BGS 1, Brachytic 1, *brh1*

Stock number: BGS 1
Locus name: Brachytic 1
Locus symbol: *brh1*

Previous nomenclature and gene symbolization:

Brachytic = *br* (12, 14).
Breviaristatum-i = *ari-i* (6, 10).
Dwarf x = *dx1* (7).

Inheritance:

Monofactorial recessive (12, 14).

Located in chromosome 7HS (4); about 9.3 cM distal from the *fch12* (chlorina seedling 12) locus (14); 0.8 cM distal from RFLP marker BCD129 (11); about 5.0 cM from AFLP marker E4134-8 in subgroup 1 of the Proctor/Nudinka map (13); about 13.6 cM proximal from SSR marker HVM04 in 7H bin 02 (2); *brh1.a* is associated with SNP markers 2_1419 to 2_0245 (positions 0.00 to 13.19 cM) in 7H bin 01 of the Bowman backcross-derived line BW074 (3); *brh1.x* is associated with SNP markers 1_0949 to 1_1495 (positions 0.00 to 8.77 cM) in 7H bin 01 of the Bowman backcross-derived line BW079 (3); *brh1.t* is associated with SNP markers 1_1495 to 1_0025 (positions 8.77 to 26.00 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW078 (3); an unnamed *brh1* mutant is associated with SNP markers 1_0851 to 2_0485 (positions 17.32 to 121.90 cM) in 7H bins 02 to 07 of the Bowman backcross-derived line BW872 (3), likely in 1H bin 01 near the border with 1H bin 02.

Description:

Plants have short leaves, culms, spikes, awns, and kernels. The seedling leaf is about 2/3 normal length. A similar reduction in the size of other organs is observed, but the awns were less than 1/2 normal length (7). The mutant phenotype was easy to classify at all stages of growth. The approximately 20% reduction in kernel weight was caused primarily by a reduction in kernel length, 7.8 vs. 9.6 mm. Grain yields of the Bowman backcross-derived lines for *brh1* mutants were about 2/3 normal and lodging was greatly reduced (2). Börner (1) reported that *ari-i.38* seedlings are sensitive to gibberellic acid. Powers (12) stated that the assigned gene symbol for this mutant is *br* and that L.J. Stadler selected this symbol.

Origin of mutant:

A spontaneous mutant in Himalaya (CIho 1312) (12, 14).

Mutational events:

brh1.a (GSHO 25) in Himalaya (14); *brh1.c* (GSHO 229) in Moravian (PI 539135) (15); *ari-i.38* (NGB 115888, GSHO 1657) in Bonus (PI 189763) (10, 16); *brh1.e* (GSHO 1690) in Aramir (PI 467786) (16); *brh1.f* (*dx1*, GSHO 1422) in Domen (CIho 9562) (7); *brh1.t* (OUM136, GSHO 1691) in Akashinriki (PI 467400, OUJ659); *brh1.x* (7125, GSHO 1692) in Volla (PI 280423); *brh1.z* (Hja80001) in Aapo; *brh1.aa* (Hja80051) in a Hja80001 cross (5, 8); *brh1.ae* (FN53, GSHO 3646) in Steptoe (CIho 15229) (5, 9); an unnamed variant of *brh1* in L50-200 (Alb Acc 67A, GSHO 1217) associated with expression of the subnodal bract 1 (*snb1.a*) gene (17).

Mutant used for description and seed stocks:

brh1.a in Himalaya (GSHO 25); *ari-i.38* (GSHO 1657, NGB 115888) in Bonus, *brh1.a* in Bowman (PI 483237)*7 (GSHO 1820, BW074, NGB 20491); *ari-i.38* in Bowman*6 (GSHO 1821, BW047, NGB 20455); *brh1.e* in Bowman*7 (GSHO 1822, BW077, NGB

20484); *brh1.t* in Bowman*7 (GSHO 1823, BW078, NGB 20485); *brh1.x* in Bowman*7 (GSHO 1824, BW079, NGB 20486); *brh1.z* in Bowman*7 (GSHO 2179, BW080, NGB 20487); *brh1.aa* in Bowman*6 (GSHO 1668, BW075, NGB 20485); *brh1.ae* in Bowman*4 (BW076, NGB 20483); an unnamed *brh1* allele in Bowman*2 (BW872, NGB 22306).

References:

1. Börner, A. 1996. GA response in semidwarf barley. Barley Genet. Newsl. 25:24-26.
2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
3. 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.
4. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.
5. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
6. 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.
7. Holm, E., and K. Aastveit. 1966. Induction and effects of the brachytic allele in barley. Adv. Front Plant Sci. 17:81-94.
8. Kivi, E. 1986. (Personal communications).
9. Kleinhofs, A. (Unpublished).
10. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
11. Li , M., D. Kudrna, and A. Kleinhofs. 2000. Fine mapping of a semi-dwarf gene brachytic 1 in barley. p. 72-74. *In* S. Logue (ed.) Barley Genetics VIII. Volume III, Proc. Eighth Int. Barley Genet. Symp., Adelaide, Dept. Plant Science, Waite Campus, Adelaide University, Glen Osmond, South Australia.
12. Powers, L. 1936. The nature of the interactions of genes affecting four quantitative characters in a cross between *Hordeum deficiens* and *vulgare*. Genetics 21:398-420.
13. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
14. Swenson, S.P. 1940. Genetic and cytological studies on a brachytic mutant in barley. J. Agric. Res. 60:687-713.
15. Szarejko, I., and M. Maluszynski. 1984. New brachytic mutant of spring barley variety Aramir. Barley Genet. Newsl. 14:33-35.
16. Tsuchiya, T. 1974. Allelic relationships of genes for short-awned mutants in barley. Barley Genet. Newsl. 4:80-81.
17. Walker, G.W.R., J. Dietrich, R. Miller, and K.J. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:104.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:100.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:44.
J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:188-189.
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:58-59.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:48-49.

BGS 9, Dense spike 1, *dsp1*

Stock number: BGS 9
Locus name: Dense spike 1
Locus symbol: *dsp1*

Previous nomenclature and gene symbolization:

Dense spike = *l* (19, 22).
Lax spike = L_1 (9).
Short spike = *e* (21).
Dense spike-ar = *dsp.ar* (2, 15).

Inheritance:

Monofactorial recessive (1, 6, 22).

Located in chromosome 7HS (7, 9); about 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (18, 19); *dsp1.a* is near molecular marker cMWG704 (11); *dsp1.a* is located near the centromere (11, 20); *dsp1.a* is near markers Bmag0359 and Bmag0321 (20); *dsp.ar* (*dsp1.ar*) is in a 0.37 cM interval between markers SC57808 (Hv_SPL14) and CAPSK06413 located in the short and long arm at the centromere of 7H (15); *dsp1.a* is associated with SNP markers 2_0671 to 2_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (2); *dsp1.ap*, *dsp1.aq*, *dsp1.ar*, and *dsp1.at* have in common from their donor parent Volla SNP markers 1_0299 to 2_0485 (positions 101.23 to 121.90 cM) in 7H bin 07 of the Bowman backcross-derived lines BW263 to BW266 (2); *dsp1.ae*, *dsp1.ag*, *dsp1.ah*, and *dsp1.af* (formerly called *Pyr.af*) have Haisa-type of SNP marker patterns in the region from 1_0128 to 1_0169 (positions 97.66 to 142.55 cM) in 7H bins 07 to 08 of the Bowman backcross-derived lines BW255, BW256, BW257, and BW654 (2); *dsp1.aa* (formerly *pyr.aa*), *dsp1.ac*, *dsp1.ay*, and *dsp1.az* (BW652, BW254, BW271, and BW272, respectively) originated from different cultivars, but retained SNP marker in the centromeric region of 7H identical to those of the Haisa-type (2); *dsp1.f* (formerly *Zeo.f*) is associated with SNP markers 1_1098 to 1_0303 (positions 68.46 to 120.92 cM) in 7H bin 07 of the Bowman backcross-derived line BW935 (2); *dsp1.a* with *nud1.a* and *fst3.c* is associated with SNP markers 2_0671 to 2_0485 (positions 93.97 to 121.90 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW375 (2), in 7H bin 07.

Description:

Spike length is reduced because rachis internode length is about 2/3 normal. The reduction in rachis internode length caused by the *dsp1.a* and *uzu1.a* (uzu 1) alleles is similar and additive (16, 19). In F_2 progenies, the *dsp1.a* gene has pleiotropic effects on coleoptile length, culm length, and grain size (16). The original mutant line for *dsp1.ah* (Mut. 4841) was associated with increased grain yield (12), but the Bowman backcross-derived line with *dsp1.ah* (BW257) yielded less than half as much as Bowman (3). The rachis internode lengths of the Bowman backcross-derived lines from Volla mutants (BW263 to BW266) averaged 2.7 mm compared to 4.5 mm for Bowman. Plants were slightly shorter than Bowman, kernels were shorter 8.7 vs. 9.8 mm and slightly wider, and kernels weights were about 10% lower (5.2 vs. 5.7 mg) (3, 15). BW264, which contains only the 7H segment from Volla, appeared to have a lower reduction in plant height and kernel weights (3). The BW lines with the donor parents Haisa (BW255, BW654), Freya (BW256), and Saale (BW257) headed about two days later than Bowman and were about 20% shorter. Kernels were shorter and about 20% lighter. Awns of BW lines having Haisa-type as a donor were shorter, 9 vs. 11 cm, and grain yields were less than 50% of the Bowman yields. The Haisa line (BW654), retaining only a 7H region from the donor parent, was later and shorter than the other Haisa-type lines (3). The BW lines with a Volla mutant differed from the BW lines with a Haisa mutant by only one SNP marker, 1_1219 at 107.44 cM (3). Phenotypically, BW254 with *dsp1.ac*, BW271 with *dsp1.ay*, and BW272 with *dsp.1.az* were similar to the BW lines from Volla, while BW652 with *dsp1.aa* was similar to the BW lines from Haisa. Since BW lines from Haisa and Volla having other phenotypic variants have the same SNP marker heterogeneities in 7H lack the dense spike trait, the mutants named in this BGS description are likely independent mutants at the *dsp1* locus (2, 3). BW935 with *dsp1.f* was morphological similar to the BW lines with the Haisa mutants. The internode lengths in BW375 with *dsp1.a* were similar to those of other presumed *dsp1* mutants, but other morphological traits were affected by the presence of the *fst3.c* (fragile stem 3) gene (3).

Origin of mutant:

Natural occurrence in cultivars from China, Japan, and Korea (22); X-ray induced mutants in Donaria and Haisa (13, 14); induced mutants in Haisa II (5).

Mutational events:

dsp1.a in many cultivars of Oriental origin, often associated with the short awn gene (16); *dsp1.f* (formerly called *Zeo.f*) (18:15:4I, GSHO 2137) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (8); *dsp1.aa* (formerly *pyr.aa*) (Betzes Erectoides, CIho 10871, GSHO 2431) in Betzes (PI 129430) (10); *dsp1.ac* (Mut. 2654, GSHO 1716) in Donaria (PI 161974) (13); *dsp1.ae* (Mut. 4014, GSHO 1717), *dsp1.af* (formerly *Pyr.af*) (Mut. 4158, GSHO 1718) in Haisa (PI 197617) (13), *dsp1.ag* (Mut. 4551, GSHO 1719) in Freya (PI 290197) (14), *dsp1.ah* (Mut. 4841) in Saale (Piroline, PI 539132) (12); *dsp1.ap* (7112, GSHO 1724), *dsp1.aq* (7113, GSHO 1725), *dsp1.ar* (7114, GSHO 1726), *dsp1.at* (7117, GSHO 1727) in Volla (PI 280423) (4, 5); *dsp1.ay* (WA11005-81, GSHO 1729) in WA9037-75 (see PI 639908 for pedigree) (23); *dsp1.az* (Wa1628-85) in Hazen (PI 483238) (23).

Mutant used for description and seed stocks:

dsp1.a in Honen 6 (OUJ469, PI 307495, GSHO 1232); *dsp1.a* in Bowman*7 (GSHO 1833, BW 277, NGB 20561); *dsp1.aa* (Betzes Erectoides, CIho 10871, GSHO 2431) in Betzes; *dsp1.ar* in Volla (GSHO 1726); *dsp1.f* in Bowman*7 (GSHO 2137, BW935, NGB 22364); *dsp1.aa* in Bowman*4 (GSHO 2236), in Bowman*6 (BW652, NGB 22217); *dsp1.ac* in Bowman*5 (GSHO 2237, BW254, NGB 22079); *dsp1.ae* in Bowman*4 (GSHO 2239), in Bowman*5 (BW255, NGB 22080); *dsp1.af* in Bowman*5 (GSHO 2142) in Bowman*6 (BW654, NGB 22219); *dsp1.ag* in Bowman*4 (GSHO 2240), in Bowman*5 (BW256, NGB 22081); *dsp1.ah* in Bowman*7 (BW257, NGB 22082); *dsp1.ap* in Bowman*4 GSHO 2245), in Bowman*5 (BW263, NGB 22088); *dsp1.aq* in Bowman*5 (GSHO 2246), in Bowman*6 (BW264, NGB 22089); *dsp1.ar* in Bowman*7 (GSHO 1942, BW265, NGB 22090); *dsp1.at* in Bowman*5 (GSHO 2247, BW267, NGB 22092); *dsp1.ay* in Bowman*3 (GSHO 2250, BW271, NGB 22096); *dsp1.az* in Bowman*5 (BW272, NGB 22097); *dsp1.a* with *nud1.a* and *fst3.c* from Kobinkatagi 4 (OUM 382, GSHO 1746) in Bowman*6 (GSHO 1842); *dsp1.a* with *nud1.a* and *fst3.c* in Bowman*7 (BW375, NGB 20614).

References:

1. Biffen, R.H. 1907. The hybridization of barleys. III. J. Agric. Sci. 2:183-206.
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. Gaul, H.P.K. 1986. (Personal communications).
5. Gaul, H. 1964. Mutations in plant breeding. Rad. Bot. 4:155-232.
6. Hayes, H.K., and H.V. Harlan. 1920. The inheritance of the length of internode in the rachis of the barley spike. U. S. Dept. Agric., Bull. 869. 26 pp.
7. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
8. Lehmann, L.C. 1985. (Personal communications).
9. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] Bot. Mag., Tokyo 36:25-38. [In Japanese.]
10. Ramage, R.T. and G.A. Wiebe. (Unpublished, see http://www.ars-grin.gov/cgi-bin/npgs/acc/display.pl?1053879).
11. Sameri, M., K. Takeda, and T. Komatsuda. 2006. Quantitative trait loci controlling agronomic traits in recombinant inbred lines from a cross of oriental- and occidental-type barley cultivars. Breed. Sci. 56:243-252.
12. Scholz, F. 1971. Utilization of induced mutations in barley. Recent information of linkage and chromosome mapping. p. 94-105. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
13. Scholz, F., and C. O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. I. Kulturpflanze 6:123-166.
14. Scholz, F., and C. O. Lehmann. 1959. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. III. Kulturpflanze 9:230-272.
15. Shahinnia, F., A. Druka, J. Franckowiak, M. Morgante, R. Waugh, and N. Stein. 2012. High resolution mapping of Dense spike-ar (*dsp.ar*) to the genetic centromere of barley chromosome 7H. Theor. Appl. Genet. 124:373-384.
16. Takahashi, R. 1951. Studies on the classification and geographic distribution of the Japanese barley varieties. II. Correlative inheritance of some quantitative characters with the ear type. Ber. Ohara Inst. landw. Forsch. 9:383-398.
17. Takahashi, R. 1987. Genetic features of East Asian barleys. pp. 7-20. *In* Yasuda, S., and T. Konishi (eds.) Barley Genetics V. Proc. Fifth Int. Barley Genetics Symp., Okayama, 1986. Sanyo Press Co. Okayama, Japan.
18. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.
19. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.
20. Taketa, S., T. Yuo, Y. Sakurai, S. Miyake, and M. Ichii. 2011. Molecular mapping of the short awn 2 (*lks2*) and dense spike 1 (*dsp1*) genes on barley chromosome 7H. Breed. Sci. 61: 80-85.
21. Takezaki, Y. 1927. [On the genetical formulae of the length of spikes and awns in barley, with reference to the computation of the valency of the heredity factors.] Rep. Agric. Exp. Sta., Tokyo 46:1-43. [In Japanese.]
22. Ubisch, G. von. 1916. Beitrag zu einer Faktorenanalyse von Gerste. Z. Indukt. Abstammungs. Vererbungsl. 17:120-152.
23. Ullrich, S.E., and A. Aydin. 1988. Mutation breeding for semi-dwarfism in barley. p. 135-144. *In* Semi-dwarf Cereal Mutants and Their Use in Cross-breeding III. IAEA-TECDOC-455. IAEA, Vienna.

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:174.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:53.
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:63-65.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:50-53.

BGS 17, Chlorina seedling 4, *fch4*

Stock number:	BGS 17
Locus name:	Chlorina seedling 4
Locus symbol:	*fch4*

Previous nomenclature and gene symbolization:

Chlorina seedling 4 = *f4* (5, 8).

Yellow viable = *yv* (8).

Inheritance:

Monofactorial recessive (8).

Located in chromosome 7HL (2, 3, 7, 8); slightly distal from the *nud1* (naked caryopsis 1) locus (3); about 4.4 cM proximal from the *lks2* (short awn 2) locus (3); *fch4.g* is associated with SNP marker 2_0042 (position 118.80 cM) in 7H bin 07 of the Bowman backcross-derived line BW360 (1); *fch4.g* is associated with SNP markers 1_0050 to 2_0042 (positions 87.33 to 118.80 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW337 (1), in 7H bin 07.

Description:

Seedlings are bright yellow-green on emergence and maintain this color until they are nearly mature. Seedlings and plants are relatively vigorous, but heading is delayed (8). Bowman backcross-derived plants with *fch4.g* gene, BW380, showed a 7 to 11 day delay in heading and are about 10% taller than Bowman. Spikes have one or two more kernels, kernels are slightly thinner and kernel weights were reduced by 10 to 20%, test weights were slightly lower, and grain yields were about half that of Bowman (4).

Origin of mutant:

A beta-ray induced mutant in Montcalm (CIho 7149) (8).

Mutational events:

fch4.g (Alb Acc 258, GSHO 1214) in Montcalm (CIho 7149) (8).

Mutant used for description and seed stocks:

fch4.g (GSHO 1214) in Montcalm; *fch4.g* in Bowman (PI 483237)*7 (GSHO 1851, BW360, NGB 20599); *fch4.g* in Bowman (PI 483237)*7 (BW337, NGB 22132).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1976. Approximate position of the chlorina mutants *f4f4* and *f8f8* on chromosome 1. Barley Genet. Newsl. 6:10-13.
3. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.
4. Franckowiak, J.D. (Unpublished).
5. Robertson, D.W. 1964. New genes in barley with their relation to linkage groups and chromosomes. p. 159-180. *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.
6. 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.
7. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. Barley Genet. Newsl. 2:93-

98.
8. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:
T.E. Haus. 1975. Barley Genet. Newsl. 5:98.

Revised:
T. Tsuchiya. 1980. Barley Genet. Newsl. 10:103.
J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:63.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:54-55.

BGS 18, Chlorina seedling 5, *fch5*

Stock number:	BGS 18
Locus name:	Chlorina seedling 5
Locus symbol:	*fch5*

Previous nomenclature and gene symbolization:

Chlorina seedling 5 = *f5* (6).
Yellow viable = *yv2* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 7HS (2, 5, 6); proximal from the *brh1* (brachytic 1) locus (2); about 25.9 cM proximal from the *Rpg1* (reaction to *Puccinia graminis* 1) locus (4); *fch5.f* is associated with SNP markers 1_0965 to 1_0451 (positions 38.08 to 41.79 cM) in 7H bin 03 of the Bowman backcross-derived line BW361 (1), likely in 7H bin 03.

Description:

Seedlings are pale yellow to ivory in color at emergence and remain this color until they are nearly mature (6). Seedlings were relatively weak and rarely survived to maturity in the field at Fargo, North Dakota, USA; however, in the greenhouse they gradually became darker green and produced late-maturing plants (3).

Origin of mutant:

A spontaneous mutant in Gateway (CIho 10072) (6).

Mutational events:

fch5.f (GSHO 1215, Alb Acc 328) in Gateway (6).

Mutant used for description and seed stocks:

fch5.f in Gateway (GSHO 1215); *fch5.f* in Bowman (PI 483237)*5 (GSHO 1827); *fch5.f* in Bowman*7 (BW361, NGB 20600).

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. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.
3. Franckowiak, J.D. (Unpublished).
4. Jin, Y., B.J. Steffenson, and J.D. Franckowiak. 1993. Linkage between the *Rpg1* gene for stem rust resistance and the *f5* locus on barley chromosome 1. Crop Sci. 33:642-643.
5. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. Barley Genet.Newsl. 2:93-98.
6. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.

Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:99.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:64.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:56.

BGS 34, Male sterile genetic 50, *msg50*

Stock number:	BGS 34
Locus name:	Male sterile genetic 50
Locus symbol:	*msg50*

Previous nomenclature and gene symbolization:

Male sterile genetic hm = *msg,,hm* (4).

Male sterile genetic gh = *msg,,gh* (4).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HL (2); about 13.6 cM from the *lks2* (short awn 2) locus (2); *msg50.hm* is associated with SNP markers 2_0230 to 2_1229 (positions 118.80 to 176.37 cM) in 7H bins 07 to 10 of the Bowman backcross-derived line BW588 (1); *msg50.gh* is associated with SNP markers 2_13350 to 2_03859 (positions 107.44 to 152.29 cM) in 7H bins 07 to 10 of the Bowman backcross-derived line BW 972 (1).

Description:

Selfing - 0% is reported (4), but occasionally 5 to 10% selfed seed set is observed.

Outcrossing - complete female fertility (4).

Stamens - anthers slightly smaller than fertile sib with filament elongation and stomium (4).

Origin of mutant:

A spontaneous mutant in Maris Mink (PI 467824) (4).

Mutational events:

msg50.gh in Maris Mink (MSS435) (2, 4); *msg50.hm* (MSS466, GSHO 2404) in Berac (PI 355136) (2, 4).

Mutant used for description and seed stocks:

msg50.hm in Berac (GSHO 2404); *msg50.hm* in Bowman (PI 483237)*7 (GSHO 1861, BW588, NGB 23448); *msg50.gh* in Maris Mink (MSS435), *msg50.gh* in Bowman*4 (BW972, NGB 23467).

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. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Franckowiak, J.D. 1993. Identification of two additional loci that control genetic male sterility in barley. Barley Genet. Newsl. 22:10-11.
4. Hockett, E. A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:83.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:57.

BGS 38, Seminudoides 1, *smn1*

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

Previous nomenclature and gene symbolization:

Seminuoides = *smn* (4, 5).

Inheritance:

Monofactorial recessive (4, 5).

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

Description:

The caryopsis of *smn1* plants is not completely covered because gaps develop between the margins of the lemma and palea. Adherence of the lemma and the palea to the pericarp is poor, but the grain does not thresh free from the hull at maturity. Tiller number and grain yield are often reduced (5). Plants of the Bowman backcross-derived line for *smn1.a*, BW871, had kernels that were slightly shorter and thinner and weighed 10 to 20% 1ess, 4.7 vs. 5.6 mg, than to Bowman kernels. The grain yield of BW871 varied from 1/3 to 3/4 that of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Haisa (PI 197617) (4, 5).

Mutational events:

smn1.a (Mut. 4128, GSHO 1602) in Haisa (PI 197617) (5).

Mutant used for description and seed stocks:

smn1.a (Mut. 4128, GSHO 1602) in Haisa; *smn1.a* in Bowman (PI 483237)*5 (GSHO 3420, BW871, NGB20786).

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. Scholz, F. 1956. Mutationsversuche an Kulturpflanzen. V. Die Vererbung zweier sich variabel manifestierender Übergangsmerkmale von bespelzter zu nackter Gerste bei röntgeninduzierten Mutanten. Kulturpflanze 4:228-246.
5. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. I. Kulturpflanze 6:123-166.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. Barley Genet. Newsl. 32:225.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:58.

BGS 43, Multiovary 1, *mov1*

Stock number: BGS 43
Locus name: Multiovary 1
Locus symbol: *mov1*

Previous nomenclature and gene symbolization:
Multiovary 5 = *mo5* (5).
Multiovary 6 = *mo6b* (3, 4).

Inheritance:
Monofactorial recessive (3).
Located in chromosome 7HL (3, 4); near the *Amy2* (alpha-amylase 2) locus (3); *mov1.f* co-segregated with molecular markers *Hsp17* and JS192.5 in 7H bin 07 (4); the plant of Bowman backcross-derived line for *mov1.f*, BW523, tested with SNP markers did not have the *mov1.f* allele, but it is present in the stock (1).

Description:
The *mov1.f* (*mov6b*) mutant has four carpels and two sepal-like structures where the lodicules should be. Stamens and lodicules are absent. It is presumed that the three stamens found in wild-type flowers have been converted into three additional carpels and that the lodicules have become leaf-like structures (4). The *mov1.f* plants appear normal, but are completely sterile. The stock must be maintained as a heterozygote (2). This mutant appears morphologically similar to the *mo5* mutant (5), which was reported to map to the same region of chromosome 7HL (6). A seed stock was, however, not available for allelism tests (4).

Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) (3).

Mutational events:
mov1.f (*mo6b*, FN01, GSHO 3641) in Steptoe (CIho 15229) (2); *mov1.e* (*mo5*) (4, 5); *mov1.i* (5102, *mo6c*), *mov1.j* (5103, *mo6d*) from the Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany (4).

Mutant used for description and seed stocks:
mov1.f (*mo6b*, FN01, GSHO 3641) in Steptoe; *mov1.f* from Steptoe in Bowman (PI 483237)*4 (BW523, NGB 22158).

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. Kleinhofs, A. (Unpublished).
3. Soule, J., I. Skodova, D. Kudrna, A. Kilian, and A. Kleinhofs. 1995. Molecular and genetic characterization of barley flower development mutants. Barley Genet. Newsl. 25:76-80.
4. Soule, J.D., D.A. Kudrna, and A. Kleinhofs. 2000. Isolation, mapping, and characterization of two barley multiovary mutants. J. Hered. 91:483-487.
5. Tazhin, O.T. 1980. The linkage of the genes *mo5* and *n* in barley. Barley Genet. Newsl. 10:69-72.
6. Tazhin, O.T. 1982. Value of crossing-over between linked genes *mo5* and *n* in barley. Barley Genet. Newsl. 12:18-21.

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:185.

Revised:

A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:59-60.

BGS 48, Reaction to *Pyrenophora teres* 4, *Rpt4*

Stock number:	BGS 48
Locus name:	Reaction to *Pyrenophora teres* 4 (*P. teres* f. *maculata*, spot form of net blotch, SFNB)
Locus symbol:	*Rpt4*

Previous nomenclature and gene symbolization:

QTL for resistance to *Pyrenophora teres* chromosome 7 = *QRpt7* (2).

Inheritance:

Monofactorial dominant (5, 6).

Located in chromosome 7HL (6); about 7.9 cM distal from RFLP marker *Xprs117 (D)* in 7H bin 09 (3, 5, 6); *Rpt4.e* is between DArT markers bPb-0027 and bPb-3484 (2).

Description:

The seedling reactions of Galleon with the *Rpt4.e* gene for resistance to *Pyrenophora teres* f. *maculata* (*Ptm*) isolates was typically measured as 2 to 4 on a scale where 1 = very resistant and 10 = very susceptible (5, 6). The *Rpt4.e* gene confers a consistent, but variable level of seedling and adult resistance to isolates of *Pyrenophora teres* f. *maculata* (*Ptm*), spot form of net blotch (SFNB) (5, 6). The adult plant resistance (APR) conferred by *Rpt4.e* was considered ineffective in controlling losses caused by *Ptm* (6). The *Rpt4.e* gene does not provide resistance to the long term standard Canadian *Ptm* isolate WRS857 and is considered ineffective in western Canada (3). The *Rpt4* region of 7HL may have four different loci involves with susceptibility to *Ptm*.

