $f_k$  (4).  
Chlorina 9 =  $f_9$  (3, 5).

Inheritance:

Monofactorial recessive (4).  
Located in chromosome 4HS (4); over 22.7 cM distal from the *Kap1* (Hooded lemma 1) locus (4); *fch9.k* is associated with SNP markers 1\_0319 and 2\_1359 (positions 11.87 and 27.52 cM) in 4H bin 02 of the Bowman backcross-derived line BW365 (1), in 4H bin 02.

Description:

Seedling leaves are yellow green in color, and the yellow green color persists until near maturity (4). Field grown plants are stunted and maturity is delayed (2). Plants of the Bowman backcross-derived line for *fch9.k*, BW365, headed 8 to 15 days later than Bowman. Plant height for BW365 varied over trials from slightly taller to slightly shorter and kernels per spike were equal to or greater than the values for Bowman. Kernels were slightly smaller and weighed 10 to 40% less than those of Bowman. Grain yields for BW365 averaged about 2/3 those for Bowman (2).

Origin of mutant:

An X-ray induced mutant in Ko A (OUJ215, PI 383935) (4).

Mutational events:

*fch9.k* (Kmut 174, OUM288, GSHO 571) in Ko A (OUJ215, PI 383935) (4).

Mutant used for description and seed stocks:

*fch9.k* (GSHO 571) in Ko A; *fch9.k* in Bowman (PI 483237)\*7 (GSHO 1996); *fch9.k* in Bowman\*9 (BW365, NGB 20604).

References:

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:137.

Revised:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:178.  
J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:92.

BGS 156, Long basal rachis internode 2, *lbi2*

Stock number: BGS 156  
Locus name: Long basal rachis internode 2  
Locus symbol: *lbi2*

Previous nomenclature and gene symbolization:

Long basal rachis internode 2 = *lb2* (5).

Erectoides-i = *ert-i* (6, 7, 8).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 4HS (1, 5, 8); less than 12.8 cM proximal from the *Kap1* (Hooded lemma 1) locus (5, 7); about 2.4 cM proximal from the *Kap1* locus (6); about 18.5 cM proximal from the *glf1* (glossy leaf 1) locus (9); *lbi2.b* is associated with SNP marker 1\_1180 (position 58.13 cM) in 4H bin 05 of the Bowman backcross-derived line BW472 (1); *ert-i.27* is associated with SNP markers 2\_1374 to 2\_1122 (positions 41.13 to 47.80 cM) in 4H bins 04 to 05 of the Bowman backcross-derived line BW311 (1), likely in 4H bin 05.

Description:

Mutant plants in the cultivar Montcalm have a marked elongation and weakness of the basal rachis internode of the spike. This region may be 10 to 13 cm long in some tillers. The spike hangs vertically downward from the collar on emergence from the sheath and is often broken off in this region by the wind. Even when not broken off, spikes have a high degree of sterility and contain poorly filled grain. Plants show delayed maturity (5). The *ert-i* mutants in Bonus have an erect, semi-compact (rachis internode length ranging from 2.3 to 2.9 mm) spike, an elongated (2 to 4 cm) basal rachis internode, and reduced plant height (3/4 normal) (8). Removal of modifiers from the Bonus and Montcalm mutants by backcrossing produced Bowman backcross-derived lines for *ert-i.27*, BW311, and *lbi2.b*, BW472, which had similar phenotypes (2, 3). Plants of the BW311 and BW472 lines were 15 to 20% shorter, had awns that were 30 to 40% shorter, and had shorter rachis internodes, 3.3 vs 4.5 mm. The number of kernels per spike was 4 to 6 fewer. Kernels of BW311 and BW472 were smaller and weighed less, 45 vs. 58 mg, than those of Bowman. Grain yields of BW311 and BW472 were 1/2 to 3/4 of those for Bowman (3).

Origin of mutant:

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

Mutational events:

*lbi2.b* (Alb Acc 1028, GSHO 572) in Montcalm (Clho 7149) (5); *ert-i.27* (NGB 112627, GSHO 482), *-i.53* (NGB 112652) in Bonus (PI 189763, NGB14657) (3, 4); *ert-i.126* (NGB 112725) in Bonus (8).

Mutant used for description and seed stocks:

*lbi2.b* (GSHO 572) in Montcalm; *ert-i.27* (NGB 112627, GSHO 482) in Bonus; *lbi2.b* in Bowman (PI 483237)\*7 (GSHO 2009, BW472, NGB 20702); *ert-i.27* in Bowman\*7 (GSHO 2008, BW311, NGB 22107).

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:142.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:183.

J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:93-94.

BGS 157, Brachytic 2, *brh2*

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

Previous nomenclature and gene symbolization:

Brachytic 2 = *br2* (11).  
Breviaristatum-1 = *ari-1* (6, 7).

Inheritance:

Monofactorial recessive (10).  
Located in chromosome 4HL (10); about 1.5 cM proximal from the *glf3* (glossy leaf 3) locus (4, 10); over 22.8 cM proximal from the *Kap1* (Hooded lemma 1) locus (10); near AFLP marker E4140-7 in subgroup 38-40 of the Proctor/Nudinka map (9), and about 15.9 cM distal from SSR marker Bmag0353 near the boundary between 4H bins 06 and 07 (2); *brh2.b* is associated with SNP markers 2\_0012 to 1\_1319 (positions 57.19 to 110.93 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW090 (3); *ari-1.3* is associated with SNP markers 2\_1374 to 2\_1332 (positions 41.13 to 112.64 cM) in 4H bins 04 to 08 of the Bowman backcross-derived line BW050 (3).

Description:

Plant height and vigor are reduced to about 2/3 normal; the awn is less than 1/4 normal length; the spike is semi-compact; and the leaf, kernel, glume and glume awn, rachilla, and coleoptile are shorter than in the original cultivar. Auricles are well developed and larger than those of the original cultivar (11). In the Bowman backcross-derived lines, the peduncle is about 1/2 normal length, kernel weights are slightly over 2/3 normal, yield is about 1/2 normal; however, rachis internode lengths are normal (2). The *ari-1.3* allele at the *brh2* locus is sensitive to gibberellic acid treatment (1). The Bowman backcross-derived for *brh2.b*, BW090, and *ari-1.3*, BW050, were morphologically similar to each other, shorter than Bowman, 65 vs. 90 cm. They also had short awns, 2.5 vs. 12 cm beyond the tip of the spike and small kernels. Compared to Bowman, kernels were shorter, 7.5 vs. 9.8 mm, and thinner, 3.61 vs. 3.83 mm, and weighed less, 40 vs. 56 mg. Grain yields for BW050 and BW090 were 1/2 to 2/3 of those produced by Bowman (5).

Origin of mutant:

An X-ray induced mutant in Svanhals (PI 5474) (11).

Mutational events:

*brh2.b* (Kmut 28, OUM283, GSHO 573) in Svanhals (PI 5474) (10); *ari-1.3* (NGB 115848) in Bonus (PI 189763, NGB14657) (7); *ari-1.132* (NGB 115942) in Foma (CIho 11333, NGB 14659) (8); *ari-1.135* (NGB 115945), *-1.145* (NGB 115956), *-1.214* (NGB 116023), *-1.237* (NGB 116047) in Foma, *-1.257* (NGB 116066) in Kristina (NGB 1500, NGB 14661) (7).

Mutant used for description and seed stocks:

*brh2.b* (GSHO 573) in Svanhals; *ari-1.3* (GSHO 1660) in Bonus; *brh2.b* in Bowman (PI 483237)\*7 (GSHO 2016, BW090, NGB 20496); *ari-1.3* in Bowman\*7 (GSHO 2017, BW050, NGB 20458).

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

4. Forster, B.P. 1993. Coordinator's report: Chromosome 4. *Barley Genet. Newsl.* 22:75-77.

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Prepared:

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

Revised:

T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:115.

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:184.

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:235-236.

J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:95-96.

BGS 161, Semi-minute dwarf 1, *min1*

Stock number: BGS 161  
Locus name: Semi-minute dwarf 1  
Locus symbol: *min1*

Previous nomenclature and gene symbolization:

Dwarf = *d* (4).  
Semi-minute = *min* (5).

Inheritance:

Monofactorial recessive (4), but interaction with the recessive allele at the *en-min* (enhancer of minute) locus is observed in some cultivars (5).  
Located in chromosome 4HL (5, 6); about 6.7 cM distal from the *glf3* (glossy leaf 3) locus (2, 6); *min1.a* is associated with SNP marker 2\_1359 to 2\_0689 (positions 27.52 to 122.99 cM) in 4H bins 02 to 08 of the Bowman backcross-derived line BW515 (1).

Description:

Plants are 1/2 as tall as the original cultivar, spikes and awns are slightly shorter, and the number of tillers, spikelets per spike, and numbers of kernels are slightly less than in the original cultivar (4). In meristematic tissues of root tips and young shoots, polyploid nuclei consisting of 4x, 8x, and sometimes many more chromosomes are found together with normal diploid cells. Epidermal cells of the leaves are sometimes irregular and variable in shape and size. The mixoploid condition of tissues is believed to result from incomplete cytokinesis following nuclear division (6). Plant vigor in the Bowman backcross-derived line is variable and very sensitive to environmental stress. When grown in the greenhouse, the plants are 2/3 normal height, spike size and length are reduced, and leaves are narrow. Under field conditions, plants can be diminutive (less than 1/4 normal height and size) and seed set is low (3). Plants of the Bowman backcross-derived line for *min1.a*, BW515, headed 4 to 5 days later than Bowman and ranged from 40 to 60% shorter. Kernels of BW515 were thin, 3.15 vs. 3.74 mm, and weighed 60 to 70% of Bowman kernels. Grain yields for BW515 varied from 3 to 15% of the Bowman yields (3).

Origin of mutant:

A spontaneous mutant in Taishomugi (OUJ 026) (4).

Mutational events:

*min1.a* (OUJ026, GSHO 987) in Taishomugi (OUJ 026) with the *En-min* gene in the genetic background (4, 6).

Mutant used for description and seed stocks:

*min1.a* (GSHO 987) in Taisho-mugi; *min1.a* in Bowman (PI 483237)\*7 (GSHO 2023, BW515, NGB 20743).

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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Nogaku Kenkyu 50:123-132. [In Japanese.]

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:186.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:187.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:97-98.

BGS 164, Hairs on lemma nerves 1, *Hln1*

Stock number: BGS 164  
Locus name: Hairs on lemma nerves 1  
Locus symbol: *Hln1*

Previous nomenclature and gene symbolization:

Hairs on lemma nerves = *Hn* (5).

Inheritance:

Monofactorial dominant when crossed to a cultivar having abundant barbs on the lemma nerves (4, 5).

Located in chromosome 4HL (4); over 8.7 cM proximal from the *yhd1* (yellow head 1) locus; over 22.5 cM distal from the *mlo* (reaction to *Erysiphe graminis hordei-o*) locus (3, 4); complete linkage with the dominant allele at the *Hsh1* (hairy leaf sheath 1) locus has been observed (5); *Hln1.a* is associated with SNP markers 1\_1066 to 1\_0269 (positions 171.3 to 176.8 cM) in 4H bin 12 of the Bowman backcross-derived line BW415 (1), in 4H bin 12. The 4HL SNP markers observed in BW415 were recorded as heterozygous, but they have the same haplotype pattern as the SNP marker retained from the donor parent in BW416 (*Hsh1.a*) (2). The BW415 plant evaluated with SNP markers did retain two other polymorphisms, in chromosomes 2HL and 7HL, from its donor parent (1).

Description:

A few hairs of 1 to 2 mm are mixed with the ordinary teeth or barbs on the lateral nerves of the lemma (4, 5). Expression of the *Hln1.a* gene may be easier to observe as 1 mm hairs on the tip of sterile lateral kernels in two-rowed barley (2). The *Hln1* gene is associated with a recessive short awn trait (2/3 of normal length). The Bowman backcross-derived line for *Hln1.a*, BW415, was similar to Bowman except awns were half normal length and kernels were slightly heavier (2).

Origin of mutant:

Natural occurrence in a number of cultivars from Japan and Korea (5).

Mutational events:

*Hln1.a* in Kogane-mugi (OUL010, GSHO 576) and in several other cultivars (5).

Mutant used for description and seed stocks:

*Hln1.a* in Kogane-mugi (PI 225020, GSHO 576, OUL010, AB1384); *Hln1.a* from AB1384 in Bowman (PI 483237)\*4 (GSHO 2027); *Hln1.a* from AB1384 in Bowman\*6 (BW 415, NGB 20648).

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Prepared:

R. Takahashi. 1972. *Barley Genet. Newsl.* 2:189.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:189.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:99-100.

BGS 166, Male sterile genetic 25, *msg25*

Stock number: BGS 166  
Locus name: Male sterile genetic 25  
Locus symbol: *msg25*

Previous nomenclature and gene symbolization:

Male sterile = *msg*,*r* (8).

Inheritance:

Monofactorial recessive (3, 8).

Located in chromosome 4HL (2, 7); near the centromere and proximal from the *Blx1* (Blue aleurone xenia 1) locus (7, 10); the Bowman backcross-derived line for *msg25.r*, BW560, did not retain any SNP markers polymorphisms compared to Bowman (1).

Description:

Selfing - 0.7% for *msg25.r* (7), 2.6% for *msg25.dz* (4).

Outcrossing - complete female fertility (7).

Stamens - anthers smaller than fertile sib, but some have stomium. Some filament elongation may occur (7).

Origin of mutant:

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

Mutational events:

*msg25.r* (MSS086, GSHO 744) in Betzes (PI 129430) (7); *msg25.dz* (MSS374) in Klages (CIho 15487) (4, 5, 6, 9).

Mutant used for description and seed stocks:

*msg25.r* (GSHO 744) in Betzes; *msg25.r* in Bowman (PI 483237)\*7 (GSHO 2020, BW560, NGB 23428).

References:

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10. Kushnak, G.D. 1974. Utilizing linkages of genetic male sterile and aleurone color genes in hybrid barley (*Hordeum vulgare* L.) systems. Ph.D. Thesis. Montana State

Univ., Bozeman.

Prepared:

E.A. Hockett. 1974. Barley Genet. Newsl. 4:135 as BGS 386.

E.A. Hockett. 1975. Barley Genet. Newsl. 5:112.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:192.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:101-102.

BGS 170, Light green 3, *lgn3*

Stock number: BGS 170  
Locus name: Light green 3  
Locus symbol: *lgn3*

Previous nomenclature and gene symbolization:

Light green 7 = *lg7* (5).

Light green 3 = *lg3*, the *lg3* stock studied by Hanson and Kramer (4) may not be the same as the *lg3* gene in the GSHO 171 stock (2).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 1HL (1); *lgn3.c* from GSHO 171 in the Bowman backcross-derived line BW480 is associated with SNP markers 1\_0552 to 2\_0229 (positions 88.33 to 106.61 cM) in 4H bins 08 to 10 (1). Since *lgn3* locus was previously mapped in chromosome 4HL (3, 4, 6, 7) [over 10.5 cM distal from the *Kap1* (Hooded lemma 1) locus (4)], the donor stock for BW480 may have been incorrect (2).

Description:

Seedlings have light or pale green color (5). The pale green color persists until near maturity, and plants are very weak (5) or non-viable in the field (2). Plants can be grown to maturity in greenhouses (6). Plants of the Bowman backcross-derived line for *lgn3.c*, BW480, showed variable responses to being grown under field conditions. In general, plants headed 4 to 5 days later, they were 10 to 20% shorter than Bowman, and rachis internodes were slightly shorter. Kernel weights of BW480 were 30 to 40% lower (36 vs. 57 mg) and grain yields ranged from none to 1/3 of those for Bowman (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (5, 6).

Mutational events:

*lgn3.c* (No 150, GSHO 171) in an unknown cultivar (5); *lgn3.g* (*lg7*) (No 154, GSHO 173) in an unknown cultivar (5).

Mutant used for description and seed stocks:

*lgn3.c* (GSHO 171) in an unknown cultivar; *lgn3.c* from an accession obtained from Montana State University and identified as *lgn3* in Bowman (PI 483237)\*5 (GSHO 2010); *lgn3.c* in Bowman\*7 (BW480, NGB 20708).

References:

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6. Tsuchiya, T., T. Fachan, and T.E. Haus. 1976. Primary trisomic analysis of *lg3* (light green) and *f3* (chlorina) in barley. *Barley Genet. Newsl.* 6:82-84.
7. Tsuchiya, T., and L.B. Hall. 1978. Telotrisomic analysis of four mutant genes in barley. *Barley Genet. Newsl.* 8:104-107.

Prepared:

T.E. Haus. 1978. *Barley Genet. Newsl.* 8:154.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:195.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:103-104.

BGS 171, Light green 4, *lgn4*

Stock number: BGS 171  
Locus name: Light green 4  
Locus symbol: *lgn4*

Previous nomenclature and gene symbolization:

Light green 1 = *lg1* (4).  
Light green 4 = *lg4* (4).  
Light green 9 = *lg9* (4, 5).

Inheritance:

Monofactorial recessive (4, 7).  
Located in chromosome 4HL (4, 6, 7, 8); about 5.0 cM distal from the *Kap1* (Hooded lemma 1) locus (4, 6); about 4.0 cM proximal from the *glf1* (glossy leaf 1) locus (4, 6); *lgn4.d* is associated with SNP markers 2\_0114 to 1\_1114 (positions 58.13 to 74.11 cM) in 4H bin 05 of the Bowman backcross-derived line BW481 (1), in 4H bin 05.

Description:

Seedlings are light green in color, and the light green color persists until near maturity (3). In the Bowman backcross-derived line for *lgn4.d*, BW481, plants had low vigor compared to normal sibs and headed 5 to 16 days later under field conditions (2). Since BW481 appeared very sensitive to environmental conditions, considerable variability in agronomic traits was observed. Plant height of BW481 ranged from 40% less to equal to Bowman with a large portion of the variability due to variable peduncle lengths. Kernel weights in field trials varied from 35 to 55 mg while those for Bowman varied from 53 to 58 mg. The grain yields of BW481 ranged from 1/4 to 3/4 of those for Bowman (2).

Origin of mutant:

A spontaneous mutant in the progeny of the cross Himalaya X Ingrescens (GSHO 681) (4).

Mutational events:

*lgn4.d* (*lg1*) (GSHO 681) in Himalaya X Ingrescens (GSHO 681) (4); *lgn4.i* (*lg9*) (GSHO 1, GSHO 94) in No 156, an unknown cultivar (3, 4).

Mutant used for description and seed stocks:

*lgn4.d* (GSHO 681) in Himalaya X Ingrescens; *lgn4.d* in Bowman (PI 483237)\*7 (GSHO 2011, BW481, NGB 20709).

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:

T.E. Haus. 1978. Barley Genet. Newsl. 8:155.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:196.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:105-106.

BGS 179, Hairy leaf sheath 1, *Hsh1*

Stock number: BGS 179  
Locus name: Hairy leaf sheath 1  
Locus symbol: *Hsh1*

Previous nomenclature and gene symbolization:

Hairy leaf sheath = *Hs* (9).

Inheritance:

Monofactorial dominant (6, 7, 8).

Located in chromosome 4HL (8), over 8.7 cM proximal from the *yhd1* (yellow head 1) locus, and over 22.5 cM distal from the *mlo* (reaction to *Erysiphe graminis hordei*-o) locus (5, 7); about 1.1 cM proximal from RFLP marker HVM067 in 4H bin 12 (2); *Hsh1.a* is associated with SNP markers 1\_1066 to 1\_1186 (positions 171.3 to 181.4 cM) in 4H bin 12 of the Bowman backcross-derived line BW416 (1), in 4H bin 12.

Description:

Short hairs (1 to 3 mm) are scattered or in rows on leaf sheaths of the basal part of the plant. The density of hairs varies considerably among cultivars and with changes in growing conditions. With few exceptions, no hairs are observed on the sheath of upper leaves (6, 7). Heterozygotes and smooth awned cultivars seem to have fewer hairs (4). Except for leaf sheath pubescence, the Bowman backcross-derived line for *Hsh1.a*, BW416, was similar morphologically and agronomically to Bowman (4).

Origin of mutant:

Natural occurrence in a few cultivars and in many accessions of *Hordeum vulgare* subsp. *spontaneum* (1, 7, 8).

Mutational events:

*Hsh1.a* was introduced into cultivated barley from its wild progenitor (7).

Mutant used for description and seed stocks:

*Hsh1.a* in Kimugi (GSHO 986, OUL012) (7, 8); *Hsh1.a* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 3450) in Bowman (PI 483237)\*10 (GSHO 2026, BW416, NGB 20649).

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which are inherited independently of the markers in the known seven linkage groups in barley.] *Nogaku Kenkyu* 45:1-10. [In Japanese.]

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Prepared:

R. Takahashi. 1972. *Barley Genet. Newsl.* 2:184 as BGS 158.

Revised:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:202.

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:240-241.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:107-108.

BGS 183, Yellow node 1, *Ynd1*

Stock number: BGS 183  
Locus name: Yellow node 1  
Locus symbol: *Ynd1*

Previous nomenclature and gene symbolization:

Yellow node = *Yn* (R.F. Eslick's collection notes) (1, 2).

Inheritance:

Monofactorial incomplete dominant (2).

Located in chromosome 4HS (3); based on incomplete data from the Harrington/Morex mapping population (3); linkage drag with the *int-c* (intermedium spike-c) locus (2); *Ynd1.a* is associated with SNP markers 1\_0409 to 2\_1122 (positions 7.91 to 47.80 cM) in 4H bins 01 to 04 of the Bowman backcross-derived line BW923 (1).