Origin of mutant:

Natural occurrence in Galleon (Clipper/Hiproly//3*Proctor/CIho 3576) (5, 6), but may have originated from CIho 3576 (a reselection from PI 57631 that originated from Egypt) (5, 6); resistant reactions to *Ptm* are conferred by CIho 5791 (PI 95095) from Ethiopia (1, 4), CIho 9214 (PI 186125), and CIho 9440 (PI 190786) from Korea (4).

Mutational events:

Rpt4.e in Galleon (5, 6); QTL for seedling and adult plant resistance to *Ptm* were located at the same chromosomal region in CIho 9214 (PI 186125) from Korea, Dairokkaku (CIho 10954) from Japan, and Chebec (Orge_Martin/2*Clipper//Schooner), Keel (CP118197/Clipper//WI2645), and Tilga (Forrest/Cantala) from Australia (6); the breeding line TR251 (TR229//AC Oxbow/ND7556) contains a resistance gene of unknown origin (2).

Mutant used for description and seed stocks:

Rpt4.e in Galleon; *Rpt4.e* in TR251.

References:

1. Buchannon, K.W., and W.C. McDonald. 1965. Sources of resistance in barley to *Pyrenophora teres*. Can. J. Plant Sci. 45:189-193.
2. Grewal, T.S., B.G. Rossnagel, C.J. Ponzniak, and G.J. Scoles. 2008. Mapping quantitative trait loci associated with barley net blotch resistance. Theor. Appl. Genet. 116: 529-539.
3. Grewal, T.S., B.G. Rossnagel, and G.J. Scoles. 2008. The utility of molecular markers for barley net blotch resistance across geographic regions, Crop Sci. 48:2321-2333.
4. Tekauz, A., and K.W. Buchannon. 1977. Distribution of and sources of resistance to biotypes of *Pyrenophora teres* in Western Canada. Can. J. Plant Sci. 57:389-395.
5. Williams, K.J., A. Lichon, P. Gianquitto, J.M. Kretschmer, A. Karakousis, S. Manning,

P. Langridge, and H. Wallwork. 1999. Identification and mapping of a gene conferring resistance to the spot form of net blotch (*Pyrenophora teres* f. *maculata*) in barley. Theor. Appl. Genet. 99:323-327.
6. Williams, K.J., G.J. Platz, A.R. Barr, J. Cheong, K. Willsmore, M. Cakir, and H. Wallwork**.** 2003. A comparison of the genetics of seedling and adult plant resistance to the spot form of net blotch (*Pyrenophora teres* f. *maculata*). Aust. J. Agric. Res. 54:1387-1394.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:61-62.

BGS 49 Slender dwarf 8, *sld8*

Stock number:	BGS 49
Locus name:	Slender dwarf 8
Locus symbol:	*sld8*

Previous nomenclature and gene symbolization:

Slender dwarf i = *sld.i* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS or 4HL (1); *sld8.i* is associated with SNP markers 1_0232 to 1_0376 (positions 44.83 to 54.30 cM) in 7H bins 03 to 04 and with SNP markers 1_0614 and 1_0510 (positions 146.91 and 149.26 cM) in 4H bin 10 of the Bowman backcross-derived line BW855 (1).

Description:

The plant height variant, *sld8.i*, was isolated from Wisconsin Pedigree 38 while it was being backcrossed into Bowman to transfer the *lbi1.a* (long basal rachis internode 1) gene (2). Plants for the Bowman backcross-derived line for *sld8.i*, BW855, were 3/4 the height of Bowman and had short coiled to kinked peduncles that were 2/3 normal length. The BW855 plants produced kernels that were 10 to15% lighter than those of Bowman. Grain yield of BW855 was 10 to 20% lower than that of Bowman (2).

Origin of mutant:

Natural occurrence in Wisconsin Pedigree 38 (Barbless, CIho 5105, GSHO 580) (2).

Mutational events:

sld8.i (GSHO 2484) in Wisconsin Pedigree 38 (Barbless, CIho 5105, GSHO 580) (2).

Mutant used for description and seed stocks:

sld8.i (GSHO 2484) in Wisconsin Pedigree 38; *sld8.i* in Bowman (PI 483237)*4 (GSHO 2356); *sld8.i* in Bowman (PI 483237)*7 (BW855, NGB 22292).

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. 2013. Barley Genet. Newsl. 43:63.

BGS 57, Elongated outer glume 1, *eog1*

Stock number:	BGS 57
Locus name:	Elongated outer glume 1
Locus symbol:	*eog1*

Previous nomenclature and gene symbolization:

Extended outer glumes = *e* (10).
Wide glumes = *w* (10).
Macrolepis = *lep-e* (*lep-a*) (7, 14, 15).
Long outer glume = *log* (16).
Elongated outer glume = *e* (3, 16).

Inheritance:

Monofactorial recessive (1, 2, 17).

Located in chromosome 2HL (6); about 30.5 cM proximal from the *vrs1* (six-rowed spike 1) locus (3, 11); *eog1.a* is associated with SNP markers 2_0387 to 2_0528 (positions 90.54 to 118.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW299 (4); *eog1.c* is associated with SNP markers 1_0996 to 2_0699 (positions 89.0 to 126.33 cM) in 2H bins 07 to 09 of the Bowman backcross-derived line BW300 (4); *eog1.d* is associated with SNP markers 1_0498 to 1_1402 (positions 81.43 to 119.86 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW301 (4); *eog1.e* is associated with SNP markers 1_1493 to 2_0476 (positions 76.05 to 96.47 cM) in 2H bins 06 to 07 of the Bowman backcross-derived line BW302 (4), likely in 2H bin 07.

Description:

A multiple allelic series exists at this locus, which controls increased size of the outer glumes (glumes) of the spikelet. Glume width varies from 2.5 to 4.0 mm depending on genetic background and specific allele (17, 18). Glume awn length varies from awnless to nearly as long as the lemma awn (92 mm) depending on the *eog1* allele present and genes at other loci (10, 17), but some confusion has occurred regarding alleles at the *eog1* locus and expression of other glume characteristics (16, 17). The size of the glume can range from less than twice normal width in CIho 14955 to lemma-like glumes in Triple Bearded Mariout (5). Kernels of the Bowman backcross-derived lines for *eog1.a* (BW299) and *eog1.c* (BW300) were slightly larger than those of Bowman in non-heat stressed environments. Other morphological and agronomic traits of BW299 and BW300 were similar to those of Bowman (5).

Origin of mutant:

A spontaneous mutant and natural occurrence in a few cultivars (1, 17).

Mutational events:

eog1.a in Triple Bearded Mariout (CIho 2523, GSHO 29) (6, 17); for additional mutants and variants at the *eog1* locus see Groups I and II mutants of Tsuchiya (17); *lep-e.1* (NGB 114210, GSHO 960), *-e.2* (NGB 114211) in Gull (CIho 1145), *-e.3* (NGB 114212), *-e.4* (NGB 114213), *-e.5* (NGB 114214), *-e.6* (NGB 114215), *-e.7* (NGB 114216), *-e.8* (NGB 114217), *-e.9* (NGB 114218), *-e.10* (NGB 114219), *-e.11* (NGB 114220), *-e.12* (NGB 114221), *-e.13* (NGB 114222), *-e.29* (NGB 114239), *-e.34* (NGB 114244), *-e.42* (NGB 114253, NGB 114386), *-e.45* (NGB 114258), *-e.49* (NGB 114265), *-e.50* (NGB 114266), *-e.51* (NGB 114267), *-e.52* (NGB 114268), *-e.53* (NGB 114269), *-e.54* (NGB 114270) in Bonus (PI 189763), *-e.14* (NGB 114223), *-e.15* (NGB 114224), *-e.16* (NGB 114225), *-e.17* (NGB 114226), *-e.18* (NGB 114227), *-e.19* (NGB 114228, NGB 114229),

-e.20 (NGB 114230), *-e.21* (NGB 114231), *-e.22* (NGB 114232), *-e.23* (NGB 114233), *-e.24* (NGB 114234), *-e.25* (NGB 114235), *-e.26* (NGB 114236), *-e.27* (NGB 114237), *-e.28* (NGB 114238), *-e.30* (NGB 114240), *-e.31* (NGB 114241), *-e.32* (NGB 114242), *-e.33* (NGB 114243), *-e.38* (NGB 114248) in Foma (CIho 11333), *-e.35* (NGB 114245), *-e.36* (NGB 114246), *-e.37* (NGB 114247), *-e.39* (NGB 114249, NGB 114250), *-e.40* (NGB 114251), *-e.41* (NGB 114252), *-e.43* (NGB 114254, NGB 114255), *-e.44* (NGB 114256), *-e.46* (NGB 114257), *-e.47* (NGB 114261, NGB 114262), *-e.48* (NGB 114263, NGB 114264) in Kristina (NGB 1500) (7, 13, 14, 15); *eog1.b* in PI 173567 (G 8) (17); *eog1.c* in CIho 14955 (enlarged outer glumes) (5); *eog1.d* (FN05, GSHO 3656), *eog1.f* (FN284, GSHO 3657), *eog1.g* (FN296, GSHO 3658), *eog1.h* (FN297, GSHO 3659), *eog1.i* (FN298, GSHO 3660) (enlarged outer glumes), *eog1.j* (FN325, GSHO 3661) (enlarged outer glumes), *eog1.k* (FN341, GSHO 3662), *eog1.l* (FN421, GSHO 3663), *eog1.m* (FN428, GSHO 3664), *eog1.n* (FN463, GSHO 3665), *eog1.o* (FN464, GSHO 3666), *eog1.p* (FN465, GSHO 3667), *eog1.q* (FN466, GSHO 3668), *eog1.r* (FN491, GSHO 3669), *eog1.s* (FN503, GSHO 3670) in Steptoe (CIho 15229) (12); *eog1.e* in AB1380 (Nuri Pori, T1-33, GSHO 285, CIho 5152) (12); *eog1.t* (Mut 3447/64) in Proctor (PI 280420) (9).

Mutant used for description and seed stocks:

eog1.a in Triple Bearded Mariout (CIho 2523, GSHO 29); *lep-e.1* (GSHO 960, NGB 114210) in Gull (CIho 1145); *eog1.a* in Bowman (PI 483237)*7 (GSHO 1891, BW299, NGB 20583); *eog1.c* from CIho 14955 in Bowman*7 (GSHO 1892, BW300, NGB 20584); *eog1.d* from Steptoe (FN05, GSHO 3656) in Bowman*3 (BW301, NGB 22101); *eog1.e* from Nuri Pori (GSHO 285, PI 87189) in Bowman*3 (BW302, NGB 22102).

References:

1. Biffen, R.H. 1906. Experiments on the hybridisation of barleys. Proc. Cambridge Phil. Soc. 13:304-308.
2. Biffen, R.H. 1907. Studies in the inheritance of disease-resistance. J. Agric. Sci. 2:109-128.
3. Bose, R.D., M.A. Aziz, and M.P. Bhatnagar. 1937. Studies in Indian barleys. IV. The inheritance of some anatomical characters responsible for lodging and of some ear-head characters in an interspecific cross between two Pusa barleys. Indian J. Agric. Sci. 7:48-88.
4. 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.
5. Franckowiak, J. (Unpublished).
6. Griffee, F. 1925. Correlated inheritance of botanical characters in barley, and the manner of reaction to *Helminthosporium sativum*. J. Agric. Res. 30:915-925.
7. 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.
8. Hang, A. 1995. List of genetic stocks in barley arranged in numerical order of BGS (Barley Genetic Stock) numbers. USDA-ARS National Small Grains Germplasm Research Facility, Aberdeen, ID 83210. (Notes from T. Tsuchiya on the collection of barley genetic stocks at Colorado State University and see Tsuchiya T. 1984. List of genetic stocks with BGS numbers. Barley Genet. Newsl. 14:100-139.)
9. Häuser, H., and G. Fischbeck. 1972. Translocations and genetic analysis of other mutants. Barley Genet. Newsl. 2:28-29.
10. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
11. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-

440.
12. Kleinhofs, A. (Unpublished).
13. Lundqvist, U. 1994. Coordinator's report: Ear morphology genes. Barley Genet. Newsl. 23:175-176.
14. Nötzel, H. 1952. Genetische Untersuchungen an röntgeninduzierten Gerstenmutanten. Kühn-Archiv. 66:72-132.
15. Nybom, N. 1954. Mutation types in barley. Acta Agric. Scand. 4:430-456.
16. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1955. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement II, 1947-1953. Agron. J. 47:418-425.
17. Tsuchiya, T. 1974. Preliminary results on genetic studies of outer glume characters in barley. Barley Genet. Newsl. 4:76-78.
18. Tsuchiya, T. 1974. Further results of allelism testing in barley. Barley Genet. Newsl. 4:82-85.

Prepared:

T. Tsuchiya. 1975. Barley Genet. Newsl. 5:101.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:92-93.
J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:64-66.

BGS 64, Desynapsis 7, *des7*

Stock number:	BGS 64
Locus name:	Desynapsis 7
Locus symbol:	*des7*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3H (1, 2); associated with the *Btr1* (brittle rachis 1) locus based on linkage drag (2); *des7.j* is associated with SNP markers 2_0742 to 1_0653 (positions 29.05 to 92.55 cM) in 3H bins 02 to 06 of the Bowman backcross-derived line BW246 (1). Previously *des7.j* was located in chromosome 2H (3).

Description:

The chromosomes are paired during the pachytene stage of microsporogenesis, but they undergo desynapsis during diplotene. The degree of desynapsis is d = 6.1 ± 2.6, ranging from 7 ring bivalents (d = 0) to 14 univalents (d = 14). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 3.0 micronuclei per tetrad with a range of 0 to 13. Female fertility is about 33%, and about 13% of the selfed seeds are trisomics (3). Grain yields of the Bowman backcross-derived line for *des7.j*, BW246, were 2/3 to 3/4 those of Bowman. BW246 and Bowman were similar for other morphological traits (2). Seed set for BW246 was about 50% when grown under greenhouse conditions (2).

Origin of mutant:

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

Mutational events:

des7.j (GSHO 598) in Betzes (PI 129430) (5).

Mutant used for description and seed stocks:

des7.j (GSHO 598) in Betzes; *des7.j* in Bowman (PI 483237)*6 (BW246, NGB 22072).

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.
4. Ramage, R.T., and J.M. Hernandez-Soriano. 1971. Desynaptic genes in Betzes barley. Barley Genet. Newsl. 1:38.
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, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:130.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:100.

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:67.

BGS 72, Globosum-c, *glo-c*

Stock number: BGS 72
Locus name: Globosum-c
Locus symbol: *glo-c*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 4).

Located in chromosome 2H (5); *glo-c.1004* is associated with SNP markers 2_0387 to 1_0823 (positions 90.54 to 133.59 cM) in 2H bins 07 to 09 of the Bowman backcross-derived line BW394 (1).

Description:

The kernels are more rounded or globe-shaped than in the parental cultivar. The spike is very lax with long rachis internodes (2). Compared to Bowman, the Bowman backcross-derived line for *glo-c.1004*, BW394, had a 10 to 15% longer rachis internodes, 5.3 vs. 4.7 mm, and four more kernels per spike. Peduncles and plants were slightly shorter and kernels were slightly shorter and lighter. BW394 plants were more susceptible to lodging than Bowman, but grain yields were similar (3).

Origin of mutant:

An X-ray induced mutant in Villa (PI 399506) (2).

Mutational events:

glo-c.1004 (1080/72, GSHO 1329) in Villa (PI 399506) (2).

Mutant used for description and seed stocks:

glo-c.1004 (GSHO 1329) in Villa; *glo-c.1004* in Bowman (PI 483237)*4 (GSHO 1879); *glo-c.1004* in Bowman*7 (BW394, NGB 20632).

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. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
3. Franckowiak, J.D. (Unpublished).
4. Häuser, H., and G. Fischbeck. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
5. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:109.

Revised:

J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:68.

BGS 73, Angustifolium-a, *fol-a*

Stock number:	BGS 73
Locus name:	Angustifolium-a
Locus symbol:	*fol-a*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2), but heterozygotes can be identified based on leaf width. Located in chromosome 2HL (2, 5); close to the *vrs1* (six-rowed spike 1) locus based on linkage drag (4); *fol-a.1* is associated with SNP markers 1_0214 to 1_1250 (positions 150.96 to 161.08 cM) in 2H bins 10 to 11 of the Bowman backcross-derived line BW370 (1).

Description:

Most organs are reduced in size. Plants have narrow, dark green leaves and a stunted, grassy growth habit (2, 5). Plant height is about 2/3 normal and spikes are 1/2 normal. Spikelets are about 2/3 normal size and the kernels were thin under greenhouse conditions (3). Plants of the Bowman backcross-derived line for *fol-a.1*, BW370, were slightly shorter than Bowman and leaf blades were about 1/2 normal width, 5 vs. 9 mm, and relatively short. Rachis internodes of BW370 were shorter 4.4 vs. 4.9 mm, kernels were smaller and 10 to15% lighter, but grain yields were slightly higher (3). BW370 plants lodged easier than Bowman (3).

Origin of mutant:

An X-ray induced mutant in Proctor (PI 280420) (2, 5).

Mutational events:

fol-a.1 (2235/64, GSHO 1744) in Proctor (PI 280420) (2, 5).

Mutant used for description and seed stocks:

fol-a.1 (GSHO 1744) in Proctor; *fol-a.1* in Bowman (PI 483237)*7 (GSHO 1927, BW370, NGB 20609).

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. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
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. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:110.

Revised:

J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:69.

BGS 90, Erectoides-j, *ert-j*

Stock number: BGS 90
Locus name: Erectoides-j
Locus symbol: *ert-j*

Previous nomenclature and gene symbolization:
Erectoides-31 = *ert-31* (4).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 2H (3); based on linkage drag with the *Gth1* (toothed lemma 1) locus (3); *ert-j.31* is associated with SNP markers 3_1205 to 1_1533 (positions 139.43 to 141.56 cM) in 2H bin 09 of the Bowman backcross-derived line BW313 (1), in 2H bin 09.
Description:
Spikes are semicompact with rachis internode length estimates of 2.4 and 2.6 mm, and culms are about 3/4 normal length (7). Compared to Bowman plants, the plants of the Bowman backcross-derived line for *ert-j.31*, BW313, were 10 to 20% shorter, peduncles were 20 to 25% shorter, the average rachis internode length was 3.4 vs. 4.6 mm, and kernels were 10% shorter. Spikes had 1 to 3 fewer kernels, kernels were 10 to 20% lighter, and grain yields were 10 to 20% lower than those of Bowman (2).
Origin of mutant:
An X-ray induced mutant in Bonus (PI 189763) (4).
Mutational events:
ert-j.31 (NGB 112632, GSHO 484) in Bonus (PI 189763) (4); *ert-j.74* (NGB 112673) in Bonus (5); *ert-j.326* (NGB 112841) in Foma (CIho 11333) (6).
Mutant used for description and seed stocks:
ert-j.31 in Bonus (NGB 112632, GSHO 484); *ert-j.31* in Bowman (PI 483237)*7 (GSHO 1902, BW313, NGB 22109).
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. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
5. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
6. Lundqvist, U. (Unpublished).
7. 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. 26:129.
Revised:
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:70.

BGS 91, Erectoides-q, *ert-q*

Stock number:	BGS 91
Locus name:	Erectoides-q
Locus symbol:	*ert-q*

Previous nomenclature and gene symbolization:

Erectoides-101 = *ert-101* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 6H (1); *ert-q.101* is associated with SNP markers 1_0061 to 2_0379 (positions 70.15 to 160.38 cM) in 6H bins 05 to 09 of the Bowman backcross-derived line BW321 (1). Previously associated with chromosome 2H based on linkage drag with the *Gth1* (toothed lemma 1) locus (3).

Description:

Spikes of *ert-q.101* plants are semicompact and have slightly irregular placement of kernels (5). Seedling leaf blades are slightly wider than normal. The plants of the Bowman-backcross-derived line for *ert-q.101*, BW321, averaged 15% shorter, 76 vs. 89 cm, than Bowman; rachis internodes were 25% shorter, 3.3 vs. 4.5 mm; and awns were 3/4 normal length. The BW321 kernels were shorter 8.5 vs. 9.3 mm, and lighter, 5.0 vs. 5.6 mg, compared to Bowman kernels. Grain yields of BW321 were nearly equal to those of Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (5).

Mutational events:

ert-q.101 (NGB 112700, GSHO 1562) in Bonus (PI 189763) (5); *ert-q.392* (NGB 112909, GSHO 491), *-q.421* (NGB 112937) in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

ert-q.101 in Bonus (NGB 112700, GSHO 1562); *ert-q.101* in Bowman (PI 483237)*7 (GSHO 1903, BW321, NGB 22116).

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. 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. 26:130.

Revised:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:71.

BGS 100, Slender dwarf 4, *sld4*

Stock number: BGS 100
Locus name: Slender dwarf 4
Locus symbol: *sld4*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (6. 7).

Located in chromosome 2HS (6, 7); *sld4.d* is associated with SNP markers 3_1169 to 1_0498 (positions 48.40 to 81.4318 cM) in 2H bins 04 to 06 of the Bowman backcross-derived line BW864 (1), likely in 2H bin 06. Previously located in chromosome 7HS (5); near AFLP marker E 4134-2 in subgroup 6 of the Proctor/Nudinka map (5).

Description:

Plants with the *sld4.d* gene have reduced vigor and are light green in color during early stages of growth (7). Plants in the Bowman derived line for the *sld4.d* mutant, BW864, are apparently very environmentally sensitive. Plants varied from less than 1/2 to 3/4 of normal height and heading was delayed over 10 days in certain environments. The number of fertile spikelets per spike varied from 2/3 normal to near normal. Depending on the delay in heading, kernels varied from very thin to near normal. Grain yield of the Bowman backcross-derived line ranged from very low to nearly normal (2).

Origin of mutant:

A neutron induced mutant in Two-row Glacier (CIho 16615) (6). (Glacier is available as CIho 6976.)

Mutational events:

sld4.d (80-T-5899-2-13, DWS1368, GSHO 2479) in Two-row Glacier (CIho 16615) (3, 4, 6).

Mutant used for description and seed stocks:

sld4.d (GSHO 2479) in Two-row Glacier; *sld4.d* in Bowman (PI 483237)*4 (GSHO 1880; *sld4.d* in Bowman*7 (BW864, NGB 22301).

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. 1999. Coordinator's report: Semidwarf genes. Barley Genet. Newsl. 29:74-79.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley *(Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
6. Ramage, R.T., and P. Curtis. 1981. A light green, dwarf mutant located on chromosome 2. Barley Genet. Newsl. 11:37-38.
7. Ramage, R.T., and R.A. Ronstadt-Smith. 1983. Location of a light green dwarf mutant on chromosome 2. Barley Genet. Newsl. 13:62-64.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:89.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:218.

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:72-73.

BGS 101, Absent lower laterals 1, *als1*

Stock number: BGS 101
Locus name: Absent lower laterals 1
Locus symbol: *als1*

Previous nomenclature and gene symbolization:

Absent lower laterals = *als* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 3HL (6, 7. 9.10); about 31.2 cM distal from the *uzu1* (uzu 1) locus (7), about 39.7 cM proximal from the *cur2* (curly 2) locus (6); near AFLP marker E4234-11 in subgroup 28 of the Proctor/Nudinka map (8); *als1.a* in BW012 is about 4.6 cM proximal from RFLP marker KFP128 (1); *als1.a* in BW012 is about 16.7 cM proximal of SSR marker GBM1050 (3); *als1.a* is associated with SNP markers 2_0628 to 2_0650 (positions 151.97 to 192.0 cM) in 3H bins 10 to 12 of the Bowman backcross-derived line BW012 (4), in 3H bin11 (3).

Description:

Lateral spikelets at the base of the spike fail to develop or are partially developed. Tillers are large, coarse, and stiff, and only 1 or 2 tillers are produced in the six-rowed stock (6). The *als1.a* plants resemble those produced by the uniculm 2 (*cul2*) mutant (6). Plants of the Bowman backcross-derived line commonly produce 3 to 4 tillers with short, malformed spikes (irregular placement of central and lateral spikelets); and seed yields are very low (1, 2). The *als1.a* plants produced primary tillers, but secondary tillers were not formed (2). Other morphological differences between BW012 and Bowman included longer awns, 17 vs. 12 cm, and 3 to 5 more kernels per spike. Kernels were slightly longer and wider, but kernel weights were about 10% lighter (5).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (CIho 7149) (6).

Mutational events:

als1.a (Alb Acc 281, GSHO 1065) in Montcalm (CIho 7149) (6).

Mutant used for description and seed stocks:

als1.a in Montcalm (GSHO 1065); *als1.a* in Bowman (PI 483237)*7 (GSHO 1990, BW012, NGB 20420).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley uniculm 2 (*cul2*) mutant. Theor. Appl. Genet. 106:846-857.
2. Dabbert, T., R.J. Okagaki, S. Cho, J. Boddu, and G.J. Muehlbauer. 2009. The genetics of barley low-tillering mutants: *absent lower laterals* (*als*). Theor. Appl. Genet. 118:1351-1360.
3. Dabbert, T., R.J. Okagaki, S. Cho, S. Heinen, J. Boddu, and G.J. Muehlbauer. 2010. The genetics of barley low-tillering mutants: *low number of tillers-1* (*lnt1*) Theor. Appl. Genet. 121:705-715.
4. 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.
5. Franckowiak, J.D. (Unpublished).
6. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their

linkages. Can. J. Genet. Cytol. 2:397-415.
7. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:251-264.
8. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
9. Shahla, A., and T. Tsuchiya. 1983. Telotrisomic analysis in Triplo 3S in barley. Barley Genet. Newsl. 13:25.
10. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 4:66-69.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:123.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:135.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:219.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:74-75.

BGS 108, Albino lemma 1, *alm1*

Stock number:	BGS 108
Locus name:	Albino lemma 1
Locus symbol:	*alm1*

Previous nomenclature and gene symbolization:

Albino lemma = *al* (12).
Eburatum = *ebu-a* (5).

Inheritance:

Monofactorial recessive (12).

Located in chromosome 3HS (12); about 16.5 cM distal from the *uzu1* (uzu 1) locus (3, 8, 10, 11, 12); about 4.8 cM proximal from RFLP marker MWG844B in 3H bin 04 (1); *alm1.a* is associated with SNP markers 2_1402 to 1_0628 (positions 78.82 to 135.80 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW011 (2), likely in 3H bin 05.

Description:

The lemma and palea are white in color and mostly devoid of chlorophyll, but they terminate into green tips with green awns. The basal part of lower leaf sheaths and stem nodes are devoid of chlorophyll. Ligules and joints between the leaf sheath and blade are white in color (12, 13). Plant vigor was reduced slightly and heading was delayed by 2 to 4 days in the Bowman backcross-derived line for *alm1.a*, BW011 (4). Kernels of BW011 were thin and weighted nearly 20% less, 4.6 vs. 5.6 mg, than those of Bowman. Grain yields of BW011 were 1/2 to 3/4 those of Bowman (4).

Origin of mutant:

Spontaneous occurrence in an unknown cultivar (Russia 82) (OUU086, NSL 43389) (12).

Mutational events:

alm1.a (GSHO 270) in Russia 82 (OUU086, NSL 43389) (12); *alm1.b* in Liberty (CIho 9549) (3); *alm1.c* (Mut 966/61) in Proctor (PI 280420) (6); *ebu-a.1* (NGB 115236), *-a.2* (NGB 115237), *-a.3* (NGB 115238) in Foma (CIho 11333) (5, 13); *ebu-a.4* (NGB 115239), *-a.5* (NGB 115240) in Foma (9); *alm1.d* (γ06-03, GSHO 3682), *alm1.e* (FN530, GSHO 3683) in Morex (CIho 15773) may be an allele based on phenotypic similarity (7).