Description:

Nodes of the culm appear to lack a coating of surface waxes in plants homozygous for the *Ynd1.a* gene. In heterozygotes, surface waxes may be observed on the upper half of the node. This trait is easier to observe in greenhouse grown plants where surface waxes are not rubbed off by wind caused leaf movements. The *Ynd1.a* allele is present in many six-rowed cultivars of Oriental origin (2). The glossy node trait is seldom found in two-rowed lines selected from two- by six-rowed crosses because the *Ynd1.a* allele is closely linked to the dominant intermedium spike-c (*Int-c.a*) allele, which causes an unacceptable increase in the size of sterile lateral spikelets (2, 3). The plants of the Bowman backcross-derived line for *Ynd1*, BW923, were similar to Bowman plants except for a slight increase in kernel weight at one site (2).

Origin of mutant:

Naturally occurring in many six-rowed barley cultivars (2).

Mutational events:

*Ynd1.a* (GSHO 1607) in a stock from R.F. Eslick's collection at Montana State University, Bozeman (2).

Mutant used for description and seed stocks:

*Ynd1.a* in Morex (CIho 15773, GSHO 2492); *Ynd1.a* from Sen 'S' (GSHO 1605) in Bowman (PI 483237)\*6 (GSHO 2363), *Ynd1.a* from Sen 'S' in Bowman\*7 (BW923, NGB 22352).

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

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:98.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:109.

BGS 185, Brachytic 5, *brh5*

Stock number: BGS 185  
Locus name: Brachytic 5  
Locus symbol: *brh5*

Previous nomenclature and gene symbolization:

Brachytic-m = *brh.m* (4).

Inheritance:

Monofactorial recessive (4, 6).

Located in chromosome 4HS (5); near the *int-c* (intermedium spike-c) locus (5); about 13.0 cM proximal from SSR marker Bmac0310 near the boundary between 4H bins 06 and 07 (1); *brh5.m* is associated with SNP markers 2\_0145 to 1\_1500 (positions 2.58 to 115.9 cM) in 4H bins 01 to 08 of the Bowman backcross-derived line BW096 (2), likely in 4H bin 06.

Description:

Plants of the Bowman backcross-derived line for *brh5.m*, BW096, were about 3/4 normal height and their awns were about 3/4 of normal length. Peduncles were less than 2/3 normal length. Seedling leaves of *brh5* plants were relatively short. The kernels of *brh5* plants were shorter than those of Bowman and weighed about 30% less. BW096 plants lodged easily and the grain yields were about 1/2 those of Bowman (1, 3).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (7).

Mutational events:

*brh5.m* (17:18:2, DWS1010, GSHO 1678 in Birgitta (NSGC 1870, NGB 14667) (6, 7).

Mutant used for description and seed stocks:

*brh5.m* (GSHO 1678 in Birgitta); *brh5.m* in Bowman (PI 483237)\*7 (GSHO 2001, BW096, NGB 20502).

References:

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3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
5. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
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7. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:100.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:242.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:110.

BGS 229, Curly dwarf 2, *cul2*

Stock number: BGS 229  
Locus name: Curly dwarf 2  
Locus symbol: *cul2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 1HL (3); about 14.6 cM proximal from the *Blp1* (Black lemma and pericarp 1) locus (3, 4); the Bowman backcross-derived line for *cul2.b*, BW199, did not retain any SNP markers polymorphisms compared to Bowman (1).

Description:

Lemmas and awns are curly or strongly twisted, and stem internodes are curved. Culms are short (1/2 normal), spikes are semi-compact, awns are short (2/3 normal length), and kernels are globe-shaped. Most leaves are short and slightly twisted (3). Compared to Bowman, plants of the Bowman backcross-derived line for *cul2.b*, BW199, were about 40% shorter, 52.8 vs. 86.4 cm. Peduncles of BW199 were short and twisted, 1/3 to 1/2 the length of those for Bowman; and leaf blades were about 2 cm shorter. The awns of BW199 were shorter 7 vs. 11 cm and slightly twisted. Rachis internodes averaged 3.6 vs. 4.4 cm. Compared to Bowman, kernels of BW199 were 20% shorter, 7.5 vs. 9.4 mm, nearly 10% wider, 4.1 vs. 3.7 mm, and weighed about 25% less, 44 vs. 56 mg. The weight test of BW199 grain was 20% lower than that for Bowman; and grain yields were 50 to 75% lower (2).

Origin of mutant

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

Mutational events:

*cul2.b* (OUM112, GSHO 1712) in Akashinriki (OUJ659, PI 467400) (3).

Mutant used for description and seed stocks:

*cul2.b* (GSHO 1712) in Akashinriki; *cul2.b* in Bowman (PI 483237)\*2 (GSHO 2062); *cul2.b* in Bowman\*7 (BW199, NGB 22031).

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. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley VI. Ten mutant genes located on chromosomes 1 to 7, except 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:227-250.
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Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:227.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:111.

BGS 257, Smooth awn 5, *raw5*

Stock number: BGS 257  
Locus name: Smooth awn 5  
Locus symbol: *raw5*

Previous nomenclature and gene symbolization:

Smooth awn e =  $r_e$ , e (3).

Smooth awn 2 =  $r_2$  (3).

Smooth awn 5 =  $r_5$  (4).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6HL (3, 4); over 31.5 cM distal from the *rob1* (orange lemma 1) locus (3); *raw5.e* is associated with SNP markers 2\_0651 to 1\_0377 (positions 89.76 to 91.91 cM) in 6H bin 06 of the Bowman backcross-derived line BW664 (1), likely in 6H bin 06.

Description:

Plants have fewer stigma hairs and seed set is reduced, but more barbs developed on the central vein of the awn than in *raw1.a* plants (4). The Bowman backcross-derived line contains both of *raw1.a* and *raw5.e* genes for smooth awn. It has very smooth awns and very few stigma hairs, and seed set is often less than 10%.

Compared to Bowman, plants of the Bowman backcross-derived line for *raw5.e*, BW664, were about 15% shorter. Selfed seed set was very low in field plots and rare in the greenhouse (2).

Origin of mutant:

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

Mutational events:

*raw5.e* (OUM195, GSHO 771) in Akashinriki (OUJ659, PI 467400) (3, 4); *raw5.e* plus *rob1.a* in GSHO 785 (from T. Konishi).

Mutant used for description and seed stocks:

*raw5.e* (GSHO 771) in Akashinriki; *raw5.e* in Bowman (PI 483237)\*6 (GSHO 2085, BW664, NGB 22472).

References:

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

T. Konishi. 1976. *Barley Genet. Newsl.* 6:131.

Revised:

T. Konishi and J. D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:238.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:112.

BGS 268, Laxatum-b, *lax-b*

Stock number: BGS 268  
Locus name: Laxatum-b  
Locus symbol: *lax-b*

Previous nomenclature and gene symbolization:

Laxatum-1 = *lax-1* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 6HL (5); about 27.3 cM distal from the *rob1* (orange lemma 1) locus (5); about 18.8 cM proximal from the *xnt5* (xantha seedling 5) locus (5); *lax-b.1* is associated with SNP markers 1\_0061 to 1\_0040 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW459 (1), SNP markers retained from the donor parent in BW459 suggest that the *lax-b* locus is close to the centromere (2).

Description:

Plants are weak and short (3/4 normal), spikes are lax and spikelet number per spike is reduced. Seeds are small and thin and have a shrunken endosperm (xenia), which is detectable in the heterozygous condition (4). Treatment of leaves after tillering with GA<sub>3</sub> increases rachis internode length (7). Seed set is reduced in the Bowman backcross-derived line (2). Plants of the Bowman backcross-derived line for *lax-b.1*, BW459, were slightly shorter and weaker than Bowman plants. Rachis internodes of BW459 were 10 to 20% longer, but fertile spikelets per spike were 10 to 50% fewer. Compared to Bowman, kernels of BW459 were thin (3.5 vs. 3.8 mm) and long 11.0 vs. 9.4 mm) and weighed less (42 vs. 59 mg). Grain yields of BW459 were about 10% those of Bowman (2).

Origin of mutant:

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

Mutational events:

*lax-b.1* (NGB 116335, GSHO 1776) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*lax-b.1* (NGB 116335, GSHO 1776) in Bonus; *lax-b.1* in Bowman (PI 483237)\*7 (GSHO 2083, BW459, NGB 20690).

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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7. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:248.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:113.

BGS 269, High lysine 6, *lys6*

Stock number: BGS 269  
Locus name: High lysine 6  
Locus symbol: *lys6*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1, 4).

Located in chromosome 6H (4); *lys6.i* is associated with SNP markers 1\_0061 to 1\_0040 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW498 (2).

Description:

At the hard dough stage, kernels homozygous for the *lys6.i* gene develop a depression near the center of the lemma, which becomes progressively more distinct as the kernels mature. Mutant plants produce grain that has a 12% increase in lysine content (1). Shrunken endosperm and high lysine content have a pleiotropic association in stocks homozygous for the *lys6.i* gene (1, 4). Plants of the Bowman backcross-derived line for *lys6.i*, BW498, were similar to Bowman plants, but kernels were lighter (43 vs. 59) mg and test weights were 20% lower. Grain yields of BW498 were about 60% of those for Bowman (3).

Origin of mutant:

A gamma-ray induced mutant in Bomi Abed (PI 43371, NGB 5096) (1).

Mutational events:

*lys6.i* (Risø 527, GSHO 1786) in Bomi Abed (PI 43371, NGB 5096) (1, 5).

Mutant used for description and seed stocks:

*lys6.i* (GSHO 1786) in Bomi Abed; *lys6.i* in Bowman (PI 483237)\*3 (GSHO 2077), *lys6.i* in Bowman\*6 (BW498, NGB 20726).

References:

1. Doll, H. 1976. Genetic studies of high lysine barley mutants. p. 542-546. *In* H. Gaul (ed.) Barley Genetics III. Proc. Third Int. Barley Genet. Symp., Garching, 1975. Verlag Karl Thieme, München.
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Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:249.

Revised:

J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:114.

BGS 303, Variegated 3, *var3*

Stock number: BGS 303  
Locus name: Variegated 3  
Locus symbol: *var3*

Previous nomenclature and gene symbolization:

Variegated 3 = *va3* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL (4); about 29.7 cM distal from the *raw1* (smooth awn 1) locus (4); Karlsson was unable to confirm the presence of *var3* in chromosome 5H (3); *var3.c* is associated with SNP markers 2\_1421 to 1\_0477 (positions 159.51 to 173.49 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW888 (1).

Description:

Narrow white stripes appear on the foliage and stems, but they are less extensive than the white streak 7 (*wst7*) type of streaks (4). Expression of *var3.c* is poor in the Bowman backcross-derived line (2). Compared to Bowman, plants of the Bowman backcross-derived line for *var3.c*, BW888, had 2 to 4 fewer kernels per spike than Bowman. Kernels of BW888 weighed less than those of Bowman, 52 vs. 58 mg, and test weight was about 10% lower. Grain yields of BW888 were about half those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Montcalm (Clho 7149) (4).

Mutational events:

*var3.c* (Alb Acc 306, GSHO 1277) in Montcalm (Clho 7149) (4).

Mutant used for description and seed stocks:

*var3.c* (GSHO 1277) in Montcalm; *var3.c* in Bowman (PI 483237)\*5 (GSHO 2143); *var3.c* in Bowman\*7 (BW888, NGB 22321).

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:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:162.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:254.  
J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:115.

BGS 313, Chlorina seedling 6, *fch6*

Stock number: BGS 313  
Locus name: Chlorina seedling 6  
Locus symbol: *fch6*

Previous nomenclature and gene symbolization:

Yellow virescent = *yv* (8).  
Chlorina seedling 6 = *f6* (2).

Inheritance:

Monofactorial recessive (8).  
Located in chromosome 5HL (2, 5, 7, 8); over 36.2 cM proximal from the *srh1* (short rachilla hair 1) locus (2); *fch6.g* is associated with SNP markers 1\_0621 to 2\_1275 (positions 56.4 to 104.7 cM) in 5H bins 03 to 06 of the Bowman backcross-derived line BW362 (1).

Description:

Seedlings appear yellowish-white initially, but green pigments develop near the leaf tip within one week. Green pigmentation is not as intense as in normal seedlings (8). The chlorophyll content is 15% of normal in 3-week old seedlings, and the free amino acid content is increased by 75% or more (4). Plants do mature in the field, but development is much delayed (3). Plants of the Bowman backcross-derived line for *fch6.g*, BW362, showed variable responses to environment. Heading dates of BW362 ranged from 2 to 17 days later than Bowman. Plant height varied from 20% shorter to 20% taller and the average number of kernels per spike varied 16 to 27 compared with 19 to 24 for Bowman. Kernels of BW362 were slightly shorter and narrower and they weighed 10 to 15% less than those of Bowman. Grain yields of BW362 ranged from 20 to 40% lower than Bowman yields (3).

Origin of mutant:

An X-ray induced mutant in Himalaya (CIho 1312) (8).

Mutational events:

*fch6.g* (GBC380, GSHO 1390) in Himalaya (CIho 1312) (6, 8).

Mutant used for description and seed stocks:

*fch6.g* (GSHO 1390) in Himalaya; *fch6.g* in GBC681 was used for linkage studies (2); *fch6.g* in Bowman (PI 483237)\*7 (GSHO 2097, BW362, NGB 20601).

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).
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8. Tuleen, N.A., L.A. Synder, R.S. Caldecott, and V.S. Haitt. 1968. Genetic investigation of suppressors of a chloroplast mutation in *Hordeum vulgare*. *Genetics* 59:45-55.

Prepared:

K.C. Falk. 1983. Barley Genet. Newsl. 13:111.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:262.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:116-117.

BGS 320, Intermedium spike-b, *int-b*

Stock number: BGS 320  
Locus name: Intermedium spike-b  
Locus symbol: *int-b*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 5HL (4); near the *raw1* (smooth awn 1) locus based on linkage drag (4); *int-b.3* is associated with SNP markers 2\_0134 to 2\_1355 (positions 163.29 to 234.98 cM) in 5H bins 10 to 13 of the Bowman backcross-derived line BW420 (2), likely in 5H bin 10.

Description:

The spike appears similar to the six-rowed spike, but developmental irregularities occur commonly in the lower portion of the spike. All lateral spikelets are reduced in size, and their lemma awns are short or reduced to a pointed tip. Commonly, only lateral spikelets in the middle of the spike set seed (5, 8). Plants of the Bowman backcross-derived line for *int-b.3*, BW420, showed reduced vigor and tillering (1). Plants of BW420 headed 2 to 3 days earlier than Bowman, but more lodging was observed. The BW420 kernels were slightly longer, but weighed less, 52 vs. 58 mg, compared to those of Bowman. Grain yields of BW420 were 10 to 30% of those recorded for Bowman (3). Combining the *int-b.3* and *cul2.b* (uniculum 2) mutants produced unicum plants having spikes without spikelets (1).

Origin of mutant:

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

Mutational events:

*int-b.3* (NGB 115421, GSHO 1764), *-b.6* (NGB 115424) in Bonus (PI 189763, NGB 14657) (5, 8); *int-b.75* (NGB 115493) in Bonus (7).

Mutant used for description and seed stocks:

*int-b.3* (NGB 115421, GSHO 1764) in Bonus; *int-b.3* in Bowman (PI 483237)\*6 (GSHO 2129); *int-b.3* in Bowman\*7 (BW420, NGB 20653).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:268.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:118-119.

BGS 331, Erectoides-n, *ert-n*

Stock number: BGS 331  
Locus name: Erectoides-n  
Locus symbol: *ert-n*

Previous nomenclature and gene symbolization:

Erectoides-51 = *ert-51* (3).

Inheritance:

Monofactorial recessive (3, 8).

Located in chromosome 5HL (4, 6, 8); about 4.8 cM proximal from the *cer-zj* (eceriferum-zj) locus (7, 8); *ert-n.51* is associated with SNP markers 1\_0580 to 2\_1244 (positions 54.27 to 91.0 cM) in 5H bins 03 to 05 of the Bowman backcross-derived line BW318 (1). The *ert-n* locus was previously reported to be very close to the *ert-g* (erectoides-g) locus (9, 10), which is located in chromosome 1H.

Description:

Semicompact spikes occur because rachis internode length is reduced. Rachis internode length values vary from 1.9 to 2.4 mm (8). Mutant lines are about 3/4 normal height. The spike has enlarged lateral spikelets that have a pointed or awnletted tip, and plants show partial sterility not associated with a translocation. Spikes tend to have a whitish color at maturity (8). GA<sub>3</sub> treatment of plants as the flag leaf emerges decreases spike density (11). In the Bowman backcross-derived line for *ert-n.51*, BW318, plants produced few tillers and matured later than Bowman (2). BW318 plants were very sensitive to environmental conditions with heading dates from 2 to 9 days later than Bowman and grain yields ranged from very little to 1/3 of those for Bowman. BW318 plants were 10 to 25% shorter than Bowman, and the number of fertile spikelets increased by about two. The awns of BW318 were shorter 8 vs. 11 cm and rachis internode length averaged 3.9 vs. 4.4 mm. Kernels of BW318 were slightly longer and thinner than Bowman kernels. Kernel weights for BW318 ranged from equal to 40% lower and test weight at one site was 10% lower than that for Bowman (2).

Origin of mutant:

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

Mutational events:

*ert-n.51* (NGB112650, GSHO 488) in Bonus (PI 189763, NGB 14657) (3); *ert-n.61* (NGB 112660), *-n.63* (NGB 112662) in Bonus (4); *ert-n.133* (NGB 112732), *-n.135* (NGB 112734) in Bonus (8); *ert-n.325* (NGB 112840), *-n.419* (NGB 112935) in Foma (Clho 11333, NGB 14659) (5); *ert-n.409* (NGB 112925), *-n.464* (NGB 112979) in Foma (8).

Mutant used for description and seed stocks:

*ert-n.51* (NGB 112650, GSHO 488) in Bonus; *ert-n.51* in Bowman (PI 483237)\*3 (GSHO 2107); *ert-n.51* in Bowman\*6 (BW318, NGB 22113).

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U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:279.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:120-121.

BGS 347, Many noded dwarf 4, *mnd4*

Stock number: BGS 347  
Locus name: Many noded dwarf 4  
Locus symbol: *mnd4*

Revised locus symbol:

The mutant named *mnd4.e* is likely an allele at the *mnd6* (many noded dwarf 6, *HvMND*) locus based a mapping-by-sequencing study (7). Phenotypic similarities (2, 7) exist and retained SNP markers in 5H of the Bowman backcross-derived lines (BW520 and BW522) overlap (1). Thus, the OUJ659 mutant in Akashinriki should be renamed *mnd6.e*. See BGS 633 for more information on the alleles at the *mnd6* locus.

Previous nomenclature and gene symbolization:

Many noded dwarf 4 = *m4* (3).  
Many noded dwarf 4 = *mnd4* (4).

Inheritance:

Monofactorial recessive (3, 6).  
Located in chromosome 5HL (3); based on close linkage to the *raw1* (smooth awn 1) locus in the Bowman backcross-derived line (3); *mnd4.e* is associated with SNP markers 1\_0024 to 1\_1200 (positions 165.44 to 180.02 cM) in 5H bin 10 of the Bowman backcrossed-derived line BW520 (1), in 5H bin 10.

Description:

Plants with the *mnd4.e* gene have 7 to 8 elongated internodes per tiller and are about 3/4 normal height. The plants produce many tillers. Spikes have 2/3 to 3/4 the normal number of rachis internodes. Awn length is slightly reduced and grain is small and thin compared to that of normal sibs (2). Plants of the Bowman backcross-derived line for *mnd4.e*, BW520, had short peduncles, 15 vs. 29 cm, short culms, 62 vs. 82 cm in length, in field trials, and awns were 2/3 normal length. They headed one to two days later than Bowman. Spikes of BW520 were short, 18 vs. 21 spikelets and average rachis internode lengths were 3.8 vs. 4.3 mm. The kernels of BW520 were small and their average weight was 44 vs. 56 mg for Bowman. The grain yields of BW520 ranged from 25% less to equal to those for Bowman (2). The Bowman backcross-derived lines for *mnd4.e* and *mnd6.6* (see BGS 633) were phenotypically similar and retained donor parent SNP markers in the same region of chromosome 5HL; however, the *mnd4.e* mutant exhibited lesser degree of effects on morphological traits and agronomic performance (2). In a mapping-by-sequencing study of mutants at the *mnd6* locus, Mascher et al. (7) demonstrated that the *mnd4.e* mutant is likely an allele at the *mnd6* (*HvMND*) locus.

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (6).

Mutational events:

*mnd4.e* (OUM168, DWS1048, GSHO 1798) in Akashinriki (OUJ659, PI 467400) (3, 5).

Mutant used for description and seed stocks:

*mnd4.e* (GSHO 1798) in Akashinriki; *mnd4.e* in Bowman (PI 483237)\*7 (GSHO 2135, BW520, NGB 20748).

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Prepared:

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Revised:

J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:122-123.

BGS 352, Glossy sheath 2, *gsh2*

Stock number: BGS 352  
Locus name: Glossy sheath 2  
Locus symbol: *gsh2*

Previous nomenclature and gene symbolization:

Glossy sheath 2 = *gs2* (18, 20).

Eceriferum-b = *cer-b* (8, 20).

Inheritance:

Monofactorial recessive (8, 17).

Located in chromosome 3HL (2, 4, 19); about 5.1 cM proximal from the *als1* (absent lower laterals 1) locus (5, 6); over 32.5 cM distal from the *uzu1* (*uzu* 1) locus (2, 5, 6); *gsh2.f* is associated with SNP markers 2\_1161 to 1\_0584 (positions 169.94 to 178.12 cM) in 3H bin 11 of the Bowman backcross-derived line BW405; *cer-b.2* is associated with SNP markers 22\_1513 to 1\_1172 (positions 190.97 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW107 (1), in 3H bin 11.

Description:

Surface wax coating appears absent on the spike, leaf sheath, and stem (wax code - - ++ ) (8, 17). The nodes of mutant plants appear to lack surface wax (3). The Bowman backcross-derived lines for the *gsh2* mutants, BW107 with *cer-b.2* and BW405 with *gsh2.f*, had agronomic traits similar to those of Bowman, but grain yields were slightly lower (3).

Origin of mutant:

Spontaneous occurrence in Vantage (Clho 7324) (16); an X-ray induced mutant in Maja Abed (PI 184884, NGB 8815) (8).

Mutational events:

*gsh2.d* in Vantage (Clho 7324), *gsh2.e* in Ymer (Clho 7275), *gsh2.f* (GSHO 736), *gsh2.g* in Atlas (Clho 4118), *gsh2.h* in Klargin (16); *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja Abed (PI 184884, NGB 8815) (7, 8, 9, 20); *cer-b.4* (NGB 110888), *-b.64* (NGB 110948), *-b.66* (NGB 110950), *-b.109* (NGB 110994 in Bonus (PI 189763, NGB 14657) (8, 9); *cer-b.79* (NGB 110963), *-b.94* (NGB 110978), *-b.96* (NGB 110980) in Bonus, *-b.209* (NGB 111096), *-b.222* (NGB 111109), *-b.319* (NGB 111206), *-b.336* (NGB 111223), *-b.337* (NGB 111224), *-b.377* (NGB 111264), *-b.418* (NGB 111306), *-b.424* (NGB 111312), *-b.427* (NGB 111315) in Foma (Clho 11333, NGB 14659) (9, 15); *cer-b.169* (NGB 111055), *-b.193* (NGB 111079) in Bonus, *-b.412* (NGB 111300), *-b.531* (NGB 111419), *-b.549* (NGB 111437) in Foma, *-b.1037* (NGB 111925), *-b.1059* (NGB 111947) in Carlsberg II (Clho 10114, NGB 5085) (9); *cer-b.751* (NGB 111639), *-b.769* (NGB 111657), *-b.791* (NGB 111679), *-b.799* (NGB 111687), *-b.800* (NGB 111688) in Bonus, *-b.1129* (NGB 112017) in Kristina (NGB 1500, NGB 14661) (10); *cer-b.910* (NGB 111798) in Bonus (11); *cer-b.932* (NGB 111820) in Bonus (12); *cer-b.147* (NGB 111033), *-b.182* (NGB 111068), *-b.623* (NGB 111511) in Bonus, *-b.1099* (NGB 111987), *-b.1267* (NGB 112155), *-b.1269* (NGB 112157) in Kristina (13); *cer-b.1699* (NGB 119343) in Bonus (14); *gsh2.ab* (OUM019), *gsh2.ah* (OUM025) in Akashinriki (OUJ659, PI 467400) (4, 6); *gsh2.bb* in the cross NDB112/Fr926-77 (3); *gsh2.bd* in Ms13551 and *gsh2.be* in PI 282610 both in *Hordeum vulgare* subsp. *spontaneum* (1, 3).

Mutant used for description and seed stocks:

*gsh2.f* (GSHO 736) in Atlas; *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja; *gsh2.f* in Bowman (PI 483237)\*7 (GSHO 1988); *gsh2.f* in Bowman\*8 (BW405, NGB 20678); *cer-b.2* in Bowman\*6 (GSHO 1989); *cer-b.2* in Bowman\*7 (BW107, NGB 20513); *gsh2.bd* from Ms13551 in Bowman\*4 (BW402, NGB 22150); *gsh2.be* from PI 282610 in Bowman\*7 (BW403, NGB 22151).

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Revised:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:294-295.  
U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:141-142.  
U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:124-125.

BGS 355, Glossy sheath 5, *gsh5*

Stock number: BGS 355  
Locus name: Glossy sheath 5  
Locus symbol: *gsh5*

Previous nomenclature and gene symbolization:

Glossy sheath 5 = *gs5* (14).  
Eceriferum-s = *cer-s* (4, 12).  
Glossy sheath 8 = *gs8* (16).

Inheritance:

Monofactorial recessive (4).  
Located in chromosome 2HL (14, 15, 16, 18); in the centromeric region about 2.5 cM proximal from the *eog1* (elongated outer glume 1) locus (14, 16); about 32.0 cM proximal from the *vrs1* (six-rowed spike 1) locus (14, 16); *gsh5.m* is associated with SNP markers 1\_0851 to 2\_1437 (positions 81.43 to 113.28 cM) in 2H bins 06 to 08 of the Bowman backcross-derived line BW408 (1); *cer-s.31* is associated with SNP markers 1\_0796 to 2\_0528 (positions 95.53 to 118.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW122 (1), in 2H bin 07.

Description:

Mutants have a reduced surface wax covering on the spikes and stems, and a bright glossy green color on all leaf sheaths (14) (wax code + - ++ (4). The nodes appear to have an excessive wax covering (3). The Bowman backcross-derived line with the *cer-s.31* allele, BW122, headed 2 to 4 days later than BW408 with the *gsh5.m* allele and Bowman (3). BW122 also had 3 to 6 more kernels per spike. Kernels of BW122 and BW408 were about 10% lighter than those of Bowman. The grain yields of BW408 were often slightly lower than those of Bowman or BW408 (3). The differences in maturity and number of kernels per spike between BW122 and BW408 were attributed to close linkage between alleles at the *gsh5* locus and those at the *Eam6* (early maturity 6 or earliness per se QTL 2S = *eps2S*) locus (3).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB 14657) (4); a radiation induced mutant in Jotun (PI 467357) (14); a spontaneous mutant in Okaiku 3 (OUL011) (17).

Mutational events:

*cer-s.24* (NGB 110908) in Bonus (PI 189763, NGB 14647) (4); *cer-s.31* (NGB 110915, GSHO 440) in Bonus (2, 4); *cer-s.41* (NGB 110925) in Bonus (4); *cer-s.287* (NGB 111174), *-s.303* (NGB 111190), *-s.372* (NGB 111259), *-s.444* (NGB 111332) in Foma (Clho 11333, NGB 14659) (12); *cer-s.1047* (NGB 111935) in Carlsberg II (Clho 10114, NGB 5085) (5); *cer-s.137* (NGB 111022) in Bonus, *-s.591* (NGB 111479) in Foma, *-s.803* (NGB 111691) in Bonus, *-s.1132* (NGB 112020) in Kristina (NGB 1500, NGB 14661) (6); *cer-s.914* (NGB 111802) in Bonus (7); *cer-s.622* (NGB 111510) in Bonus, *-s.1054* (NGB 111942) in Carlsberg II, *-s.1153* (NGB 117264) in Kristina (8); *cer-s.1323* (NGB 112211) in Bonus (9); *cer-s.1134* (NGB 112022) in Kristina (10); *cer-s.1754* (NGB 112568) in Bonus (11); *gsh5.m* (GSHO 739) in Jotun (PI 467357) (14); *gsh5.n* (GSHO 832) in Okaiku 3 (OUL011) (13, 17).

Mutant used for description and seed stocks:

*gsh5.m* (GSHO 739) in Jotun; *cer-s.31* (GSHO 440, NGB 110915) in Bonus; *cer-s.31* in Bowman (PI 483237)\*5 (GSHO 1888); *cer-s.31* in Bowman\*8 (BW122, NGB 20528); *gsh5.m* in Bowman\*8 (GSHO 1889, BW408, NGB 20644).

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Revised:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:300-301.

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BGS 359, Male sterile genetic 3, *msg3*

Stock number: BGS 359  
Locus name: Male sterile genetic 3  
Locus symbol: *msg3*

Previous nomenclature and gene symbolization:

Male sterile 10 = *ms10* (3, 8).

Male sterile 3 = *ms3* (3, 5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 2HS (5); about 4.6 cM distal from the *eog1* (elongated outer glume 1) locus (5); 0.6 cM distal from the *fch1* (chlorina seedling 1) locus (5); *msg3.cc* is associated with SNP markers 1\_1493 to 1\_1046 (positions 76.05 to 96.47 cM) in 2H bins 06 to 07 of a heterozygous plant from the Bowman backcross-derived line BW565 and with small regions of 1H and 3H (1, 2).

Description:

Selfing - none (3, 5).

Outcrossing - complete female fertility (3, 5).

Stamens - anthers much smaller than fertile sib (3), no stomium or filament elongation (6).

Pollen - non-staining, no free pollen grains (7).

The male sterile plants are also about 1/3 normal size with short, wide leaves (3, 5).

Spikes are dense and spikelets are small and malformed, awns are 1/3 normal length, and double or triple pistils (fasciation) occur in some spikelets (5). The fused double and triple kernels, which developed after pollination of male sterile plants, were likely caused by failure of rachilla abortion and partial fusion of adjacent florets (2). Partial fertility was observed in mutant plants of the BW565 stock when they were grown in Lund, Sweden in 2013 and 2014 (6).

Origin of mutant:

An acetone induced mutant in Gateway (CIho 10072) (5).

Mutational events:

*msg3.cc* (MSS051, GSHO 1130) in Gateway (CIho 10072) (4, 5).

Mutant used for description and seed stocks:

*msg3.cc* (GSHO 1130) in Gateway; *msg3.cc* from Gateway in Bowman (PI 483237)\*7 (GSHO 1885); *msg3.cc* in Bowman\*8 (BW565, NGB 24806).

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. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. *Crop Sci.* 8:218-220.
4. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.
5. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. *Can. J. Genet. Cytol.* 2:397-415.
6. Lundqvist, U. (Unpublished).
7. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. *Crop Sci.* 11:200-203.
8. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III. 1954-1963.

Crop Sci. 5:33-43.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:176.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:307.

J.D. Franckowiak and U. Lundqvist. 2014. Barley Genet. Newsl. 44:128-129.

BGS 375, Male sterile genetic 20, *msg20*

Stock number: BGS 375  
Locus name: Male sterile genetic 20  
Locus symbol: *msg20*

Previous nomenclature and gene symbolization:

Male sterile ad = *msg,,ad* (3, 4, 6).

Male sterile 20 = *ms 20* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 4HL (1); *msg20.ad* is associated with SNP markers 1\_0028 to 1\_0846 (positions 69.62 to approximately 92 cM) in 4H bins 05 to 06 of the of the Bowman backcross-derived line BW555 (1). Previously the *msg20* locus was placed in chromosome 1H (3).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3).

Stamens - anthers smaller than fertile sib (3). Selfed seed set in the Bowman backcross-derived line for *msg20.ad*, BW555, is 50 to 75%; thus, it is maintained as an inbred line. Both the original mutant stock and BW555 have short awns (3/4 normal length) (2).

Origin of mutant:

An X-ray induced mutant in Hannchen (Clho 531) (3).

Mutational events:

*msg20.ad* (MSS096, GSHO 2372) in Hannchen (Clho 531) (3, 5).

Mutant used for description and seed stocks:

*msg20.ad* (GSHO 2372) in Hannchen; *msg20.ad* in Bowman (PI 483237)\*5 (GSHO 2059, BW555, NGB 23424).

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. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) *Barley Genetics II. Proc. Second Int. Barley Genet. Symp.*, Pullman, WA, 1969. Washington State Univ. Press.
4. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. *Crop Sci.* 8:754-755.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.
6. Robertson, D.W. 1971. Recent information of linkage and chromosome mapping. p. 220-242. *In* R.A. Nilan (ed.) *Barley Genetics II. Proc. Second Int. Barley Genet. Symp.*, Pullman, WA, 1969. Washington State Univ. Press.

Prepared:

E.A. Hockett. 1971. *Barley Genet. Newsl.* 1:188.

Revised:

- T. Tsuchiya. 1982. *Barley Genet. Newsl.* 12:107.  
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:323.  
J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 43:139.  
J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:130.

BGS 388, Desynapsis 9, *des9*

Stock number: BGS 388  
Locus name: Desynapsis 9  
Locus symbol: *des9*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 7HL (1); *des9.n* is associated mainly with SNP markers 1\_0861 to 2\_1363 (positions 183.9 to 198.7 cM) in 7H bins 11 to 12 of the Bowman backcross-derived line BW249 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis is 0.9, ranging from 7 ring bivalents ( $d = 0$ ) to 5 rod bivalents ( $d = 5$ ). Ovule fertility is about 90% (4). Compared to Bowman, plants of the Bowman backcross-derived line for *des9.n*, BW249, were 10% shorter and kernels were 10% lighter. Average seed set for BW249 was about 25%. Grain yields of BW249 were 10 to 40% of those for Bowman (2).

Origin of mutant:

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

Mutational events:

*des9.n* (GSHO 600) in Betzes (PI 129430) (3, 5).

Mutant used for description and seed stocks:

*des9.n* (GSHO 600) in Betzes; *des9.n* in Bowman (PI 483237)\*5 (BW249, NGB 22074).

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 388, Normal vs. desynapsis 9, *des9*. *Barley Genet. Newsl.* 4:137.
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.

Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1974. *Barley Genet. Newsl.* 4:137.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:336.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:131.

BGS 390, Desynapsis 11, *des11*

Stock number: BGS 390  
Locus name: Desynapsis 11  
Locus symbol: *des11*

Previous nomenclature and gene symbolization:

Desynapsis  $r = des_{,,r}(3, 5)$ .

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 3HL (1); *des11.r* is associated with SNP markers 2\_0931 to 2\_0168 (positions 104.39 to 173.82 cM) in 3H bins 07 to 11 of the Bowman backcross-derived line BW231 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis is 5.7, ranged from 6 ring bivalents plus one rod bivalent ( $d = 1$ ) to 2 rod bivalents plus 10 univalents ( $d = 12$ ). Ovule fertility is about 40% (4). When crossed with the non-allelic desynaptic mutants *des4.d* and *des5.e*, the  $F_1$ 's frequently showed a low degree of desynapsis (up to 3 rod bivalents). When crossed with *des7.j*, the  $F_1$ 's show a low to medium degree of desynapsis ( $d = 1.8$ ), ranging from 7 ring bivalents ( $d = 0$ ) to 4 ring bivalents plus 4 rod bivalents ( $d = 5$ ), and there are lagging chromosomes and micronuclei at telophase I (4). Plants of the Bowman backcross-derived line for *des11.r*, BW231, were slightly taller than Bowman and kernels often weighed slightly more. Grain yields of BW231 were 20% lower than those for Bowman (2).

Origin of mutant:

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

Mutational events:

*des11.r* (GSHO 602) in Betzes (PI 129430) (3, 5).

Mutant used for description and seed stocks:

*des11.r* (GSHO 602) in Betzes; *des11.r* in Bowman (PI 483237)\*6 (BW231, NGB 22058).

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 390, Normal vs. desynapsis 11, *des11*. *Barley Genet. Newsl.* 4:139.
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.

Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1974. *Barley Genet. Newsl.* 4:139.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:338.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:132.

BGS 391, Desynapsis 12, *des12*

Stock number: BGS 391  
Locus name: Desynapsis 12  
Locus symbol: *des12*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 3H (1); *des12.s* is associated with SNP markers 2\_0742 to 2\_1277 (positions 29.05 to 173.82 cM) in 3H bins 06 to 11 of the Bowman backcross-derived line BW232 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis is 4.7, ranging from 7 ring bivalents ( $d = 0$ ) to 1 rod bivalent plus 12 univalents ( $d = 13$ ). Ovule fertility is about 35% (4). Under greenhouse conditions, selfed set was about 50% for main tillers of the Bowman backcross-derived line for *des12.s*, BW232, but later tillers had much higher levels of seed set (2).

Origin of mutant:

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

Mutational events:

*des12.s* (GSHO 603) in Betzes (PI 129430) (3, 5). The mutant *des.w* in Betzes was recorded as an allele at the *des12* locus (3, 5), but seed set of the Bowman backcross derived line for *des.w*, BW233, is less than 10% and the SNP markers retained are largely in 7H (1, 2).

Mutant used for description and seed stocks:

*des12.s* (GSHO 603) in Betzes; *des12.s* in Bowman (PI 483237)\*4 (BW232, NGB 22059). The *des.w* mutant in Betzes is not an allele at the *des12* locus (see above), but there is a Bowman backcross-derived stock for *des.w* in six crosses to Bowman (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.M. Hernandez-Soriano and R.T. Ramage. 1974. *Barley Genet. Newsl.* 4:140.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:339.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:133.

BGS 392, Desynapsis 13, *des13*

Stock number: BGS 392  
Locus name: Desynapsis 13  
Locus symbol: *des13*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 3H (1); *des13.t* is associated with SNP markers 1\_0886 to 2\_1502 (positions 17.49 to 100.48 cM) in 3H bins 02 to 06 and with markers 2\_0115 to 1\_0747 (positions 126.83 to 144.3 cM) in 3H bins 08 to 09 of the Bowman backcross-derived line BW234 (1).

Description:

There are two types of microspore mother cells in mutant plants. About 58% have normal early prophase and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis is 0.8, ranging from 7 ring bivalents ( $d = 0$ ) to 4 ring bivalents plus 2 rod bivalents plus 2 univalents ( $d = 4$ ). The other type of microspore mother cells has chromosomes that appear "sticky" at metaphase I. The stickiness is accompanied by very elongated ring bivalents and by extensive chromosome fragmentation. Ovule fertility is about 20 to 30% (4). Seed set of the Bowman backcross-derived line for *des13.t*, BW234, was about 50% and its grain yields were reduced by about 50%. Other traits of BW234 were similar to those of Bowman (2).

Origin of mutant:

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

Mutational events:

*des13.t* (GSHO 604) in Betzes (PI 129430) (3, 5).

Mutant used for description and seed stocks:

*des13.t* (GSHO 604) in Betzes; *des13.t* in Bowman (PI 483237)\*6 (BW234, NGB22061).

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 392, Normal vs. desynapsis 13, *des13*. *Barley Genet. Newsl.* 4:141.
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.

Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1974. *Barley Genet. Newsl.* 4:141.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:340.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:134.

BGS 393, Desynapsis 14, *des14*

Stock number: BGS 393  
Locus name: Desynapsis 14  
Locus symbol: *des14*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 7H (1); *des14.u* is associated mainly with SNP markers 1\_0838 to 1\_0485 (positions 49.53 to 121.90 cM) in 7H bins 04 to 07 of the Bowman backcross-derived line BW235 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis is 4.8, ranging from 7 ring bivalents ( $d = 0$ ) to 1 rod bivalent plus 12 univalents ( $d = 13$ ). Lagging chromosomes and micronuclei are observed frequently at telophase I. Ovule fertility is about 35% (4). The selfed seed set of the Bowman backcross-derived line for *des14.u*, BW235, was 40 to 50% and it yielded about half as much grain as Bowman. Kernels of BW235 averaged 5 to 10% lighter than those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (4).

Mutational events:

*des14.u* (GSHO 605) in Betzes (PI 129430) (3, 5).

Mutant used for description and seed stocks:

*des14.u* (GSHO 605) in Betzes; *des14.u* in Bowman (PI 483237)\*6 (BW235, NGB 22062).

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 393, Normal vs. desynapsis 14, *des14*. *Barley Genet. Newsl.* 4:142.
5. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. *Barley Genet. Newsl.* 2:65-68.

Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1974. *Barley Genet. Newsl.* 4:142.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:341.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:135.

BGS 394, Desynapsis 15, *des15*

Stock number: BGS 394  
Locus name: Desynapsis 15  
Locus symbol: *des15*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 3HL probably (1); *des15.x* is associated mainly with SNP markers 1\_1436 to 2\_1362 (positions 230.99 to 255.13 cM) in 3H bins 15 to 16 of the Bowman backcross-derived line BW236 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene and diakinesis. The average degree of desynapsis is 7.5, ranging from 5 ring bivalents plus 2 rod bivalents ( $d = 2$ ) to 1 rod bivalent plus 12 univalents ( $d = 13$ ). Ovule fertility is about 25% (4). Under greenhouse conditions, selfed set was about 20% for the Bowman backcross-derived line for *des15.x*, BW236 (2).

Origin of mutant:

A spontaneous mutant in Ingrid (CIho 10083, NGB 2671) (3).

Mutational events:

*des15.x* (GSHO 606) in Ingrid (CIho 10083, NGB 2671) (3, 5). The mutant *des.y* in Ingrid was reported as an allele at the *des15* locus (3, 5), but seed set of the Bowman backcross derived line for *des.y*, BW237, was 30 to 50% and the SNP markers retained are largely in 2HL (1, 2).

Mutant used for description and seed stocks:

*des15.x* (GSHO 606) in Ingrid; *des15.x* in Bowman (PI 483237)\*3 (BW236, NGB 22063). The *des.y* mutant in Ingrid is not an allele at the *des15* locus (see above), but there is a Bowman backcross-derived stock for *des.y* with five crosses to Bowman (BW237, NGB 22064).

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. 1975. BGS 394, Normal vs. desynapsis 15, *des15*. *Barley Genet. Newsl.* 5:113.
5. Scheuring, J.R., and R.T. Ramage. 1975. Reports from coordinators: Desynaptic genes. *Barley Genet. Newsl.* 5:86.

Prepared:

J.M. Hernandez-Soriano and R.T. Ramage. 1975. *Barley Genet. Newsl.* 5:113.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:342.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:136.

BGS 395, Male sterile genetic 26, *msg26*

Stock number: BGS 395  
Locus name: Male sterile genetic 26  
Locus symbol: *msg26*

Previous nomenclature and gene symbolization:

Male sterile u = *msg,u* (7).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 7HS (3, 4); linked to the *nud1* (naked caryopsis 1) locus (3); linked to the *ant1* (anthocyanin-less 1) locus based on linkage drag (4); *msg26.u* is associated with SNP markers 2\_0790 to 1\_1098 (positions 73.69 to 93.97 cM) in 7H bins 05 to 06 of Bowman backcross-derived line BW561 (1).

Description:

Selfing - none (6).

Outcrossing - complete female fertility (6).

Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (6).

The Bowman backcross-derived line for *msg26.u*, BW561, has adequate self-fertility so that it can be maintained as an inbred line (2).

Origin of mutant:

A spontaneous mutant in Unitan (CIho 10421) (7).

Mutational events:

*msg26.u* (MSS088, GSHO 745, GSHO 2378) in Unitan (CIho 10421) (5, 7, 8).

Mutant used for description and seed stocks:

*msg26.u* (GSHO 745, GSHO 2378) in Unitan; *msg26.u* in Bowman (PI 483237)\*6 (GSHO 1858, BW561, NGB 23429).