Mutant used for description and seed stocks:

alm1.a (GSHO 270) in Russia 82; *alm1.a* in Bowman (PI 483237)*8 (GSHO 1953, BW011, NGB 20419).

References:

1. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. Theor. Appl. Genet. 103:415-424.
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. Eslick, R.F., W.L. McProud. 1974. Positioning of the male sterile 5 (*msg5*) on chromosome 3. Barley Genet. Newsl. 4:16-23.
4. Franckowiak, J.D. (Unpublished).
5. 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.
6. Häuser, H., and G. Fischbeck. 1972. Translocations and genetic analysis of other mutants. Barley Genet. Newsl. 2:28-29.
7. Kleinhofs, A. (Unpublished).
8. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:251-264.
9. Lundqvist, U. (Unpublished).
10. Moriya, I., and R. Takahashi. 1980. Linkage studies of three barley mutants. Barley Genet. Newsl. 10:47-51.
11. Nonaka, S. 1973. A new type of cultivar, Mitake, with very few in number, but thick and stiff culms. Barley Genet. Newsl. 3:45-47.
12. Takahashi, R., and J. Hayashi. 1959. Linkage study of albino lemma character in barley. Ber. Ohara Inst. landw. Biol., Okayama Univ. 11:132-140.
13. Tsuchiya, T. 1973. Allelism testing between established marker stocks and Swedish mutants. Barley Genet. Newsl. 3:67-68.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:130.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:111.
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:143.
J.D. Franckowiak and U. Lundqvist. 2007. Barley Genet. Newsl. 37:222-223.
J.D. Franckowiak and A. Kleinhofs. 2013. Barley Genet. Newsl. 43:76-77.

BGS 115, Non-brittle rachis 1, *btr1*

Stock number: BGS 115
Locus name: Non-brittle rachis 1
Locus symbol: *btr1*

Previous nomenclature and gene symbolization:

Non-brittle rachis = *r* (14).
Non-brittle rachis = *b* (8).
Non-brittle rachis 1 = *bt1* (3).

Inheritance:

Monofactorial recessive in crosses to *Hordeum vulgare* subsp. *spontaneum* (8, 10, 14). Located in chromosome 3HS (12, 13); very close or semi-allelic to the *btr2* (non-brittle rachis 2) locus (12, 13); the *Btr1/Btr2* complex is about 15.4 cM distal from the *alm1* (albino lemma 1) locus (13); *btr2.b* is in a 4.3 cM interval between markers KFP216-RisP114 (4); *btr1.a* was placed within 0.8 cM of AFLP markers e09m25-08 and e45m11-11 (1, 5, 6, 9); the e09m25-08STS-ext sequence is tightly linked with *btr1*/*btr2* locus (1); *Btr* is associated with SNP markers 2_0742 to 1_0081 (positions 29.05 to 61.77 cM) in 3H bins 030 to 05 of the Bowman backcross-derived line BW102 (2); likely in 3H bin 04.

Description:

Joints at the rachis nodes are tough or non-brittle, which prevents segmentation or disarticulation of the rachis prior to maturity. Plants homozygous for the *btr1.a* allele do not shatter prior to harvest in contrast to wild barley (*Hordeum vulgare* subsp. *spontaneum*) (12). All cultivars with the *btr1.a* allele have a dominant allele at the *Btr2* locus. When crossed to cultivars with the *btr2.b* allele at the *Btr2* locus (genotype *Btr1Btr1btr2btr2*), F_1 plants have a brittle rachis. The segregation ratio in the F_2 generation is 1 brittle: 1 tough rachis (12). The majority of the cultivars distributed in Occidental region of the Old World have the *btr1.a* allele (11, 13). Failure to identify recombinants between the *btr1* and *btr2* loci is attributed to close linkage (5, 9). The abscission layer in barley is probably similar to that described in *Oryza sativa* (7).
The e09m25-08STS-ext sequence is tightly linked with *btr1*/*btr2* locus and exhibits a high amount of sequence diversity in wild barley, but is less polymorphic within either the East- or the West-type groups (1).

Origin of mutant:

A spontaneous mutant in *Hordeum vulgare* subsp. *spontaneum* (1, 3, 8, 14).

Mutational events:

btr1.a in an unknown race of *Hordeum vulgare* subsp. *spontaneum* (10, 13); the line A222 (CIho 11555) is recommended as the source line for the *btr1.a* gene.

Mutant used for description and seed stocks:

btr1.a in A 222 (GSHO 1233); *Btr1Btr2* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)*10 (GSHO 1937, BW102, NGB 20508).

References:

1. Azhaguvel, P., and T. Komatsuda. 2007. A phylogenetic analysis based on nucleotide sequence of a marker linked to the brittle rachis locus indicates a diphyletic origin of barley. Ann. Bot. 2007 100:1009-1015.
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. Johnson, I.J., and E. Åberg. 1943. Inheritance of brittle rachis in barley. J. Am. Soc. Agron. 35:100-106.
4. Kandemir, N., A. Yildirim, D.A. Kudrna, P.M. Hayes, and A. Kleinhofs. 2004: Marker assisted genetic analysis of non-brittle rachis trait in barley. Hereditas 141:272-277.
5. Komatsuda, T., and Y. Mano, 2002. Molecular mapping of the intermedium spike (*int-c*) and non-brittle rachis1 (*btr1*) loci in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 105:85-90.
6. Komatsuda, T., P. Maxim, N. Senthil, and Y. Mano, 2004. High-density AFLP map of nonbrittle rachis 1 (*btr1*) and 2 (*btr2*) genes in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 109:986-995.
7. Li, C., A. Zhou, and T. Sand. 2006. Rice domestication by reduced shattering. Science 311:1936-1939.
8. Schieman, E. 1921. Genetische Studien an Gerste. I. Zur Frage der Brüchigkeit an Gerste. Z. Indukt. Abstammungs. Vererbungsl. 26:109-143.
9. Senthil, N., and T. Komatsuda. 2005. Inter-subspecific maps of non-brittle rachis genes *btr1*/*btr2* using occidental, oriental and wild barley lines. Euphytica 145:215-220.
10. Takahashi, R. 1955. The origin and evolution of cultivated barley. p. 227-266. *In* M. Demerec (ed.) Advances in Genetics, Vol. 7. Academic Press, New York.
11. Takahashi, R. 1964. Further studies on the phylogenetic differentiation of cultivated barley. p. 19-26. *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.
12. Takahashi, R., and J. Hayashi. 1959. Linkage study of the complementary genes for brittle rachis in barley. Preliminary note. Nogaku Kenkyu 46:113-119. [In Japanese with English summary.]
13. Takahashi, R., and J. Hayashi. 1964. Linkage study of two complementary genes for brittle rachis in barley. Ber. Ohara Inst. landw. Biol., Okayama Univ. 12:99-105.
14. Ubisch, G. von. 1915. Analyse eines Falles von Bastardatavismus und Faktorenkoppelung bei Gerste. Z. Indukt. Abstammungs. Vererbungsl. 14:226-237.

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:181.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:149.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:78-79.

BGS 116, Non-brittle rachis 2, *btr2*

Stock number:	BGS 116
Locus name:	Non-brittle rachis 2
Locus symbol:	*btr2*

Previous nomenclature and gene symbolization:

Non-brittle rachis = *r* (14).
Non-brittle rachis = *b* (8).
Non-brittle rachis 2 = *bt2* (3).

Inheritance:

Monofactorial recessive in crosses to *Hordeum vulgare* subsp. *spontaneum* (8, 10, 14). Located in chromosome 3HS (12, 13); very close or semi-allelic to the *btr1* (non-brittle rachis 1) locus (12, 13); the *Btr1/Btr2* complex is about 15.4 cM distal from the *alm1* (albino lemma 1) locus (13); *btr2.b* is in a 4.3 cM interval between markers KFP216-RisP114 (4); *btr1.a* was placed within 0.8 cM of AFLP markers e09m25-08 and e45m11-11 (1, 5, 6, 9); the e09m25-08STS-ext sequence is tightly linked with *btr1*/*btr2* locus (1); *Btr* is associated with SNP markers 2_0742 to 1_0081 (positions 29.05 to 61.77 cM) in 3H bins 030 to 05 of the Bowman backcross-derived line BW102 (2); likely in 3H bin 04.

Description:

Joints at the rachis nodes are tough or non-brittle, which prevents segmentation or disarticulation of the rachis prior to maturity. Plants homozygous for the *btr2.b* allele do not shatter prior to harvest in contrast to wild barley (*Hordeum vulgare* subsp. *spontaneum*) (12). All cultivars with the *btr2.b* allele have a dominant allele at the *Btr1* locus. When crossed to cultivars with the *btr1.a* allele at the *Btr2* locus (genotype *btr1btr1Btr2Btr2*), F_1 plants have a brittle rachis. The segregation ratio in the F_2 generation is 1 brittle: 1 tough rachis (12). The majority of the cultivars distributed in Oriental region of the Old World have the *btr2.b* allele (11, 13). Failure to identify recombinants between the *btr1* and *btr2* loci is attributed to close linkage (5, 9). The abscission layer in barley is probably similar to that described in *Oryza sativa* (7). The e09m25-08STS-ext sequence is tightly linked with *btr1*/*btr2* locus and exhibits a high amount of sequence diversity in wild barley, but is less polymorphic within either the East- or the West-type groups (1).

Origin of mutant:

A spontaneous mutant in *Hordeum vulgare* subsp. *spontaneum* (1, 3, 8, 14).

Mutational events:

btr2.b in an unknown race of *Hordeum vulgare* subsp. *spontaneum* (10, 13).

Mutant used for description and seed stocks:

btr2.b in Sakigoke (OUJ349, GSHO 842); *btr2.b* in Bowman (PI 483237); *Btr1Btr2* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1565) in Bowman*10 (GSHO 1937, BW102, NGB 20508).

References:

1. Azhaguvel, P., and T. Komatsuda. 2007. A phylogenetic analysis based on nucleotide sequence of a marker linked to the brittle rachis locus indicates a diphyletic origin of barley. Ann. Bot. 2007 100:1009-1015.
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. Johnson, I.J., and E. Åberg. 1943. Inheritance of brittle rachis in barley. J. Am. Soc. Agron. 35:100-106.
4. Kandemir, N., A. Yildirim, D.A. Kudrna, P.M. Hayes, and A. Kleinhofs. 2004: Marker assisted genetic analysis of non-brittle rachis trait in barley. Hereditas 141:272-277.
5. Komatsuda, T., and Y. Mano, 2002. Molecular mapping of the intermedium spike (*int-c*) and non-brittle rachis1 (*btr1*) loci in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 105:85-90.
6. Komatsuda, T., P. Maxim, N. Senthil, and Y. Mano, 2004. High-density AFLP map of nonbrittle rachis 1 (*btr1*) and 2 (*btr2*) genes in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 109:986-995.
7. Li, C., A. Zhou, and T. Sand. 2006. Rice domestication by reduced shattering. Science 311:1936-1939.
8. Schieman, E. 1921. Genetische Studien an Gerste. I. Zur Frage der Brüchigkeit an Gerste. Z. Indukt. Abstammungs. Vererbungsl. 26:109-143.
9. Senthil, N., and T. Komatsuda. 2005. Inter-subspecific maps of non-brittle rachis genes *btr1*/*btr2* using occidental, oriental and wild barley lines. Euphytica 145:215-220.
10. Takahashi, R. 1955. The origin and evolution of cultivated barley. p. 227-266. *In* M. Demerec (ed.) Advances in Genetics, Vol. 7. Academic Press, New York.
11. Takahashi, R. 1964. Further studies on the phylogenetic differentiation of cultivated barley. p. 19-26. *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.
12. Takahashi, R., and J. Hayashi. 1959. Linkage study of the complementary genes for brittle rachis in barley. Preliminary note. Nogaku Kenkyu 46:113-119. [In Japanese with English summary.]
13. Takahashi, R., and J. Hayashi. 1964. Linkage study of two complementary genes for brittle rachis in barley. Ber. Ohara Inst. landw. Biol., Okayama Univ. 12:99-105.
14. Ubisch, G. von. 1915. Analyse eines Falles von Bastardatavismus und Faktorenkoppelung bei Gerste. Z. Indukt. Abstammungs. Vererbungsl. 14:226-237.

Prepared:
R. Takahashi. 1972. Barley Genet. Newsl. 2:182.

Revised:
J.D. Franckowiak and T. Konishi. 1996. Barley Genet. Newsl. 26:150.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:80-81.

BGS 118, Low number of tillers, *lnt1*

Stock number:	BGS 118
Locus name:	Low number of tillers 1
Locus symbol:	*lnt1*

Previous nomenclature and gene symbolization:

Reduced number of tillers = *rnt* (7).
Intermedium spike-l = *int-l* (6).

Inheritance:

Monofactorial recessive (7).

Located in chromosome 3HL (7); about 30.5 cM distal from the *uzu1* (uzu 1) locus (7, 8); lnt1.a mapped about 7.8 cM from SSR marker GBM1043 in 3HL (4); *lnt1.a* was not associated with any SNP markers in the Bowman backcross-derived line BW494 (2); *int-l.81* is associated with SNP markers 2_1517 to 2_1405 (positions 158.21 to 187.28 cM) in 3H bins 11 to12 of the Bowman backcross-derived line BW428 (2), in 3H bin11 (1).

Description:

The tiller number is reduced to 2 to 4 per plant. These tillers are formed soon after seedling emergence; hence, no late-emerging tillers are observed. Culms are thick and stiff and leaves are dark green (7). Plants mutants at the *lnt1* locus fail to produce secondary tillers (1). Occasional spike malformations occur in most environments. The spike may have irregular rachis internode lengths and is relatively short. The lower portion of the spike appears more compact than the upper portion (1, 6). Lateral spikelets in two-rowed cultivars are enlarged and have a pointed apex. Plants homozygous for a recessive allele at the *lnt1* locus headed slightly earlier than normal sibs (6). Compared to Bowman, the grain yields of the backcross-derived lines for *lnt1.a* (BW494) and *int-l.81* (BW428) were about 10% of those of Bowman. Kernels were longer and wider and weighed up to 20% more (3). Double mutant plants with the *lnt1.a* and *int-b.3* (intermedium spike-b) genes produced uniculm plants (1). The *lnt1.a* gene showed an epistatic interaction with high tillering mutants *gra-a.1* (granum-a) *int-m.85* (intermedium spike-m), *mnd1.a* (many noded dwarf 1) and *mnd6.*6 (many noded dwarf 6), producing double mutant plants with 2 to3 tillers (1). Reduced transcript levels for Contig12274, Bell-like homeodomain protein (*JuBel2*) in *lnt1.a* plants and co-segregation with *JuBel2* were observed (1).

Origin of mutant:

A spontaneous mutant in the hybrid Chikurin Ibaragi 2/Miho Hadaka (7).

Mutational events:

lnt1.a (GSHO 833) in Mitake (OUJ408) (7); *int-l.81* (NGB 115499, GSHO 1771) in Bonus (PI 189763) (3, 6); *lnt1.b* (FN468, GSHO 3678) in Steptoe (CIho 15229) may be an allele based on phenotypic similarity (5).

Mutant used for description and seed stocks:

lnt1.a (GSHO 833) in Mitake; *int-l.81* (NGB 115499, GSHO 1771) in Bonus; *lnt1.a* in Bowman (PI 483237)*8 (GSHO 1984, BW494, NGB 22157); *int-l.81* in Bowman*6 (GSHO 1961, BW428, NGB 22152).

References:

1. Dabbert, T., R.J. Okagaki, S. Cho, S. Heinen, J. Boddu, and G.J. Muehlbauer. 2010. The genetics of barley low-tillering mutants: *low number of tillers-1* (*lnt1*). Theor. Appl. Genet. 121:705-715.

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. (Unpublished).
4. Liu, Y.X., X.-H. Sun, B.-L. Xu, and G.-Y. Chen. 2012. Genetic analysis and molecular mapping of low-tillering mutants (*cul2.b* and *lnt1.a*) in barley (*Hordeum vulgare* L.). J. Plant Sci. 7:105-112.
5. Kleinhofs, A. (Unpublished).
6. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. Hereditas 108:13-26.
7. Nonaka, S. 1973. A new type of cultivar, Mitake, with very few in number, but thick and stiff culms. Barley Genet. Newsl. 3:45-47.
8. Nonaka, S. 1974. Further information of the *rnt* locus on chromosome 3. Barley Genet. Newsl. 4:56-58.

Prepared:

S. Nonaka. 1973. Barley Genet. Newsl. 3:120.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:113.
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:153.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:82-83.

BGS 119, Desynapsis 2, *des2*

Stock number:	BGS 119
Locus name:	Desynapsis 2
Locus symbol:	*des2*

Previous nomenclature and gene symbolization:

Desynaptic chromosomes = *ds* (2, 3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 3H (2, 3); *des2.b* is associated with SNP markers 1_0825 to 1_0312 (positions 61.77 to 173.82 cM) in 3H bins 05 to 11 of the Bowman backcross-derived line BW238 (1);

Description:

Synapsed homologous chromosomes disjoin precociously because of an apparent lack of chiasmata (2). The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is d = 6.0 " 3.3 with a range from 7 ring bivalents (d = 0) to 2 rod bivalents plus 10 univalents (d = 12). Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore tetrads contain an average of 1.8 micronuclei per tetrad and a range of 0 to 7. Ovule fertility is about 1% and highly variable from spike to spike on the same plant (5). The very low fertility trait occurs infrequently in the F_2 progeny from the cross to Bowman, but nearly 1/4 the plants show reduced seed set (about 60%) (4). Grain yields of the Bowman backcross-derived line for *des2.b*, BW238, varied from less than 10% to nearly 1/2 those of Bowman. BW238 and Bowman were similar for other morphological traits, except kernels weighed slightly more (4).

Origin of mutant:

An X-ray induced mutant in Husky (CIho 9537) (2).

Mutational events:

des2.b (GSHO 593) in Husky (CIho 9537) (2, 6).

Mutant used for description and seed stocks:

des2.b (GSHO 593) in Husky; *des2.b* in Bowman (PI 483237)*5 (BW238, NGB 22065).

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. Enns, H., and E.N. Larter. 1960. Note on the inheritance of *ds*; a gene governing meiotic chromosome behaviour in barley. Can. J. Plant Sci. 40:570-571.
3. Enns, H., and E.N. Larter. 1962. Linkage relations of ds: A gene governing chromosome behaviour in barley. Can. J. Genet. Cytol. 4:263-266.
4. Franckowiak, J.D. (Unpublished).
5. Hernandez-Soriano, J.M. 1973. Desynaptic mutants in Betzes barley. M.S. Thesis. Univ. of Arizona, Tucson.
6. Ramage, R.T., and J.M. Hernandez-Soriano. 1972. Desynaptic genes in barley. Barley Genet. Newsl. 2:65-68.

Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:125.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:154.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:84-85.

BGS 120, Zebra stripe 1, *zeb1*

Stock number: BGS 120
Locus name: Zebra stripe 1
Locus symbol: *zeb1*

Previous nomenclature and gene symbolization:

Zebra stripe = *zb* (1, 6).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 3HL (1, 5, 6); about 7.0 cM proximal from the *uzu1* (uzu 1) locus (4); *zeb1.a* is associated with SNP markers 1_0444 to 1_0312 (positions 135.80 to 173.82 cM) in 3H bins 08 to 10 of the Bowman backcross-derived line BW930 (2).

Description:

Seedlings may have pale green to yellow bands across the leaf blades when germinated under cold conditions in the field (1). Cold room studies show that development of the mutant phenotype in seedlings can be induced by 10 to 15 days of cold treatment (0° to 1°C) if initiated within one day after wetting of the seed (7). Alternating cold and warm temperatures in the field induce diagnostic symptoms (7). Compared to Bowman, plants of the Bowman backcross-derived line for *zeb1.a*, BW930, were slightly taller and kernels weighed slightly more. Grain yields of BW930 and Bowman were similar (3).

Origin of mutant:

A radiation induced mutant in Mars (CIho 7015) (1).

Mutational events:

zeb1.a (C3-1, GSHO 1279) in Mars (CIho 7015) (4, 5).

Mutant used for description and seed stocks:

zeb1.a (GSHO 1279) in Mars; *zeb1.a* in Bowman (PI 483237)*3 (GSHO 1964); *zeb1.a* in Bowman*4 (BW930, NGB 22359).

References:

1. Burnham, C.R. 1958. New linkages found. Barley Newsl. 1:44-47.
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. Kasha, K.J., and C.R. Burnham. 1965. The location of interchange breakpoints in barley. I. Linkage studies and map orientation. Can. J. Genet. Cytol. 7:62-77.
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. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 4:66-69.
7. Tsuchiya T., and R.J. Singh. 1974. Identification of zebra (*zb*) stripe character at early seedling stage. Barley Genet. Newsl. 4:96-97.

Prepared:

T. Tsuchiya. 1975. Barley Genet. Newsl. 5:100.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:155.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:86.

BGS 125, Lazy dwarf 1, *lzd1*

Stock number:	BGS 125
Locus name:	Lazy dwarf 1
Locus symbol:	*lzd1*

Previous nomenclature and gene symbolization:

Dwarf 4 = *dw4* (3).

Inheritance:

Monofactorial recessive (4, 6).

Located in chromosome 3H (5, 6); over 16.3 cM distal from the *alm1* (albino lemma 1) locus (5, 6); *lzd1.a* is associated with SNP markers 2_0356 to 2_1120 (positions 72.36 to 98.41 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW499 (1).

Description:

Plants have a very procumbent growth habit prior to the boot stage. Plants are 3/4 normal height, maturity is delayed, and seedlings are very responsive to gibberellic acid (4, 6). Leaf blades of the Bowman backcross-derived line for *lzd1.a*, BW499, were about 2/3 the length of those of Bowman. BW499 plants headed 3 to 4 days later than Bowman under long days, but up to 10 days later under short-day conditions (2). The spike of BW499 often had 2 to 3 more kernels than Bowman, plants were 5 to 10% shorter, and kernels had slight smaller dimensions and weighed about 10% less, 5.0 vs. 5.6 mg. The grain yields of BW499 were 2/3 to 3/4 those of Bowman (2).

Origin of mutant:

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

Mutational events:

lzd1.a (OUM005, GSHO 1787) in Akashinriki (OUJ659, PI 467400) (4, 6).

Mutant used for description and seed stocks:

lzd1.a (GSHO 1787) in Akashinriki; *lzd1.a* in Bowman (PI 483237)*8 (GSHO 1938, BW499, NGB 20727).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Konishi, T. 1970. Studies on EMS-induced mutation in barley III. Nogaku Kenkyu 53:141-152.
4. Konishi, T. 1975. Characteristics and inheritance of EMS-induced mutants in barley. Nogaku Kenkyu 55:53-56.
5. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:251-264.
6. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:161.

Revised:

J.D. Franckowiak. Barley Genet. Newsl. 43:87.

BGS 138, Necrotic leaf spot 4, *nec4*

Stock number:	BGS 138
Locus name:	Necrotic leaf spot 4
Locus symbol:	*nec4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3, 5).

Located in chromosome 3H (2, 5); *nec4.f* is associated with SNP markers in both arms of 3H and the long arm of 2H of the Bowman backcross-derived line BW631 (1).

Description:

Small black spots develop on the leaves (2, 5). The spots persist until maturity, but they do not appear to reduce plant vigor (4).

Origin of mutant:

An X-ray induced mutant in Proctor (PI 280420) (2, 5.

Mutational events:

nec4.f (728/63, OUM371) in Proctor (PI 280420) (2, 3, 5, 6).

Mutant used for description and seed stocks:

nec4.f in Proctor (OUM371); *nec4.f* in Bowman (PI 483237)*2 (BW631, NGB 22197).

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. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
3. Fischbeck, G., and H. Häuser. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
4. Franckowiak, J.D. (Unpublished).
5. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.
6 Søgaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. Carlsberg Res. Comm. 52:123-196.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:175.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:88.

BGS 139, Necrotic leaf spot 5, *nec5*

Stock number: BGS 139
Locus name: Necrotic leaf spot 5
Locus symbol: *nec5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3, 5).

Located in chromosome 3H (2, 5), *nec5.g* is associated with SNP markers 2_0607 to 2_0410 (positions 52.41 to 61.77cM) in 3H bins 04 to 05 of the Bowman backcross-derived line BW632 and with SNP marker on all other chromosomes except 2H (1).

Description:

Circular dark brown spots develop on the leaves (2, 5). Leaf tissue in the large spots gradually darkens and dies, but plants vigor appears normal (4).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Diamant (PI 330397, PI 467775) (2, 5).

Mutational events:

nec5.g (HLN$_{EP}$71/48, OUM372) in Diamant (PI 330397, PI 467775) (2, 3, 5, 6).

Mutant used for description and seed stocks:

nec5.g (OUM372) in Diamant; *nec5.g* in Bowman (PI 483237)*2 (BW632, NGB 22198).

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. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
3. Fischbeck, G., and H. Häuser. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
4. Franckowiak, J.D. (Unpublished).
5. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.
6. Søgaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. Carlsberg Res. Comm. 52:123-196.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:176.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:89.

BGS 143, Shrunken endosperm xenia 8, *sex8*

Stock number:	BGS 143
Locus name:	Shrunken endosperm xenia 8
Locus symbol:	*sex8*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia-j = *sex.j* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3HS (3); based on linkage drag with the *Btr1* (non-brittle rachis 1) locus (3); *sex8.j* is associated with SNP markers 2_1259 to 2_0093 (positions 69.14 to 127.914 cM) in 3H bins 05 to 08 and with SNP markers 2_0653 to 2_117 (positions 199.04 to 203.85 cM) in 5H bin 11 of the Bowman backcross-derived line BW848 (1).

Description:

After the hard dough stage, the grain develops a slight depression in the dorsal or lemma side. In plants heterozygous for *sex8.j*, a xenia pattern of expression is observed. Seeds with a small depression in the dorsal side are homozygous for *sex8* (2). Kernels of the Bowman backcross-derived line for *sex8.j,* BW848, were 10 to 15% lighter than those of Bowman. Grain yields of BW848 were about 3/4 those of Bowman (2).

Origin of mutant:

A spontaneous mutant in a selection from cross I89-633 (lax-69/3*Bowman) (2).

Mutational events:

sex8.j (GSHO 2471) in I89-633-1 (2, 3); the origin could be from the Bonus (PI 189763) mutant *lax.69* (NGB 116402).

Mutant used for description and seed stocks:

sex8.j (GSHO 2471) in I89-633-1; *sex8.j* in Bowman (PI 483237)*6 (GSHO 1945); *sex8.j* in Bowman*7 (BW848, NGB 22284).

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.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:93.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:90.