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. 1988. Mapping four male sterile genes on chromosome 1. *Barley Newsl.* 31:111.
4. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
5. Hockett, E.A. 1974. The genetic male sterile collection. *Barley Genet. Newsl.* 4:121-123.
6. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) *Barley Genetics II*. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press.
7. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. *Crop Sci.* 8:754-755.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1974. *Barley Genet. Newsl.* 4:136 as BGS 387, Male sterile genetic 26, *msg26*.

E.A. Hockett. 1975. *Barley Genet. Newsl.* 5:170.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:343.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:137.

BGS 396, Shrunken endosperm genetic 6, *seg6*

Stock number: BGS 396  
Locus name: Shrunken endosperm genetic 6  
Locus symbol: *seg6*

Previous nomenclature and gene symbolization:

Shrunken endosperm = *se6* (5).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL (6); *seg6.g* is mainly associated with SNP markers 1\_0762 to 2\_0168 (positions 58.56 to 173.82 cM) in 3H bins 04 to 11 of the Bowman backcross-derived line BW838, other small polymorph segments were retained in BW838 (1).

Description:

Seed size is reduced, but the degree reduction is affected by environment. Seed weights of 25, 50, and 75% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (4). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg6.g* plants can be used to establish stands under field conditions (6). Light microscopy revealed that *seg6* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (2). The kernel weights for the Bowman backcross-derived line for *seg6.g*, BW838, varied from 35 to 70% of those for Bowman. Kernel length was similar, but BW838 kernels were very thin, 3.14 vs. 3.86 mm. The test weight of BW838 grain was 40% that of Bowman grain and yields ranged from 20 to 50% those of Bowman (3).

Origin of mutant:

A spontaneous mutant in Ingrid (Clho 10083, NGB2671) (5).

Mutational events:

*seg6.f* in an unknown hybrid, *seg6.g* (GSHO 2467) in Ingrid (Clho 10083, NGB 2671) (5).

Mutant used for description and seed stocks:

*seg6.g* (GSHO 2467) in Ingrid; *seg6.g* in Bowman (PI 483237)\*4 (GSHO 1975, BW838, NGB 22275).

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Revised:

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BGS 402, Eceriferum-g, *cer-g*

Stock number: BGS 402  
Locus name: Eceriferum-g  
Locus symbol: *cer-g*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HL (2, 14); about 15.9 cM distal from the *vrs1* (six-rowed spike 1) locus (14, 15); *cer-g.10* is associated with SNP markers 1\_0317 to 2\_0374 (positions 98.35 to 104.81 cM) in 2H bin 08 and SNP markers 1\_0619 to 1\_0533 (positions 133.59 to 141.56 cM) in 2H bin 09 of the Bowman backcross-derived line BW111 (1), in 2H bin 08.

Description:

Mutants have reduced surface wax coating on spike, leaf sheath, and stem (wax code + + ++ ) with the wax coating of the leaf sheath and stem wax present in broad horizontal bands (4). Double and triple stomatal complexes are produced during stomatal development (4, 16). All *cer-g* mutants have globe-shaped or globosum kernels (4). Plants of the Bowman backcross-derived line for *cer-g.10*, BW111, headed 1 to 2 days later than Bowman and about 10% shorter. Kernels of BW111 were shorter (8.2 vs. 9.5 mm), narrower (3.5 vs. 3.8 mm) and weighed 15 to 20% less. Grain yields of BW111 were 2/3 to 3/4 of those for Bowman (3).

Origin of mutant:

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

Mutational events:

*cer-g.10* (NGB 110894, GSHO 428), *-g.11* (NGB 110895), *-g.23* (NGB 110907), *-g.47* (NGB 110931), *-g.55* (NGB 110939) in Bonus (PI 189763, NGB 14657) (4); *cer-g.106* (NGB 110991) in Bonus, *-g.202* (NGB 111089), *-g.208* (NGB 111095), *-g.210* (NGB 111097), *-g.494* (NGB 111382) in Foma (CIho 11333, NGB 14659) (13); *cer-g.166* (NGB 111052) in Bonus, *-g.553* (NGB 111441), *-g.568* (NGB 111456), *-g.700* (NGB 111588), *-g.709* (NGB 111597), *-g.710* (NGB 111598) in Foma, *-g.1026* (NGB 111914) in Carlsberg II (CIho 10114, NGB 5085) (5); *cer-g.746* (NGB 111634), *-g.818* (NGB 111706), *-g.875* (NGB 111763) in Bonus, *-g.1033* (NGB 111921), *-g.1071* (NGB 111959) in Carlsberg II, *-g.1097* (NGB 111985), *-g.1116* (NGB 112004) in Kristina (NGB 1500, NGB 14661) (6); *cer-g.893* (NGB 111781), *-g.976* (NGB 111864) in Bonus, *-g.1172* (NGB 112060) in Kristina (7); *cer-g.1161* (NGB 117265), *-g.1169* (NGB 112057) in Kristina (8); *cer-g.1038* (NGB 111926) in Carlsberg II, *-g.1289* (NGB 112177) in Kristina, *-g.1332* (NGB 112220) in Bonus (9); *cer-g.1410* (NGB 112298), *-g.1451* (NGB 112339), *-g.1454* (NGB 112342) in Bonus (10); *cer-g.1495* (NGB 112383) in Bonus, *-g.1510* (NGB 112398) in Nordal (NGB 13680, NGB 4704), *-g.1736* (NGB 112549), *-g.1740* (NGB 112553), *-g.1741* (112554) in Bonus (11); *cer-g.1573* (NGB 112461) in Nordal (12).

Mutant used for description and seed stocks:

*cer-g.10* (GSHO 428, NGB 110894) in Bonus; *cer-g.10* in Bowman (PI 483237)\*6 (GSHO 1906); *cer-g.10* in Bowman\*7 (BW111, NGB 20517).

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Hereditas 61:327-337.

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Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:349-350.

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BGS 406, Eceriferum-I, *cer-1*

Stock number: BGS 406  
Locus name: Eceriferum-I  
Locus symbol: *cer-1*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3HL possibly (1); *cer-1.14* is associated with several groups of SNP markers in Bowman backcross-derived line, BW 116, the largest segment is from markers 1\_0681 to 2\_1362 (positions 247.13 to 255.13 cM) in 3H bins 15 to 16 of (1).

Description:

Surface wax coating on the spike is slightly reduced (wax code + ++ ++ ) (3). Identification of mutant plants is difficult in the Bowman backcrossed-derived progenies (2). Agronomic and morphological differences between the Bowman backcross-derived line for the *cer-1.14* mutant, BW116, and Bowman were not observed (2).

Origin of mutant:

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

Mutational events:

*cer-1.14* (NGB 110898, GSHO 433) in Bonus (PI 189763, NGB 14657) (3, 4).

Mutant used for description and seed stocks:

*cer-1.14* (NGB 110898, GSHO 433) in Bonus; *cer-1.14* in Bowman (PI 483237)\*3 (GSHO 2191); *cer-1.14* in Bowman\*4 (BW116, NGB 20522).

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Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:124.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:355.  
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BGS 408, Eceriferum-n, *cer-n*

Stock number: BGS 408  
Locus name: Eceriferum-n  
Locus symbol: *cer-n*

Previous nomenclature and gene symbolization:

Eceriferum-zm = *cer-zm* (16).

Glossy sheath 9 = *gs9* (5, 6).

Inheritance:

Monofactorial recessive (7), except *Cer-n.969* (12).

Located in chromosome 2HL (3, 17, 18); *gsh9.al* is about 8.8 cM distal from the *eog1* (elongated outer glume 1) locus (1); about 23.3 cM proximal from the *vrs1* (six-rowed spike 1) locus (1, 5); *cer-n.20* is associated with SNP markers 2\_0674 to 1\_1533 (positions 85.71 to 141.56 cM) in 5H bins 07 to 10 of the Bowman backcrossed-derived line BW118 (2); *gsh9.al* is associated with SNP markers 1\_1493 to 2\_0734 (positions 76.05 to 122.02 cM) in 2H bins 06 to 09 of the Bowman backcrossed-derived line BW412 (2).

Description:

Mutants appear to lack surface wax coating on the spike, and surface wax on the leaf sheath may be reduced or absent (wax codes - - ++ and - +/- ++ ) (7, 16). The original stock *cer-n.20* has a translocation breakpoint that is closely linked to the gene (7).

The agronomic and morphological attributes of the Bowman backcross-derived line for *cer-n.20*, BW118, were similar to Bowman. BW118 did not exhibit the reduced seed set trait frequently associated with a translocation (4). However, the Bowman backcross-derived line for *gsh9.ad*, BW412, had variable kernel weights, slightly less to much less as compared to Bowman, and its grain yields were 20 to 40% of those recorded for Bowman (4).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763, NGB 14657) (7).

Mutational events:

*cer-n.20* (trans) (NGB 110904, GSHO 435), *-n.26* (NGB 110910), *-n.53* (NGB 110937), *-n.101* (NGB 110986) in Bonus (PI 189763, NGB 14657) (7); *cer-n.86* (*cer-zm.86*) (NGB 110970), *cer-n.731* (*cer-zm.731*) (NGB 111619) in Bonus (8, 9, 16, 17); *cer-n.93* (trans) (NGB 110977), *-n.97* (NGB 110981) in Bonus, *-n.211* (NGB 111098), *-n.236* (NGB 111123), *-n.289* (NGB 111176) in Foma (CIho 11333, NGB 14659) (16); *cer-n.155* (NGB 111041), *-n.162* (NGB 111048), *-n.163* (NGB 111049), *-n.170* (NGB 111056) in Bonus, *-n.422* (NGB 111310), *-n.529* (NGB 111417), *-n.547* (NGB 111435), *-n.562* (NGB 111450), *-n.580* (NGB 111468), *-n.599* (NGB 111487), *-n.666* (NGB 111554) in Foma, *-n.715* (NGB 111603) in Bonus, *-n.1077* (NGB 111965) in Carlsberg II (CIho 10114, NGB 5085) (8); *cer-n.608* (NGB 111496) in Foma, *-n.829* (NGB 111717), *-n.877* (NGB 111765), *-n.880* (NGB 111768) in Bonus, *-n.1085* (NGB 111973), *-n.1139* (NGB 112027) in Kristina (NGB 1500, NGB14661) (9); *cer-n.624* (NGB 111512), *-n.926* (NGB 111814), *-n.948* (NGB 111836), *-n.954* (NGB 111842), *-n.957* (NGB 111845) in Bonus, *-n.1173* (NGB 112061) in Kristina (10); *cer-n.963* (NGB 111851), *-n.985* (NGB 111873) in Bonus, *-n.1133* (NGB 112021) in Kristina (11); *Cer-n.969* (NGB 111857), *cer-n.97* (NGB 110981) in Bonus, *-n.1296* (NGB 112184), *-n.1303* (NGB 112191), *-n.1307* (NGB 112195) in Kristina, *-n.1337* (NGB 112225) in Bonus (12); *cer-n.998* (NGB 111886) in Bonus, *-n.1093* (NGB 111981) in Kristina, *-n.1391* (NGB 112279), *-n.1437* (NGB 112325), *-n.1449* (NGB 112337), *-n.1456* (NGB 112344) in Bonus (13); *cer-n.996* (NGB 111884), *-n.1438* (NGB 112326) in Bonus, *-n.1700* (NGB 112513) in Kristina, *-n.1787* (NGB 117335) in Bonus (14); *cer-n.1765* (NGB 112580) in Bonus (15); *gsh9.al* (OUM029, GSHO 1761) in

Akashinriki (PI 467400, OUJ659) (5).

Mutant used for description and seed stocks:

*cer-n.20* (GSHO 435, NGB 110904) in Bonus; *gsh9.al* (GSHO 1761, OUM029) in Akashinriki; *cer-n.20* in Bowman (PI 483237)\*8 (GSHO 1893; BW118, NGB 20524); *gsh9.al* in Bowman\*7 (GSHO 1894; BW412, NGB 20645).

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9. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. *Barley Genet. Newsl.* 3:110-112.
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Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:120.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:357-358.

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BGS 411, Eceriferum-r, *cer-r*

Stock number: BGS 411  
Locus name: Eceriferum-r  
Locus symbol: *cer-r*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL (1); about 4.3 cM distal from the *uzu1* (*uzu 1*) locus (11, 12, 13, 14); *cer-r.19* is associated with SNP markers 1\_0601 to 1\_0047 (positions 71.29 to 119.1 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW121 (1); likely in 3H bin 06.

Description:

Surface wax coating on the spike appears greatly reduced or absent, while the wax coating on the leaf sheath and stem appears greatly reduced (wax code +/- +++) (4, 10). The wax coating on the spike appeared absent in the Bowman backcross-derived line for *cer-r.19*, BW121 (3). Except for surface waxes, BW121 was similar to Bowman for agronomic and morphological traits (3).

Origin of mutant:

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

Mutational events:

*cer-r.19* (NGB 110903, GSHO 439) in Bonus (PI 189763, NGB 14657) (4, 5); *cer-r.127* (NGB 111012) in Bonus (5, 10); *cer-r.181* (NGB 111067) in Bonus (5); *cer-r.231* (NGB 111118) in Foma (CIho 11333, NGB 14659) (5, 10); *cer-r.801* (NGB 111689) in Bonus (6); *cer-r.773* (NGB 111661) in Bonus (7); *cer-r.911* (NGB 111799) in Bonus, -*r.1300* (NGB 112188) in Kristina (NGB 1500, 14661) (8); *cer-r.1290* (NGB 112178) in Kristina (9).

Mutant used for description and seed stocks:

*cer-r.19* (GSHO 439, NGB 110903) in Bonus; *cer-r.19* in Bowman (PI 483237)\*7 (GSHO 1977, BW121, NGB 20527).

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Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:129.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:361.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:145-146.

BGS 414, Eceriferum-v, *cer-v*

Stock number: BGS 414  
Locus name: Eceriferum-v  
Locus symbol: *cer-v*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HS (8); near the *fch15* (chlorina seedling 15) locus (9); *cer-v.49* is associated with SNP markers 2\_1187 to 2\_1338 (positions 51.62 to 74.97 cM) in 2H bins 05 to 06 of the Bowman backcross-derived line BW124 (1), likely in 2H bin 06.

Description:

Surface wax coating on the spike appears absent or greatly reduced (wax code +/- ++ ++). Pointed lateral spikelets are observed in the original stock, but not in the Bowman backcross-derived line (2). The vigor of the Bowman backcross-derived line for *cer-v.49*, BW124, appeared reduced somewhat (2). Compared to Bowman, BW124 plants were about 10% shorter and had slightly shorter awns. Kernel weights for BW124 were 10 to 15% lower than those of Bowman; and grain yields were less than half (2).

Origin of mutant:

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

Mutational events:

*cer-v.49* (NGB 110933, GSHO 443) in Bonus (PI 189763, NGB 14657) (3); *cer-v.489* (NGB 111377), *-v.590* (NGB 111478) in Foma (Clho 11333, NGB 14659) (4); *cer-v.515* (NGB 111403) in Foma (5); *cer-v.752* (NGB 111640) in Bonus (6); *cer-v.1434* (NGB 112322) in Bonus (7).

Mutant used for description and seed stocks:

*cer-v.49* (GSHO 443, NGB 110933) in Bonus; *cer-v.49* in Bowman (PI 483237)\*7 (GSHO 1895, BW124, NGB 20530).

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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:132.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:366.

U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:147-148.

BGS 417, Eceriferum-y, *cer-y*

Stock number: BGS 417  
Locus name: Eceriferum-y  
Locus symbol: *cer-y*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 1HS probably (1); *cer-y.72* is associated mainly with SNP markers 1\_0873 to 1\_0562 (positions 32.99 to 88.33 cM) in 1H bins 04 to 08 of the Bowman backcross-derived line BW131 (1).

Description:

Surface wax coating on the spike appears greatly reduced, and the wax coating on the leaf sheath and stem is reduced or normal (wax code + +/++ ++). The original *cer-y.72* stock showed semi-sterility (6). The Bowman backcross-derived line for *cer-y.72*, BW131, has normal fertility and surface wax on the leaf sheath and stem appears normal (wax code + ++ ++). BW131 plants were agronomically and morphologically similar to Bowman (2).

Origin of mutant:

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

Mutational events:

*cer-y.72* (NGB 110956, GSHO 446) in Bonus (PI 189763, NGB 14657) (3, 6); *cer-y.884* (NGB 111772) in Bonus (4); *cer-y.828* (NGB 111716) in Bonus (5).

Mutant used for description and seed stocks:

*cer-y.72* (GSHO 446, NGB 110956) in Bonus; *cer-y.72* in Bowman (PI 483237)\*5 (GSHO 2195); *cer-y.72* in Bowman\*6 (BW131, NGB 20537).

References:

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6. Lundqvist, U., P. von Wettstein-Knowles, and D. von Wettstein. 1968. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. II. *Hereditas* 59:473-504.

Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:135.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:368.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:149.

BGS 418, Eceriferum-z, *cer-z*

Stock number: BGS 418  
Locus name: Eceriferum-z  
Locus symbol: *cer-z*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HS (3); close to the *ant1* (anthocyanin-less 1) locus based on linkage drag (3); *cer-z.52* is not associated with any SNP markers in the Bowman backcross-derived line BW156 (1); likely located between SNP markers 1\_0726 and 1\_0346 (positions 75.21 to 82.82 cM, a gap with no heterogeneities between Bonus and Bowman) in 7H bins 05 to 06 of BW156 (2).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears absent (wax code - - ++). The original stock shows leaf streaks, late maturity, and semi-sterility (partial seed set) (4). The Bowman backcross-derived line has waxy nodes, normal maturity and fertility, and no leaf streaks (2). Kernels of the Bowman backcross-derived line for *cer-z.52*, BW156, were 5 to 10% lighter than those of Bowman. Grain yields of BW156 were about 60% those of Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763, NGB 14657) (4).

Mutational events:

*cer-z.52* (NGB 110936, GSHO 447) in Bonus (PI 189763, NGB 14657) (4, 5); *cer-z.74* (NGB 110958) in Bonus (5); *cer-z.113* (NGB 110998) in Bonus (5, 8); *cer-z.512* (NGB 111400) in Foma (Clho 11333, NGB 14659) (6); *cer-z.705* (NGB 111593), *-z.981* (NGB 111869), *-z.988* (NGB 111876), *-z.989* (NGB 111877), *-z.990* (NGB 111878) in Bonus (7).

Mutant used for description and seed stocks:

*cer-z.52* (GSHO 447, NGB 110936) in Bonus; *cer-z.52* in Bowman (PI 483237)\*7 (GSHO 1838, BW156, NGB 21988).

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. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
4. 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. 5:136.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:369.

U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:150-151.

BGS 423, Eceriferum-ze, *cer-ze*

Stock number: BGS 423  
Locus name: Eceriferum-ze  
Locus symbol: *cer-ze*

Previous nomenclature and gene symbolization:

Glossy seedling 5 = *gl5* (3, 4).

Inheritance:

Monofactorial recessive (4, 14).

Located in chromosome 7HS (4, 15); over 23.7 cM proximal from the *brh1* (brachytic 1) locus (4); *cer-ze.81* is associated with SNP markers 2\_0495 to 1\_0451 (positions 32.35 to 41.79 cM) in 7H bins 02 to 03 of the Bowman backcross-derived line BW161 (1); *glf5.e* is associated with SNP markers 2\_0495 to 2\_0758 (positions 32.35 to 41.79 cM) in 7H bins 02 to 03 of the Bowman backcross-derived line BW387 (1), likely in 7H bin 03.

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (14).

Concerning the chemical epicuticular wax composition, the reduction in the amount of surface wax is accompanied by a decrease in the size and morphological complexity of the wax bodies. The wax body structure is arranged in single, double, and triple finger-like forms (16). Plants of the Bowman backcross-derived line for *cer-ze.81*, BW161, occasionally showed slightly delayed heading, but delayed heading of the stock for *glf5.e*, BW387, was not observed. The grain yields of both BW161 and BW387 were about 3/4 of those for Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB 14657) (14).

Mutational events:

*cer-ze.81* (NGB 110965, GSHO 452), *-ze.145* (NGB 111031), *-ze.152* (NGB 111038) in Bonus (PI 189763, NGB 14657), *-ze.203* (NGB 111090), *-ze.247* (NGB 111134), *-ze.253* (NGB 111140), *-ze.298* (NGB 111185), *-ze.331* (NGB 111218), *-ze.333* (NGB 111220), *-ze.391* (NGB 111278), *-ze.392* (NGB 111279), *-ze.460* (NGB 111348), *-ze.506* (NGB 111394) in Foma (Clho 11333, NGB 14659) (6, 14); *cer-ze.179* (NGB 111065), *-ze.196* (NGB 111082), *-ze.660* (NGB 111548), *-ze.662* (NGB 111550), *-ze.694* (NGB 111582), *-ze.714* (NGB 111602), *-ze.725* (NGB 111613), *-ze.729* (NGB 111617), *-ze.736* (NGB 111624), *-ze.745* (NGB 111633) in Bonus, *-ze.584* (NGB 111472) in Foma (6); *cer-ze.620* (NGB 111508) in Foma, *-ze.816* (NGB 111704), *-ze.817* (NGB 111705), *-ze.824* (NGB 111712), *-ze.834* (NGB 111722), *-ze.864* (NGB 111752), *-ze.885* (NGB 111773) in Bonus, *-ze.1086* (NGB 111974) in Kristina (NGB 1500, NGB 14661) (7); *cer-ze.621* (NGB 111509) in Foma, *-ze.638* (NGB 111526), *-ze.918* (NGB 111808) in Bonus (8); *cer-ze.934* (NGB 111822) in Bonus, *-ze.1241* (NGB 112129), *-ze.1274* (NGB 112174) in Kristina (9); *cer-ze.1160* (NGB 112048), *-ze.1297* (NGB 112185), *-ze.1298* (NGB 112186), *-ze.1299* (NGB 112187) in Kristina, *-ze.1322* (NGB 112210) in Bonus (10); *cer-ze.1349* (NGB 112237), *-ze.1350* (NGB 112238), *-ze.1367* (NGB 112255), *-ze.1380* (NGB 112268), *-ze.1392* (NGB 112280), *-ze.1417* (NGB 112305), *-ze.1422* (NGB 112310), *-ze.1432* (NGB 112320) in Bonus (11); *cer-ze.1781* (NGB 112596), *-ze.1782* (NGB 112597), *-ze.1804* (NGB 117352), *-ze.1809* (NGB 117357), *-ze.1814* (NGB 117362), *-ze.1815* (NGB 117363) in Bonus (12); *cer-ze.1817* (NGB 117365) in Bonus, *-ze.1832* (NGB 117380), *-ze.1834* (NGB 117382), *-ze.1836* (NGB 117384), *-ze.1838* (NGB 117386), *-ze.1840* (NGB 117388), *-ze.1842* (NGB 117390), *-ze.1845* (NGB 117393), *-ze.1846* (NGB 117394), *-ze.1848* (NGB 117396), *-ze.1849* (NGB 117397), *-ze.1851* (NGB 117399), *-ze.1854* (NGB 117402), *-ze.1855* (NGB 117403), *-ze.1856* (NGB 117404), *-ze.1869* (NGB 117417)

in Sv 79353 (13); *glf5.e* in Kirin Choku 1 (Kmut 239, OUM294, GSHO 1753) (4, 5).

Mutant used for description and seed stocks:

*cer-ze.81* (GSHO 452, NGB 110965) in Bonus; *cer-ze.81* in Bowman (PI 483237)\*6 (GSHO 1831); *cer-ze.81* in Bowman\*7 (BW161, NGB 21993); *glf5.e* in Bowman\*7 (GSHO 1830, BW387, NGB 20625).

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. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley VI. Ten mutant genes located on chromosomes 1 to 7, except 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:227-250.
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Prepared:

U. Lundqvist and P. von Wettstein-Knowles. 1975. *Barley Genet. Newsl.* 5:141.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:374-375.

U. Lundqvist and J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:514-515.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:152-153.

BGS 432, Eceriferum-zo, *cer-zo*

Stock number: BGS 432  
Locus name: Eceriferum-zo  
Locus symbol: *cer-zo*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3HS (1); *cer-zo.229* is associated with SNP markers 2\_1197 to 1\_0601 (positions 19.75 to 71.29 cM) in 3H bins 03 to 05 of the Bowman backcross-derived line BW170 (1).

Description:

Surface wax coating on the spike appears absent in the original stock (wax code - ++ ++ ) (5). Pointed lateral spikelets were observed in the original stock (5), but not in the Bowman backcross-derived line (2). Only reduced surface wax coating on the spike occurs in the Bowman backcross-derived line (wax code + ++ ++ ) (2). No significant agronomic differences were observed between the Bowman backcross-derived line for *cer-zo.229*, BW170, and Bowman, except BW170 tended to yield less grain (2).

Origin of mutant:

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

Mutational events:

*cer-zo.229* (NGB 111116, GSHO 462), *-zo.352* (NGB 111239) in Foma (CIho 11333, NGB 14659) (3, 5); *cer-zo.565* (NGB 111453) in Foma (3); *cer-zo.718* (NGB 111606), *-zo.882* (NGB 111770) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*cer-zo.229* (GSHO 462, NGB 111116) in Foma; *cer-zo.229* in Bowman (PI 483237)\*3 (GSHO 2201); *cer-zo.229* in Bowman\*5 (BW170, NGB 22002).

References:

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5. Lundqvist, U., P. von Wettstein-Knowles, and D. von Wettstein. 1968. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. II. *Hereditas* 59:473-504.

Prepared:

U. Lundqvist, U. 1975. *Barley Genet. Newsl.* 5:150.

Revised:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:384.  
U. Lundqvist and J.D. Franckowiak. 2013. *Barley Genet. Newsl.* 43:148.  
U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:154.

BGS 435, Eceriferum-zr, *cer-zr*

Stock number: BGS 435  
Locus name: Eceriferum-zr  
Locus symbol: *cer-zr*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL (1); *cer-zr.260* is associated with SNP markers 2\_0134 to 1\_1200 (positions 163.74 to 180.02 cM) in 5H bin 10 of the Bowman backcross-derived line BW173 (1), in 5H bin 10.

Description:

Surface wax coating on the spike appears reduced or absent (wax code +/- ++ ++)  
(4). In the Bowman backcross-derived line for *cer-zr.260*, BW173, the wax coating appeared absent on the spike and nodes and may be reduced on stem and leaf sheath (wax code - +/++ ++)  
(2). Besides surface waxes, BW173 and Bowman were morphologically and agronomically similar (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333, NGB14659) (4).

Mutational events:

*cer-zr.260* (NGB 111147, GSHO 1525) in Foma (CIho 11333, NGB14659) (3, 4); *cer-zr.528* (NGB 111416) in Foma (3).

Mutant used for description and seed stocks:

*cer-zr.260* (GSHO 1525, NGB 111147) in Foma; *cer-zr.260* in Bowman (PI 483237)\*3 (GSHO 2203); *cer-zr.260* in Bowman\*6 (BW173, NGB 22005).

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., P. von Wettstein-Knowles, and D. von Wettstein. 1968. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. II. *Hereditas* 59:473-504.

Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:153.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:387.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:155.

BGS 436, Eceriferum-zs, *cer-zs*

Stock number: BGS 436  
Locus name: Eceriferum-zs  
Locus symbol: *cer-zs*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Location is unknown; large chromosomal segments from the donor parent were retained in chromosomes 2H, 3H, and 5H in the Bowman backcross-derived line for *cer-zs.467*, BW174 (1).

Description:

Surface wax coating on the spike is reduced (wax code + ++ ++), maturity is delayed, and vigor is somewhat reduced (4). Compared to Bowman, plants of the Bowman backcross-derived line for *cer-zs.467*, BW174, headed about three days later and had 2 to 5 more kernels per spike. Kernel weights for BW174 averaged 10% less than those for Bowman. The grain yields for BW174 were about 2/3 of those for Bowman (2).

Origin of mutant:

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

Mutational events:

*cer-zs.467* (NGB 111355, GSHO 1526), *-zs.474* (NGB 111362), *-zs.475* (NGB 111363) in Foma (CIho 11333, NGB 14659) (4); *cer-zs.594* (NGB 111482) in Foma (5).

Mutant used for description and seed stocks:

*cer-zs.467* (GSHO 1526, GSHO 2204, NGB 111355) in Foma; *cer-zs.467* in Bowman (PI 483237)\*3 (BW174, NGB 22006).

References:

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5. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. *Barley Genet. Newsl.* 7:92-96.

Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:154.

Revised:

U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:388.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:156.

BGS 437, Eceriferum-zt, *cer-zt*

Stock number: BGS 437  
Locus name: Eceriferum-zt  
Locus symbol: *cer-zt*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Location in chromosome 2HS (1); about 16.8 distal from SSR marker Bmac0134 in 2H bin 01 (1); *cer-zt.389* is associated with SNP markers 1\_0326 to 1\_0399 (positions 16.91 to 66.78 cM) in 2H bins 02 to 05 of the Bowman backcross-derived line BW175 (2), likely in 2H bin 02.

Description:

Surface wax coating on the spike appears slightly reduced (wax code + ++ ++ ) (5). The reduction in the surface wax seemed greater in plants selected from backcrosses to Bowman (wax code +/- ++ ++ ) (3). Except for the difference in surface waxes, plants of the Bowman backcross-derived line for *cer-zt.389*, BW175, and Bowman were similar (3).

Origin of mutant:

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

Mutational events:

*cer-zt.389* (NGB 111276, GSHO 1527), *-zt.479* (NGB 111367) in Foma (CIho 11333, NGB 14659) (4).

Mutant used for description and seed stocks:

*cer-zt.389* (GSHO 1527, NGB 111276) in Foma; *cer-zt.389* in Bowman (PI 483237)\*2 (GSHO 2205); *cer-zt.389* in Bowman\*5 (BW175, NGB 22007).

References:

1. Dahleen, L.S., and J.D. Franckowiak. 2006. SSR linkages to eight additional morphological marker traits. *Barley Genet. Newsl.* 36:12-16.
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. Lundqvist, U. (Unpublished).
5. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. *Barley Genet. Newsl.* 1:97-102.

Prepared:

U. Lundqvist. 1975. *Barley Genet. Newsl.* 5:155.

Revised:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:389.  
U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:270.  
U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:157.

BGS 441, Eceriferum-zx, *cer-zx*

Stock number: BGS 441  
Locus name: Eceriferum-zx  
Locus symbol: *cer-zx*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3H (1); *cer-zx.100* is associated largely with SNP markers 1\_0728 to 2\_0523 (positions 96.85 to 173.82 cM) in 3H bins 06 to 11 of the Bowman backcross-derived line BW179 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears reduced (wax code + + ++ ) (4). The only noted difference between the Bowman backcross-derived line for *cer-zx.100*, BW179, was the reduction in surface waxes on the spike and leaf sheath (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-zx.100* (NGB 110984, GSHO 1531) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

*cer-zx.100* (GSHO 1531, NGB 110984) in Bonus; *cer-zx.100* in Bowman (PI 483237)\*2 (GSHO 2209); *cer-zx.100* in Bowman\*5 (BW179, NGB 22011).

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.* 5:159.

Revised:

U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:393.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:158.

BGS 443, Eceriferum-zz, *cer-zz*

Stock number: BGS 443  
Locus name: Eceriferum-zz  
Locus symbol: *cer-zz*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Chromosomal location is unknown (1); *cer-zz.615* is associated with SNP markers from its donor in many chromosomes, but the largest ones are in chromosomes 3HL, 6H, and 7HS (1) in the Bowman backcrossed derived line BW181.

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (4). The Bowman backcross-derived line for *cer-zz.615*, BW181, was similar to Bowman, except kernels were slightly heavier (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (CIho 11333, NGB14659) (3).

Mutational events:

*cer-zz.615* (NGB 111503, GSHO 1533) in Foma (CIho 11333, NGB14659) (4).

Mutant used for description and seed stocks.

*cer-zz.615* (GSHO 1533, NGB 111503) in Foma; *cer-zz.615* in Bowman (PI 483237)\*2 (GSHO 2210); *cer-zz.615* in Bowman \*4 (BW181, NGB 22013).

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.* 5:161.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:395.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:159.

BGS 449, Eceriferum-yf, *cer-yf*

Stock number: BGS 449  
Locus name: Eceriferum-yf  
Locus symbol: *cer-yf*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7H (1); *cer-yf.652* is associated with SNP markers 1\_0394 to 1\_0531 (positions 107.44 to 116.68 cM) in 7H bin 07 of the Bowman backcross-derived line BW137 (1), near the centromere in 7H bin 07.

Description:

Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (4). ). Plants of the Bowman backcross-derived line for *cer-yf.652*, BW137, had slightly pale green leaf blades, headed 3 to 5 days later, and had 2 to 5 more kernels per spike (2). were slightly shorter than Bowman. Kernels of BW137 were 10 to 20% lighter, and grain yields were 1/2 to 2/3 of those for Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-yf.652* (NGB 111540, GSHO 1539), *-yf.804* (NGB 111692) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*cer-yf.652* (GSHO 1539, NGB 111540) in Bonus; *cer-yf.652* in Bowman (PI 483237)\*3 (GSHO 2212); *cer-yf.652* in Bowman\*5 (BW137, NGB 20543).

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.* 5:167.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:401.

U. Lundqvist. 2007. *Barley Genet. Newsl.* 37:271.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:160.

BGS 450, Eceriferum-yg, *cer-yg*

Stock number: BGS 450  
Locus name: Eceriferum-yg  
Locus symbol: *cer-yg*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosomes 7HS (1); based on linkage drag with the *ant1* (anthocyanin-less 1) locus (3); *cer-yg.1014* is associated with SNP markers 1\_0576 to 2\_1270 (positions 54.30 to 93.97 cM) in 7H bins 05 to 06 and with SNP markers 2\_1495 to 1\_0754 (positions 160.37 to 190.87 cM) in 3H bins 11 to 12 of the Bowman backcross-derived line BW138 (1).

Description:

Surface wax coating on the spike, leaf sheath, stem, and leaf blade appears absent (wax code - - -) (5). The Bowman backcross-derived line BW138 is semidwarf (3/4 normal), surface wax is present on the leaf blades (wax code - - ++), and surface wax appears absent on the nodes (2). Plants of the Bowman backcross-derived line for *cer-yg.1014*, BW138, were similar to Bowman, except they were slightly shorter and rachis internodes were slightly shorter (2).

Origin of mutant:

A diethyl sulfate induced mutant in Carlsberg II (Clho 10114, NGB 5085) (4).

Mutational events:

*cer-yg.1014* (NGB 111902, GSHO 1540) in Carlsberg II (Clho 10114, NGB 5085) (5).

Mutant used for description and seed stocks:

*cer-yg.1014* (GSHO 1540, NGB 111902) in Carlsberg II; *cer-yg.1014* in Bowman (PI 483237)\*5 (GSHO 1839); *cer-yg.1014* in Bowman\*7 (BW138, NGB 20544).

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. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
4. Lundqvist, U. (Unpublished).
5. 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.* 5:168.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:402.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:161.

BGS 453, Few roots 1

Stock number: BGS 453  
Locus name: Few roots 1  
Locus symbol: *fer1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants produce one to three seminal roots as six-day old seedlings while normal segregates produce four to nine seminal roots. Older plants grown in gravel do not develop a secondary root system (1). Older plants are phenotypically normal, but inclined to overturn or lodge easily (1).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bomi Abed (PI 43371, NGB 5096) (1).

Mutational events:

*fer1.a* (2076/04-10) in Bomi Abed (PI 43371, NGB 5096) (1).

Mutant used for description and seed stocks:

*fer1.a* (2076/04-10) in Bomi Abed.

References:

1. Linde-Laursen, I. Barley mutant with few roots. Barley Genet. Newsl. 7:43-45.

Prepared:

I. Linde-Laursen. 1978. Barley Genet. Newsl. 8:162.

Revised:

J.D. Franckowiak and U. Lundqvist. 2014. Barley Genet. Newsl. 44:162.

BGS 462, Yellow streak 3, *yst3*

Stock number: BGS 462  
Locus name: Yellow streak 3  
Locus symbol: *yst3*

Previous nomenclature and gene symbolization:

Yellow streak *c* = *yst,,c* (4).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 3HS (3); linked to the *btr2* (non-brittle rachis 2) locus based on linkage drag (3); trisomic analyses of the *yst3* locus have not been successful (5, 6, 7); *yst3.c* is associated with SNP markers 2\_1101 to 2\_0704 (positions 74.51 to 98.41 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW926 (1).

Description:

Yellow streaks of variable width and number develop in the leaves, stems, and spikes of homozygous plants. Some plants are almost entirely yellow, similar to chlorina plants. Penetrance is 100%, but expressivity is highly variable and finding streaks may require careful observation. Colder environments increase the number and width of the yellow streaks (2). Plants of the Bowman backcross-derived line for *yst3.c*, BW926, headed 3 to 4 days later than Bowman. Spikes had about 3 more kernels and kernel weight were about 10% lower, 48 vs. 55 mg. The grain yields for BW926 were 40 to 60% of the Bowman yields (2).

Origin of mutant:

A spontaneous mutant in Lion (CIho 923) (4).

Mutational events:

*yst3.c* (GSHO 48) in Lion (CIho 923) (4).

Mutant used for description and seed stocks:

*yst3.c* (GSHO 48) in Lion; *yst3.c* in Bowman (PI 483237)\*6 (GSHO 1939); *yst3.c* in Bowman\*7 (BW926, NGB 22355).

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. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
4. Singh, R.J., and T. Tsuchiya. 1973. Allelism testing among three yellow streak mutants. *Barley Genet. Newsl.* 3:54-55.
5. Tsuchiya, T., and J.V. Alanko. 1976. Genetic studies of two mutations by means of primary trisomic analysis. *Barley Genet. Newsl.* 6:84-85.
6. Tsuchiya, T., and A. Hang. 1979. Telotrisomic analysis of *yst3* and *i* in barley. *Barley Genet. Newsl.* 9:106-108.
7. Tsuchiya, T., and A. Shahla. 1982. Primary trisomic analysis of the gene *yst3* in barley. *Barley Genet. Newsl.* 12:31-32.

Prepared:

Tsuchiya, T. 1984. *Barley Genet. Newsl.* 14:99.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:409.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:163.

BGS 463, Gigas 1, *gig1*

Stock number: BGS 463  
Locus name: Gigas 1  
Locus symbol: *gig1*

Previous nomenclature and gene symbolization:

Female sterile = *sf* (4, 6).

Gigas = *gig* (8).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 2HL possibly (5, 6, 9, 10); a possible linkage drag association with the *Gth1* (Toothed lemma 1) locus in chromosome 2H was noted (3); *gig1.a* is associated with SNP markers 1\_0780 to 1\_0085 (positions 189.37 to 247.86 cM) in 2H bins 12 to 14 of the Bowman backcross-derived line BW381 (1).

Description:

Culm length and diameter, leaves, spikes, and glumes are greater than the control; awns are shorter than the control; leaf blades are dark green; spikes are lax; spikes, culms, and leaf sheaths have a heavy wax coating (7). Anther development is good, but the stigma has few hairs and seed set is poor (4, 7). Stigma hairs were few, and selfed seed set was 10 to 15%. Hand pollination increased seed set (2). In the Bowman backcross-derived line for *gig1.a*, BW381, plants were slightly shorter and awns were considerably shorter (8 vs. 12 cm) compared to Bowman. The surface wax coating of BW381 is abnormally heavy. Lemma were large and long and average kernel length was 12.7 vs. 9.4 mm. Kernel width was slightly reduced, 3.59 vs. 3.84 mm, and kernel weights were 70 to 85% of those for Bowman. Grain yields of BW381 were reduced to only 15 to 30% of those for Bowman and the test weight was slightly less than 1/2 of that for Bowman (2).

Origin of mutant:

A spontaneous mutant in a population from the cross Montcalm//Galore/Daples (GB96) (4); an X-ray induced mutant in Tochigi Golden Melon (OUJ808) (7, 8).

Mutational events:

*gig1.a* (Kmut 72, GSHO 1650) in Tochigi Golden Melon (OUJ808) (7, 8); *gig1.b* in Montcalm//Galore/Daples (4, 8).

Mutant used for description and seed stocks:

*gig1.a* (GSHO 1650) in Tochigi Golden Melon; *gig1.a* in Bowman (PI 483237)\*7 (GSHO 1924, BW381, NGB 20620).

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. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
4. Harvey, B.L., E. Reinbergs, and B.H. Somaroo. 1968. Inheritance of female sterility in barley. *Can. J. Plant Sci.* 48:417-418.
5. Shim, J.W., E. Furst, and T. Tsuchiya. 1983. Primary trisomic analysis of a mutant "gigas" in barley. *Barley Genet. Newsl.* 13:49.
6. Shim, J.W., A. Shahla, and T. Tsuchiya. 1984. Additional information on the primary trisomic analysis of *sf* (female sterile or gigas) in barley. *Barley Genet. Newsl.* 14:42-43.
7. Tsuchiya, T. 1962. Annual report on breeding of malting barley. *Kihara Inst. Biol.*

Res., Japan. 28 p. with 8 tables, Mimeo.

8. Tsuchiya, T. 1975. Allelic relationships of some morphological and chlorophyll mutants in barley. *Barley Genet. Newsl.* 5:64-67.

9. Tsuchiya, T., and R.L. Haines. 1975. Trisomic analysis of nine mutant genes in barley. *Barley Genet. Newsl.* 5:67-69.

10. Wang, S. 1992. Telotrismic analysis of the mutant *gigas (gig)* in barley. *Barley Genet. Newsl.* 21:76-77.

Prepared:

T. Tsuchiya. 1985. *Barley Genet. Newsl.* 15:88 as BGS 460, *Gigas, gig*.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:410.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:164-165.

BGS 501, Male sterile genetic 38, *msg38*

Stock number: BGS 501  
Locus name: Male sterile genetic 38  
Locus symbol: *msg38*

Previous nomenclature and gene symbolization:

Male sterile *jl* = *msg,,jl* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3HL (3); *msg38.jl* is associated with SNP markers 2\_1533 to 1\_0728 (positions 67.01 to 96.85 cM) in 3H bins 05 to 06 of Bowman backcross-derived line BW574 (1).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3).

Stamens - anthers nearly normal in size, but without stomium, filament elongates (3).

Origin of mutant:

A spontaneous mutant in Ingrid (Clho 10083, NGB 2671) (3).

Mutational events:

*msg38.jl* (MSS517, GSHO 2390) in Ingrid (Clho 10083, NGB 2671) (2, 3).

Mutant used for description and seed stocks:

*msg38.jl* (GSHO 2390, MSS517) in Ingrid; *msg38.jl* in Bowman (PI 483237)\*7 (GSHO 2304, BW 574, NGB 23437).

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., and E.A. Hockett. 1988. Identification of three new loci which control male sterility of barley. *Barley Genet. Newsl.* 18:11-13.
3. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:105.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:427.

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:166.

BGS 524, Eceriferum-yk, *cer-yk*

Stock number: BGS 524  
Locus name: Eceriferum-yk  
Locus symbol: *cer-yk*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HL (1); *cer-yk.627* is associated with SNP markers 2\_0385 to 1\_0861 (positions 152.29 to 183.9 cM) in 7H bins 09 to 11 of the Bowman backcross-derived line BW142 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears reduced (wax code + +++) (4). The original stock has narrow leaves, a lax spike, and extra wax coating on the kernels. Plants of the Bowman backcross-derived line BW142 seemed to lack surface wax on the nodes (glossy node) (2). Compared to Bowman, plants of the Bowman backcross-derived line for *cer-yk.627*, BW142, are 10 to 15% shorter and rachis internodes were slightly longer. BW142 had slightly narrower leaf blades and kernels. Kernel weights were 10 to 15% less and grain yields were 30 to 50% lower than those for Bowman (2).