BGS 147, Multiovary 2, *mov2*

Stock number: BGS 147
Locus name: Multiovary 2
Locus symbol: *mov2*

Previous nomenclature and gene symbolization:
Multi-ovary = *mo* (4).
Multiovary 7 = *mo7a* (5, 6).
Inheritance:
Monofactorial recessive (2, 4, 5, 6).
Located in chromosome 3HS (6); co-segregation with molecular markers ABC171A and JS001B in 3H bin 02 (6).
Description:
The *mov2.g* (*mo7a*) mutant has between five and seven carpel-like structures and normal lodicules. Stamens are not present, but some carpels are terminated with stamen-like structures. Pollination using wild-type flowers results in a few seeds (6). The plant appears abnormal with a twisted and compact spike and reduced awn length. The frequency of mutant plants in the two F_2 progenies examined was much lower than expected (6). The stock must be maintained as a heterozygote (3). The mutants reported by Moh and Nilan (4) and Kamra and Nilan (2) may be alleles, but seed stocks were unavailable for testing (6).
Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) (5).
Mutational events:
mov2.g (FN243, *mo7a*, GSHO 3642) in Steptoe (CIho 15229) (5, 6); *mov2.a* (*mo1*) (4, 6); *mov2.c* (*mo3*) (1, 2, 6).
Mutant used for description and seed stocks:
mov2.g (FN243, GSHO 3642) in Steptoe.
References:
1. Kamra, P. 1966. Genetic control of the development of floral organs in *Hordeum vulgare*. p. 213-215. *In* A. Lengerova (ed.) Mechanisms of Mutation and Inducing Factors. Academia, Prague.
2. Kamra, O.P., and R.A. Nilan 1959. Multi-ovary in barley. Floral anatomy and embryo-sac development. J. Hered. 50:159-165.
3. Kleinhofs, A. (Unpublished).
4. Moh, C.C., and R.A. Nilan. 1953. Multi-ovary in barley. A. mutant induced by atomic radiation. J. Hered. 44:183-184.
5. Soule, J., I. Skodova, D. Kudrna, A. Kilian, and A. Kleinhofs. 1995. Molecular and genetic characterization of barley flower development mutants. Barley Genet. Newsl 25:76-80.
6. Soule, J.D., D.A. Kudrna, and A. Kleinhofs. 2000. Isolation, mapping, and characterization of two barley multiovary mutants. J. Hered. 91:483-487.
Prepared:
A. Kleinhofs. 2005. Barley Genet. Newsl. 35:190.
Revised:
A. Kleinhofs . 2013. Barley Genet. Newsl. 43:91.

BGS 165, Glossy leaf 3, *glf3*

Stock number: BGS 165
Locus name: Glossy leaf 3
Locus symbol: *glf3*

Previous nomenclature and gene symbolization:

Glossy leaf = *gl* (5).
Glossy leaf 3 = *gl3* (17).
Glossy leaves 4 = *gl4* (5, 20, 21, 22).
Eceriferum-j = *cer-j* (5, 8).

Inheritance:

Monofactorial recessive (17, 19).

Located in chromosome 4HL (2, 7, 17); about 1.5 cM distal from the *brh2* (brachytic 2) locus (6); over 13.7 cM from the *sid1* (single elongated internode 1) locus (6); *glf3.d* is associated with SNP markers 1_1180 to 1_1513 (positions 58.13 to 101.44 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW386 (1); *cer-j.59* is associated with SNP markers 2_1122 to 2_1332 (positions 47.80 to 112.64 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW114 (1).

Description:

Surface wax coating on the leaf blades appears absent from the seedling stage to near maturity, and leaf blades have a shiny appearance (wax code ++ ++ -) (8). Concerning the chemical epicuticular wax composition, the *cer-j* mutant in Bonus produces 34% less wax compared to the wild type, the primary alcohols are the largest wax class. The wax occurs as many very thin plates and as few large irregularly shaped bodies (4, 16, 23). Compared to Bowman, plants of the Bowman backcross-derived line for *glf3.d*, BW386, had kernels that were slightly lighter in some environments. Plants of the Bowman backcross-derived line for *cer-j.59*, BW114, were slightly shorter, headed about 2 days later, and had slightly lighter kernel weights (3).

Origin of mutant:

A spontaneous mutant in Goseshikoku (OUJ128) (17).

Mutational events:

glf3.c (Goseshikoku-hen, OUL032, GSHO 577) in Goseshikoku (OUJ128) (18); *glf3.d (gl4*, GSHO 1376*)* in Gateway (CIho 10072) (22); *cer-j.59* (NGB 110943, GSHO 431), -*j.62* (NGB 110946) in Bonus (PI 189763) (8, 9); *cer-j.71* (NGB 110955)*, -j.142* (NGB 111028)*, -j.148* (NGB 111034) in Bonus, *-j.274* (NGB 111161)*, -j.288* (NGB 111175)*, -j.301* (NGB 111188)*, -j.311* (NGB 111198)*, -j.340* (NGB 111227)*, -j.346* (NGB 111233)*, -j.349* (NGB 111236), *-j.358* (NGB 111245)*, -j.370* (NGB 111257)*, -j.390* (NGB 111277)*, -j.429* (NGB 111317), *-j.447* (NGB 111335)*, -j.470* (NGB 111358) in Foma (CIho 11333) (9, 16); *cer-j.183* (NGB 111069)*, -j.184* (NGB 111070)*, -j.696* (NGB 111584) in Bonus, -*j.275* (NGB 111162)*, -j.399* (NGB 111286)*, -j.517* (NGB 111405)*, -j.521* (NGB 111409)*, -j.558* (NGB 111446) in Foma, *-j.1024* (NGB 111912)*, -j.1081* (NGB 111969) in Carlsberg II (CIho 10114) (11); *cer-j.458* (NGB 111346) in Foma, *-j.780* (NGB 111668)*, -j.797* (NGB 111685)*, -j.832* (NGB 111720) in Bonus, *-j.1090* (NGB 111978)*, -j.1102* (NGB 111990) in Kristina (NGB 1500) (12); *cer-j.909* (NGB 111797) in Bonus, *-j.1152* (NGB 112040) in Kristina (11); *cer-j.1204* (NGB 112092)*, -j.1231* (NGB 112119)*, -j.1233* (NGB 112121)*, -j.1239* (NGB 112127)*, -j.1251* (NGB 112139) in Kristina (12); *cer-j.997* (NGB 111885)*, -j.1331* (NGB 112219)*, -j.1361* (NGB 112249)*, -j.1388* (NGB 112276)*, -j.1405*

(NGB 112293)*, -j.1433* (NGB 112321)*, -j.1469* (NGB 112357) in Bonus (12); *cer-j.1712* (NGB 112525)*, -j.1744* (NGB 112558)*, -j.1761* (NGB 112576)*, -j.1803* (NGB 117351)*, -j.1808* (NGB 117356) in Bonus (12); *cer-j.1827* (NGB 117375) in Bonus, *-j.1831* (NGB 117379)*, -j.1835* (NGB 117383)*, -j.1839* (NGB 117387)*, -j.1841* (NGB 117389)*, -j.1843* (NGB 117391)*, -j.1844* (NGB 117392)*, -j.1847*(NGB 117395)*, -j.1850* (NGB 117398)*, -j.1852* (NGB 117400)*, -j.1857* (NGB 117405)*, -j.1858* (NGB 117406), *-j.1859* (NGB 117407), *-j.1860* (NGB 117408)*, -j.1861* (NGB 117409)*, -j.1862* (NGB 117410) in Sv 79353 (15).

Mutant used for description and seed stocks:

glf3.c (GSHO 577) in Goseshikoku; *cer-j.59* (NGB 110943, GSHO 431) in Bonus is used for allelic localization tests and for wax chemistry and wax structure studies; *glf3.d* from Gateway in Bowman (PI 483237)*5 (GSHO 2019); *glf3.d* in Bowman*8 (BW386, NGB 20624); *cer-j.59* in Bowman*3 (GSHO 2021); *cer-j.59* in Bowman*7 (BW114, NGB 20520).

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. Fester, T., and B. Søgaard. 1969. The localization of eceriferum loci in barley. Hereditas 61:327-337.
3. Franckowiak, J.D. (Unpublished).
4. Giese, B.N. 1976. Roles of the *cer-j* and *cer-p* loci in determining the epicuticular wax composition on barley seedling leaves. Hereditas 82:137-148.
5. Haus, T.E. 1974. Allelism tests of chromosome 4 mutants. Barley Genet. Newsl. 4:31-33.
6. 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.
7. Jensen, J. 1987. Linkage map of barley chromosome 4. p. 189-199*. In* S. Yasuda and T. Konishi (eds.) Barley Genetics V. Proc. Fifth Int. Barley Genet. Symp., Okayama, 1986. Sanyo Press Co., Okayama.
8. Lundqvist, U., and D. von Wettstein. 1962. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. Hereditas 48:342-362.
9. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl.1:97-102.
10. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.
11. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
12. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
13. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
14. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
15. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.
16. 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.
17. Takahashi, R., J. Hayashi, and I. Moriya. 1962. Linkage studies. Barley Newsl. 5:41-42.
18. Takahashi, R., J. Hayashi, and I. Moriya. 1971. Linkage studies in barley. Barley Genet. Newsl. 1:51-58.
19. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1972. Inheritance and linkage studies in barley V. Locating of seven new mutant genes. Ber. Ohara Inst. landw. Biol., Okayama Univ. 15:147-168.
20. Tsuchiya, T. 1973. Allelic relationship between two glossy seedling genes, *gl3* and *gl4* in barley. Barley Genet. Newsl. 3:66-67.
21. Tsuchiya, T., and T.E. Haus. 1973. Allelism testing in barley. I. Analysis of ten mapped genes. J. Hered. 64:282-284.
22. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.
23. Wettstein-Knowles, P. von, 1971. The molecular phenotypes of the *eceriferum* mutants. p. 146-193. *In* R.A. Nilan (ed). Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:190.

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:159 as BGS 256, Glossy leaf 4, *gl4*.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:117 as BGS 165, Glossy seedling 3, *gl3*; and Barley Genet. Newsl. 10:123 as BGS 256, Glossy leaf 4, *gl4*.

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:190-191.

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:92-94.

BGS 177, Chlorina seedling 10, *fch10*

Stock number:	BGS 177
Locus name:	Chlorina seedling10
Locus symbol:	*fch10*

Revised locus symbol:

The *fch10.s* is an allele at the *zeb2* (zebra stripe 2) locus based on phenotypic expression and retained SNP markers in 4H of the Bowman backcross-derived lines BW 352 with *fch10.s* and BW931 line with *zeb2.b* (1). See BGS 461 for further information on the *zeb2* locus.

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 4H (3, 4, 5); about 9.3 cM distal from the *Kap1* (hooded lemma 1) locus (3, 4); about 17.0 cM proximal from the *glf3* (glossy leaf 3) locus (3, 4); no recombination with the *lgn4* (light green 4) locus (3, 4); *fch10.s* is associated with SNP markers 1_0668 to 1_1224 (positions 63.19 to 91.93 cM) in 4H bins 05 and 06 of the Bowman backcross-derived line BW352 (1), in 4H bin 05 near the centromere.

Description:

Plants are nearly normal green on emergence at 20°C gradually fading to light green, which is maintained to adult stages. Viable, though somewhat weak under outdoor conditions, and develops chlorina leaves from seedling to near maturity (5). When compared to Bowman, the Bowman backcross-derived line for *fch10.s* (BW352) headed about 17 days later and produced little or no seed. Rachis internodes were slightly shorter and plants were 1/2 to 3/4 of normal height (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar isolated by R.W. Woodward (4, 5, 6).

Mutational events:

fch10.s (GSHO 1737, T. 95) in an unknown six-rowed cultivar (4, 5); based on SNP patterns the *fch10.s* mutant studied by Woodward originated in six-rowed barley Himalaya (1).

Mutant used for description and seed stocks:

fch10.s (GSHO 1737) in an unknown six-rowed cultivar; *fch10.s* in Bowman (PI 483237)*7 (BW352, NGB 20591).

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.
4. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.
5. Takahashi, R., J. Hayashi, and I. Moriya. 1973. Two new mutant genes on chromosome 4. Barley Genet. Newsl. 3:65-66.

6. Woodward, R.W. 1957. Linkages in barley. Agron. J. 49:28-32.

Prepared:

T.E. Haus. 1984. Barley Genet. Newsl. 14:93.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:95-96.

BGS 180, Single internode dwarf 1, *sid1*

Stock number:	BGS 180
Locus name:	Single internode dwarf 1
Locus symbol:	*sid1*

Previous nomenclature and gene symbolization:

Node-less described by Schmalz (7) and Gaul (4).

Node-less dwarf = *nls* (9).

Inheritance:

Monofactorial recessive (5, 8).

Located in chromosome 4HL (8); over 13.2 cM distal from the *glf3* (glossy leaf 3) locus (5, 8); over 29.5 cM proximal from the *Kap1* (hooded lemma 1) locus (8. 9); *sid1.a* is associated with SNP markers 1_0262 to 2_0072 (positions 76.26 to 95.92 cM) in 4H bin 06 of the Bowman backcross-derived line BW849 (1); *sid1.b* is associated with SNP markers 1_0309 to 2_0358 (positions 110.93 to 128.85 cM) in 4H bins 07 to 09 of the Bowman backcross-derived line BW850 (1); *sid1.c* associated with a large segment of 4H in the Bowman backcross-derived line BW851 (1), likely in 4H bin 07.

Description:

All stem nodes are crowded together close to the secondary root system and the stem is formed from a single elongated terminal internode (4, 7). The mature plant has several culms, each having only a single elongated internode, the peduncle (9). Some of the elongated peduncles are much longer than normal. Plants are relatively weak and partially sterile, and have very lax spikes (2). The expression of mutant traits is less extreme in *sid1.b* plants, tillers often have two elongated internodes, fertility is better, and the spike is not as lax (2). The peduncle was approximately 80% of plant height in the Bowman backcross derived lines for *sid1.a* (BW849) and *sid1.b* (BW850). Plant height of BW849 was about 2/3 that of Bowman while BW850 was 85% as tall. Compared to Bowman, kernels of *sid1* mutants were thinner and 10 to 15% lighter and grain yield ranged from less than 1/3 to nearly 1/2 (2).

Origin of mutant:

An X-ray induced mutant in Akashinriki (OUJ659, PI 467400) from Dr. Ohta (9).

Mutational events:

sid1.a (R101, OUX052, GSHO 2477) in Akashinriki (OUJ659, PI 467400) (5); *sid1.b* (GSHO 2478) in Birgitta (NSGC 1870) (3); *sid1.c* (FN249, GSHO 3685) in Steptoe (CIho 15229) (6).

Mutant used for description and seed stocks:

sid1.a (GSHO 2477) in Akashinriki; *sid1.b* in (GSHO 2478) in Birgitta; *sid1.a* in Bowman (PI 483237)*7 (GSHO 2024, BW849, NGB 22286); *sid1.b* in Bowman*8 (GSHO 2025, BW850, NGB 22287); *sid1.c* from Steptoe mutant FN249 in Bowman*1 (BW851, NGB 22288)

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. (Unpublished).

3. Franckowiak, J.D. 1992. Allelism tests among selected semidwarf barleys. Barley Genet. Newsl. 21:17-23.

4. Gaul, H. 1964. Mutations in plant breeding. Rad. Bot. 4:155-232.
5. 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.
6. Kleinhofs, A. (Unpublished).
7. Schmalz, H. 1962. Makromutationen bei Sommergeste und Sommerweizen. Züchter 32:133-146.
8. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.
9. Takahashi, R., and I. Moriya. 1973. Two new mutant genes on chromosome 4. Barley Genet. Newsl. 3:65.

Prepared:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:203.

Revised:

J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:97-98.

BGS 187, Brachytic 9, *brh9*

Stock number: BGS 187
Locus name: Brachytic 9
Locus symbol: *brh9*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 4HL (1); about 11.7 cM distal from SRR marker Bmac0310 in 4H bin 06 (1); *brh9.k* is associated with SNP markers 1_1180 to 2_0906 (positions 58.13 to 92.93 cM) in 4H bins 05 to 06 of the Bowman backcross-derived line BW101 (2).

Description:

Culms and peduncles are about 3/4 normal length and awns are 3/4 to 5/6 of normal length. Rachis internodes are slightly shorter than those of normal sibs. Seedling leaves of *brh9.k* plants of Bowman backcross-derived line BW101 are relatively short (1, 3). The kernels of BW101 plants were shorter and kernel weights were about 20% lower than those of normal sibs. Grain yields averaged less than 1/2 normal (1, 3); however, plants appeared nearly normal when grown in Dundee, Scotland (3). The *brh9.k* gene was found to be non-allelic at *brh5* locus, which is located in the same region of 4HS (1).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (6).

Mutational events:

brh9.k (17:14:4, DWS1006, GSHO 1676) in Birgitta (NSGC 1870, NGB 14667) (4, 5).

Mutant used for description and seed stocks:

brh9.k (GSHO 1676) in Birgitta; *brh9.k* in Bowman (PI 483237)*5 (GSHO 2170); *brh9.k* in Bowman*7 (BW101, NGB 20507).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
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. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
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. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:244.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:99.

BGS 193, Viviparoides-b, *viv-b*

Stock number: BGS 193
Locus name: Viviparoides-b
Locus symbol: *viv-b*

Previous nomenclature and gene symbolization:

Viviparoides-6 = *viv-6* (4, 5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 4HS (2); *viv-b.6* is associated with SNP markers 1_0738 to 2_0210 (positions 26.58 to 38.41 cM) in 4H bins 02 to 04, SNP markers 2_1377 and 2_0563 (positions 20.11 and 21.19 cM) in 2H bin 2, and with SNP markers 1_0376 to 2_1274 (positions 209.87 to 218.47 cM) in 2H bin 13 of the Bowman backcross-derived line BW894 (2).

Description:

Tillers of the *viv-b.6* plants in the original mutant stock may remain vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as new phytomers are added, but occasionally a short, malformed spike is formed. In these spikes, many spikelets are replaced by plantlets. In the spikes that produce kernels, arrangement of spikelets is irregular and partial sterility occurs (1, 5). In the Bowman backcross-derived line for *viv-b.6* (BW894), some multiflorous spikes are observed and seed set is reduced. Compared to Bowman, BW894 plants headed 7 days later, were slightly shorter and had about 3 fewer kernels per spike (3).

Origin of mutant:

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

Mutational events:

viv-b.6 (NGB 115365) in Foma (CIho 11333) (5).

Mutant used for description and seed stocks:

viv-b.6 (NGB 115365) in Foma; *viv-b.6* in Bowman (PI 483237)*4 (BW894, NGB 22327).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. 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. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:100.

BGS 194, Slender dwarf 7, *sld7*

Stock number:	BGS 194
Locus name:	Slender dwarf 7
Locus symbol:	*sld7*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4HL (4); based on linkage drag with the *Int-c* (intermedium sapike-c) locus (4); *sld7.f* is associated with SNP markers 2_0762 to 2_0089 (positions 143.75 to 183.54 cM) in 4H bins 10 to 13 of Bowman backcross-derived line BW853 (1).

Description:

The original *sld7.f* mutant was isolated based on reduced plant height and exhibited reduced tillering (2). Plants of the Bowman backcross-derived line for *sld7.f*, BW853, were 80 to 90% for normal height. Grain yields of BW853 were 1/4 to 3/4 those of Bowman. Other morphological traits of BW853 were similar to those of Bowman (3).

Origin of mutant:

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

Mutational events:

sld7.f (GSHO 2481) in Glenn (CIho 15769) (2, 3).

Mutant used for description and seed stocks:

sld7.f (GSHO 2481) in Glenn; *sld7.f* in Bowman (PI 483237)*5 (GSHO 1997), *sld7.f* in Bowman*8 (BW853, NGB 22290).

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.

Prepared:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:101.

BGS 195, Shrunken endosperm xenia 9, *sex9*

Stock number:	BGS 195
Locus name:	Shrunken endosperm xenia 9
Locus symbol:	*sex9*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia I = *sex.l* (1).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 4HL (1); *sex9.l* is associated with SNP markers 1_1180 to 2_0062 (positions 58.13 to 91.93 cM) in 4H bins 05 to 06 and with SNP markers 2_0206 to 1_1381 (positions 9.61 to 11.21 cM) in 5H bin 01 of the Bowman backcross-derived line BW842 (1).

Description:

The *sex9.l* mutant was isolated based on the shrunken endosperm trait in progeny from the second backcross of Alf mutant *ant19.109* to Bowman (2). As the kernels matured, they develop a depression in the center of the lemma which becomes gradually more distinct and depressed (2). Plants of the Bowman backcross-derived line for *sex9.l*, BW842, had kernels that were the same dimensions as those of Bowman, but weighed much less, 3.8 vs. 5.7 mg. BW842 plants headed about 2 days later than Bowman plants and were about 10% shorter. Grain yields of BW842 were averaged about 1/4 those of Bowman and test weights were very low (2).

Origin of mutant:

Likely a sodium azide induced mutant in Alf (NGB 13682) (2).

Mutational events:

sex9.l (GSHO 2473) in Alf (NGB 13682) mutant *ant19.109* (NGB 13703) (2).

Mutant used for description and seed stocks:

sex9.l (GSHO 2473) in Alf; *sex9.l* in Bowman (PI 483237)*3 (GSHO 2354), *sex9.l* in Bowman*7 (BW842, NGB 22279).

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. 2013. Barley Genet. Newsl. 43:102.

BGS 196, Semidwarf 7, *sdw7*

Stock number:	BGS 196
Locus name:	Semidwarf 7
Locus symbol:	*sdw7*

Previous nomenclature and gene symbolization:

Semidwarf u = *sdw.u* (3).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4HL (4); based on linkage drag with the *Int-c* (intermedium spike-c) locus (4); *sdw7.u* is associated with SNP markers 1_0738 to 2_1397 (positions 26.58 to 47.80 cM) in 4H bins 02 to 04 of the Bowman backcross-derived line BW821 (1).

Description:

The original *sdw7.u* mutant was isolated based on reduced plant height (2). Plants of the Bowman backcross-derived line for *sdw7.u*, BW821, had slightly longer rachis internodes than Bowman. Grain yields of BW821 were about 2/3 those of Bowman. Other morphological traits of BW821 were similar to those of Bowman (2).

Origin of mutant:

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

Mutational events:

sdw7.u (GSHO 2462, DWS1072, SA6102-2-4-8) in Glenn (CIho 15769) (2, 3).

Mutant used for description and seed stocks:

sdw7.u (GSHO 2462) in Glenn; *sdw7.u* in Bowman (PI 483237)*4 (GSHO 2000, BW821, NGB 22258).

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.

Prepared:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:103.

BGS 197, Necrotic leaf spot 34, *nec34*

Stock number:	BGS 197
Locus name:	Necrotic leaf spot 34
Locus symbol:	*nec34*

Previous nomenclature and gene symbolization:

Necrotic leaf spot k = *nec.k* (1).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 4HS (1); *nec34.k* is associated with SNP markers 1_0738 to 1_0221 (positions 26.58 to 29.67 cM) in 4H bin 02 of the Bowman backcross-derived line BW625 (1), in 4H bin 02.

Description:

The original *nec34.k* variant in breeding line ND13917 (ND10278/ND11231) develops numerous small black flecks on the leaf blades, leaf sheathes, and awns (2). Plants of the Bowman backcross-derived line for *nec34.k*, BW625, were phenotypically similar to Bowman except for the necrotic flecks (2).

Origin of mutant:

A spontaneous variant in ND13917 (ND10278/ND11231), ND10278 is held as PI 643259 and ND11231 is a Logan (PI 592784) sib (2).

Mutational events:

nec34.k in ND13917 (2).

Mutant used for description and seed stocks:

nec34.k in ND13917; *nec34.k* in Bowman (PI 483237)*6 (BW625, NGB 22191).

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. 2013. Barley Genet. Newsl. 43:104.

BGS 198, Reaction to *Pyrenophora teres* 8, *Rpt8*

Stock number:	BGS 198
Locus name:	Reaction to *Pyrenophora teres* 8 (*P. teres* f. *maculata*, spot form of net blotch, SFNB)
Locus symbol:	*Rpt8*

Previous nomenclature and gene symbolization:

QTL for resistance to *Pyrenophora teres* seedling 4H = *QRpts4* (2).

Inheritance:

Monofactorial dominant (1).

Location in chromosome 4HS (1, 2); *Rpt8.j* is less than 3 cM from SSR markers HVM03 and Bmac181 (1); *Rpt8.j* is close to SSR marker HVM03 in bin 04 (2),

Description:

The reactions of seedlings with the *Rpt8.j* gene from Q21861 to *Pyrenophora teres* f. *maculata* (*Ptm*) isolates were often measured as 2 to 3 on a scale where 1 = very resistant and 9 = very susceptible (1). A similar disease reaction was recorded for TR251, which may have *Rpt8.j* gene in combination with the *Rpt4.e* (reaction to *Pyrenophora teres* 4) gene (2). A QTL located in chromosome 4H from VB9104 was reported to increase resistance to *Ptm* in a doubled-haploid population segregating for the *Rpt4.e* gene (4).

Origin of mutant:

Natural occurrence in Q21861 [PI 584766, selected in 1983 from a barley breeding nursery established at the International Maize and Wheat Improvement Center (CIMMYT) in Mexico] (1, 3).

Mutational events:

Rpt8.j in Q21861 (PI 584766) (1); possible *Rpt8* alleles are present in TR251 (TR229//AC Oxbow/ND7556) (2) and in VB9104 (Europa/IBON7.148) (4).

Mutant used for description and seed stocks:

Rpt8.j in Q21861.

References:

1. Friesen, T.L., J.D. Faris, Z. Lai, and B.J. Steffenson. 2006. Identification and chromosomal location of major genes for resistance to *Pyrenophora teres* in a doubled-haploid barley population. *Genome*, 49:855-859.
2. Grewal, T.S., B.G. Rossnagel, C.J. Ponzniak, and G.J. Scoles. 2008. Mapping quantitative trait loci associated with barley net blotch resistance. Theor. Appl. Genet. 116: 529-539.
3. Steffenson, B.J., Y. Jin, B.G. Rossnagel, J.B. Rasmussen, and K. Kao. 1995. Genetics of multiple disease resistance in a doubled-haploid population of barley. Plant Breed. 114:50-54.
4. Williams, K.J., G.J. Platz, A.R. Barr, J. Cheong, K. Willsmore, M. Cakir, and H. Wallwork**.** 2003. A comparison of the genetics of seedling and adult plant resistance to the spot form of net blotch (*Pyrenophora teres* f. *maculata*). Aust. J. Agric. Res. 54:1387-1394.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:105.

BGS 215, Desynapsis 6, *des6*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 1HL (1, 3) or 5HL (1); *des6.i* is associated with SNP markers 2_0603 to 2_0772 (positions 199.4 to 205.07 cM) in 1H bins 14 to 15 and with SNP markers 2_0127 to 2_0934 (positions 189.10 to 254.07 cM) in 5H bins 10 to 13 of the Bowman backcross-derived line BW244 (1); *des6.o* is associated with SNP markers 2_0383 to 2_0772 (positions 192.78 to 205.07 cM) in 1H bins 13 to 15 and with SNP markers 2_0127 to 2_1355 (positions 189.10 to 235.0 cM) in 5H bins 10 to 12 of the Bowman backcross-derived line BW245 (1).

Description:

The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is 7.9 ± 2.1 ranging from 7 ring bivalents (d = 0) to 14 univalents (d = 14). Many univalents split longitudinally during anaphase I. Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore quartets contain an average of 3.3 micronuclei per quartet with a range of 0 to 12. Ovule fertility is about 16%, and about 22% of the selfed seeds are trisomics (3). Compared to Bowman plants of the Bowman backcross-derived line for *des6.i*, BW244, were slightly shorter. Kernels of BW244 were on average slightly lighter. Grain yields of BW244 were 1/5 to 1/4 those of Bowman (3). Seed set for BW244 and BW245 was 15 to 20% when grown under greenhouse conditions (3).

Origin of mutant:

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

Mutational events:

des6.i (GSHO 597) in Betzes (PI 129430) (5, 6); *des6.m* in OAC 21 (CIho 1740), *des6.o* in Betzes (4, 6).

Mutant used for description and seed stocks:

des6.i (GSHO 597) in Betzes; *des6.i* in Bowman (PI 483237)*6 (BW244, NGB 22070); *des6.o* in Bowman*5 (BW245, NGB 22071).

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.
4. Hernandez-Soriano, J.M., and R.T. Ramage. 1973. Coordinator's report. Desynaptic genes. Barley Genet. Newsl. 3:91.
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.