Origin of mutant:

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

Mutational events:

*cer-yk.627* (NGB 111515, GSHO 1544) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*cer-yk.627* (GSHO 1544, NGB 111515) in Bonus; *cer-yk.627* in Bowman (PI 483237)\*4 (GSHO 2215); *cer-yk.627* in Bowman\*7 (BW142, NGB 20548).

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.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. *Barley Genet. Newsl.* 12:169-172.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:451.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:167.

BGS 528, Eceriferum-yo, *cer-yo*

Stock number: BGS 528  
Locus name: Eceriferum-yo  
Locus symbol: *cer-yo*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 4HS most likely (1); the largest donor parent chromosomal segment associated with *cer-yo.647* has SNP markers 2\_0145 to 2\_0210 (positions 26.58 to 38.91 cM) in 4H bins 02 to 04 of the Bowman backcross-derived line BW146 (1).

Description:

Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (4). The original stock in Bonus exhibited a high level of sterility. Seedlings of the original stock and the Bowman backcross-derived line have slightly pale green color (2). Bowman and the Bowman backcross-derived line for *cer-yo.647*, BW146, were agronomically similar except the BW146 kernels were slightly lighter (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-yo.647* (NGB 111535, GSHO 1548) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*cer-yo.647* (GSHO 1548, NGB 111535) in Bonus; *cer-yo.647* in Bowman (PI 483237)\*3 (GSHO 2219); *cer-yo.647* in Bowman\*4 (BW146, NGB 20552).

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. 1979. Stock list for the eceriferum mutants V. *Barley Genet. Newsl.* 9:135-137.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:455.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:168.

BGS 529, Eceriferum-yp, *cer-yp*

Stock number: BGS 529  
Locus name: Eceriferum-yp  
Locus symbol: *cer-yp*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HS most likely (1); *cer-yp.949* is associated with SNP markers 1\_0974 to 2\_0392 (positions 41.29 to 109.27 cM) in 5H bins 03 to 06 and with SNP markers 2\_1398 to 2\_0742 (positions 13.67 to 29.05 cM) in 3H bins 01 to 02 of the Bowman backcross-derived line BW147 (1).

Description:

Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (4). Leaf blades have a pale green color similar to that of some chlorina mutants (2). Compared to Bowman, the Bowman backcross-derived line for *cer-yp.949*, BW147, was 10 to 15% shorter and had 3 to 5 fewer kernels per spike. Kernels weighed about 10% less and grain yields averaged about 1/3 of those for Bowman (2).

Origin of mutant:

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

Mutational events:

*cer-yp.949* (NGB 111837, GSHO 1549), *-yp.955* (NGB 111843) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*cer-yp.949* (GSHO 1549, NGB 111837) in Bonus; *cer-yp.949* in Bowman (PI 483237)\*2 (GSHO 2220); *cer-yp.949* in Bowman\*5 (BW147, NGB 20553).

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. 1979. Stock list for the eceriferum mutants V. *Barley Genet. Newsl.* 9:135-137.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:456.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:169.

BGS 530, Eceriferum-yq, *cer-yq*

Stock number: BGS 530  
Locus name: Eceriferum-yq  
Locus symbol: *cer-yq*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5H probably (1); the Bowman backcross-derived line for *cer-yq.1246*, BW148, retained two large donor parent segments of chromosome 5H, one in each arm, based on SNP markers, and small segments in other chromosomes (1).

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (4). In the Bowman backcross-derived line for *cer-yq.1246*, BW148, the wax coating is reduced only on upper leaf blades (wax code ++ ++ +) (2). The phenotype associated with the *cer-yq.1246* was difficult to observe in progeny from crosses to Bowman; thus, BW148 represents only two crosses to Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500, NGB 14661) (3).

Mutational events:

*cer-yq.1246* (NGB 112134, GSHO 1550) in Kristina (NGB 1500, NGB 14661) (4).

Mutant used for description and seed stocks:

*cer-yq.1246* (GSHO 1550, NGB 112134) in Kristina; *cer-yq.1246* in Bowman (PI 483237)\*3 (GSHO 2221); *cer-yq.1246* in Bowman\*2 (BW148, NGB 20554).

References:

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

Prepared:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:457.  
U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:170.

BGS 531, Eceriferum-yr, *cer-yr*

Stock number: BGS 531  
Locus name: Eceriferum-yr  
Locus symbol: *cer-yr*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL (1); *cer-yr.492* is associated with SNP markers 1\_0622 to 1\_0477 (positions 158.46 to 173.49 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW149 (1).

Description:

Surface wax coating on the spike appears greatly reduced or absent, and surface wax coating on the leaf sheath and stem is reduced (wax code -/+ +++) (4). Nodes are glossy and appear to lack surface wax (2). Kernels of the Bowman backcross-derived line for *cer-yr.492*, BW149 were slightly smaller and lighter than those of Bowman. Except for surface waxes, BW 149 and Bowman were agronomically and morphologically in other characters similar (2).

Origin of mutant:

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

Mutational events:

*cer-yr.492* (NGB 111380, GSHO 1551) in Foma (CIho 11333, NGB 14659), *-yr.1418* (NGB 112306) in Bonus (PI 189763, NGB 14657) (4).

Mutant used for description and seed stocks:

*cer-yr.492* (GSHO 1551, NGB 111380) in Foma; *cer-yr.492* in Bowman (PI 483237)\*5 (BW149, NGB20555).

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.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. *Barley Genet. Newsl.* 15:89-93.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:458.

Revised:

U. Lundqvist and J.D. Franckowiak. 2013. *Barley Genet. Newsl.* 43:155.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:171.

BGS 532, Eceriferum-ys, *cer-ys*

Stock number: BGS 532  
Locus name: Eceriferum-ys  
Locus symbol: *cer-ys*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HL (1, 2); *cer-ys.680* is associated mainly with SNP markers 2\_0674 to 1\_1250 (positions 85.71 to 161.08 cM) in 2H bins 07 to 11 of the Bowman backcross-derived line BW150 (1).

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (4). The original stock has a lax spike. Plants of the Bowman backcross-derived line for *cer-ys.680*, BW150, headed one to two days later than Bowman, were about 5 cm taller, and had 2 to 4 more kernels per spike. Compared to Bowman, kernel weights for BW150 were variable, 10% less to slightly more. The grain yields of BW150 were often slightly more than those for Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-ys.680* (NGB 111568, GSHO 1552), *-ys.1352* (NGB 112240) in Bonus (PI 189763, NGB14657) (4); *cer-ys.1182* (NGB 117268), *-ys.1247* (NGB 112135) in Kristina (NGB 1500, NGB14661) (5); *cer-ys.1826* (NGB 117374) in Bonus (6).

Mutant used for description and seed stocks:

*cer-ys.680* (GSHO 1552, NGB 111568) in Bonus; *cer-ys.680* in Bowman (PI 483237)\*3 (GSHO 2222); *cer-ys.680* in Bowman\*5 (BW150, NGB 20556).

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:459.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:172.

BGS 537, Eceriferum-*yz*, *cer-yz*

Stock number: BGS 537  
Locus name: Eceriferum-*yz*  
Locus symbol: *cer-yz*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosomes 1H or 5H (1); *cer-yz.1452* is associated with SNP markers 2\_1067 to 1\_0520 (positions 3.18 to 82.35 cM) in 1H bins 01 to 08 and with SNP markers 1\_1048 to 2\_0713 (positions 46.35 to 101.69 cM) in 5H bins 03 to 06 of the Bowman backcross-derived line BW155 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem appears slightly reduced (wax code + + +) (4). The Bowman backcross-derived line for *cer-yz.1452*, BW155, and Bowman were agronomically similar except BW155 headed slightly later and its kernels were about 10% lighter (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-yz.1452* (NGB 112340, GSHO 1557), *-yz.1453* (NGB 112341) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

*cer-yz.1452* (GSHO 1557, NGB 112340) in Bonus; *cer-yz.1452* in Bowman (PI 483237)\*2 (GSHO 2226); *cer-yz.1452* in Bowman\*3 (BW155, NGB 21987).

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:464.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:173.

BGS 538, Eceriferum-xa, *cer-xa*

Stock number: BGS 538  
Locus name: Eceriferum-xa  
Locus symbol: *cer-xa*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosomes 2HL, 4H, or 5HL (1); *cer-xa.585* is associated with SNP markers 1\_0786 to 2\_0182 (positions 133.59 to 185.53 cM) in 2H bins 09 to 12, with SNP markers 1\_0221 to 1\_0829 (positions 29.67 to 107.76 cM) in 4H bins 02 to 07, and with SNP markers 1\_0845 to 1\_0869 (positions 217.82 to 264.33 cM) in 5H bins 11 to 13 of the Bowman backcross-derived line BW127 (1).

Description:

Surface wax coating on the leaf blade appears absent only on upper leaves (wax code ++ ++ -) (4). The Bowman backcross-derived line for *cer-xa.585*, BW127, appeared to have more surface on the leaf blades (wax code ++ ++ +) than the original mutant. Plants of line BW127 and Bowman were similar in other agronomic and morphological traits, except BW127 had slightly lighter kernels and yielded slightly more grain (2).

Origin of mutant:

A gamma-ray induced mutant in Foma (CIho 11333, NGB 14659) (3).

Mutational events:

*cer-xa.585* (NGB 111473, GSHO 1558) in Foma (CIho 11333, NGB 14659), *-xa.838* (NGB 111726) in Bonus (PI 189763, NGB14657), *-xa.1113* (NGB 112001) in Kristina (NGB 1500, NGB 14661) (4).

Mutant used for description and seed stocks:

*cer-xa.585* (GSHO 1558, NGB 111473) in Foma; *cer-xa.585* in Bowman (PI 483237)\*2 (GSHO 2227); *cer-xa.585* in Bowman\*3 (BW127, NGB 20533).

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:465.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:174.

BGS 539, Eceriferum-xb, *cer-xb*

Stock number: BGS 539  
Locus name: Eceriferum-xb  
Locus symbol: *cer-xb*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 4H (1); *cer-xb.943* is associated with SNP markers 1\_0394 to 1\_0531 (positions 107.44 to 116.68 cM) in 4H bin 07 of the Bowman backcross-derived line BW128 (1), in 4H bin 07.

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++ ) (4). In the Bowman backcross-derived line for *cer-xb.943*, BW128, peduncles appeared to lack surface wax (2). Compared to Bowman, BW128 plants were slightly shorter and had slightly shorter rachis internodes. Kernels of BW128 were about 5% lighter and test weights were nearly 10% lower. Grain yields of BW128 were about 3/4 those for Bowman (2).

Origin of mutant:

An isopropyl methanesulfonate induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-xb.943* (NGB 111831, GSHO 1559) in Bonus (PI 189763, NGB14657), *-xb.1166* (NGB 112054) in Kristina (NGB 1500, NGB14661) (4).

Mutant used for description and seed stocks:

*cer-xb.943* (GSHO 1559, NGB 111831) in Bonus; *cer-xb.943* in Bowman (PI 483237)\*4 (GSHO 2228); *cer-xb.943* in Bowman\*6 (BW128, NGB 20534).

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. 1988. Stock list for the eceriferum mutants VIII. *Barley Genet. Newsl.* 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:466.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:175.

BGS 540, Eceriferum-xc, *cer-xc*

Stock number: BGS 540  
Locus name: Eceriferum-xc  
Locus symbol: *cer-xc*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 1H likely (1); *cer-xc.1371* is associated with SNP markers 2\_0479 to 2\_1126 (positions 0.54 to 110.10 cM) in 1H bins 01 to10 of Bowman backcross-derived line BW129 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem is reduced (wax code + + ++ ) (4). Plants of the Bowman backcross-derived line for *cer-xc.1371*, BW129, headed two to four later than Bowman and had kernels that were 5 to 10% lighter (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-xc.1371* (NGB 112259, GSHO 1560), *-xc.1457* (NGB 112345) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

*cer-xc.1371* (GSHO 1560, NGB 112259) in Bonus; *cer-xc.1371* in Bowman (PI 483237)\*2 (GSHO 2229); *cer-xc.1371* in Bowman\*4 (BW129, NGB 20535).

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. 1988. Stock list for the eceriferum mutants VIII. *Barley Genet. Newsl.* 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:467.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:176.

BGS 541, Eceriferum-xd, *cer-xd*

Stock number: BGS 541  
Locus name: Eceriferum-xd  
Locus symbol: *cer-xd*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4H or 5HL (1); *cer-xd.1455* is associated with donor parent SNP markers in two large segments, 2\_0289 to 2\_1332 (positions 69.62 to 112.64 cM) in 4H bins 05 to 07 and 2\_0884 to 1\_0310 (positions 210.59 to 286.68 cM) in 5H bins 11 to 15 of the Bowman backcross-derived line BW130 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem is reduced (wax code + + ++ ) (4). Plants of the Bowman backcross-derived line for *cer-xd.1455*, BW130, appeared to have extra surface wax on their nodes (2). BW130 plants headed up to 3 days later than Bowman and were about 10% shorter. Most of the height reduction was caused by short peduncles. Kernels of BW130 were slightly shorter and 10 to 20% lighter than those of Bowman. Grain yields of BW130 were about 2/3 of those for Bowman (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*cer-xd.1455* (NGB112343, GSHO 1561), *-xd.1492* (NGB 112380) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

*cer-xd.1455* (GSHO 1561, NGB 112343) in Bonus; *cer-xd.1455* in Bowman (PI 483237)\*2 (GSHO 2230); *cer-xd.1455* in Bowman\*4 (BW130, NGB 20536).

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. 1988. Stock list for the eceriferum mutants VIII. *Barley Genet. Newsl.* 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:468.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:177.

BGS 543, Intermedium spike-f, *int-f*

Stock number: BGS 543  
Locus name: Intermedium spike-f  
Locus symbol: *int-f*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 2HS or 3HL (1); *int-f.19* is associated with SNP markers 2\_0929 to 2\_1286 (positions 86.79 to 96.47 cM) in 2H bin 07 and with SNP markers 1\_0754 to 1\_1141 (positions 190.87 to 197.25 cM) in 3H bin 13 of the Bowman backcross-derived line BW424 (1).

Description:

The spike appears six-rowed, but the lateral spikelets are much smaller, less than half the size of the central spikelets. Lateral spikelets are pointed and often have short awns. Seed set occurs in the lateral spikelets in the upper third of the spike. The base of the spike has shortened rachis internodes and appears erectoides-like (5).

Average kernels of the Bowman backcross-derived line for *int-f.19*, BW424, were slightly smaller than Bowman kernels and weighed 15 to 20% less, 50 vs. 58 mg. Grain yields of BW424 were variable ranging from 1/3 to 3/4 of the Bowman yields (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (CIho 11333, NGB 14659) (5).

Mutational events:

*int-f.19* (NGB 115437, GSHO 1767) in Foma (CIho 11333, NGB 14659) (4, 5).

Mutant used for description and seed stocks:

*int-f.19* (NGB 115437, GSHO 1767) in Foma; *int-f.19* in Bowman (PI 483237)\*3 (GSHO 2270); *int-f.19* in Bowman\*6 (BW424, NGB 20657).

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. Gustafsson, Å., and U. Lundqvist. 1980. Hexastichon and intermedium mutants in barley. *Hereditas* 92:229-236.
5. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:469.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:178.

BGS 544, Intermedium spike-h, *int-h*

Stock number: BGS 544  
Locus name: Intermedium spike-h  
Locus symbol: *int-h*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5H (1); *int-h.42* is associated with SNP markers 2\_1324 to 2\_1075 (positions 47.4 to 104.7 cM) in 5H bins 02 to 06 of the Bowman backcross-derived line BW425 (1).

Description:

Lateral spikelets are enlarged and have an inconspicuously pointed apex, but they do not set seed. Induced mutants show early heading and have an elongated basal rachis internode. The spike appears lax with shortened rachis internodes at the base (3). The Bowman backcross-derived line is slightly shorter (5/6 normal) and produces extra spikelets (up to five fertile ones) at several rachis nodes in the lower half of the spike. Some double and occasionally triple kernels are formed likely caused by presence of more than one floret in certain spikelets (2). Plants of the Bowman backcross-derived line for *int-h.42*, BW425, varied across test locations from slightly taller than Bowman to 20% shorter. Kernels per spike ranged from 4 less to 6 more.. Kernels of BW425 were slightly shorter and thinner than Bowman kernels and weighed about 20% less, 47 vs. 58 mg. Grain yields of BW425 were 1/2 to 2/3 of those for Bowman (2).

Origin of mutant:

A neutron induced mutant in Kristina (NGB 1500, NGB14661) (3, 5).

Mutational events:

*int-h.42* (NGB 115460, GSHO 1768), *-h.43* (NGB 115461), *-h.44* (NGB 115462) in Kristina (NGB 1500, NGB14661) (3, 5); *int-h.83* (NGB 115501) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

*int-h.42* (NGB 115460, GSHO 1768) in Kristina; *int-h.42* in Bowman (PI 483237)\*5 (GSHO 2271); *int-h.42* in Bowman\*6 (BW425, NGB 20658).

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., and U. Lundqvist. 1980. Hexastichon and intermedium mutants in barley. *Hereditas* 92:229-236.
4. Lundqvist, U. (Unpublished).
5. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:470.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:179.

BGS 546, Intermedium spike-k, *int-k*

Stock number: BGS 546  
Locus name: Intermedium spike-k  
Locus symbol: *int-k*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7H (1); in the centromeric region closely linked to markers Bmag0217 and Bmac0162 in 7H bins 06 to 07 (1); *int-k.47* is associated with SNP markers 1\_0721 to 2\_0485 (positions 82.82 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcrossed-derived line BW427 (2).

Description:

The spike is short and dense in the original mutant. Lateral spikelets are enlarged and the apex is pointed, and they occasionally have short awns. Seed set does not occur in lateral spikelets and the central spikelets are semi-sterile (4). Plants of the original stock have a dense coating of surface waxes (3). In the Bowman backcross-derived line for *int-k.47*, BW427, plants appeared small and weak (about 3/4 normal height) and had short spikes (2 to 6 fewer spikelets), reduced awn length (4 vs. 12 cm), and very poor seed set. Awns of BW427 plants are semi-rough, but F1 hybrids with Bowman have semi-smooth awns (3). BW427 plants headed 1 to 2 days earlier than Bowman. The flag minus one leaf blades were shorter (14 vs. 19 cm) and narrower (0.6 vs. 0.8 cm) and had less surface area (84 vs. 152 cm<sup>2</sup>). BW427 kernels were short (8.6 vs. 9.4 mm) and narrow (3.3 vs. 3.8 mm) and weighed less (36 vs. 58 mg). Grain yields for BW427 were 1/4 to 1/3 of those for Bowman (3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500, NGB14661) (4).

Mutational events:

*int-k.47* (NGB 115465, GSHO 1770) in Kristina (NGB 1500, NGB14661) (4).

Mutant used for description and seed stocks:

*int-k.47* (GSHO 1770, NGB 115465) in Kristina; *int-k.47* in Bowman (PI 483237)\*7 (BW427, NGB 20660).

References:

1. Dahleen, L.S., and J.D. Franckowiak. 2006. SSR Linkages to eight additional morphological marker traits. *Barley Genet. Newsl.* 36:12-16.
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. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:472.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:279.  
J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:180.

BGS 547, Intermedium spike-m, *int-m*

Stock number: BGS 547  
Locus name: Intermedium spike-m  
Locus symbol: *int-m*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5HL (2); *int-m.85* is associated with SNP markers 2\_0988 to 2\_1138 (positions 247.08 to 274.74 cM) in 5H bins 13 to 14 of the Bowman backcross-derived line BW429 (2); *int-m.la* is associated with SNP markers 2\_0571 to 1\_1249 (positions 69.76 to 109.27 cM) in 5H bins 04 to 06 and with SNP markers 2\_1177 to 1\_0869 (positions 203.85 to 264.33 cM) in 5H bins 11 to 13 of the Bowman backcross-derived line BW430 (2), likely in 5H bin 13.

Description:

The spike is very short and has irregular rachis internode lengths. Lateral spikelets are enlarged and pointed, but they do not set seed. Spikelet density at the base of the spike is increased (5). Tillering of *int-m* plants is increased and heading is slightly earlier (5). Rachis internodes at the tip of the spike are very short, and the spike appears to have two or three fused or fasciated terminal spikelets (1, 3). Plants of the Bowman backcross-derived line for *int-m.85*, BW429, had more tillers, 13 vs. 26 (1). Combining the *int-m.85* and *cul2.b* (uniculm 2) mutants produced unculm plants having long spikes with fused or fasciated terminal spikelets (1). Spikes of the Bowman backcross-derived line for *int-m.85*, BW430, had slightly less than half as many kernels as Bowman spikes. The shorter spikes caused the awns of BW430 to extend 3 to 5 cm more beyond the upper most spikelet. Kernel of BW430 were 10 to 15% lighter than Bowman kernels. Grain yields of BW430 were about 1/3 of those for Bowman (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763, NGB14657) (4).

Mutational events:

*int-m.85* (NGB 115503, GSHO 1772) in Bonus (PI 189763, NGB14657) (4); *int-m.la* (GSHO 1773) in Lamont (PI 512036) (3).

Mutant used for description and seed stocks:

*int-m.85* (GSHO 1772, NGB 115503) in Bonus; *int-m.85* in Bowman (PI 483237)\*7 (GSHO 2273, BW429, NGB 20661); *int-m.la* from Lamont in Bowman (PI 483237)\*5 (GSHO 2274, BW430, NGB 20662).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unculm 2 (*cul2*) mutant. *Theor. Appl. Genet.* 106:846-857.
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. Lundqvist, U. (Unpublished).
5. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:473.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:280.

U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:181-182.