Prepared:

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

Revised:

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

BGS 222, Necrotic leaf spot 1, *nec1*

Stock number:	BGS 222
Locus name:	Necrotic leaf spot 1
Locus symbol:	*nec1*

Previous nomenclature and gene symbolization:

Mutant no. 10 (4).
Parkland spot = *sp,,b* (2).

Inheritance:

Monofactorial recessive (4, 6).

Located in chromosome 1HL (2, 4, 6); near the centromere (2); about 34.5 cM proximal from the *wst5* (white streak 5) locus (5, 8); about 10.0 cM distal from the *msg1* (male sterile genetic 1) locus (6, 9); near EST marker BF630384 in 1H bin 09 (10); *nec1.c* is associated with SNP markers 1_0516 to 2_0657 (positions 96.74 to 115.07 cM) in 1H bins 09 to 10 of the Bowman backcross-derived line BW628 (1); *nec1.i* is associated with SNP markers 2_1072 to 2_0625 (positions 55.85 to 157.02 cM) in 1H bins 06 to 12 of the Bowman backcross-derived line BW627 (1), in 1H bin 09 (10).

Description:

Small black-brown spots develop on all light-exposed parts of the plant starting near the leaf tip at the three-leaf stage (2, 4). The spots are oval (the longest dimension is parallel to the leaf veins) and generally less than 1 to 2 mm in size. The spots are concentrated in awn and the most distal parts of the leaf blade, but may occur on all plant parts (4, 6). No other consistent agronomic or morphological differences between BW628 (*nec1.c*) and Bowman were observed (3). The *nec1* locus is an orthologue of *Arabidopsis* necrotic mutant *HLM1* that encodes the cyclic nucleotide-gated ion channel 4 and over-expresses the pathogenesis-related gene *PR-1* (10). Keiša et al. (7) suggest that the *nec1.c* mutation alters activation of systemic acquired resistance-related physiological markers and non-host resistance while not altering compatible interaction with host pathogens.

Origin of mutant:

A mutant induced by combined treatment with gamma-rays and diethyl sulfate of Carlsberg II (CIho 10114, NGB 5085) (4).

Mutational events:

nec1.a (Mutant no 10, GSHO 989) in Carlsberg II (CIho 10114, NGB 5085) (4, 5); *nec1.c* (*sp,,b*, GSHO 1284) in Parkland (CIho 10001) (2, 6); a mutant in Morex (CIho 15773) (8); *nec1.i* (FN338, GSHO 3602) in Morex (CIho 15773) (10); *nec1.j* (FN085, GSHO 3603) and *nec1.y* (FN370, GSHO 3604) in Steptoe (CIho 15229) (10).

Mutant used for description and seed stocks:

nec1.a (GSHO 989) in Carlsberg II; *nec1.c* from Parkland (CIho 10001) via R.I. Wolfe's Multiple Marker Stock for Chromosome 5 in Bowman (PI 483237)*7 (GSHO 2052, BW628, NGB 22194); *nec1.i* in Bowman*2 (BW627, NGB 22193).

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. Fedak, G., T. Tsuchiya, and S.B. Helgason. 1972. Use of monotelotrisomics for linkage mapping in barley. Can. J. Genet. Cytol. 14:949-957.

3. Franckowiak, J.D. (Unpublished).
4. Jensen, J. 1971. Mapping of 10 mutant genes for necrotic spotting in barley by means of translocation. p. 213-219. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
5. Jensen, J. 1992. Coordinator's report: Chromosome 5. Barley Genet. Newsl. 21:89-92.
6. Jensen, J., and J.H. Jørgensen. 1973. Locating some genes on barley chromosome 5. Barley Genet. Newsl. 3:25-27.
7. Keiša, A., K. Kanberga-Silina, I. Nakurte, L. Kunga, and N. Rostoks. 2011. Differential disease resistance response in the barley necrotic mutant *nec1*. BMC Plant Biol. 11:66.
8. Nielsen, G., H. Johansen, and J. Jensen. 1983. Localization on barley chromosome 5 of the locus *Pgd2* coding for phosphogluconate dehydrogenase. Barley Genet. Newsl. 13:57-59.
9. Ramage, T., and J.L.A. Eckhoff. 1985. Assignment of mutants in Morex to chromosomes. Barley Genet. Newsl. 15:22-25.
10. Rostoks, N., D. Schmierer, S. Mudie, T. Drader, R. Brueggeman, D. Caldwell, R. Waugh, and A. Kleinhofs. 2006. Barley necrotic locus *nec1* encodes the cyclic nucleotide-gated ion channel 4 homologous to the *Arabidopsis Hlm1.* Mol. Gen. Genomics 275:159-168.

Prepared:

J. Jensen. 1981. Barley Genet. Newsl. 11:101.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:220.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:251-252.
A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:108-109.

BGS 237, Reaction to *Pyrenophora teres* 2, *Rpt2*

Stock number:	BGS 237
Locus name:	Reaction to *Pyrenophora teres* 2 (*P. teres* f. *teres*, net form of net blotch, NFNB)
Locus symbol:	*Rpt2*

Previous nomenclature and gene symbolization:

Resistance to *Pyrenophora teres* 2c = *Rpt2c* (3).

Inheritance:

Monofactorial incomplete dominant (3, 5).

Located in chromosome 1HS (3); associated with 1HS based on molecular markers (8).

Description:

The seedling reactions of CIho 9819 to *Pyrenophora teres* f. *teres* (*Ptt*) isolates was described as 1 on a scale where 0 = very resistant and 4 = susceptible (3, 4); however, some (*Ptt*) isolates produced susceptible seedling reactions (2, 3). Two genes conferring resistance to *Ptt* were reported to be present in CIho 9819 (5). One gene was associated with chromosome 3H and named *Rpt1.b* and another gene was associated with chromosome 1H and named *Rpt2.c* (3). Using different *Ptt* isolates, CIho 9819 was reported by Manninen et al. (8) to have another *Rpt* gene (*Rpt5*) with a major effect in chromosome 6H, but a minor effect QTL was reported in 1HS. Using several *Ptt* isolates, two dominant and one recessive resistance genes were found in CIho 9819 by Afanasenko et al. (2). A QTL for *Ptt* resistance from Steptoe was found in 1H (9), but other reports of QTL for *Ptt* reaction in 1H are rare (7). CIho 9819 was reported to show resistant seedling responses to *Ptt* isolates from many countries (1).

Origin of mutant:

Natural occurrence in CIho 9819 (PI 195985) collected from Welo, Ethiopia (3, 4).

Mutational events:

Rpt2.c from CIho 9819 (PI 195985) collected from Welo, Ethiopia (3, 4); a possible allele present as a QTL in Arapiles (PI 591926) (6).

Mutant used for description and seed stocks:

Rpt2.c from CIho 9819 (PI 195985).

References:

1. Afanasenko, O.S., M. Jalli, H.O. Pinnschmidt, O. Filatova, and G.J. Platz. 2009. Development of an international standard set of barley differential genotypes for *Pyrenophora teres* f. *teres*. Plant Pathol. 58:665-676.
2. Afanasenko, O.S., I.G. Makarova, and A.A. Zubkovich. 1999. The number of genes controlling resistance to *Pyrenophora teres* Drechs. strains in barley. Russ. J. Genet. 35:274-283.
3. Bockelman, H.E., E.L. Sharp, and R.F. Eslick. 1977. Trisomic analysis of genes for resistance to scald and net blotch in several barley cultivars. Can. J. Bot. 55:2142-2148.
4. Buchannon, K.W., and W.C. McDonald. 1965. Sources of resistance in barley to *Pyrenophora teres*. Can. J. Plant Sci. 45:189-193.
5. Khan, T.N., and W.J.R. Boyd. 1969. Inheritance of resistance to net blotch in barley II. Genes conditioning resistance against race W.A.-2. Can. J. Genet. Cytol. 11:592-597.
6. Lehmensiek, A., G.J. Platz, E. Mace, D. Poulsen, and M.W. Sutherland. 2007. Mapping of adult plant resistance to net form of net blotch in three Australian barley populations. Aust. J. Agric. Res. 58:1191-1197.

7. Liu, Z., S.R. Ellwood, R.P. Oliver, and T.L. Friesen. 2011. *Pyrenophora teres*: profile of an increasingly damaging barley pathogen. Mol. Plant Pathol. 12:1-19.
8. Manninen, O.M., M. Jalli, R. Kalendar, A. Schulman, O. Afanasenko, and J. Robinson. 2006. Mapping of major spot-type and net-type net-blotch resistance genes in Ethiopian barley line CI 9819. Genome 49: 1564-1571.
9. Steffenson, B.J., Hayes, P.M., and Kleinhofs, A. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:110-111.

BGS 253, Uniculm 2, *cul2*

Stock number:	BGS 253
Locus name:	Uniculm 2
Locus symbol:	*cul2*

Previous nomenclature and gene symbolization:

Uniculm 2 = *uc2* (13).

Inheritance:

Monofactorial recessive (13).

Located in chromosome 6HL (6, 8); about 1.3 cM distal from the *gsh4* (glossy sheath 4) locus (4, 7); about 11.4 cM from the *msg36* (male sterile genetic 36) locus (4, 7); about 2.2 cM proximal from the *rob1* (orange lemma 1) locus (4, 6, 7); about 8.8 cM from RFLP markers cMWG679 and ABG458 and between *rob1* and RFLP marker KFP128 (1); about 6.2 cM from AFLP marker E4343-10 in subgroup 54 of the Proctor/Nudinka map (12); *cul2.l* is located between SSR markers GBM1212 and Bmag 0613 (10); *cul2.b* is associated with SNP markers 2_0291 to 1_0469 (positions 81.35 to 119.40 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW205 (3); *cul2.b* is associated with SNP markers 2_0675 to 1_1246 (positions 82,43 to 135.62 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW206 (3); since BW205 and BW206 originated as the same mutant, the *cul2* locus is likely located in 6H bin 06 because the same SNP markers are retained in both stocks, 2_1339 to 2_1310 (96.12 to 98.16 cM).

Description:

The *cul2* plants have a single elongated culm (stem), the culm is usually straight and has a much greater diameter than normal, and plants are usually head earlier than normal (13). Kernels of the backcross-derived line for *cul2.b*, BW205, were longer and wider than Bowman kernels and weighed on average slightly more (5). The *cul2.b* plants initiate vegetative axillary meristems, but tillers fail to develop (1). Irregular placement of some spikelets and partial female sterility of lateral spikelets occur in the original stock (7) and in the Bowman backcross-derived line (1). Yield of uniculm plants is not restored when grown under high plant populations (2). Double mutant combinations with most other mutants that affect tiller number resulted in a uniculm vegetative phenotype (1). Stress response genes are up regulated in *cul2.b* mutants (11).

Origin of mutant:

A thermal neutron induced mutant in Kindred (CIho 6969) (13).

Mutational events:

cul2.b (GBC379, CIho 115530, GSHO 531) in Kindred (CIho 6969) (7), *cul2.k* (*unc*^{k}) in an unknown cultivar from the Max-Planck-Institut für Züchtungsforschung (12); *cul2.l* (FN237, GSHO 3648) in Steptoe (CIho 15229) (9).

Mutant used for description and seed stocks:

cul2.b (CIho 115530, GSHO 531) in Kindred; *cul2.b* in Bowman (PI 483237)*4 (GSHO 2074); *cul2.b* in Bowman*7 (BW205, NGB 22033); *cul2.b* plus *rob1.a* from sel 79Cal in Bowman*8 (GSHO 2075, BW206, NGB 22034).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley uniculm2 (*cul2*) mutant. Theor. Appl. Genet. 106:846-857.

2. Dofing, S.M. 1996. Near-isogenic analysis of uniculm and conventional-tillering barley lines. p. 617-619. *In* A.E. Slinkard, G.J. Scoles, and B.G. Rossnagel (eds.) Proc. Fifth

Int. Oat Conf. & Seventh Int. Barley Genet. Symp., Saskatoon. Univ. of Saskatchewan, Saskatoon.
3. 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.
4. Falk, D.E., M.J. Swartz, and K.J. Kasha. 1980. Linkage data with genes near the centromere of barley chromosome 6. Barley Genet. Newsl. 10:13-16.
5. Franckowiak, J.D. (Unpublished).
6. 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.
7. Kasha, K.G., D.E. Falk, and A. Ho-Tsai. 1978. Linkage data with genes on chromosome 6. Barley Genet. Newsl. 8:61-65.
8. Kirby, E.J. 1973. Effect of temperature on ear abnormalities in uniculm barley. J. Exp. Bot. 24:935-947.
9. Kleinhofs, A., and G.J. Muehlbauer (Unpublished).
10. Liu, Y.X., X.-H. Sun, B.-L. Xu, and G.-Y. Chen. 2012. Genetic analysis and molecular mapping of low-tillering mutants (*cul2.b* and *lnt1.a*) in barley (*Hordeum vulgare* L.). J. Plant Sci. 7:105-112.
11. Okagaki, R.J., S. Cho, W.M. Kruger, W.W. Xu, S. Heinen, and G.J. Muehlbauer. 2013. The barley UNICULM2 gene resides in a centromeric region and may be associated with signaling and stress response. Funct. Integr. Genomics 13:33-41.
12. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
13. Shands, R.G. 1963. Inheritance and linkage of orange lemma and uniculm characters. Barley Newsl. 6:35-36.

Prepared:

C.R. Burnham. 1971. Barley Genet. Newsl. 1:156.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:234.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:253-254.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:112-113.

BGS 258, Dense spike 9, *dsp9*

Stock number: BGS 258
Locus name: Dense spike 9
Locus symbol: *dsp9*

Revised locus symbol:

The *dsp9.i* mutant is likely an allele at the *ert-e* (erectoides-e) locus based on allelism tests (2), phenotypic expression (2), and retained SNP markers in 6HL of the Bowman backcross-derived line (BW279) (1). See BGS 266 for more information about the alleles at the *ert-e* locus.

Previous nomenclature and gene symbolization:

Dense spike = *la* (3).
Dense spike 9 = *l9* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6HL (3), about 27.2 cM distal from the *xnt5* (xantha seedling 5) locus (4); over 26.9 cM distal from the *Aat2* (aspartate aminotransferase 2) locus (7); *dsp9.i* is associated with SNP markers 1_0645 to 2_1425 (positions 190.39 to 207.0 cM) in 6H bins 11 to 15 of the Bowman backcross-derived line BW279 (1).

Description:

Extremely dense spikes are easily distinguished from normal types when grown in the field or greenhouse (3). A photo of the original spike phenotypes is presented in Saisho and Takeda (6). The spike often emerges from the side of the sheath. Compared to Bowman, plants of the Bowman backcross-derived line for *dsp9.i*, BW279, were about 2/3 as tall and had very short rachis internodes, 2.3 vs. 4.6 mm. Peduncles averaged about 3/4 normal length, kernels were 10 to 20% lighter, and grain yields were about 2/3 those of Bowman (2).

Origin of mutant:

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

Mutational events:

dsp9.i (OUM113, GSHO 1774) in Akashinriki (3); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118) in Akashinriki (5).

Mutant used for description and seed stocks:

dsp9.i in Akashinriki (GSHO 1774, OUM113); *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090, BW279, NGB 20563).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.
4. Konishi, T. 1978. New linkage data on chromosome 6 of barley. Barley Genet. Newsl. 8:71-72.
5. Konishi, T. (Unpublished).
6. Saisho, D., and K. Takeda. 2011. Barley: Emergence of a new research material of crop science. Plant Cell Physiol. 52:724-727.

7. Yoshimi, R., and T. Konishi. 1995. Linkage analysis of several isozyme loci in barley. Barley Genet. Newsl. 24:35-37.

Prepared:

T. Konishi. 1976. Barley Genet. Newsl. 6:132.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:239.

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:114-115.

BGS 265, Necrotic leaf spot 3, *nec3*

Stock number: BGS 265
Locus name: Necrotic leaf spot 3
Locus symbol: *nec3*

Previous nomenclature and gene symbolization:

Necrotic leaf spot 3 = *nec3a* (4, 5, 9).
Necrotic leaf spot 3 = *nec3b* (5, 9).

Inheritance:

Monofactorial recessive (4, 7).

Located in chromosome 6HS (4, 7); about 29.2 cM distal from the *rob1* (orange lemma 1) locus (2, 4, 6); about 16.7 cM distal from the *msg36* (male sterile genetic 36) locus (2); *nec3.d* is associated with SNP markers 1_00616 to 1_0882 (position 70.15 cM) in 6H bin 05 of the Bowman backcross-derived line BW629 (1); *nec3.e* is associated with SNP markers 1_0427 to 1_0494 (positions 56.64 to 70.15 cM) in 6H bin 05 of the Bowman backcross-derived line BW630 (1), in 6H bin 05.

Description:

Tan or brown necrotic blotches develop on the leaf sheath and blade prior to heading and persist to maturity (4, 5). Plants homozygous for *nec3.d* develop brown blotches having irregular margins. Plants homozygous for *nec3.e* develop large tan or faded blotches having distinct margins. After maturation, plants expressing the *nec3.d* gene can be identified easily by brown blotches on the leaves, but those expressing the *nec3.e* gene are difficult to identify (3). In the Bowman backcross-derived lines, vigor is reduced more in *nec3.e* plants than in *nec3.d* ones. Keiša et al. (8) suggested that the nec3 mutations affect expression of genes involved in abiotic stress response. Plants of the Bowman backcross-derived line for *nec3.d*, BW629, were slightly taller than Bowman, but their kernels weighed slightly less. Plants of the Bowman backcross-derived line for *nec3.e*, BW630, were slightly shorter than Bowman, but had 2 to 3 more kernels per spike. The kernels of BW630 averaged 10 to15% lighter than those of Bowman, 5.4 vs. 5.8 mg (3).

Origin of mutant:

An X-ray induced mutant in Proctor (PI 280420) (4, 7).

Mutational events:

nec3.d (1339/62, GSHO 1330) in Proctor (PI 280420) (4, 7); *nec3.e* (1558/74, GSHO 2423) in Villa (PI 399506) (5); *nec3.l* (FN362, GSHO 3605) and *nec3.m* (FN363, GSHO 3606) in Steptoe (CIho 15229) (8).

Mutant used for description and seed stocks:

nec3.d (GSHO 1330) in Proctor; *nec3.e* (GSHO 2423) in Villa; *nec3.d* in Bowman (PI 483237)*4 (GSHO 2065); *nec3.d* in Bowman*6 (BW629, NGB 22195); *nec3.e* in Bowman*3 (GSHO 2066); *nec3.e* in Bowman*6 (BW630, NGB 22196).

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. Falk, D.E., M.J. Swartz, and K.J. Kasha. 1980. Linkage data with genes near the centromere of barley chromosome 6. Barley Genet. Newsl. 10:13-16.
3. Franckowiak, J.D. (Unpublished).

4. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
5. Fischbeck, G., and H. Häuser. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
6. Häuser, H., and G. Fischbeck. 1980. Genetic analysis of induced mutations. Barley Genet. Newsl. 10:30-31.
7. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.
8. Keiša, A., R. Brueggeman, T. Drader, A. Kleinhofs, and N. Rostoks. 2010. Transcriptome analysis of the barley *nec3* mutant reveals a potential link with abiotic stress response related signaling pathways. Environ. Exper. Biol. 8:1-16.
9. Søgaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. Carlsberg Res. Comm. 52:123-196.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:245.
J.D. Franckowiak and A. Kleinhofs. 2013. Barley Genet. Newsl. 43:116-117.

BGS 266, Erectoides-e, *ert-e*

Stock number: BGS 266
Locus name: Erectoides-e
Locus symbol: *ert-e*

Previous nomenclature and gene symbolization:
Erectoides-17 = *ert-17* (3).
Dense spike = *la* (5).
Dense spike 9 = *l9* (5).
Dense spike 9 = dsp9 (8).

Inheritance:
Monofactorial recessive (3, 5, 10).
Located in chromosome 6HL (4, 9, 10), about 27.2 cM distal from the *xnt5* (xantha seedling 5) locus (4), over 26.9 cM distal from the *Aat2* (aspartate aminotransferase 2) locus (13); *ert-e.17* is associated with SNP markers 2_0467 to 2_0733 (positions 169.88 to 180.69 cM) in 6H bin 11 of the Bowman backcross-derived line BW307 (1); *dsp9.i* is associated with SNP markers 1_0645 to 2_1425 (positions 190.39 to 207.0 cM) in 6H bins 11 to 15 of the Bowman backcross-derived line BW279 (1).

Description:
Spikes are very compact with rachis internode length values from 1.2 to 1.5 mm. Plants are about 2/3 normal height. Partial fertility and reduced vigor are noted among *ert-e* mutants. The peduncle is very short and spikes often emerge from the side of the flag sheath (9, 11). A large deficiency of mutant plants is frequently noted in segregating populations (9). Spike density decreases greatly when plants are treated with gibberellic acid (GA_3) as the flag leaf emerges (12). The mutant *ert-e.17* is allelic to mutant *dsp9.i* (dense spike 9, see BGS 258) (2). Compared to Bowman, plants of the Bowman backcross-derived line for *ert-e.17*, BW307, were about 2/3 as tall and had very short rachis internodes, 2.0 vs. 4.4 mm. Peduncles were 3/4 normal length, kernels were10 to 20% lighter, and grain yields were 1/3 to 1/2 those of Bowman (2).

Origin of mutant:
An X-ray induced mutant in Bonus (PI 189763) (3); an ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (5).

Mutational events:
ert-e.17 (GSHO 477, NGB112619), *-e.65* (NGB 112664) in Bonus (PI 189763) (2); *ert-e.94* (NGB 112693)*, -e.143* (NGB 112742) in Bonus, *-e.331* (NGB112846)*, -e.396* (NGB 114150) in Foma (CIho 11333) (11); *dsp9.i* (OUM113) in Akashinriki (5); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118,GSHO 1774) in Akashinriki (7).

Mutant used for description and seed stocks:
ert-e.17 (GSHO 477, NGB 112619) in Bonus; *ert-e.17* in Bowman (PI 483237)*6 (GSHO 2091); *ert-e.17* in Bowman*7 (BW307, NGB 22103); *dsp9.i* (GSHO 1774) in Akashinriki; *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090, BW279, NGB 20563).

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

3. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
4 Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
5. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.
6. Konishi, T. 1978. New linkage data on chromosome 6 of barley. Barley Genet. Newsl. 8:71-72.
7. Konishi, T. (Unpublished).
8. Konishi, T., and J.D. Franckowiak. 1997. BGS 258, Dense spike 9, *dsp9*. Barley Genet. Newsl. 26:239.
9. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. Hereditas 62:25-96.
10. Persson, G., and A. Hagberg. 1962. Linkage studies with the erectoides loci. Barley Newsl. 5:46-47.
11. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
12. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.
13. Yoshimi, R., and T. Konishi. 1995. Linkage analysis of several isozyme loci in barley. Barley Genet. Newsl. 24:35-37.

Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:246.

Revised as BGS 258:
T. Konishi and J.D. Franckowiak. 1997. BGS 258, Dense spike 9, *dsp9*. Barley Genet. Newsl. 26:239.

Revised:
J.D. Franckowiak and U. Lundqvist. 2007. Barley Genet. Newsl. 37:257-258.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:118-119.

BGS 272, Reaction to *Pyrenophora teres* 5, *Rpt5*

Stock number: BGS 272
Locus name: Reaction to *Pyrenophora teres* 5
(*P. teres* f. *teres*, net form of net blotch, NFNB)
Locus symbol: *Rpt5*

Previous nomenclature and gene symbolization:

Resistance to *Pyrenophora teres* a = Pt_a (14).
QTL for resistance to *Pyrenophora teres* f. *teres* seedling 6L = *QRpts6L* (24).
QTL for resistance to *Pyrenophora teres* 6 = *QRpt6* (11).
Reaction to *Pyrenophora teres* f. *teres* Kombar = *rpt.k* (1).
Reaction to *Pyrenophora teres* f. *teres* Rika = *rpt.r* (1).

Inheritance:

Monofactorial dominant (20, 21); two complementary genes in CIho 5791 (13, 14, 19); dominance or recessive gene action is dependent on the isolate used for screening (7). Located in chromosome 6HL (16, 24); the *Rpt5* locus is between microsatellite markers HVM14 and HVM65 (16); between RFLP markers MWG916 and WG223 (29); near SSR marker Bmag173 (5, 8, 9); *Rpt5.i* is closely linked to HVM74 (11); *Rpt5.i* is near DArT marker bPb-9051 (26); the *rpt5.k* and *rpt5.r* alleles are in a 0.8 cM region near EST marker *ABC04320* (1).

Description:

The 6HL gene from CIho 9819, which confers resistance to many *Pyrenophora teres* f. *teres* (*Ptt*) isolates, was named *Rpt5* (21). The *Rpt5* locus was reported by many researchers as the main locus controlling the response to *Ptt*. Accessions from Ethiopia, CIho 5791 and CIho 9819, were identified as resistant to a mixture of North American isolates of *Ptt* (4, 14, 15). Duplicate factors in CIho 5791 and CIho 9819 control resistance to *P. teres*, but one of these factors Pt_a is not allelic to previously reported genes (14, 15). Resistance to *Ptt* is conferred by one dominant gene in 6HL of CIho 9819 with the infection type (IT) of 1 for CIho 9819 on a 10 point scale and an IT of 10 for Rolfi (20). Subsequent reports have associated this region of 6HL with both dominant and recessive interactions to various *Ptt* isolates (17). Abu Qamar et al. (1) demonstrated that at least two recessive *Rpt* loci were expressed in this region of 6HL in doubled-haploid progeny from a Rika/Kombar cross. Based on expressed sequence tag (EST) markers, Liu et al. (18) reported that in the *Rpt5* region of 6HL, Kombar (CIho 15694) is identical to that of closely related cultivars, Atlas (CIho 4118, PI 539108) and Beecher (CIho 6566), and the *Rpt5* region of Rika (CIho 11200, PI 263575) is identical to that of Tifang (CIho 4407-1, PI 69426), Manchuria (CIho 2330), and Manchurian (CIho 1251, PI 20824). The *Rpt5.f* allele from CIho 5791 and CIho 9819 is named because it confers a high level of resistance to many *Ptt* isolates (2, 3, 14, 22, 23). This source was used by Metcalfe (23) and led to the development in the development of two-rowed cultivars such as Norbert (PI 452125), TR251 (TR229//AC Oxbow/ND7556), Conlon (PI 597789), Vlamingh (76T110-409/TR118, CN 45884) (10, 22) and six-rowed cultivars Heartland (32) and M120 (26, 32). CIho 5791 and CIho 9819 are still resistance to a diverse set of *Ptt* isolates (2), but the derived cultivars are not as resistant to a smaller spectrum of *Ptt* isolates (2, 6).

Origin of mutant:

Natural occurrence in CIho 5791 (PI 95095) and CIho 9819 (PI 195985) (4, 14, 21, 31);

natural occurrence in Steptoe (30), in Hor 9088 (25), in Kaputar (5), in ND11231 (a Logan sib) (5, 8), in Halcyon (24), in Chevron (19), in SM89010 (9), in TR251 (11, 12), in Rika and Kombar (1).

Mutational events:

Rpt5.f in CIho 9819 (PI 195985) (4, 14); *Rpt5.f* in CIho 5791 (PI 95095) (4, 14, 23) and TR251 (TR229//AC Oxbow/ND7556) (11); *rpt5.k* in Kombar (CIho 15694) from California and *rpt5.r* in Rika (CIho 11200, PI 263575) from Sweden (18, 30); other possible alleles include *Rph5* in Steptoe (27, 30); *Rpt5* from HOR 9088 from Ethiopia (25); *Rpt5* in TR306 (CN 44323, Abee//TR451/WM793-1776) (27, 29); *Rpt5* in Chevron (CIho 1111) (19).

Mutant used for description and seed stocks:

Rpt5.f in CIho 9819, CIho 5791, Heartland, and TR251; *rpt5.k* in Kombar; *rpt5.r* in Rika; *Rpt5.f* from CIho 5791 via Heartland (PI 552963) (32) in M120 (CDC Tisdale/Lacey) (26).

References:

1. Abu Qamar, M., Z.H. Liu, J.D. Faris, S. Chao, M.C. Edwards, Z. Lai, J.D. Franckowiak, and T.L. Friesen. 2008. A region of barley chromosome 6H harbors multiple major genes associated with net type net blotch resistance. Theor. Appl. Genet. 117:1261-1270.

2. Afanasenko, O.S., M. Jalli, H.O. Pinnschmidt, O. Filatova, and G.J. Platz. 2009. Development of an international standard set of barley differential genotypes for *Pyrenophora teres* f. *teres*. Plant Pathol. 58:665-676.

3. Afanasenko, O., N. Mironenko, O. Filatova, D. Kopahnke, I. Krämer, and F Ordon. 2007. Genetics of host-pathogen interactions in the *Pyrenophora teres* f. *teres* (net form) – barley (*Hordeum vulgare*) pathosystem.117:267-280.

4. Buchannon, K.W., and W.C. McDonald. 1965. Sources of resistance in barley to *Pyrenophora teres*. Can. J. Pl. Sci. 45:189-193.

5. Cakir, M., S. Gupta, C. Li, M. Hayden, D.E. Mather, G.A. Ablett, G.J. Platz, S. Broughton, K.J. Chalmers, R. Loughman, M.G.K. Jones, and R.C.M. Lance. 2011. Genetic mapping and QTL analysis of disease resistance traits in the barley population Baudin x AC Metcalfe. Crop Pasture Sci. 62:152-161.

6. Cromey, M.G., and R.A. Parkes. 2003. Pathogenic variation in *Drechslera teres* in New Zealand. New Zealand Plant Protect. 56:251-256.

7. Douiyssi, A., D.C. Rasmusson, and R.D. Wilcoxson. 1996. Inheritance of resistance to net blotch in barley in Morocco. Plant Dis. 80:1269-1272.

8. Emebiri, L.C., G. Platz, and D.B. Moody. 2005. Disease resistance genes in a doubled haploid population of two-rowed barley segregating for malting quality attributes. Aust. J. Agric. Res. 56:49-56.

9. Friesen, T.L., J.D. Faris, Z. Lai, and B.J. Steffenson. 2006. Identification and chromosomal location of major genes for resistance to *Pyrenophora teres* in a doubled-haploid barley population Genome 49:855-859.

10. Franckowiak et al. (Unpublished).

11. Grewal, T.S., B.G. Rossnagel, C.J. Ponzniak, and G.J. Scoles. 2008. Mapping quantitative trait loci associated with barley net blotch resistance. Theor. Appl. Genet. 116: 529-539.

12. Grewal, T.S., B.G. Rossnagel, and G.J. Scoles. 2008. The utility of molecular markers for barley net blotch resistance across geographic regions. Crop Sci. 48:2321-2333.

13. Jonsson, R., T. Säll, T. Kraft, and M. Gustafsson. 1999.. Inheritance of resistance to

Pyrenophora teres f. *teres* in spring barley. Plant Breed. 118:313-317.
14. Khan, T.N., and W.J.R. Boyd. 1969. Inheritance of resistance to net blotch in barley. II. Genes conditioning resistance against race W.A.-2. Can. J. Genet. Cytol. 11:592-597.
15. Khan, T.N., and W.J.R. Boyd. 1971. Genetics of host resistance to net blotch in barley. p. 484-492. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
16. Liu, Z.W., R.M. Biyashev, and M.A. Saghai Maroof. 1996. Development of simple sequence repeat DNA markers and their integration into a barley linkage map. Theor. Appl. Genet. 93:869-876.
17. Liu, Z., S.R. Ellwood, R.P. Oliver, and T.L. Friesen. 2011. *Pyrenophora teres*: profile of an increasingly damaging barley pathogen. Mol. Plant Pathol. 12:1-19.
18. Liu, Z., L., J.D. Faris, M.C. Edwards, and T.L. Friesen. 2010. Development of expressed sequence tag (EST)–based markers for genomic analysis of a barley 6H region harboring multiple net form net blotch resistance genes. The Plant Genome 3:41-52.
19. Ma, Z.Q., N.L.V. Lapitan, and B. Steffenson. 2004. QTL mapping of net blotch resistance genes in a doubled-haploid population of six-rowed barley. Euphytica 137:291-296.
20. Manninen, O., R. Kalendar, J. Robinson, and A.H. Schulman. 2000. Application of BARE-1 retrotransposon markers to the mapping of a major resistance gene for net blotch in barley. Mol. Gen. Genet. 264:325-334.
21. Manninen O.M., M. Jalli, R. Kalendar, A. Schulman, O. Afanasenko, and J. Robinson. 2006. Mapping of major spot-type and net-type net-blotch resistance genes in Ethiopian barley line CI 9819. Genome 49:1564-1571.
22. Metcalfe, D.R., and V.M. Bendlow. 1981. Norbert barley. Can. J. Pl. Sci. 81:1005-1007.
23. Metcalfe, D.R., K.W. Buchannon, W.C. McDonald, and E. Reinbergs. 1970. Relationships between the ‘Jet” and ‘Milton” genes for resistance to loose smut and genes for resistance to other barley diseases. Can. J. Pl. Sci. 50:23-427.
24. Raman, H., G.J. Platz, K.J. Chalmers, R. Raman, B.J. Read, A.R. Barr, and D.B. Moody. 2003. Mapping of genomic regions associated with net form of net blotch resistance in barley. Aust. J. Agric. Res. 54:1359-1367.
25. Richter, K., J. Schondelmaier, and C. Jung. 1998. Mapping of quantitative trait loci affecting *Drechslera teres* resistance in barley with molecular markers. Theor. Appl. Genet. 97:1225-1234.
26. St. Pierre, S., C. Gustus, B. Steffenson, R. Dill-Macky, and K.P. Smith. 2010. Mapping net form net blotch and Septoria speckled leaf blotch resistance loci in barley. Phytopathology 100:80-84.
27. Sato, K., K. Takeda, and P.M. Hayes. 1996. QTL analysis for net blotch resistance in barley. Vol 1 p. 298-300. *In* A.E. Slinkard, G.J. Scoles, and B.G. Rossnagel (eds.) Barley Genetics VII. Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp. Proceed., Saskatoon. Univ. Ext. Press, Univ. of Saskatchewan, Saskatoon, Canada.
28. Schaller, C.W. 1955. Inheritance of resistance to net blotch of barley. Phytopathology 45:174-176.
29. Spaner, D., L.P. Shugar, T.M. Choo, I. Falak, K.G. Briggs, W.G. Legge, D.E. Falk, S.E. Ullrich, N.A. Tinker, B.J. Steffenson, and D.E. Mather. 1998. Mapping of disease resistance loci in barley based on the visual assessment of naturally occurring symptoms. Crop Sci. 38:843-850.
30. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs, 1996. Genetics of seedling and adult

plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.

31. Steffenson, B.J., and R.K. Webster. 1992. Pathotype diversity of *Pyrenophora teres* f. *teres* on barley. Phytopathology 82:170-177.

32. Therrien, M. C., and R.I. Wolfe. 1985. Heartland barley. Can. J. Pl. Sci. 65:445-446.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:120-123.

BGS 274, Breviaristatum-x, *ari-x*

Stock number:	BGS 274
Locus name:	Breviaristatum-x
Locus symbol:	*ari-x*

Previous nomenclature and gene symbolization:

Breviaristatum-22 = *ari-22* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 6H (1); ar*i-x.22* is associated with SNP markers 1_0061 to 2_0379 (positions 70.15 to 163.56 cM) in 6H bins 05 to 10 of the Bowman backcross-derived line BW030 (1).

Description:

Awns of *ari-x.22* plants about 1/2 normal length and are curled (3, 4). Compared to Bowman, plants of the Bowman backcross-derived line for *ari-x.22*, BW030, were 10 to 15% shorter and had awns that were 1/2 to 2/3 as long and slightly twisted. Awn barbs were slightly more prominent than those of Bowman. BW030 had kernels that were slightly smaller than those of Bowman and weighted less, about 4.7 vs. 5.8 mg. Grain yields of BW030 were 1/2 to 3/4 those of Bowman and test weights were slightly lower (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (3, 4).

Mutational events:

ari-x.22 (NGB 115870) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

ari-x.22 (NGB 115870) in Bonus; *ari-x.22* in Bowman (PI 483237)*5 (BW030, NGB 20438).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:124.

BGS 308, Long basal rachis internode 1, *lbi1*

Stock number: BGS 308
Locus name: Long basal rachis internode 1
Locus symbol: *lbi1*

Previous nomenclature and gene symbolization:

Curved peduncle = *cr* (1).
Long basal spike internode = *bi* (5).
Long basal spike internode = *lb* (7).
Rachisextensum = *rac-a* and *rac-b* (4, 8).

Inheritance:

Monofactorial recessive (1, 5).

Located in chromosome 5HL (5); about 16.0 cM distal from the *raw1* (smooth awn 1) locus (5); the *lbi1.a* phenotype in Bowman backcross-derived line BW471 may be associated with retained SNP markers 1_0238 to 2_0550 (positions 55.85 to 130.68 cM) of 1H bins 06 to 11 or with 5HS bin 01 with SNP markers 2_0226 to 2_0553 (positions 3.14 to 26.06 cM) (2); the *lbi1* phenotype is associated with the *sdw8.ah* (semidwarf 8) mutant and with SNP markers 2_0097 to 1_0477 (positions 154.37 to 173.49 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW786 (NGB 20763, BGS 708) (2, 3); the *lbi1* phenotype is associated with the *ari-v.137* (breviaristatum-v) mutant and with SNP markers 2_1065 to 2_1244 (positions about 40.91 to 92.0 cM) in 5H bins 02 to 05 of Bowman backcrossed-derived line BW026 (2, 3).

Description:

The first or basal rachis internode is much longer than the other rachis internodes. Basal internode lengths range from less than 1 cm to more than 20 cm (5, 9). Genotype, environmental conditions, and tiller health alter basal rachis internode elongation in plants homozygous for the *lbi1.a* gene. Expression of the *lbi1.a* gene is commonly more pronounced in six-rowed cultivars than in two-rowed ones. In many environments, plants of the Bowman backcross-derived line BW471 were about 10% taller than Bowman and had longer peduncles. Rachis internodes were slightly longer and spikes often had one or two more fertile rachis nodes. Kernels of BW471 plants were often slightly longer and heavier than those of Bowman (3). The marker data for BW471 conflicts with the previously reported chromosomal location for *lbi1.a*, but the SNP marker pattern of the donor parent segments in BW471 suggests a six-rowed origin of the retained segments (2). This indicates more than one locus may be involved in expression of the long basal rachis internode trait.

Origin of mutant:

Natural occurrence in Wisconsin Pedigree 38 (Barbless, CIho 5105, GSHO 580) (5), and in many other six-rowed cultivars of Manchurian origin (5, 8).

Mutational events:

lbi1.a in Wisconsin Pedigree 38 (CIho 5105, GSHO 580) (5); *rac-a.2* (NGB 114845) and *rac-b.1* (NGB 114844) in Bonus (PI 189763) are not alleles of each other (6); but both *rac-a.2 and rac-b.1* are reported to be alleles at the *lbi1* locus (8).

Mutant used for description and seed stocks:

lbi1.a in Wisconsin Pedigree 38 (GSHO 580); *lbi1.a* in Bowman (PI 483237)*5 (GSHO 2144); *lbi1.a* in Bowman*6 (BW471, NGB 20701).

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.
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. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
5. Hehn, E.R. 1948. The inheritance of agronomic characters in barley. Iowa State Coll. Jour. Sci. 23:39-40. (Abstr.).
6. Lundqvist, U. (Unpublished).
7. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1955. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement II, 1947-1953. Agron. J. 47:418-425.
8. Tsuchiya, T. 1974. Further results of allelism testing in barley. Barley Genet. Newsl. 4:82-85.
9. Wiebe G.A., and D.A. Reid. 1961. Classification of barley varieties grown in the United States and Canada in 1958. U.S. Dep. Agric. Tech. Bull. 1224. 234 pp.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:167.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:258.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:88-89.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:125-126.

BGS 339, High lysine 3, *lys3*

Stock number:	BGS 339
Locus name:	High lysine 3
Locus symbol:	*lys3*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia 3 = *sex3* (18, 19).

Inheritance:

Monofactorial recessive (3, 5, 18).

Located in 5HL (9, 13, 20); near the *msg19* (male sterile genetic 19) locus (18); about 14.5 cM proximal from the *fst1* (fragile stem 1) locus; about 20.7 cM proximal from the *ddt1* (reaction to DDT 1) locus (9, 11); likely in the cluster of hordein genes in 1H bin 02. A second variant isolated from Risø 1508 is associated with SNP markers 2_0479 to 3_0918 (positions 0.54 to 17.27 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW496 (6).

Description:

After the hard dough stage, kernels develop a depression in the dorsal side or lemma which becomes progressively more distinct with maturity. The 1000-kernel weight of the mutant is about 75% of normal. The mutant expresses xenia permitting classification of kernels from heterozygous plants as normal or shrunken with an expected 3:1 ratio (3). Field establishment and growth of mutant plants is normal (3, 5). Mutant kernels have a higher lysine content than normal kernels (3) and a pleiotropic the association with shrunken endosperm (13, 19). The endosperm is nearly devoid of B- and C-hordeins (8, 14, 16). The B-hordein genes in developing barley endosperm were highly methylated in the *lys3.a* mutant compared to wild-type endosperm (17). A deficiency of kernels with shrunken endosperm occurs in some crosses (1, 2, 5, 18) and was caused likely highly distorted male gamete transmission (4). The gamete lethal factor in Risø 1508 was named *Gam3* (gametophyte factor 3) and was position in 5HL about 6.5 cM from the *lys3* locus (21). Based on SNP mapping information (6), the Bowman backcross-derived line from Risø 1508, BW496, may also contain a shrunken endosperm mutant near the *Hor2* locus in the 1HS cluster of hordein genes (15), which is not the *lys3.a* mutant. The Bowman backcross-derived line BW496 is apparently more sensitive to environmental stress than Bowman. Heading of BW496 is delayed by 6 to 10 days, plants are 2/3 to almost normal in height, and peduncles are 1/2 to normal in length. Kernel weights for BW496 were 30% lower than those for Bowman. Grain yields of BW496 were about half of normal (6).

Origin of mutant:

An induced mutant in Bomi (PI 43371) (3).

Mutational events:

lys3.a (Risø 1508, GSHO 1785) in Bomi (PI 43371) (3, 9); *lys3.b* (Risø 18), *lys3.c* (Risø 19) in Bomi (9, 12).

Mutant used for description and seed stocks:

lys3.a (GSHO 1785, Risø 1508) in Bomi; *lys3.*a from Risø 1508 in Bowman (PI 483237) (GSHO 2096); *lys3.a* in Bowman*6 (BW496, NGB 20724).

References:

1. Ahokas, H. 1979. Further results on the suppression of shrunken endosperm in high lysine mutants. Barley Genet. Newsl. 9:3-7.

2. Ahokas, H. 1988. High-lysine gene segregation distorted in the barley cross Risø 1508 x Crypt CI 1090: Patterns of endosperm proteins by an electrophorectic method. Hereditas 108:129-131.
3. Doll, H. 1973. Inheritance of a high-lysine character of a barley mutant. Hereditas 74:293-294.
4. Doll, H. 1991. A factor on barley chromosome 7 causing distorted male segregation of gene *lys3a*. Barley Genet. Newsl. 20:23-24.
5. Doll, H., and R. Oram. 1989. Deviating Mendelian segregation of barley gene *lys3a*. Hereditas 110:97-99.
6. 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.
7. Franckowiak, J.D. (Unpublished).
8. Hopp, H.E., S.K. Rasmussen, and A. Brandt. 1983. Organization and transcription of B1 hordein genes in high lysine mutants of barley. Carlsberg Res. Commun. 48:201-216.
9. Jensen, J. 1979. Location of a high-lysine gene and the DDT-resistant gene on barley chromosome 7. Euphytica 28:47-56.
10. Jensen, J. 1979. Chromosomal location of one dominant and four recessive high-lysine genes in barley mutants. Vol. 1. p. 89-96. *In* Seed Protein Improvement in Cereals and Grain Legumes. Proc. Int. Symp., Neuherberg, Germany, 1978. Int. Atomic Energy Agency, Vienna.
11. Jensen, J. 1981. Construction of a barley chromosome 7 linkage map. p. 927-939. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.) Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp., Edinburgh. Edinburgh Univ. Press, Edinburgh.
12. Jensen, J., and H. Doll. 1979. Gene symbols for barley high-lysine mutants. Barley Genet. Newsl. 9:33-37.
13. Karlsson, K.-E. 1977. Linkage studies in a gene for high lysine content in Risø barley mutant 1508. Barley Genet. Newsl. 7:40-41.
14. Kries, M., P.R. Shewry, B.G. Forde, S. Rahman, M.B. Bahramian, and B.J. Miflin. 1984. Molecular analysis of the effects of the *lys3a* gene on the expression of *Hor* loci in developing endosperms of barley (*Hordeum vulgare* L.). Biochem. Genet. 22:231-255.
15: Pelger, S., T. Säll, and B.O. Bengtsson. 1993. Evolution of hordein gene organization in three *Hordeurn* species. Hereditas 119:219-231.
16. Shewry, P.R., A.J. Faulks, and B.J. Miflin. 1980. Effect of high-lysine mutations on the protein fractions of barley grains. Biochem. Genet. 18:133-151.
17. Sørensen, M.B. 1992. Methylation of B-hordein genes in barley endosperm is inversely correlated with gene activity and affected by the regulatory gene *Lys3*. Proc. Natl. Acad. Sci. USA. 89:4119-4123.
18. Ullrich, S.E., and R.F. Eslick. 1977. Inheritance of the shrunken endosperm character, *sex3c*, of Bomi Risø mutant 1508 and its association with lysine content. Barley Genet. Newsl. 7:66-73.
19. Ullrich, S.E., and R.F. Eslick. 1978. Chromosome location evidence for Risø induced high lysine shrunken endosperm mutants of barley. Barley Genet. Newsl. 8:114-125.
20. Ullrich, S.E., and R.F. Eslick. 1978. Inheritance of the associated kernel characters, high lysine and shrunken endosperm, of the barley mutant Bomi, Risø 1508. Crop Sci. 18:828-831.
21. Yamae, G., and T. Konishi. 1993. Distorted segregation of the *lys3a* mutant in barley kernels. Barley Genet. Newsl. 22:68-70.

Prepared:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:287-288.
Revised:
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:138-139.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:127-129.

BGS 346, Yellow streak 5, *yst5*

Stock number:	BGS 346
Locus name:	Yellow streak 5
Locus symbol:	*yst5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 7HS (1); *yst5.e* is associated with SNP markers 1_0327 to 1_1348 (positions 55.54 to 96.67 cM) in 7H bins 05 to 07 of the Bowman backcross-derived line BW928 (1). Previously *yst5* was located in chromosome 5HL (2); based on linkage drag with the *raw1* (smooth awn 1) locus (2).

Description:

Beginning with the second leaf, emerging leaf blades are very pale yellow-green in color. As the leaf blade matures, fine vertical green streaks develop. More greening of the leaf blade occurs along the midrib than near the margins. This pattern of greenish streaks in a yellow background persists until heading; then, leaf blades gradually develop a normal green in color (2). The *yst5* plants of the Bowman backcross-derived line for *yst5.e*, BW928, varied from 15% shorter to equal height compared to Bowman. BW928 headed up to three days later in some environments. Kernels were slightly lighter in some trials and grain yields varied from 3/4 those of Bowman to similar (2).

Origin of mutant:

A spontaneous mutant isolated from a Bowman/*ant10.30* cross (2).

Mutational events:

yst5.e (GSHO 2501) in Bowman/*ant10.30* (2).

Mutant used for description and seed stocks:

yst5.e (GSHO 2501) in Bowman/*ant10.30*; *yst5.e* in Bowman (PI 483237)*3 (GSHO 2366); *yst5.e* in Bowman*7 (BW928, NGB 22357).

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. 32:107.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:130.

BGS 351, Glossy sheath 1, *gsh1*

Stock number: BGS 351
Locus name: Glossy sheath 1
Locus symbol: *gsh1*

Previous nomenclature and gene symbolization:

Glaucous sheath = *gs* (5).
Glossy sheath and spike = *gs* (25).
Glossy sheath 1 = *gs1* (17).
Eceriferum-q = *cer-q* (7).

Inheritance:

Monofactorial recessive (5, 7), except *Cer-q.1440* (14).

Located in chromosome 2HS (21, 22); in a sub-terminal position (20) over 36.5 cM distal from the *Eam1* (early maturity 1) locus (1); associated with SNP markers 2_0562 to 1_0943 (positions 22.43 to 34.31 cM) in 2HS of the Bowman backcross-derived line BW404 (2), in 2H bins 02 or 03.

Description:

A bright, green glossy color is apparent on the spike, leaf sheath, and stem (wax code - - ++) (7, 17). The *gsh1* locus is the *cer-q* component of the complex locus named *cer-cqu* (3, 16), which controls formation of β-diketone lipids in epicuticular wax layer (23). The *cer-q* mutants affect the β-ketoacyl condensing enzyme (18, 24). Morphological differences, except for surface waxes, were not observed between Bowman and its backcross-derived line BW404 (4).

Origin of mutant:

A spontaneous mutant in PI 95285 (5), an iodine vapor induced mutant in Bonus (PI 189763) (7).

Mutational events:

gsh1.a (GSHO 735) in PI 95285 (5, 17, 19); *gsh1.b* in Piroline (PI 539132) (17); *gsh1.c* in Velvon (CIho 6109) (17, 25); *gsh1.y* in Minn 549 (17, 19); *cer-q.35* (GSHO 438, NGB 110919) in Bonus (PI 189763) (3, 7, 8); *cer-q.42* (NGB 110926), *-q.50* (NGB 110934), *-q.56* (NGB 110940), *-q.103* (NGB 110988) in Bonus (7, 8); *cer-q.82* (NGB 110966), *-q.83* (NGB 110967), *-q.84* (NGB 110968), *-cqu.124* (NGB 111009), *-q.128* (NGB 111013), *-q.131* (NGB 111016), *-q.132* (NGB 111017), *-q.133* (NGB 111018), *-q.141* (NGB 111027), *-q.151* (NGB 111037) in Bonus, *-q.213* (NGB 111100), *-q.217* (NGB 111104), *-q.218* (NGB 111105), *-q.239* (NGB 111126), *-q.241* (NGB 111128), *-q.245* (NGB 111132), *-q.246* (NGB 111133), *-q.261* (NGB 111148), *-q.262* (NGB 111149), *-q.292* (NGB 111179), *-q.295* (NGB 111182), *-q.297* (NGB 111184), *-q.299* (NGB 111186), *-q.310* (NGB 111197), *-q.320* (NGB 111207), *-q.326* (NGB 111213), *-q.327* (NGB 111214), *-q.334* (NGB 111221), *-q.335* (NGB 111222), *-q.341* (NGB 111228), *-q.365* (NGB 111252), *-q.395* (NGB 111282), *-q.396* (NGB 111283), *-q.400* (NGB 111287), *-q.403* (NGB 111291), *-q.411* (NGB 111299), *-cqu.416* (NGB 111304), *-cqu.420* (NGB 111308), *-q.425* (NGB 111313), *-q.440* (NGB 111328), *-q.488* (NGB 111376), *-q.509* (NGB 111397), *-qu.510* (NGB 111398) in Foma (CIho 11333) (8, 16); *cer-q.129* (NGB 111014), *-q.176* (NGB 111062) in Bonus, *-q.483* (NGB 111371), *-q.516* (NGB 111404), *-q.519* (NGB 111407), *-q.524* (NGB 111412), *-q.527* (NGB 111415), *-q.533* (NGB 111421), *-q.536* (NGB 111424), *-q.548* (NGB 111436), *-q.555* (NGB 111443), *-q.557* (NGB 111445), *-q.566* (NGB 111454), *-q.574* (NGB 111462), *-q.579*

(NGB 111467), *-q.597* (NGB 111485) in Foma, *-q.675* (NGB 111563), *-q.683* (NGB 111571), *-q.688* (NGB 111576), *-cqu.724* (NGB 111612), *-cqu.733* (NGB 111621) in Bonus, *-q.1016* (NGB 111904), *-q.1018* (NGB 111906), *-q.1040* (NGB 111928), *-q.1061* (NGB 111949), *-q.1063* (NGB 111951), *-q.1064* (NGB 111952), *-q.1065* (NGB 111953), *-q.1068* (NGB 111956), *-q.1070* (NGB 111958), *-q.1073* (NGB 111961), *-q.1074* (NGB 111962), *-q.1083* (NGB 111971) in Carlsberg II (CIho 10114) (8); *cer-q.153* (NGB 111039), *-q.754* (NGB 111642), *-q.755* (NGB 111643), *-q.756* (NGB 111644), *-q.757* (NGB 111645), *-q.759* (NGB 111647), *-q.772* (NGB 111660), *-qu.813* (NGB 111701), *-q.822* (NGB 111710), *-q.827* (NGB 111715), *-q.837* (NGB 111725), *-q.848* (NGB 111736), *-q.876* (NGB 111764) in Bonus, *-q.401* (NGB 111289) in Foma, *-q.1079* (NGB 111967) in Carlsberg II, *-q.1105* (NGB 111993), *-q.1128* (NGB 112016), *-q.1131* (NGB 112019), *-q.1141* (NGB 112029), *-q.1143* (NGB 112031) in Kristina (NGB 1500) (9); *cer-q.629* (NGB 111517), *-q.634* (NGB 111522), *-q.636* (NGB 111524), *-cq.645* (NGB 111533), *-q.900* (NGB 111788), *-cqu.925* (NGB 111813), *-cqu.944* (NGB 111832) in Bonus, *-q.1158* (NGB 112046), *-q.1167* (NGB 112055) in Kristina (10); *cer-q.1011* (NGB 111899) in Carlsberg II, *-q.1121* (NGB 112009), *-q.1193* (NGB 112081), *-q.1209* (NGB 112097), *-q.1225* (NGB 112113), *-q.1234* (NGB 112122), *-q.1238* (NGB 112126), *-q.1242* (NGB 112130), *-q.1243* (NGB 112131) in Kristina (11); *cer-q.598* (NGB 111486) in Foma, *-q.1260* (NGB 112148), *-q.1281* (NGB 112169), *-q.1283* (NGB 112171), *-q.1285* (NGB 112173) in Kristina, *-q.1320* (NGB 112208), *-q.1330* (NGB 112218) in Bonus (12); *cer-q.1230* (NGB 112118) in Kristina, *-q.1345* (NGB 112233), *-q.1358* (NGB 112246, 116826, 117275), *-q.1362* (NGB 112250), *-q.1363* (NGB 112251), *-q.1368* (NGB 112256), *-q.1369* (NGB 112257), *-q.1375* (NGB 112263), *-q.1400* (NGB 112288), *-q.1406* (NGB 112294), *-q.1412* (NGB 112300), *-q.1430* (NGB 112318), *-q.1459* (NGB 112347), *-q.1464* (NGB 112352) in Bonus, *-q.1504* (NGB 112392), *-q.1512* (NGB 112400), *-q.1514* (NGB 112402) in Nordal (13); *Cer-q.1440* (NGB 112328), *cer-q.1490* (NGB 112378), *-q.1499* (NGB 112387), *-q.1706* (NGB 112519), *-q.1708* (NGB 112521), *-q.1742* (NGB 112555), *-q.1748* (NGB 112562), *-q.1753* (NGB 112567) in Bonus (14), *-q.1517* (NGB 112405), *-q.1521* (NGB 112409), *-q.1522* (NGB 112410), *-q.1527* (NGB 112415), *-q.1528* (NGB 112416), *-q.1533* (NGB 112421), *-q.1534* (NGB 112422), *-q.1537* (NGB 112425), *-q.1538* (NGB 112426), *-q.1539* (NGB 112427), *-q.1542* (NGB 112430), *-q.1551* (NGB 112439), *-q.1556* (NGB 112444), *-q.1572* (NGB 112460) in Nordal (14); *cer-q.571* (NGB 111459) in Foma (15); *gsh1.aa* (OUM018), *gsh1.ad* (OUM021), *gsh1.ak* (OUM028) in Akashinriki (PI 467400, OUJ659), *gsh1.an* (T119, OUL045) in a tester line, *gsh1.ap* (PI 95285, OUE093), *gsh1.ar* (PI 151791, OUE121), *gsh1.as* (PI 151815, OUE128), *gsh1.at* (PI 194916, OUE168), *gsh1.au* (CIho 14093, OUE330), *gsh1.av* (CIho 14139, OUE370), *gsh1.ax* (CIho 14094, OUE630), *gsh1.ay* (CIho 14140, OUE670), *gsh1.az* (CIho 4361, OUE676) in Ethiopian introductions, *gsh1.ba* in Bozu Omugi 1 (OUJ655) (6).