BGS 549, Long glume awn 1, *Lga1*

Stock number: BGS 549  
Locus name: Long glume awn 1  
Locus symbol: *Lga1*

Previous nomenclature and gene symbolization:

Long glume awn = *L* (4, 5).

Long outer glume = *Log* (3); this gene symbol was recommended by Helgason (3), but the symbol was already used for the *eog1* (elongated outer glume 1) gene (6).

Inheritance:

Monofactorial dominant (3, 4).

Located in chromosome 7HS (1); *Lga1.a* is associated with SNP markers 1\_0838 to 1\_0576 (positions 49.53 to 54.30 cM) in 7H bin 04 of BW479 (1), in 7H bin 04.

Description:

In spikelets of plants with the dominant allele (*Lga1.a*), the glume (outer) plus its awn is much longer than the kernel. Heterozygotes have a glume awn of intermediate length. In the short glume awn phenotype (*lga1.b*), the glume length and width are unaltered, but the glume plus its awn are about the same length as the kernel (4, 5). Tsuchiya (6) reported that the glume awn length is 4 to 6 mm for the short type and 11 to 13 mm for the long type. Recessive alleles at the *eog1* locus (see BGS 57) produce an array of glume sizes, some of which have glumes phenotypically similar to those associated with the dominant allele at the *Lga1* locus. However, large glumes controlled by *eog1* alleles are wider than normal and show a recessive inheritance pattern (2). Besides long glume awns, plants of the Bowman backcross-derived line for *Lga1.a*, BW479, were similar to Bowman, except for heading two days later and being slightly taller in some environments (2).

Origin of mutant:

The short glume awn appears to be the mutant phenotype and occurs commonly in two-rowed cultivars of Occidental origin.

Mutational events:

*Lga1.a* in Guy Mayle (CIho 620, GSHO 835) (2, 3); *lga1.b* in Canadian Thorpe (PI 2710) (4, 5).

Mutant used for description and seed stocks:

*Lga1.a* in Guy Mayle (CIho 620, GSHO 835); *lga1.b* in Canadian Thorpe (GSHO 834); *lga1.b* from Hector (CIho 15514) is present in Bowman (PI 483237); *Lga1.a* from Akashinriki (OUJ659, PI 467400) mutant OUM113 in Bowman (PI 483237)\*8 (GSHO 2147, BW479, NGB 20707).

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. Helgason, S.B. 1964. Inheritance of glume characteristics in some barley crosses. p. 181-185. *In* S. Broekhuizen, G. Dantuma, H. Lamberts, and W. Lange (eds.) *Barley Genetics I. Proc. First Int. Barley Genet. Symp.*, Wageningen, 1963. Centre for Agricultural Publications and Documentation, Wageningen.
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6. Tsuchiya, T. 1974. Preliminary results on genetic studies of outer glume characters in barley. *Barley Genet. Newsl.* 4:76-78.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:475.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:183-184.

BGS 550, Breviaristatum-b, *ari-b*

Stock number: BGS 550  
Locus name: Breviaristatum-b  
Locus symbol: *ari-b*

Previous nomenclature and gene symbolization:

Breviaristatum-11 = *ari-11* (3, 4).

Inheritance:

Monofactorial recessive (4).

Location is unknown (1); *ari-b.11* is associated with SNP molecular markers in large DNA segments of chromosomes 3H, 4H, and 5H of the Bowman backcross-derived line BW039 (1).

Description:

Plants are semidwarf with reduced viability and fertility; leaves are broad, but shortened and lighter green in color; and awns are about 3/4 normal length. Growth is markedly retarded during warm seasons and relatively good during cool seasons (4). Development of reproductive organs is delayed and sterility makes the Bowman backcross-derived line for *ari-b.11*, BW039, difficult to maintain (2). In field experiments, BW039 plants were about 2/3 the height of Bowman and headed 4 to 6 days later. Rachis internodes were short, 3.2 vs. 4.7 mm, peduncles were short, 22 vs. 32 cm, and flag minus one leaf blades were short, 14 vs. 20 cm. Awns of BW039 were 1/2 to 3/4 normal length. Kernels of BW039 were short, 8.3 vs. 9.6 mm, narrow, 3.6 vs. 3.8 mm, and weighed 1/2 to 2/3 of those for Bowman. Grain yields of BW039 were almost none (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763, NGB14657) (4).

Mutational events:

*ari-b.11* (NGB 115856, GSHO 1649), *-b.13* (NGB 115859), *-b.17* (NGB 115863), *-b.19* (115866), *-b.29* (115877) in Bonus (PI 189763, NGB14657) (4); *ari-b.175* (NGB 115985), *-b.226* (NGB 116035), *-b.238* in Foma (CIho 11333, NGB14659) (4).

Mutant used for description and seed stocks:

*ari-b.11* (NGB 115856, GSHO 1649) in Bonus; *ari-b.11* in Bowman (PI 483237)\*3 (GSHO 2157, BW039, NGB 20447). (The NGB 20447 backcross derived line was segregating in the glasshouse in Lund and stored as a segregating stock).

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:476.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:185.

BGS 552, Breviaristatum-j, *ari-j*

Stock number: BGS 552  
Locus name: Breviaristatum-j  
Locus symbol: *ari-j*

Previous nomenclature and gene symbolization:

Breviaristatum-32 = *ari-32* (3, 4).

Inheritance:

Monofactorial recessive (4).

Chromosome location is unknown (1); *ari-j.32* is not associated with any SNP markers in the Bowman backcross-derived line BW048 (1).

Description:

Plants are semidwarf (3/4 of normal culm length) and awns are about 5/6 normal length. The peduncle is short and coiled or kinked, and as a result the spike rarely emerges above the flag leaf (4). Plants of the Bowman backcross-derived line for *ari-j.32*, BW048, headed 3 to 4 days later than Bowman. BW048 plants and their peduncles were about 2/3 normal length and awns were about 2 cm shorter. Compared to Bowman, kernels of BW048 were shorter and thinner and weighed less, 47 vs. 59 mg. Grain yields for BW048 were 1/2 to 2/3 of those for Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763, NGB14657) (4).

Mutational events:

*ari-j.32* (NGB 115881, GSHO 1658) in Bonus (PI 189763, NGB14657) (4); *ari-j.101* (NGB 115914) in Foma (CIho 11333, NGB 14659) (3); *ari-j.167* (NGB 115977) in Foma (4).

Mutant used for description and seed stocks:

*ari-j.32* (NGB 115881, GSHO 1658) in Bonus; *ari-j.32* in Bowman (PI 483237)\*5 (GSHO 2159); *ari-j.32* in Bowman\*8 (BW048, NGB 20456).

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:478.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:186.

BGS 553, Breviaristatum-k, *ari-k*

Stock number: BGS 553  
Locus name: Breviaristatum-k  
Locus symbol: *ari-k*

Previous nomenclature and gene symbolization:

Breviaristatum-504 = *ari-504* (3, 4).

Dearistatum-k = *ari-k* (3, 6).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 3H (1); *ari-k.280* is associated with SNP markers 1\_0672 to 2\_0063 (positions 58.66 to 133.92 cM) in 3H bins 05 to 08 of the Bowman backcrossed-derived line BW049 (1).

Description:

Awns often are normal in length, but they are dehiscent (dearistatum) at maturity. Variability in awn length is observed over environments and awns seem thinner than normal (4). Awns of plants grown in fall greenhouse nurseries at Fargo, North Dakota, USA, are very short and thread-like (2). The awns of the Bowman backcross-derived line for *ari-k*, BW049, extend about 9 cm beyond the tip of the spike while awns of Bowman extend about 12 cm. The rachis internodes of BW049 were slightly longer. Differences between BW049 and Bowman for kernel size and weight and for grain yield were not observed (2).

Origin of mutant:

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

Mutational events:

*ari-k.501* (NGB 116330, GSHO 1659), *-k.502* (NGB 116331), *-k.503* (NGB 116332), *-k.504* (NGB 116333) in Bonus (PI 189763, NGB 14657) (3).

Mutant used for description and seed stocks:

*ari-k.504* (NGB 116330, GSHO 1659) in Bonus; *ari-k.504* in Bowman (PI 483237)\*3 (GSHO 2160); *ari-k.504* in Bowman\*5 (BW049, NGB 20457).

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. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.
5. Lundqvist, U. (Unpublished).
6. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. *Hereditas* 62:25-96.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet Newsl.* 26:479.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:187.

BGS 558, Breviaristatum-q, *ari-q*

Stock number: BGS 558  
Locus name: Breviaristatum-q  
Locus symbol: *ari-q*

Previous nomenclature and gene symbolization:

Breviaristatum-271 = *ari-271* (3).

Inheritance:

Monofactorial recessive (3).

Location in chromosome 4H (1); *ari-q.280* is associated with SNP markers 2\_0289 to 1\_0588 (positions 69.62 to 130.65 cM) in 4H bins 05 to 09 of the Bowman backcrossed-derived line BW055 (1).

Description:

The spike is short with irregular placement of spikelets. Awns are about 3/4 normal length. Lateral spikelets are missing from a few basal rachis nodes and two awns occur occasionally on the terminal spikelet (3). Compared to Bowman, plants of the Bowman backcross-derived line for *ari-q.280*, BW055, headed 3 to 4 days later, were 15 to 20% shorter, and had 2 to 4 fewer kernels per spike. Kernels of BW055 weighed less, 52 vs. 59 mg, than those of Bowman and grain yields of BW055 were about 25% lower (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500, NGB 14661) (3).

Mutational events:

*ari-q.271* (NGB 119347), *-q.280* (NGB 116094, GSHO 1665), *-q.281* (NGB 116096, 116097) in Kristina (NGB 1500, NGB 14661) (3, 4).

Mutant used for description and seed stocks:

*ari-q.280* (NGB 116094, GSHO 1665) in Kristina; *ari-q.280* in Bowman (PI 483237)\*4 (GSHO 2164); *ari-q.280* in Bowman\*7 (BW055, NGB 20463).

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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4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:484.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:188.

BGS 561, Erectoides-h, *ert-h*

Stock number: BGS 561  
Locus name: Erectoides-h  
Locus symbol: *ert-h*

Previous nomenclature and gene symbolization:

Erectoides-25 = *ert-25* (3).

Inheritance:

Monofactorial recessive (3).

Located likely in chromosome 5HL (1); *ert-h.25* is associated with a large number of donor parent SNP markers in 5H bins 11 to 14, markers 1\_1090 to 2\_0536 (positions 203.85 to 271.24 cM), of the Bowman backcross-derived line BW310 (1).

Description:

Plants are semidwarf (about 3/4 normal height), and spike density is increased only slightly (5). Plants of the Bowman backcross-derived line for *ert-h.25*, BW310, headed 5 to 7 days later than Bowman. The number of kernels per spike for BW310 increased by 3 to 5, but rachis internodes were slightly shorter, 3.9 vs. 4.4 mm. Grain yields for BW310 were up to 20% lower than the Bowman yields (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB14657) (3).

Mutational events:

*ert-h.25* (NGB 112626, GSHO 481) in Bonus (PI 189763, NGB14657) (3); *ert-h.68* (NGB 112667) in Bonus (4).

Mutant used for description and seed stocks:

*ert-h.25* (GSHO 481, NGB 112626) in Bonus; *ert-h.25* in Bowman (PI 483237)\*3 (GSHO 2252, BW310, NGB 22106).

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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5. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:487.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:189.

BGS 571, Erectoides-za, *ert-za*

Stock number: BGS 571  
Locus name: Erectoides-za  
Locus symbol: *ert-za*

Previous nomenclature and gene symbolization:

Erectoides-102 = *ert-102* (4).

Brachytic 7 = *br7* (5).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 5H (1); *ert-za.102* is associated with SNP markers 1\_0974 to 2\_1244 (positions 41.99 to 93.00 cM) in 5H bins 03 to 05 of the Bowman backcross-derived line BW330 (1).

Description:

Plants are semidwarf (3/4 normal height) and can be placed in the brachytic class of semidwarfs (3, 5). Peduncles are relatively short, the leaf blade attachment appears more erect than normal, and kernels are slightly rounded or globe-shaped (2). Plants of the Bowman backcross-derived line for *ert-za.102*, BW330, were 20 to 25% shorter than Bowman and their awns were 4 to 5 cm shorter, but BW330 had only slightly shorter rachis internodes. Kernels were slightly shorter and wider and kernel weights varied from 15% less to 10% more than those for Bowman. BW330 headed 2 days later than Bowman and its grain yields were about 30% lower (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB14657) (4).

Mutational events:

*ert-za.102* (NGB 112701, GSHO 501), *-za.146* (NGB 112745) in Bonus (PI 189763, NGB14657) (4).

Mutant used for description and seed stocks:

*ert-za.102* (NGB 112701, GSHO 501) in Bonus; *ert-za.102* in Bowman (PI 483237)\*6 (GSHO 2261); *ert-za.102* in Bowman\*7 (BW330, NGB 22125).

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. 1997. *Barley Genet. Newsl.* 26:497.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:190.

BGS 612, Gigas 2, *gig2*

Stock number: BGS 612  
Locus name: Gigas 2  
Locus symbol: *gig2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Location in chromosome 4HL (1); *gig2.c* is associated with SNP marker 3\_0554 (position 102.93 cM) in 4H bin 07 of the Bowman backcross-derived line BW382 (1), in 4H bin 07.

Description:

Plants with the *gig2* gene are tall and robust. Most plant parts are larger than those of normal sibs and spikes have 4 to 8 more fertile spikelets. In the greenhouse, heading is delayed by two to three weeks and plants are nearly twice as tall as normal sibs. Under field conditions, plants are tall and late and lodge easily. If planted late in North Dakota, *gig2.c* plants may remain vegetative until the end of the growing season (2). Compared to Bowman, the Bowman backcross-derived line for *gig2.c*, BW382, headed 14 days later at Aberdeen, Idaho and 27 days later at Dundee, Scotland. Upper leaf blades of BW382 were 25 to 50% wider and plants were taller, 107 vs. 88 cm. The awns were slightly shorter and spikes had 2 to 9 more kernels at various locations. Kernels of BW382 were shorter (8.7 vs. 9.4 mm) and narrower (3.43 vs. 3.86 mm) and lighter (47 vs. 59 mg). Test weights of BW382 were about 25% lower and grain yields 25 to 50% lower than those for Bowman (2). Based on a similar phenotype and retained SNP markers in 4HL, BW380 contains an allele at the *gig2* locus, tentatively named *gig2.e* (1, 2).

Origin of mutant:

A spontaneous mutant in the breeding line ND12463 (ND7556/4/ND5835//ND4064/ND2199/3/Bowman/5/ND8879) (2).

Mutational events:

*gig2.c* in ND12463 (GSHO 1750, DWS1372) (3), *gig2.e* in ND18365 (2B91-4947/ND15403) (2).

Mutant used for description and seed stocks:

*gig2.c* in ND12463 (GSHO 1750); *gig2.c* in Bowman (PI 483237)\*6 (GSHO 2266); *gig2.c* in Bowman\*8 (BW382, NGB 20621); *gig2.e* in Bowman\*2 (BW380, NGB 20619).

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.

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:113.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:191.

BGS 617, Uniculme 4, *cul4*

Stock number: BGS 617  
Locus name: Uniculme 4  
Locus symbol: *cul4*

Previous nomenclature and gene symbolization:

Uniculme-5 = *uc-5* (4).

Uniculme-3 = *uc-3* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL (7); near AFLP marker E4143-4 in subgroup 32 of the Proctor/Nudinka map (5); *cul4.3*, *cul4.5*, *cul4.15*, and *cul4.16* mapped near RFLP markers CDO0394a and CDO105 (8); *cul4.5* is associated with SNP markers 1\_0646 to 2\_0339 (positions 239.73 to 248.51 cM) in 3H bin 15 of the Bowman backcross-derived line BW212 (2); *cul4.3* is associated with SNP markers 2\_0136 to 1\_0044 (positions 138.00 to 190.80) in 3H bins 08 to 13 and with markers 1\_0646 to 2\_1362 (positions 239.73 to 255.13 cM) in 3H bins 15 and 16 of the Bowman backcross-derived line BW211 (2), likely in 3HL bin 15.

Description:

Plants produce 1 to 4 tillers that are twisted and have slightly bowed culm internodes. All secondary tillers are shorter than the primary tiller and have a curly appearance. Often secondary tillers are trapped at the base of the primary tiller (3, 6). Compared to normal sibs, *cul4* plants have peduncles that are slightly to 50% longer. Rachis internodes are slightly elongated, and kernels are slightly longer. Plant height varies from 2/3 normal to slightly taller than Bowman (3). Under greenhouse conditions, the Bowman line for *cul4.5*, BW212, developed only two axillary tillers, and it was unicum when combined with the *cul2.b* (unicum 2) gene (1). The *cul4* mutants cause reduced tillering, deregulation of the number of axillary buds in an axil, and alterations in leaf proximal-distal patterning (9). Only one or two axils of BW212 plants contained axillary buds, but often two buds instead of one bud were present. These axillary buds were sometimes associated with the development of leafy shoots. All *cul4* mutants had a liguleless phenotype (9). The *Cul4* gene was isolated by positional cloning and shown to encode a BTB-ankyrin protein closely related to Arabidopsis BLADE-ON-PETIOLE1 (BOP1) and BOP2. Morphological, histological and in situ RNA expression analyses indicated that the dominant allele at the *Cul4* locus acts at axil and leaf boundary regions to control axillary bud differentiation, as well as development of the ligule (9).

Origin of mutant:

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

Mutational events:

*cul4.3* (NGB 115062, GSHO 2495), *cul4.5* (NGB 115063, GSHO 2493) in Bonus (PI 189763, NGB 14657), *cul4.15* (NGB 115064) in Foma (CIho 11333, NGB 14659), *cul4.16* (NGB 115065) in Bonus (6, 8); *cul4.24* (NGB 119360) in Flare (NGB 1518) (6, 9, 10).

Mutant used for description and seed stocks:

Mutant used for description and seed stocks:

*cul4.3* (NGB 115062, GSHO 2495) in Bonus; *cul4.5* (GSHO 2493, NGB 115063) in Bonus; *cul4.3* in Bowman (PI 483237)\*3 (GSHO 2360); *cul4.3* in Bowman\*4 (BW211, NGB 22038); *cul4.5* in Bowman\*4 (GSHO 2361); *cul4.5* in Bowman\*7 (BW212, NGB 22039); *cul4.15* in Bowman\*3 (BW208, NGB 22036); *cul4.16* in Bowman\*2 (BW209, NGB 20559); *cul4.24* in Bowman\*3 (BW210, NGB 22037).

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1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unculm2 (*cul2*) mutant. *Theor. Appl. Genet.* 106:846–857.
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.
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Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. *Barley Genet. Newsl.* 32:118.

Revised:

J.D. Franckowiak and U. Lundqvist. 2007. *Barley Genet. Newsl.* 37:289.

J.D. Franckowiak and U. Lundqvist. 2013. *Barley Genet. Newsl.* 43:162-163.

J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:192-193.

BGS 618, Many noded dwarf 3, *mnd3*

Stock number: BGS 618  
Locus name: Many noded dwarf 3  
Locus symbol: *mnd3*

Previous nomenclature and gene symbolization:

Many noded dwarf 3 = *mn3* (6).  
Many noded dwarf = *m3* (5).  
Many noded dwarf 3 = *mnd3* (3).

Inheritance:

Monofactorial recessive (6, 7).  
Located in chromosome 4HS likely (1); the largest group of SNP markers associated with *mnd3.d* includes 2\_1056 to 2\_0001 (positions 5.42 to 41.26 cM) in 4H bins 01 to 04 of the Bowman backcross-derived line BW519 (1). Previously the *mnd3* locus was placed in chromosome 3H (7) over 36.7 cM from the *uzu1* (*uzu* 1) locus (7).

Description:

In plants homozygous for the *mnd3.d* gene, all plant parts are somewhat reduced in size. The number of elongated culm internodes is increased by 1 or 2 compared to normal sibs. Plants are short, 2/3 to 3/4 normal height (2). However, the *mnd3.d* gene does not reduce fertility and spike appears normal in R.I. Wolfe's Multiple Marker Stock for chromosome 2H (2). In the Bowman backcross-derived line for *mnd3.d*, BW519, plants were shorter, 77 vs. 92 cm, and spikes had fewer spikelets, 12 vs. 21. BW519 often showed partial seed set. Kernels of BW519 were smaller, 7.4 vs. 9.9 mm in length and 3.6 vs. 3.8 mm in width, than those of Bowman and weighed less, 42 vs. 58 mg. Grain yields of BW519 were about 20% of those for Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (Clho 7149) (7).

Mutational events:

*mnd3.d* from Montcalm (Clho 7149), but isolated from R.I. Wolfe's Multiple Marker Stock for chromosome 2H (DWS1346) (2, 3).

Mutant used for description and seed stocks:

*mnd3.d* from R.I. Wolfe's 2.1 Multiple Marker Stock crossed to Bowman (GSHO 1797); *mnd3.d* in Bowman (PI 483237)\*7 (GSHO 1949, BW519, NGB 20747).

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. 2002. Barley Genet. Newsl.32:119.

Revised:

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:194-195.

BGS 619, Bracteatum-a, *bra-a*

Stock number: BGS 619  
Locus name: Bracteatum-a  
Locus symbol: *bra-a*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 7H (3); based on linkage drag with the *ant1* (anthocyanin-less 1) locus (3); *bra-a.001* is associated with SNP markers 1\_0056 to 2\_0385 (positions 51.93 to 152.29 cM) in 7H bins 04 to 09 of the Bowman backcross-derived line BW067 (2).

Description:

Leaf-like structures or bracts develop from the rachis slightly below the rachis node at which the spikelets are attached (1). The bract associated with the lowest spikelet is always the largest and the bracts become progressively smaller toward the tip of the spike (5). Development of the bracts is poor in the Bowman backcross-derived line for *bra-a.001*, BW067 (3). Compared to Bowman, plants of BW067 headed 5 to 12 days later and were 3/4 normal height, 65 vs. 90 cm. Leaf blades were slightly shorter and narrower, peduncles were 1/3 to 1/2 normal length, and the number of kernels per spike was reduced, 16 vs. 22. BW067 had slightly shorter rachis internodes, 3.9 vs. 4.5 mm. Its kernels were relatively thin, 3.5 vs. 3.9 mm, and weighed up to 30% less than those of Bowman. Grain yields of BW067 were about half normal (3).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763, NGB 14657) (4, 5).

Mutational events:

*bra-a.001* (NGB 114318), *bra-a.003* (NGB 114320) in Bonus (PI 189763, NGB 14657) (5).

Mutant used for description and seed stocks:

*bra-a.001* (GSHO 1693, NGB 114318) in Bonus; *bra-a.001* in Bowman (PI 483237)\*6 (GSHO 2183); *bra-a.001* in Bowman\*7 (BW067, NGB 20475).

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.
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5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:120.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:196.

BGS 620, Calcaroides-b, *cal-b*

Stock number: BGS 620  
Locus name: Calcaroides-b  
Locus symbol: *cal-b*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 5HL (7); about 4.2 cM proximal from AFLP marker E4040-4 and probably near molecular marker CDO749 in 5H bin 04 (7); *cal-b.2* 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 backcrossed-derived line BW104 (2), likely in 5H bin 05.

Description:

At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, *cal-b* mutants have a knee-like ectopic structure (1, 7). In mutant *cal-b.2*, frequently only an enlargement of the basal third of the awn is evident and the enlargement is expressed more in terminal and subterminal spikelets. Leaf knots and leaf curling occurs also (7). The awn malformation of the *cal-b.2* mutant is associated with developmental activation of the phytomeric triad separating the lemma from awn (4). In the Bowman backcross-derived line for *cal-b.2*, BW104, plants were slightly shorter and spikes had a more lax arrangement of spikelets (3). The awns of BW104 were slightly shorter, 10 vs. 12 cm, than those of Bowman. Leaf blades were 1/2 to 2/3 as wide, and the spikes had about 5 fewer rachis internodes with fertile spikelets than those of Bowman. Kernels were shorter and thinner and weighed about 20% less. Grain yields of BW104 were about 1/3 of normal (3).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB14657) (5, 6).

Mutational events:

*cal-b.2* (NGB 114282, GSHO 1697), *cal-b.19* (NGB 114298) in Bonus (PI 189763, NGB14657) (6).

Mutant used for description and seed stocks:

*cal-b.2* (GSHO 1697, NGB 114282) in Bonus; *cal-b.2* in Bowman (PI 483237)\*4 (GSHO 2187, BW104, NGB 20510).

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.
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Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:121.

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:197-198.

BGS623, Eligulum-a, *eli-a*

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

Previous nomenclature and gene symbolization:

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

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

Inheritance:

Monofactorial recessive (3).

Location is unknown; no consent pattern of SNP markers retained in backcross-derived lines assumed to be alleles at the *eli-a* locus was observed (1).

Description:

Plants do not have ligules in the junction between the sheath and leaf blade, auricles are rudimentary and asymmetrically displaced. Plants are about 2/3 of normal height and have very wide leaves (4, 5). The peduncle is short and spike emergence from the sheath of the flag leaf is poor. Spikes have a compact arrangement of spikelets and are extremely compacted near the tip (2, 4). The culm breaks very easily between the upper and lower halves of the nodes. The Bowman backcross-derived lines have glume awns that are nearly twice as long as those of Bowman, but the lemma awns are about 2/3 of normal (2).

Origin of mutant:

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

Mutational events:

*eli-a.2* (NGB 115389), *eli-a.3* (NGB 115390), *-a.7* (NGB 115392), *-a.9* (NGB 115393), *-a.10* (NGB 115394) in Foma (CIho 11333, NGB 14659) (5); *eli-a.11* (NGB 115395), *-a.14* (NGB 115397) in Kristina (NGB 1500, NGB 14661); *eli-a.15* (NGB 115398), *-a.16* (NGB 151399) in Bonus (PI 189763) (5), *eli-a.216* (FN216, GSHO 3647) in Steptoe (CIho 15229) (2, 4).

Mutant used for description and seed stocks:

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

References:

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5. Lundqvist, U. (Unpublished).

Prepared:

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

Revised:

J.D. Franckowiak and A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:192.

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:290.

U. Lundqvist and J.D. Franckowiak. 2013. *Barley Genet. Newsl.* 43:164.

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:199.

BGS 625, Scirpoides-a, *sci-a*

Stock number: BGS 625  
Locus name: Scirpoides-a  
Locus symbol: *sci-a*

Previous nomenclature and gene symbolization:

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

Scirpoides-3 = *sci-3* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 5H (1); *sci-a.3* is associated with SNP markers 1\_1198 to 2\_1121 (positions 73.70 to 105.91 cM) in 5H bins 04 to 06 of the Bowman backcrossed-derived line BW773 (1); *sci-a.1* is associated with SNP markers 1\_0686 to 2\_1480 (positions 52.12 to 137.96 cM) in 5H bins 03 to 08 of the Bowman backcrossed-derived line BW772 (1).

Description:

Plants expressing the *sci-a* gene appear to have very narrow, inward folded leaf blades. The tip of emerging leaf blade is sometimes trapped inside the previous one. Folding of the leaf blade persists until maturity. Premature yellowing of leaf blade tips may occur shortly after heading. Spikes appeared 1/2 to 2/3 normal length and plant height is reduced slightly (2, 4). Compared to Bowman, plants of the Bowman backcross-derived lines for *sci-a.1*, BW772, and *sci-a.3*, BW773, were slightly shorter, with slightly shorter rachis internodes, and had 1 to 3 fewer kernels per spike. Kernel weights for BW772 and BW773 were slightly lower than those of Bowman in some trials. Grain yields ranged from 40 to 70% of those for Bowman; however, BW772 often yielded slightly less than BW773 (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763, NGB14657) (4).

Mutational events:

*sci-a.3* (NGB 117097) in Bonus (PI 189763, NGB14657) (4); *sci-a.1* (NGB 117095) in Gull (Clho 1145, GSHO 466, NGB 1480) (4).

Mutant used for description and seed stocks:

*sci-a.3* (NGB 117097) in Bonus; *sci-a.1* (NGB 117095) in Gull; *sci-a.3* in Bowman (PI 483237)\*4 (GSHO 3430; BW773, NGB 22241); *sci-a.1* in Bowman\*4 (BW772, NGB 22240).

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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4. Lundqvist, U. (Unpublished).

Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:200.

BGS 626, Scirpoides leaf-a, *scl-a*

Stock number: BGS 626  
Locus name: Scirpoides leaf-a  
Locus symbol: *scl-a*

Previous nomenclature and gene symbolization:

Scirpoides leaf-6 = *scl.6* (3).  
Scirpoides leaf-1 = *scl.1* (3).  
Scirpoides leaf-2 = *scl.2* (3).  
Scirpoides leaf-4 = *scl.4* (3).

Inheritance:

Monofactorial recessive (2).  
Located in chromosome 1HL (1); *scl-a.6* is associated with SNP markers 1\_0433 to 1\_0396 (positions 139.25 to 143.47 cM) in 1HL bin 11 of Bowman backcross-derived line BW778 (1); *scl-a.2* is associated with SNP marker 2\_0780 (position 154.89 cM) in 1H bin 12 of the Bowman backcross-derived line BW775 (1); *scl-a.4* is associated with SNP markers 1\_0006 and 2\_1126 (position 110.10 cM) in 1HL bin 10 of the Bowman backcross-derived line BW776 (1), likely in 1H bin 11.

Description:

Leaf blades of *scl-a* plants are folded inward and are narrow compared to those of normal sibs. Folding of the leaf blade persists until maturity (2, 3). Plants of Bowman backcross-derived line BW778 were slightly shorter than Bowman, kernels were slightly thinner and lighter, and grain yields were about 20% lower. Plants of BW778 have inward folded leaf blades that are about 2/3 as wide as those of Bowman (2). The mutant stocks *scl.1*, *scl.2*, and *scl.4* are alleles based on allelism tests (2). Their phenotypic similarities to the *scl-a.6* mutant and SNP markers retained in the same region of 1HL suggesting they are alleles at the *scl-a* locus (1, 2).

Origin of mutant:

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

Mutational events:

*scl-a.6* (NGB 117105) in Foma (CIho 11333, NGB14659) (3); *scl-a.1* (NGB 117100), *scl-a.2* (NGB 117101), *scl-a.4* (NGB 117102) in Bonus (PI 189763, NGB 14657) (1, 2, 3).

Mutant used for description and seed stocks:

*scl-a.6* (NGB 117105) in Foma; *scl-a.6* in Bowman (PI 483237)\*5 (GSHO 3431); *scl-a.6* in Bowman\*6 (BW778, NGB 20755); *scl-a.1* (NGB 117100) in Bonus; *scl-a.1* in Bowman\*4 (BW774, NGB 22242); *scl-a.2* (NGB 117101) in Bonus; *scl-a.2* in Bowman\*5 (BW775, NGB 22243); *scl-a.4* (NGB 117102) in Bonus; *scl-a.4* in Bowman\*5 (BW776, NGB 20753).

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2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:127.  
U. Lundqvist and J. D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:142.  
U. Lundqvist and J. D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:201.

BGS 632, Many noded dwarf 5, *mnd5*

Stock number: BGS 632  
Locus name: Many noded dwarf 5  
Locus symbol: *mnd5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HL (1); *mnd5.g* is associated with SNP markers 2\_0092 to 1\_1440 (positions 152.29 to 198.70 cM) in 7H bins 09 to 12 of the Bowman backcrossed-derived line BW521 (1).

Description:

When grown in the field, plants are about 1/2 normal height and have numerous tillers. Each tiller has numerous small leaves and a spike of about 1/3 normal size. Plants head late under field conditions. Culm branches with 4 to 7 leaves each may develop at the uppermost culm node, but these branches develop late and have very small spikes. When grown in the greenhouse, plants are tall and late compared with normal sibs. Each culm may have 15 to 20 elongated internodes (2). In field trials, plants of the Bowman backcross-derived line for *mnd5.g*, BW521, headed 9 to 13 days later than Bowman and were 1/2 to 2/3 the height of Bowman. Peduncles were very short, 3 vs. 25 cm, awns were short, 7 vs. 11 cm, and kernels per spike were less, 13 vs. 23. Rachis internodes of BW521 were slightly shorter, 4.1 vs. 4.7 mm, and leaf blades were smaller, 3 mm by 11 cm vs. 7 mm by 18 cm for the flag minus one leaves. Kernels of BW521 were smaller, 8.3 vs. 9.4 mm in length and 3.2 vs. 3.8 mm in width, and lighter, 39 vs. 59 mg, than those of Bowman. Grain yields of BW521 were 1/3 to 2/3 of those for Bowman (2).

Origin of mutant:

A spontaneous mutant in the cross C2-95-199 [Logan (PI 592784)/ND15053] (2).

Mutational events:

*mnd5.g* (C2-95-199-1) in C2-95-199 (2).

Mutant used for description and seed stocks:

*mnd5.g* (C2-95-199-1) in C2-95-199; *mnd5.g* in Bowman (PI483237)\*4 (BW521, NGB 20749).

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, 2002. *Barley Genet. Newsl.* 32:133.

Revised:

J.D. Franckowiak. 2014. *Barley Genet. Newsl.* 44:202.

BGS 633, Many noded dwarf 6, *mnd6*

Stock number: BGS 633  
Locus name: Many noded dwarf 6  
Locus symbol: *mnd6*

Previous nomenclature and gene symbolization:

Densinodosum-6 = *den-6* (5, 6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5HL (7, 8); near AFLP marker E3743-3 in subgroup 65 of the Proctor/Nudinka map (8); *mnd6.6* is associated with SNP markers 2\_0134 to 2\_0795 (positions 163.29 to 166.96 cM) in 5H bin 10 of the Bowman backcrossed-derived line BW522 (3); associated with position 97 cM of the POPSEQ map (7), in 5H bin 10.

Description:

Plants with the *mnd6.6* gene are about 2/3 normal height and have many elongated internodes in each culm (2, 6). The number of elongated internodes can be up to 20 in the original stock when grown in Sweden. Kernels are thin and small (6). The Bowman backcross derived line for *mnd6.6*, BW522, produced thin culms and leaf blades and axillary branches developed from the crown as well as from upper culm nodes. The number of tillers per plant for BW522 was three the number produced by Bowman (1). BW522 had 9 to 10 elongated internodes per tiller and the blades of the flag minus one leaves were small, 3.5 vs. 6.5 mm wide and 11 vs. 19 cm long. Peduncles of BW522 were very short, 11 vs. 29 cm, awns were about 1/2 normal length, and plants were about 2/3 as tall as Bowman plants. Spikes were short, 17 vs. 21 spikelets and average rachis internode lengths were 3.9 vs. 4.3 mm. BW522 plants headed about 2 days later than Bowman. The kernels of BW522 were small and their average weight was 36 vs. 56 mg for Bowman. The grain yields of BW522 were 1/2 to 2/3 of those recorded for Bowman (4). The double mutant plants for *mnd6.6* and *cul2.b* (uniculm 2) were unculm with short spikes and awns (1). Mapping-by-sequencing of a series of *mnd6* mutants demonstrated that loss-of-function for MLOC\_64838.2 is associated with the *mnd6* phenotype (7). This gene was named the *HvMND* (*mnd6*) locus and shown to be a member of the CYP78A subfamily of cytochrome P450 enzymes (7). Bowman backcross-derived lines for *mnd6.6* and *mnd4.e* (see BGS 347) are phenotypically similar and *mnd4.e* mutant in Akashinriki is likely an allele at the *mnd6* locus (7).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763, NGB14657) (5); an X-ray induced mutant in Saale (PI 194554) (7, 9, 10).

Mutational events:

*mnd6.6* (NGB 114514, GSHO 1713) in Bonus (PI 189763, NGB14657) (5); *mnd6.8* (NGB 114516) in Foma (CIho 11333, NGB 14659) (5, 6); *mnd6.47* (Mut. 4899, MHOR474) in Saale (PI 194554) (7, 9); *mnd6.3* (NGB 114513) in an unknown cultivar (6, 7); *mnd6.7* (NGB 114515) in Bonus; *mnd6.9* (NGB 114517), *mnd6.10* (NGB 114518), *mnd6.11* (NGB 114519), *mnd6.12* (NGB114520), *mnd6.13* (NGB 114521), *mnd6.19* (NGB114526) in Foma (6, 7); *mnd6.20* (NGB 114527) in Kristina (NGB 1500, NGB14661) (6); *mnd6.21* (NGB 114528) in Foma (6, 7); *mnd6.22* (NGB 114529), *mnd6.24* (NGB 114530), *mnd6.25* (NGB 114531), *mnd6.26* (NGB 114532), *mnd6.27* (NGB 114533), *mnd6.28* (NGB 114534), *mnd6.29* (NGB 114535), *mnd6.30* (NGB 114536), *mnd6.33* (NGB 114538), *mnd6.34* (NGB 114539), *mnd6.36* (NGB 114541), *mnd6.37* (NGB 114542) in Kristina (6, 7); *mnd6.38* (NGB 114543) in Sv 71120 (6, 7); *mnd6.41* (NGB 114545), *mnd6.42* (NGB 114546), *mnd6.44* (NGB

114548), *mnd6.45* (NGB 114550) in Bonus (6, 7); *mnd6.46* (NGB 119361) in Lina (NGB 1517) (6, 7).

Mutant used for description and seed stocks:

*mnd6.6* (GSHO 1713, NGB 114514) in Bonus; *mnd6.6* in Bowman (PI 483237)\*7 (GSHO 2235, BW522, NGB 20750); *mnd6.47* (Mut. 4899, MHOR474) in Saale.

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Prepared:

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Revised:

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:291.

J.D. Franckowiak and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:203-204.

BGS 657, Brachytic 15, *brh15*

Stock number: BGS 657  
Locus name: Brachytic 15  
Locus symbol: *brh15*

Previous nomenclature and gene symbolization:

Brachytic-u = *brh.u* (4).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosomes 2HL most likely (1); *brh15.u* is associated with SNP markers 1\_0876 to 2\_0182 (positions 161.10 to 185.33 cM) in 2H bins 11 to 12 and with small groups of SNP markers in other chromosomes of Bowman backcross-derived line BW086 (1).

Description:

Plants have numerous tillers with small leaves, spikes, and kernels. Prior to heading plants appear to be grassy culms similar to those produced by the *sld2* (slender dwarf 2) and *sld4* (slender dwarf 4) mutants, but heading is not drastically delayed.

Compared to Bowman, culms and peduncles of the Bowman backcross-derived line for *brh15.u*, BW086, were about 1/2 normal length. Awns and rachis internodes were slightly shorter than those of normal sibs. Leaf blades were narrow and about 1/2 normal length. Mutant plants headed 2 to 3 days later than Bowman. Spikes of BW086 plants had nearly 4 fewer kernels than those of Bowman. The kernels of BW086 were slightly shorter (8.6 vs. 9.6 mm), thinner (3.4 vs. 3.8 mm), and about 30% lighter. The grain yields of the BW086 averaged about 2/3 of that recorded for Bowman (2, 3).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Julia (PI 339811) (6, 7).

Mutational events:

*brh15.u* (409 JK, DWS1156, GSHO 1685) in Julia (PI 339811) (5, 7).

Mutant used for description and seed stocks:

*brh15.u* (GSHO 1685) in 409 JK/Bowman; *brh15.u* in Bowman (PI 483237)\*5 (GSHO 2176, BW086, NGB 20493).

References:

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Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:297.

Revised:

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:205-206.

BGS 675, Mottled leaf 9, *mtt9*

Stock number: BGS 675  
Locus name: Mottled leaf 9  
Locus symbol: *mtt9*

Previous nomenclature and gene symbolization:

Mutant 2721 (2).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown (3). The Bowman line for *mtt9.2721* (BW598) differs from Bowman only for SNP markers near the *Rph3* (reaction to *Puccinia hordei* 3) locus (1).

Description:

Leaf blades of the *mtt9.2721* plants are characterized by chlorotic leaf spots and bands that coalesce and eventually form large white patches. The phenotype is displayed on all leaves. As the leaves mature, the white regions gradually become darker, seeming to undergo necrosis and death. Often the necrosis affects the leaf edges, resulting in wrinkled leaf edges. Under short day conditions, expression of the mutant phenotype is delayed by several days and is reduced in severity (2, 3). Initially the chlorosis of *mtt9.2721* plants appears similar to that produced by the *mtt2* (mottled leaf 2) and *mtt6* (mottled leaf 6) mutants (2, 3). Autofluorescence is clearly noticeable in the cell walls or apoplastic compartments of the bleached leaf tissues, and is more pronounced in the vascular tissues. The green tissues display little or no autofluorescence. The cell walls of leaf blade lesions are clearly thickened (3). The *mtt9.2721* plants were more susceptible to *Pyrenophora teres* f. *teres* than Bowman-*Rph3.c* based on counting the number of spores produced on leaf surfaces (3).

Origin of mutant:

A fast neutron induced mutant in Bowman-*Rph3.c* (Bowman\*11//Estate/3.2 uz als MM) (BW746, PI 643152, NGB 22452) (2, 3).

Mutational events:

*mtt9.2721* (GSHO 3598, NGB 23524) in Bowman-*Rph3.c* (Bowman\*11//Estate/3.2 uz als MM) (PI 643152, NGB 22452) (2, 3).

Mutant used for description and seed stocks:

*mtt9.2721* (GSHO 3598, NGB 23524) in Bowman-*Rph3.c* (BW746, PI 643152, NGB 22452); *mtt9.2721* from Bowman *Rph3.c* in Bowman (PI 483237) (BW597, NGB 22163).

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Prepared:

S.A.I. Wright, A.B. Falk, J.D. Franckowiak, and U. Lundqvist. 2013. *Barley Genet. Newsl.* 43:183.

Revised:

S.A.I. Wright, A.B. Falk, J.D. Franckowiak, and U. Lundqvist. 2014. *Barley Genet. Newsl.* 44:207.

BGS 729, Dusky 2, *dsk2*

Stock number: BGS 729  
Locus name: Dusky 2  
Locus symbol: *dsk2*

Previous nomenclature and gene symbolization:

Male sterile genetic *df* = *msg,,df* (5).

Inheritance:

Monofactorial recessive (5), but an additional recessive gene may be involved in expression (3, 4).

Location in chromosome 7HL (1); *dsk2.b* is associated with SNP markers1\_0861 to 2\_0365 (positions 183.90 to 229.66 cM) in 7H bins 11 to 13 of the Bowman backcross-derived line BW252 (1).

Description:

The original *dsk2.b* mutant was identified as a male sterile genetic mutant and assigned the temporary gene symbol *msg,,df* (3) (now converted to *msg.df*). Hockett reported deficiencies of mutant plants in segregating progenies of MSS354 for *msg.df*: 133 fertile to 15 male sterile in 1975 (3) and 222 to 18 in 1977 (4). When grown under greenhouse conditions, the mutant segregates were weak and developed severe necrotic lesions on the leaves shortly before heading (2). Plant vigor is a little better in Bowman backcross-derived line for *dsk2.b*, BW252, but mutant gene is still maintained in a heterozygous stock. The mutant plants in BW252 are very weak and self-fertile, but premature dying of the mutants limits seed production to very small kernels with poor viability. Spraying the fungicide Tilt on *dsk2.b* segregates of BW252 caused severe bleaching of leaf blades (2). The original stock, MSS354, may have contained two mutants: one associated with male sterility and a second for severe leaf necrosis.

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) isolated by R.F. Eslick (3).

Mutational events:

*dsk2.b* (MSS 354) in Betzes (PI 129430) (3).

Mutant used for description and seed stocks:

*dsk2.b* (MSS 354) in Betzes; *dsk2.b* in Bowman (PI 483237)\*5 (BW252, NGB 22077).

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Prepared:

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