Mutant used for description and seed stocks:

gsh1.a (GSHO 735) in PI 95285; *cer-q.35* (GSHO 438, NGB 110919) in Bonus (PI 189763); *cer-q-42* (NGB 110926) in Bonus is used for wax chemistry and wax structure studies (23, 24); *gsh1.a* in Bowman (PI 483237)*7 (GSHO 1868, BW404, NGB 20637).

References:

1. Doney, D.L. 1961. An inheritance and linkage study of barley with special emphasis on purple pigmentation on the auricle. M.S. Thesis. Utah State Univ., Logan.
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. 2010. Genetic dissection of barley morphology and development. Plant Physiol. *155*:617-627.

3. Eslick, R.F. 1974. Allele tests of *gs* and *cer* mutants. Barley Genet. Newsl. 4:9-11.
4. Franckowiak, J.D. (Unpublished).
5. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.
6. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.
7. Lundqvist, U., and D. von Wettstein. 1962. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. Hereditas 48:342-362.
8. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
9. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.
10. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
11. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
12. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.
13. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
14. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
15. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91
16. 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.
17. McProud, W.L., and R.F. Eslick. 1971. Allelism within a series of glossy sheath mutants. Barley Genet. Newsl. 1:31-34.
18. Mikkelsen, J.D. 1984. Biosynthesis of esterified alkan-2-ols and β-diketones in barley spike epicuticular wax: synthesis of radioactive intermediates. Carlsberg Res. Commun. 49:391-416.
19. Rasmusson, D.C, and J.W. Lambert. 1965. Inheritance of the glossy-sheath character in barley, *Hordeum vulgare* L. Crop Sci. 5:251-253.
20. Schondelmaier, J., G. Fischbeck, and A. Jahoor. 1993. Linkage studies between morphological and RFLP markers in the barley genome. Barley Genet. Newsl. 22:57-62.
21. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.
22. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. Barley Genet. Newsl. 2:93-98.
23. Wettstein-Knowles, P. von. 1972. Genetic control of β-diketone and hydro-β-diketone synthesis in epicuticular waxes of barley. Planta 106:113-130.
24. Wettstein-Knowles, P. von. 1992. Molecular genetics of the lipid synthesis in barley. p.753-771. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.) Barley Genetics, Vol. II. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Sweden. Munksgaard International Publishers Ltd., Copenhagen.
25. Woodward, R.W. 1957. Linkage studies in barley. Agron. J. 49:28-32.

Prepared:

W.L. McProud and R.F. Eslick. 1971. Barley Genet. Newsl. 1:168-169.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:292-293.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:92-94.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:131-134.

BGS 356, Glossy sheath 6, *gsh6*

Stock number: BGS 356
Locus name: Glossy sheath 6
Locus symbol: *gsh6*

Previous nomenclature and gene symbolization:

Glossy sheath 6 = *gs6* (16).
Eceriferum-c = *cer-c* (5).
Eceriferum-cqu = *cer-cqu* (14, 22).

Inheritance:

Monofactorial recessive (5, 16, 18).

Located in chromosome 2HS (18, 19, 20); in a subterminal position (17); associated with SNP markers 1_0326 to 2_0563 (positions 16.91 to 21.19 cM) in 2HS of the Bowman backcross-derived line BW409 (1), in 2H bin 02.

Description:

A bright, glossy green color is apparent on the spike, leaf sheath, and stem (16). The *gsh6* locus is the *cer-c* component of the complex locus *cer-cqu* (2), which controls formation of β-diketone lipids in epicuticular wax layer (21, 22). Most alleles have the wax code - - ++, but a few alleles show delayed development of surface waxes on the sheath (wax code - +/- ++) (5, 15). The only observed morphological difference between Bowman and the backcross-derived line BW409 was an increase in kernel length (3).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (5), a radiation induced mutant in Domen (CIho 9562) (16).

Mutational events:

cer-c.3 (GSHO 212. GSHO 424, GSHO 959, NGB 110887) in Bonus (PI 189763) (2, 5); *cer-c.7* (NGB 110891), *-c.29* (NGB 110913), *-c.36* (NGB 110920), *-c.44* (NGB 110928), *-c.61* (NGB 110945), *-c.63* (NGB 110947) in Bonus (5, 6); *cer-c.73* (NGB 110957), *-c.89* (NGB 110973), *-c.95* (NGB 110979), *-cu.108* (NGB 110993), *-c.115* (NGB 111000), *-c.123* (NGB 111008), *-cqu.124* (NGB 111009) in Bonus, *-c.201* (NGB 111088), *-c.206* (NGB 111093), *-c.220* (NGB 111107), *-c.223* (NGB 111110), *-c.234* (NGB 111121), *-c.238* (NGB111125), *-c.240* (NGB 111127), *-c.250* (NGB 111137), *-c.270* (NGB 111157), *-c.282* (NGB 111169), *-c.283* (NGB 111170), *-c.284* (NGB 111171), *-c.290* (NGB 111177), *-c.291* (NGB 111178), *-c.293* (NGB 111180). *-c.306* (NGB 111193), *-c.315* (111202), *-c.332* (NGB 111219), *-c.343* (NGB 111230), *-c.354* (NGB 111241), *-c.361* (NGB 111248), *-c.364* (NGB 111251), *-c.367* (NGB 111254), *-c.368* (NGB 111255), *-c.374* (NGB 111261), *-c.379* (NGB 111266), *-c.398h* (NGB 111285), *-c.398l* (NGB 111288), *-c.405* (NGB 111293), *-c.406* (NGB 111294), *-c.413* (NGB 111301), *-cqu.416* (NGB 111304), *-cqu.420* (NGB 111308), *-c.431* (NGB 111319), *-c.445* (NGB 111333), *-c.455* (NGB 111343), *-c.469* (NGB 111357), *-c.471* (NGB 111359), *-c.502* (NGB 111390) in Foma (CIho 11333) (6, 14); *cer-c.143* (NGB 111029), *-c.171* (NGB 111057), *-c.175* (NGB 111061) in Bonus, *-c.345* (NGB 111232), *-c.451* (NGB 111339), *-c.459* (NGB 111347), *-c.508* (NGB 111396), *-c.513* (NGB 111401), *-c.514* (NGB 111402), *-c.520* (NGB 111408), *-c.526* (NGB 111414), *-c.544* (NGB 111432), *-c.550* (NGB 111438), *-c.563* (NGB 111451), *-c.596* (NGB 111484), *-c.601* (NGB 111489), *-c.661* (NGB 111549) in Foma, *-c.669* (NGB 111557), *-c.673* (NGB 111561), *-c.690* (NGB 111578), *-c.693* (NGB 111581), *-c.698* (NGB 111586), *-c.703* (NGB 111591), -

c.711 (NGB 111499), *-cqu.724* (NGB 111612), *-cqu.733* (NGB 111621) in Bonus, *-c.1001* (NGB 111889), *-c.1004* (NGB 111892), *-c.1008* (NGB 111896), *-c.1010* (NGB 111898), *-c.1015* (NGB 111903), *-c.1022* (NGB 111910), *-c.1029* (NGB 111917), *-c.1034* (NGB 111922), *-c.1035* (NGB 111923), *-c.1039* (NGB 111927), *-c.1062* (NGB 111950), *-c.1067* (NGB 111955), *-c.1082* (NGB 111970) in Carlsberg II (CIho 10114) (6); *cer-c.589* (NGB 111477) in Foma, *-c.748* (NGB 111636), *-c.760* (NGB 111648), *-c.764* (NGB 111652), *-c.767* (NGB 111655), *-c.770* (NGB 111658), *-c.774* (NGB 111662), *-c.786* (NGB 111674), *-c.793* (NGB 111681), *-c.794* (NGB 111682), *-c.841* (NGB 111729), *-c.845* (NGB 111733) -, *c.847* (NGB 111735), *-c.851* (NGB 111739), *-c.860* (NGB 111748), *-c.870* (NGB 111758), *-c.881* (NGB 111769), *-c.883* (NGB 111771) in Bonus, *-c.1032* (NGB 111920) in Carlsberg II, *-c.1098* (NGB 111986), *-c.1100* (NGB 111988), *-c.1109* (NGB 111997), *-c.1117* (NGB 112005), *-c.1123* (NGB 112011), *-c.1125* (NGB 112013), *-c.1135* (NGB 112023), *-c.1136* (NGB 112024), *-c.1140* (NGB 112028), *-c.1147* (NGB 112035) in Kristina (NGB 1500) (7); *cer-c.499* (NGB 111387), *-c.609* (NGB 111497) in Foma, *-c.630* (NGB 111518), *-c.635* (NGB 111523), *-c.640* (NGB 111528), *-cu.644* (NGB 111532), *-cq.645* (NGB 111533), *-c.648* (NGB 111536), *-c.890* (NGB 111778), *-c.897* (NGB 111785), *-c.902* (NGB 111790), *-c.903* (NGB 111791), *-c.904* (NGB 111792), *-c.907* (NGB 111795), *-c.912* (NGB 111800), *-c.915* (NGB 111803), *-cqu.925* (NGB 111813), *-c.942* (NGB 111830), *-cqu.944* (NGB 111832), *-c.945* (NGB 111833), *-c.980* (NGB 111868) in Bonus, *-c.1156* (NGB 112044), *-c.1187* (NGB 112075) in Kristina (8); *cer-c.144* (NGB 111030), *-cu.947* (NGB 111835), *-c.987* (NGB 111875) in Bonus, *-c.1110* (NGB 111998), *-c.1212* (NGB 112100), *-c.1229* (NGB 112117), *-c.1248* (NGB 112136), *-c.1258* (NGB 112146), *-c.1264* (NGB 112152), *-c.1276* (NGB 112164) in Kristina (9); *cer-c.511* (NGB 111399) in Foma, *-c.1200* (NGB 112088), *-c.1254* (NGB 112271, 1168212), *-c.1278* (NGB 116824, 117273), *-c.1287* (NGB 112175), *-c.1291* (NGB 112179) in Kristina, *-c.1319* (NGB 112207), *-c.1325* (NGB 112213), *-c.1329* (NGB 112217), *-c.1334* (NGB 112222), *-c.1338* (NGB 112226) in Bonus (10); *cer-c.993* (NGB 111881), *-c.994* (NGB 111882), *-c.995* (NGB 111883), *-c.999* (NGB 111887), *-c.1348* (NGB 112236), *-c.1355* (NGB 112243), *-c.1359* (NGB 112247), *-c.1365* (NGB 112253), *-c.1376* (NGB 112264), *-c.1381* (NGB 112269), *-c.1382* (NGB 112270), *-c.1385* (NGB 112273), *-c.1386* (NGB 112274), *-c.1389* (NGB 112277), *-c.1416* (NGB 112304), *-c.1421* (NGB 112309), *-c.1439* (NGB 112327), *-c.1448* (NGB 112336), *-c.1460* (NGB 112348), *-c.1462* (NGB 112350), *-c.1466* (NGB 112354), *-c.1467* (NGB 112355) in Bonus, *-c.1501* (NGB 112389), *-c.1502* (NGB 112390), *-c.1503* (NGB 112391), *-c.1505* (NGB 112393), *-c.1506* (NGB 112394), *-c.1511* (NGB 112399), *-c.1515* (NGB 112403) in Nordal (11); *cer-c.1491* (112379), *-c.1701* (NGB 112514), *-c.1702* (NGB 112515), *-c.1703* (NGB 112516), *-c.1705* (NGB 112518), *-c.1707* (NGB 112520), *-c.1714* (NGB 112527), *-c.1737* (NGB 112550, 117329), *-c.1739* (NGB 112552), *-c.1749* (NGB 112563), *-c.1755* (NGB 112569), *-c.1757* (NGB 112572) in Bonus, *-c.1516* (NGB 112404), *-c.1520* (NGB 112408), *-c.1525* (NGB 112413), *-c.1526* (NGB 112414), *-c.1532* (NGB 112420), *-c.1553* (NGB 112441), *-c.1555* (NGB 112443), *-c.1560* (NGB 112448) in Nordal (12); *cer-c.602a* (NGB 119348) in Foma (13); *gsh6.o* in Domen (CIho 9562), *gsh6.p* in PI 184877, *gsh6.q* in Kogane Mugi (OUL010, PI 225020), *gsh6.r* in Barbless (CIho 5105), *gsh6.s* (GSHO 740) in Betzes (PI 129430), *gsh6.t* in Heines Hanna (PI 539131), *gsh6.u, gsh6.v, gsh6.w*, and *gsh6.x* in Compana (PI 539111) (15); *gsh6.z* (OUM017), *gsh6.ac* (OUM020), *gsh6.ai* (OUM026) in Akashinriki (PI 467400, OUJ659) (4); *gsh6.aq* in an Ethiopian introduction (PI 151787, OUE 120) (4).

Mutant used for description and seed stocks:

cer-c.3 (GSHO 212, GSHO 424, GSHO 959, NGB 110887) in Bonus; *cer-c.36* (NGB 110920 is used for wax chemistry and wax structure studies (21, 22); *gsh6.s* (GSHO 740) in Betzes, *gsh6.s* via R.I. Wolfe's Multiple Marker Stock for chromosome 2 in Bowman (PI 483237)*7 (GSHO 1869, BW409, NGB 20642).

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. Eslick, R.F. 1974. Allele tests of *gs* and *cer* mutants. Barley Genet. Newsl. 4:9-11.
3. Franckowiak, J.D. (Unpublished).
4. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.
5. Lundqvist, U., and D. von Wettstein. 1962. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. Hereditas 48:342-362.
6. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
7. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.
8. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
9. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
10. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.
11. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
12. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
13. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.
14. 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.
15. McProud, W.L., and R.F. Eslick. 1971. Allelism within a series of glossy sheath mutants. Barley Genet. Newsl. 1:31-34.
16. Rasmusson, D.C., and J.W. Lambert. 1965. Inheritance of the glossy-sheath character in barley, *Hordeum vulgare* L. Crop Sci. 5:251-253.
17. Schondelmaier, J., G. Fischbeck, and A. Jahoor. 1993. Linkage studies between morphological and RFLP markers in the barley genome. Barley Genet. Newsl. 22:57-62.
18. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 4:66-69.
19. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.
20. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. BGN 2:93-98.
21. Wettstein-Knowles, P. von. 1972. Genetic control of β-diketone and hydro-β-diketone synthesis in epicuticular waxes of barley. Planta 106:113-130.
22. Wettstein-Knowles, P. von. 1992. Molecular genetics of the lipid synthesis in barley. p. 753-771. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.) Barley Genetics VI, Vol. II. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, Sweden, 1991. Munksgaard

International Publishers Ltd., Copenhagen.

Prepared:

W. L. McProud and R.F. Eslick. 1971. Barley Genet. Newsl. 1:172-173.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:302-303.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:95-97.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:135-138.

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 2_1073 to 1_0846 (positions 69.62 to approximately 93.5 cM) in 4H bins 02 to 04 of the Bowman backcross-derived line BW555 (1). Previously located 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 70 to 90% (2). Both the original stock and BW555 have short awns (3/4 normal length) (2).
Origin of mutant:
An X-ray induced mutant in Hannchen (CIho 531) (3).
Mutational events:
msg20.ad (MSS096, GSHO 2372) in Hannchen (CIho 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, Pullman.
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. 2013. Barley Genet. Newsl. 43:139.

BGS 386, Desynapsis 3, *des3*

Stock number: BGS 386
Locus name: Desynapsis 3
Locus symbol: *des3*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 2H or 5HL (1); *des3.c* is associated with SNP markers 1_0796 to 2_0528 (positions 95.53 to 118.80 cM) in 2H bins 07 to 08 and with SNP markers 1_0104 to 2_0644 (positions 223.60 to 266.0 cM) in 5H bins 11 to 13 of the Bowman backcross-derived line BW239 (1).

Description:

The chromosomes are paired during the pachytene stage of microsporogenesis, but they undergo desynapsis during diplotene and diakinesis. The degree of desynapsis is 0.9 ± 1.7, ranging from 7 ring bivalents (d = 0) to 4 ring bivalents plus 2 rod bivalents and 2 univalents (d = 4). Ovule fertility ranges from 1% to 33%, much too low to be explained by the low degree of desynapsis observed in microsporocytes (3). Compared to Bowman, plants of the Bowman backcross-derived line for *des3.c*, BW239, headed three days later and had about three more kernels per spike. Kernel weights were often slight lighter than those of Bowman. The grain yield of BW239 was about 1/2 that of Bowman (2). Seed set for BW239 was 20 to 40% when grown under greenhouse conditions, but late tillers had very low or no seed set (2).

Origin of mutant:

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

Mutational events:

des3.c (GSHO 594) in Betzes (PI 129430) (4, 5).

Mutant used for description and seed stocks:

des3.c (GSHO 594) in Betzes; *des3.c* in Bowman (PI 483237)*6 (BW239, NGB 22066).

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.
4. Ramage, R.T., and J.M. Hernandez-Soriano. 1971. Desynaptic genes in Betzes barley. Barley Genet. Newsl. 1:38.
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, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:126.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:334.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:140.

BGS 413, Glossy sheath 8, *gsh8*

Stock number: BGS 413
Locus name: Glossy sheath 8
Locus symbol: *gsh8*

Previous nomenclature and gene symbolization:

Eceriferum-u = *cer-u* (6).
Glossy sheath 8 = *gs8* (4).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 2HS (17, 18); based on close association with the *gsh6* (glossy sheath 6) locus (2, 5, 17, 18); in a subterminal position (16); *gsh8.ag* is associated with SNP markers 2_1377 to 1_0919 (positions 20.11 to 66.78 cM) in 2H bin 02 to 03 of the Bowman backcross-derived line BW411 (1), in 2H bins 02 or 03.

Description:

The wax coating on the spike, stem and leaf sheath appears reduced (wax code + + ++) (6). The *gsh8* locus is the *cer-u* component of the complex locus *cer-cqu* which controls epicuticular wax layer formation on the surface of the spike, leaf sheath, and stem (19, 20). Deposition of β-diketone lipids is reduced or eliminated by mutants in the *cer-cqu* locus (20), specifically the *cer-u* mutants have impaired hydroxyl group insertion (19). The original *cer-u.21* stock has reduced seed set (6). Morphological differences, except for surface waxes, were not observed between Bowman and its backcross-derived line BW411 (3).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (6).

Mutational events:

cer-u.21 (NGB 110905, GSHO 442), *-u.58* (NGB 110942) in Bonus (PI 189763) (6, 7); *cer-u.69* (NGB 110953), *-u.76h* (NGB 110960), *-u.76l* (NGB 110985), *-u.80* (NGB 110964), *-u.99* (NGB 110983), *-u.107* (NGB 110992), *-cu.108* (NGB 110993), *-u.119* (NGB 111004), *-u.120* (NGB 111005) in Bonus, *-u.204* (NGB 111091), *-u.237* (NGB 111124), *-u.258* (NGB 111145), *-u.265* (NGB 111152), *-u.281* (NGB 111168), *-u.304* (NGB 111191), *-u.305* (NGB 111192), *-u.307* (NGB 111194), *-u.324* (NGB 111211), *-u.330* (NGB 111217), *-u.338* (NGB 111225), *-u.344* (NGB 111231), *-u.371* (NGB 111258), *-u.376* (NGB 111263), *-u.387* (NGB 111274), *-cqu.416* (NGB 111304), *-cqu.420* (NGB 111308), *-u.443* (NGB 111331), *-u.446* (NGB 111334), *-u.452* (NGB 111340), *-u.464* (NGB 111352), *-u.466* (NGB 111354), *-u.468* (NGB 111356), *-u.472* (NGB 111360),*-u.485* (NGB 111373), *-u.491* (NGB 111379), *-u.497* (NGB 111385), *-u.498* (NGB 111386), *-u.505* (NGB 111393), *-qu.510* (NGB 111398) in Foma (CIho 11333) (7, 15); *cer-cqu.124* (NGB 111009), *-u.177* (NGB 111063), *-u.178* (NGB 111064), *-u.189* (NGB 111075) in Bonus, *-u.525* (NGB 111413), *-u.538* (NGB 111426), *-u.542* (NGB 111430), *-u.543* (NGB 111431), *-u.556* (NGB 111444), *-u.570* (NGB 111458), *-u.581* (NGB 111469), *-u.600* (NGB 111488), *-u.605* (NGB 111493), *-u.606* (NGB 111494) in Foma, *-u.677* (NGB 111565), *-u.686* (NGB 111574), *-u.689* (NGB 111577), *-u.697* (NGB 111585), *-cqu.724* (NGB 111612), -cqu.733 (NGB 111621) in Bonus, *-u.1003* (NGB 111891), *-u.1009* (NGB 111897), *-u.1042* (NGB 111930), *-u.1043* (NGB 111931), *-u.1048* (NGB 111936), *-u.1060* (NGB 111948), *-u.1076* (NGB 111964), *-u.1078* (NGB 111966) in Carlsberg II (CIho 10114) (7); *cer-u.610* (NGB 111498), *-u.613*

(NGB 111501) in Foma, *-u.737* (NGB 111625), *-u.766* (NGB 111654), *-u.775* (NGB 111663), *-u.779* (NGB 111667), *-u.784* (NGB 111672), *-u.789* (NGB 111677), *-u.798* (NGB 111686), *-qu.813* (NGB 111701), *-u.823* (NGB 111711), *-u.825* (NGB 111713), *-u.830* (NGB 111718), *-u.835* (NGB 111723), *-u.839* (NGB 111727), *- u.840* (NGB 111728), *-u.842* (NGB 111730), *-u.843* (NGB 111731), *-u.844* (NGB 111732), *-u.855* (NGB 111743), *-u.861* (NGB 111749) in Bonus, *-u.1091* (NGB 111979), *-u.1096* (NGB 111984), *-u.1101* (NGB 111989), *-u.1107* (NGB 111995), *-u.1108* (NGB 111996), *-u.1111* (NGB 111999), *-u.1114* (NGB 112002), *-u.1120* (NGB 112008), *-u.1137* (NGB 112025), *-u.1146* (NGB 112034), *-u.1148* (NGB 112036) in Kristina (NGB 1500) (8); *cer-cu.644* (NGB 111532), *-u.695* (NGB 111583), *-u.850* (NGB 111738), *-u.887* (NGB 111775), *-u.892* (NGB 111780), *-u.895* (NGB 111783), *-u.901* (NGB 111789), *-cqu.925* (NGB 111813), *-cqu.944* (NGB 111832), *-cu.947* (NGB 111835) in Bonus, *-u.1177* (NGB 112065) in Kristina (9); *cer-u.699* (NGB 111587), *-u.776* (NGB 111664), *-u.986* (NGB 111874) in Bonus, *-u.1165* (NGB 112053), *-u.1184* (NGB 112072), *-u.1188* (NGB 112076), *-u.1202* (NGB 112090), *-u.1215* (NGB 112103), *-u.1227* (NGB 112115), *-u.1232* (NGB 112120), *-u.1237* (NGB 112125), *-u.1253* (NGB 112141), *-u.1272* (NGB 112160) in Kristina (10); *cer-u.1208* (NGB 112096), *-u.1261* (NGB 112149), *-u.1268* (NGB 112156), *-u.1282* (NGB 112170), *-u.1288* (NGB 112176), *-u.1295* (NGB 112183), *-u.1306* (NGB 112194), *-u.1309* (NGB 112197), *-u.1310* (NGB 112198) in Kristina, *-u.1327* (NGB 112215), *-u.1340* (NGB 112228), *-u.1341* (NGB 112229) in Bonus (11); *cer-u.457* (NGB 111345), *-u.578* (NGB 111466) in Foma, *-u.1364* (NGB 112252), *-u.1370* (NGB 112258), *-u.1372* (NGB 112260), *-u.1373* (NGB 112261), *-u.1390* (NGB 112278), *-u.1402* (NGB 112290), *-u.1409* (NGB 112297), *-u.1411* (NGB 112299), *-u.1420* (NGB 112308), *-u.1429* (NGB 112317) in Bonus (12); *cer-u.1496* (NGB 112384), *-u.1500* (NGB 112388), *-u.1734* (NGB 112547), *-u.1759* (NGB 112574), *-u.1763* (NGB 112567) in Bonus, *-u.1540* (NGB 112428), *-u.1541* (NGB 112429) in Nordal (13); *cer-u.678* (NGB 111566), *-u.1825* (NGB 117373) in Bonus, *-u.602b* (NGB 111490) in Foma, *-u.1870* (NGB 117418) in Sv 79353 (14); *gsh8.ag* (OUM024, GSHO 1760), *gsh8.am* (OUM031) in Akashinriki (PI 467400, OUJ659) (4, 5).

Mutant used for description and seed stocks:

cer-u.21 (NGB 110905, GSHO 442) in Bonus; *cer-u.69* (NGB 110953) in Bonus is used for wax chemistry and wax structure studies (19, 20); *gsh8.ag* (OUM024, GSHO 1760) in Akashinriki; *gsh8.ag* in Bowman (PI 483237)*4 (GSHO 1870); *gsh8.ag* in Bowman*5 (BW411, NGB 20644).

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. Eslick, R.F. 1974. Allele tests of *gs* and *cer* mutants. Barley Genet. Newsl. 4:9-11.
3. Franckowiak, J.D. (Unpublished).
4. Konishi, T. 1973. Genetic analyses of EMS-induced mutants in barley. Barley Genet. Newsl. 3:28-31.
5. Lundqvist, U. 1995. Coordinator's report: *Eceriferum* genes. Barley Genet. Newsl. 24:159.
6. Lundqvist, U., and D. von Wettstein. 1962. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. Hereditas 48:342-362.
7. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
8. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II.

Barley Genet. Newsl. 3:110-112.
9. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
10. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
11. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.
12. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
13. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
14. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.
15. 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.
16. Schondelmaier, J., G. Fischbeck, and A. Jahoor. 1993. Linkage studies between morphological and RFLP markers in the barley genome. Barley Genet. Newsl. 22:57-62.
17. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw. Forsch. 10:29-52.
18. Tsuchiya, T. 1972. Cytogenetics of telotrisomics in barley. Barley Genet. Newl. 2:93-98.
19. Wettstein-Knowles, P. von. 1972. Genetic control of β-diketone and hydro-β-diketone synthesis in epicuticular waxes of barley. Planta 106:113-130.
20. Wettstein-Knowles, P. von. 1992. Molecular genetics of the lipid synthesis in barley. p. 753-771. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.) Barley Genet. VI, Vol. II. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, Sweden, 1991. Munksgaard International Publishers Ltd., Copenhagen.

Prepared:
U. Lundqvist and P. von Wettstein-Knowles. 1975. Barley Genet. Newsl. 5:131 as BGS 413, Eceriferum-u, *cer-u.*

Revised:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:364-365.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:107-109.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:141-143.

BGS 419, Eceriferum-za, *cer-za*

Stock number: BGS 419
Locus name: Eceriferum-za
Locus symbol *cer-za*

Previous nomenclature and symbolization:
None.

Inheritance:
Monofactorial recessive (11).
Located in chromosome 5HL (3); close to the *raw1* (smooth awn 1) locus based on linkage drag (3); *cer-za.227* is associated with SNP markers 1_0360 to 2_0188 (positions 199.04 to 210.59 cM) in 5H bins 10 to 11 of the Bowman backcross-derived line BW157 (1).

Description:
Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (11). Plants of the Bowman backcross-derived line for *cer-za.227*, BW157, headed slightly later than Bowman and were slightly taller. BW157 plants were similar to Bowman for other morphological traits and grain yield (2).

Origin of mutant:
An ethylene imine induced mutant in Foma (CIho 11333) (11).

Mutational events:
cer-za.126 (NGB 111011; GSHO 1521), *-za.173* (NGB 111059), *-za.185* (NGB 111071), *-za.186* (NGB 111072) in Bonus (PI 189763) (4); *cer-za.227* (NGB 111114, GSHO 1521), *-za.232* (NGB 111119), *-za.318* (NGB 111205), *-za.323* (NGB 111210), *-za.328* (NGB 111215), *-za.441* (NGB 111329), *-za.462* (NGB 111350), *-za.482* (NGB 111370), *-za.490* (NGB 111378), *-za.504* (NGB 111392) in Foma (CIho 11333) (4, 11); *cer-za.378* (NGB 111365), *-za.465* (NGB 111353), *-za.530* (NGB 111418), *-za.541* (NGB 111429), *-za.552* (NGB 111440), *-za.572* (NGB 111460), *-za.575* (NGB 111463), *-za.583* (NGB 111471), *-za.587* (NGB 111475), *-za.588* (NGB 111476) in Foma, *-za.672* (NGB 111560), *-za.676* (NGB 111564), *-za.685* (NGB 111573), *-za.735* (NGB 111623), *-za.739* (NGB 111627), *-za.741* (NGB 111629) in Bonus (4); *cer-za.681* (NGB 111569), *-za.768* (NGB 111656), *-za.782* (NGB 111670), *-za.812* (NGB 111700), *-za.831* (NGB 111719), *-za.833* (NGB 111721), *-za.853* (NGB 111741), *-za.854* (NGB 111742), *-za.869* (NGB 111757) in Bonus, *-za.1122* (NGB 112010), *-za.1126* (NGB 112014) in Kristina (NGB 1500) (5); *cer-za.628* (NGB 111516), *-za.637* (NGB 111525), *-za.639* (NGB 111527), *-za.643* (NGB 111531), *-za.917* (NGB 111807) in Bonus, *-za.1159* (NGB 112047), *-za.1186* (NGB 112074), *-za.1190* (NGB 112078), *-za.1191* (NGB 112079) in Kristina (6); *cer-za.478* (NGB 117257) in Foma, *-za.1157* (NGB 112045), *-za.1178* (NGB 112066), *-za.1189* (NGB 112077), *-za.1203* (NGB 112091), *-za.1224* (NGB 112109), *-za.1228* (NGB 112116), *-za.1252* (NGB 112140) in Kristina (7); *cer-za.1286* (NGB 112174) in Kristina, *-za.1324* (NGB 112212), *-za.1346* (NGB 112234) in Bonus (8); *cer-za.1284* (NGB 112172) in Kristina, *-za.1357* (NGB 112245), *-za.1399* (NGB 112287), *-za.1407* (NGB 112295), *-za.1408* (NGB 112296), *-za.1431* (NGB 112319) in Bonus (9); *cer-za.1546* (NGB 112434) in Nordal, *-za.1713* (NGB 112526, *-za.1738* (NGB 117330), *-za.1745* (NGB 117331), *-za.1747* (NGB 112561), *-za.1800* (NGB 117348), *-za.1805* (NGB 117353), *-za.1806* (NGB 117354), *-za.1807* (NGB 117355), *-za.1812* (NGB 117360, *-za.1813* (NGB 117361) in Bonus (10).

Mutant used for description and seed stocks:

cer-za.227 in Foma (GSHO 1521, NGB 111114); *cer-za.227* in Bowman (PI 483237)*6 (GSHO 2126); *cer-za.227* in Bowman*7 (BW157, NGB 21989).

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. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
5. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.
6. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
7. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
8. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.
9. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
10. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
11. 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. 5:137.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:370.

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:144-145.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (9).

Located in chromosome 2HL (1, 2); based on the presence of the *gth1.a* allele at the *Gth1* (toothed lemma 1) locus in the BC_3F_3 stock (2); *cer-zk.85* is associated with SNP markers 2_0667 to 2_0528 (positions 117.73 to 118.78 cM) in 2H bin 08 of the Bowman backcross-derived line BW167 (1), in 2H bin 08.

Description:

Surface wax coating on the spike, leaf sheath, and stem is greatly reduced, and surface wax on the leaf blade is greatly reduced or absent (wax code + + +/-) (9). In the Bowman backcross-derived line for *cer-zk.85*, BW167, the distinct reduction in surface waxes on the leaf sheath and stem was not observed (wax code + ++ +/-). BW167 plants were similar to Bowman for all other traits evaluated including yield (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (9).

Mutational events:

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

Mutant used for description and seed stocks:

cer-zk.85 (GSHO 458, NGB 110969) in Bonus; *cer-zk.85* in Bowman (PI 483237)*4 (GSHO 2199); *cer-zk.85* in Bowman*6 (BW167, NGB 21999).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol. 155*:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
4. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.
5. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. Barley Genet. Newsl. 5:88-91.
6. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
7. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI.

Barley Genet. Newsl. 12:169-172.
8. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
9. 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. 5:147.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:381.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:146-147.

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 1_0112 to 1_0601 (positions 17.49 to 71.29 cM) in 3H bins 02 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 are observed in the original stock (5), but not in the Bowman backcross-derived line (2). Only reduced surface wax coating on the spike occurred (wax code + ++ ++) in the Bowman backcross-derived line for *cer-zo.229*, BW170. Other traits of BW170 including yield were not significantly different from those of Bowman (2).

Origin of mutant:

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

Mutational events:

cer-zo.229 (NGB 111116, GSHO 462), *-zo.352* (NGB 111239) in Foma (CIho 11333) (3, 5); *cer-zo.565* (NGB 111493) in Foma (3); *cer-zo.718* (NGB 111606)*, -zo.882* (NGB 111770 in Bonus (PI 189763) (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:

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

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

3. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.

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

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.

BGS 448, Eceriferum-ye, *cer-ye*

Stock number:	BGS 448
Locus name:	Eceriferum-ye
Locus symbol:	*cer-ye*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 4H (1); *cer-ye.267* is associated with SNP markers 2_1122 to 1_0569 (positions 47.80 to 78.18 cM) in 4H bins 05 to 06 of the Bowman backcross-derived line BW136 (1). Previously located in chromosome 5HL based on linkage drag with the *raw1* (smooth awn 1) locus (3).

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (5). Plants of the Bowman backcross-derived line for *cer-ye.267*, BW136, lack normal surface waxes on the leaf blades (2). BW136 plants were slightly shorter and later and had slightly lighter kernels in some trials (2).

Origin of mutant:

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

Mutational events:

cer-ye.267 (NGB 111154, GSHO 1538), *-ye.582* (NGB 111470) in Foma (CIho 11333, *cer-ye.792* (NGB 111680) in Bonus (PI 189763) (5); *cer-ye.1103* (NGB 111991) in Kristina (NGB 1500) (6); *cer-ye.1395* (NGB 112283) in Bonus (7).

Mutant used for description and seed stocks:

cer-ye.267 (GSHO 1538, NGB 111154) in Foma; *cer-ye.267* in Bowman (PI 483237)*7 (GSHO 2127); *cer-ye.267* in Bowman*7 (BW136, NGB 20542).

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.
6. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
7. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.

Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:166.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:400.

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:149.

BGS 455, Shrunken endosperm genetic 8, *seg8*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7H (7); *seg8.k* is associated with SNP markers 1_0772 to 1_0169 (positions 71.81 to 142.56 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW840 (1).

Description:

Seed size is reduced and maturity is delayed. Seed weights of 24, 23, and 27% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (7). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg8.k* plants can be used to establish stands under field conditions (7). Endosperms of *seg8.k* plants developed as two-filled lateral lobes with no central endosperm lobe, resulting in a distinct dorsal crease (2). This is evidence that the endosperm is divided into three lobes as explained by the phytomeric triad model (4). Kernels of the Bowman backcross-derived line for *seg8.k*, BW840, were very thin 3.01 vs. 3.84 mm in width and weighed much less, 1.7 vs. 5.6 mg, compared to those of Bowman. BW840 plants were similar to Bowman morphologically, but their grain yield was about 1/20 (3).

Origin of mutant:

A spontaneous mutant in 60Ab1810-53 (CIho 15686) (6).

Mutational events:

seg8.k (GSHO 2469) in 60Ab1810-53 (CIho 15686) (6, 7).

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D., B.P. Forster, U. Lundqvist, J. Lyon, I. Pitkethly, and W.T.B. Thomas. 2010. Developmental mutants as a guide to the barley phytomer. pp. 46-60. In: S. Ceccarelli and S. Grando (eds), Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt. ICARDA, PO Box 5466, Aleppo, Syria.
5. Ramage, R.T. 1983. Chromosome location of shrunken endosperm mutants *seg6g* and *seg8k*. Barley Genet. Newsl. 13:64-65.
6. Ramage, R.T., and C.L. Crandall. 1981. BGS 453, Shrunken endosperm, *seg8*. Barley Genet. Newsl. 11:103.
7. Ramage, R.T., and C.L. Crandall. 1981. Shrunken endosperm mutant *seg8*. Barley

Genet. Newsl. 11:34.

Prepared:

R.T. Ramage and C.L. Crandall. 1981. Barley Genet. Newsl. 11:103 as BGS 453.

Revised:

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

BGS 461, Zebra stripe 2, *zeb2*

Stock number:	BGS 461
Locus name:	Zebra stripe 2
Locus symbol:	*zeb2*

Previous nomenclature and gene symbolization:

Zoned leaf = *zd* (4).
Zoned leaf = *z* (5, 7, 14).
Zoned leaf c = zb_c (7, 13, 15).
Zebra leaf or zoned Colorado = z_c (6, 14).
Zebra striped leaves = *zd* (8).
Zebra stripe 2 =*zb2* (14).
Chlorina seedling 10 = *f10* (3, 11, 15).

Inheritance:

Monofactorial recessive (4, 5, 11).

Located in chromosome 4HS (3, 4); between the *lgn4* (light green 4) and *lgn3* (light green 3) loci (9); about 9.3 cM distal from the *Kap1* (hooded lemma 1) locus (3, 10); about 17.0 cM proximal from the *glf3* (glossy leaf 3) locus (3, 10); no recombination with the *lgn4* locus (3, 10); *zeb2.b* is associated with SNP markers 1_1180 to 1_0946 (positions 58.13 to 74.11 cM) in 4H bin 05 of the Bowman backcross-derived line BW931 (1); *fch10.s* is associated with SNP markers 1_0668 to 1_1224 (positions 63.19 to 91.93 cM) in 4H bins 05 and 06 of the Bowman backcross-derived line BW352 (1), in 4H bin 05 near the centromere.

Description:

Leaves are chlorina throughout the life cycle, independent of light and temperature (4). Plants may be killed by low temperature during the winter when normal plants are unaffected (4). A zonate pattern of different degrees of chlorina is observed in seedling leaves. After much confusion about this gene, the locus was named zebra stripe 2 = *zb2* (14). Plants are very weak or non-viable in the field in North Dakota, but only reduced vigor is noted when grown in the greenhouse (2). When compared to Bowman in the field, the Bowman backcross-derived line for *zeb2.b* (BW931) headed about 11 days later and produced only little very thin seed. Rachis internodes were slightly shorter and plants were 3/5 to 3/4 of normal height (2).

Origin of mutant:

Spontaneous mutants in an unknown cultivar (4, 15).

Mutational events:

zeb2.b (GSHO 93) in an unknown cultivar (4, 5, 12, 14); *fch10.s* in an unknown six-rowed cultivar (GSHO 1234) (10, 11); based on SNP patterns the *fch10.s* mutant studied by Woodward (10, 15) originated in six-rowed barley and the *zeb2.b* mutant first isolated by Immer and Henderson (4) originated in Bonus or a closely related line (1).

Mutant used for description and seed stocks:

zeb2.b (GSHO 93) in an unknown two-rowed cultivar; *zeb2.b* in Bowman (PI 483237)*4 (GSHO 2012); *zeb2.b* in Bowman*7 (BW931, NGB 22360); *fch10.s* (GSHO 1737) in an unknown six-rowed cultivar; *fch10.s* in Bowmnan (PI 483237)*7 (BW352, NGB 20591).

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.
4. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.
5. Kasha, K.J., and G.W. Walker. 1960. Several recent barley mutants and their linkages. Can. J. Genet. Cytol. 2:397-415.
6. Robertson, D.W. 1964. New genes in barley with their relation to linkage groups and chromosomes. p. 159-180. *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.
7. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.
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.
9. Smith, L. 1951. Cytology and genetics of barley. Bot. Rev. 17:1-55, 133-202, 285-355.
10. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.
11. Takahashi, R., J. Hayashi, and I. Moriya. 1973. Two new mutant genes on chromosome 4. Barley Genet. Newsl. 3:65-66.
12. Tsuchiya, T. 1975. Allelic relationships of some morphological and chlorophyll mutants in barley. Barley Genet. Newsl. 5:64-67.
13. Tsuchiya, T. 1983. Proposed new gene symbol for two different mutant types for zebra Colorado, or zoned leaf. Barley Genet. Newsl. 13:84.
14. Tsuchiya, T. 1984. Zebra striped leaves: Problems in gene and stock designation and proposed new symbols for zoned or zebra mutants in barley. Barley Genet. Newsl. 14:21-24.
15. Woodward, R.W. 1957. Linkages in barley. Agron. J. 49:28-32.

Prepared:

T.E. Haus. 1984. Barley Genet. Newsl. 14:93 as BGS 177, Chlorina 10, *f10*.
T. Tsuchiya. 1984. Barley Genet. Newsl. 14:98 as BGS 461, Zebra or zoned leaves 2, *zb2*.

Revised:

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:407-408.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:152-153.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4, 5).

Located in chromosome 2H (6); *mnd1.a* is associated with SNP markers 1_0638 to 1_0624 (positions 86.79 to 96.47 cM) in 2H bin 07 and SNP markers 2_0998 to 1_0999 (positions 160 to 222.50 cM) in 7H bins 10 to 13 of the Bowman backcross-derived line BW518 (2).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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

Prepared:

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

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:154.

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).

Location in chromosome 5HL (1, 2); associated with 5HL based on linkage drag with the *raw1* (smooth awn 1) locus (2); *cer-yr.492* is associated with SNP markers 1_0622 to 1_0477 (positions 158.46 to 174.49 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. Other morphological traits and grain yields were similar to those of Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333) (3).

Mutational events:

cer-yr.492 (NGB 111380, GSHO 1551) in Foma (CIho 11333), *-yr.1418* (NGB 112306) in Bonus (PI 189763) (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. 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. 26:458.

Revised:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:155.

BGS 562, Erectoides-k, *ert-k*

Stock number:	BGS 562
Locus name:	Erectoides-k
Locus symbol:	*ert-k*

Previous nomenclature and gene symbolization:

Erectoides-32 = *ert-32* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 6H (3, 5, 9), *ert-k.32* 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 BW314 (2).

Description:

Spikes of *ert-k* mutants are semicompact with rachis internode length values varying from 2.4 to 2.8 mm compared to 3.1 for Bonus (10). Culm length was 3/4 to 5/6 of normal (10). The improved straw strength of this mutant has potential agronomic value as indicated by the release of the *ert-k.32* stock as the cultivar Pallas (1, 7). In the Bowman backcross-derived line for *ert-k.32*, BW314, plants were about 15% shorter, kernels were 10 to 15% lighter, and rachis internodes were shorter, 3.5 vs. 4.5 mm, than those of Bowman (4). The grain yields of BW314 and Bowman were similar (4).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (6).

Mutational events:

ert-k.32 (NGB 112633, GSHO 485) in Bonus (PI 189763) (6); *ert-k.76* (NGB 112675) in Bonus (7); *ert-k.93* (NGB 112692) in Bonus, *-k.309* (NGB 112825) in Foma (CIho 11333) (10); *ert-k.302* (NGB 112819), *-k.435* (NGB 112951), *-k.459* (NGB 112974), *-k.477* (NGB 112993) in Foma (8).

Mutant used for description and seed stocks:

ert-k.32 (NGB 112633, GSHO 485) in Bonus; *ert-k.32* in Bowman (PI 483237)*6 (GSHO 2253, BW314, NGB 20589).

References:

1. Borg, G., K. Fröier, and Å. Gustafsson. 1958. Pallas barley, a variety produced by ionizing radiation: its significance for plant breeding and evolution. p. 1-17. Proc. 2nd Int. Conf. Peaceful Uses Atomic Energy Geneva, 1958, (A/CONF. 15/P/2468).
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. Forster, B.J. 2001. Mutation genetics of salt tolerance in barley: An assessment of Golden Promise and other semi-dwarf mutants. Euphytica 120:317-328.
4. Franckowiak, J.D. (Unpublished).
5. Gustafsson, A., A. Hagberg, G. Persson, and K. Wiklund, 1971.Induced mutations and barley improvement. Theor. Appl. Genet. 41:239-248.
6. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
7. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.

8. Lundqvist, U. (Unpublished).
9. Nilan, R.A. 1964. The Cytology and Genetics of Barley, 1951-1962. Monographic Supplement No. 3 Research Studies. Washington State University Press. Note: the chromosome association of *ert-k.32* is based on summarized information from A. Hagberg.
10. 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. 26:488.

Revised:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:156-157.

BGS 593, Awned palea 1, *adp1*

Stock number:	BGS 593
Locus name:	Awned palea 1
Locus symbol:	*adp1*

Previous nomenclature and gene symbolization:

Awned palea = *adp* (1).

Inheritance:

Monofactorial recessive (1, 4).

Located in chromosome 3HL (4); about 5.8 cM distal from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (4); *adp1.a* is associated with SNP markers 1_1016 to 1_1319 (positions 90.67 to 107.40 cM) in 3H bins 06 to 07 and with SNP markers 2_1348 to 1_1503 (positions 135.8 to 173.82 cM) in 3H bins 08 to 11 of the Bowman backcross-derived line BW010 (2).

Description:

This mutant was isolated as a partially female sterile plant with abnormal spikes. The palea is elongated to form two awns (4), which are derived from two fused bracts that form from the palea (5). Pistils are often transformed into leafy buds and result in low female fertility and greatly reduced seed set (1). Two of the anthers appear normal and the third is deformed to some extent. Pollen fertility is good (1). Plants of the Bowman backcross-derived line for *adp1.a*, BW010, compared to Bowman plants produced spikes with slightly longer rachis internodes. Kernels BW010 were slightly thinner and weighted 30% less. Grain yields of BW010 were 5 to 15% of the Bowman yields (3).

Origin of mutant:

A spontaneous mutant in an inbred line (1).

Mutational events:

adp1.a (GSHO 1618) in an unknown inbred line (1).

Mutant used for description and seed stocks:

adp1.a in a selection, with the *eog1.a* (elongated outer glume 1) gene from Svalöfs Guldkorn 91 [AHOR 226, a mutant of Gull (CIho 1145, GSHO 466)] (1), crossed to the unknown line (GSHO 1618); *adp1.a* in Bowman*5 (GSHO 1950; BW010, NGB 20418).

References:

1. Ahokas, H. 1977. A mutant of barley: Awned palea. Barley Genet. Newsl. 7:8-10.
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. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
5. Williams, R.F. 1975. The Shoot Apex and Leaf Growth. Cambridge University Press, Cambridge.

Prepared:

J.D. Franckowiak. 1998. Barley Genet. Newsl. 28:34.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:285.

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:158.

BGS 611, Necrotic leaf spot 6, *Nec6*

Stock number:	BGS 611
Locus name:	Necrotic leaf spot 6
Locus symbol:	*Nec6*

Previous nomenclature and gene symbolization:

Spotted = *Sp* (3).

Inheritance:

Monofactorial dominant (3).

Located in chromosome 7HS (1); *Nec6.h* is associated with SNP markers 1-0949 to 1-1031 (positions 0.00 to 7.83 cM) in 7H bin 01 of the Bowman backcrossed-derived line BW633 (1), in 7H bin 01.

Description:

Numerous dark-brown, oval to elongated spots form on all foliar parts of plants homozygous or heterozygous for the *Nec6* gene. The spots are pinpoint in size when they first appear and gradually enlarge to a diameter of 10 to 15 mm. The spots appear on the first leaf when seedlings are at a three to four-leaf stage and on succeeding leaf when the leaf blade has partially expanded. The spots may cover 20 to 30% of the leaf blade area, but areas adjacent to the spots remain green. Average grain yield reduction in spotted isogenic lines was 13.6% (3). Plant height and kernel plumpness are slightly reduced in the Bowman backcross-derived line BW633 (2).

Origin of mutant:

A spontaneous mutant in Awnless Atlas (CIho 10965) (3).

Mutational events:

Nec6.h (GSHO 977) in Awnless Atlas (CIho 10965) (3).

Mutant used for description and seed stocks:

Nec6.h in Spotted Quarter-awned Atlas (GSHO 2424); *Nec6.h* in Bowman (PI 483237)*7 (GSHO 3429, BW633, NGB 22199).

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. Schaller, C.W., and C.O. Qualset. 1975. Isogenic analysis of productivity in barley: Interaction of genes affecting awn length and leaf-spotting. Crop. Sci. 15:378-382.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:112.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:159.

BGS 615, Waxy spike 1, *wxs1*

Stock number:	BGS 615
Locus name:	Waxy spike 1
Locus symbol:	*wxs1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Location is limited to chromosomes 7H or 2HL (1); *wxs1.a* is associated with SNP markers 1_0924 to 2_0247 (positions 107.44 to 159.73 cM) in 7H bins 07 to 09 and between 1_1118 and 2_1088 (positions 180.85 to 204.58 cM) in 2HL bins 12 to 13 of the Bowman backcross-derived line BW917 (1).

Description:

Plants with the *wxs1.a* gene accumulate excess surface waxes on the spike. Spikes appear normal at heading, but gradually they accumulate more surface waxes. Spikes have a distinctive white hue prior to ripening. The kernels have an irregular surface caused by poor adherence of the lemma to the caryopsis (2, 3). The *wxs1.a* plants of Bowman backcross-derived line BW917 were slightly shorter and lodge easier than their normal sibs. Their kernel weights were 10 to 20% lighter and grain yield was reduced by about 30% (2). Expression of *wxs1.a* gene is suppressed by the glossy spike mutants (2).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (3).

Mutational events:

wxs1.a (FN16, GSHO 3649) in Steptoe (CIho 15229) (3); *wxs1.b* (FN323, GSHO 3679), *wxs1.c* (FN331, GSHO 3680), *wax1.d* (FN444, GSHO 3681) in Steptoe (CIho 15229) may be alleles based on phenotypic similarity (3).

Mutant used for description and seed stocks:

wxs1.a (FN16, GSHO 3649) in Steptoe; *wxs1.a* in Bowman (PI 483237)*5 (GSHO 3432, BW917, NGB 22348).

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. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:205.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:141.

A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:160.

BGS 616, Uniculme 3, *cul3*

Stock number: BGS 616
Locus name: Uniculme 3
Locus symbol: *cul3*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (5).
Located in chromosome 3HL (1); *cul3.c* is associated with SNP markers 2_0023 to 2_0168 (positions 169.94 to 173.82 cM) in 3H bin 11 of the Bowman backcross-derived line BW207 (1), likely in 3H bin 11.
Description:
Plants have only one tiller, which is taller and thicker than those of normal sibs. Spikes are lax and malformed with extra lateral spikelets at some rachis nodes and none at others. The first basal rachis internode is sometimes curved (5). Seed set is very low in the Bowman backcross-derived line, which causes a problem with maintenance of the line (2).
Origin of mutant:
An X-ray induced mutant in Donaria (PI 161974) (5).
Mutational events:
cul3.c (Mut. 3170, DWS 1343, GSHO 2494) in Donaria (PI 161974) (3, 5); *cul3.m* (FN498, GSHO 3677) in Steptoe (CIho 15229) may be an allele based on phenotypic similarity (4).
Mutant used for description and seed stocks:
cul3.c (GSHO 2494) in Donaria; *cul3.c* in Bowman (PI 483237)*7 (BW207, NGB 22035).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Kleinhofs, A. (Unpublished).
5. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. I. Kulturpflanze 6:123-166.
Prepared:
J.D. Franckowiak and U. Lundqvist. 2002. Barley Genet. Newsl. 32:117.
Revised:
J.D. Franckowiak and A. Kleinhofs. 2013. Barley Genet. Newsl. 43:161.

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 (7); *cul4.3*, *cul4.5*, *cul4.15*, and *cul4.16* mapped near RFLP markers CDO0394a and CDO105 (8, 9); *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). The mutant *cul4.15* exhibits the most variation in height over environments (3). Under greenhouse conditions, Bowman line for *cul4.5* developed only two axillary tillers, and it was uniculm when combined with the *cul2.b* (uniculm 2) gene (1).

Origin of mutant:
An ethylene oxide induced mutant in Bonus (PI 189763) (6).

Mutational events:
cul4.3 (NGB 115062, GSHO 2495), *cul4.5* (NGB 115063, GSHO 2493) in Bonus (PI 189763), *cul4.15* (NGB 115064) in Foma (CIho 11333), *cul4.16* (NGB 115065) in Bonus (6, 8).

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)*4 (GSHO 2360, BW211, NGB 22038); *cul4.5* in Bowman (PI 483237)*7 (GSHO 2361, BW212, NGB 22039); *cul4.16* in Bowman*2 (BW210, NGB 20559).

References:
1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley uniculm2 (*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. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system

of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
5. Hussien, A., E. Tavakol, D.S. Horner, M. Muñoz-Amatriaín, G.J. Muehlbauer, and L. Rossini. 2014. Genetics of tillering in rice and barley. The Plant Genome 7. doi: 10.3835/plantgenome2013.10.0032.
6. Lundqvist, U. (Unpublished).
7. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
8. Rossini, L., A. Vecchietti, L. Nicoloso, N. Stein, S. Franzago, F. Salamini, and C. Pozzi. 2006. Candidate genes for barley mutants involved in plant architecture: An *in silico* approach. Theor. Appl. Genet. 112:1073-1085.
9. Tavakol, E., G. Verderio, T. Fusca, S. Ciannamea, T.J. Close, A. Druka, R. Waugh, M. Mihaela, K. Mayer, R. Ariyadasa, D. Schulte, R. Zhou, N. Stein, G.J. Muehlbauer, and L. Rossini. 2012. Positional cloning of the barley tillering gene *uniculme 4*. http://www.triticeaegenome.eu/file/Tavakol-Poster_Versailles_2012.pdf.

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.

BGS 623, 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 just below 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) (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) (5); *eli-a.11* (NGB 115395), *-a.14* (NGB 115397) in Kristina (NGB 1500); *eli-a.15* (NGB 115398), *-a.16* (NGB 151399) in Bonus (PI 189763) (5), *-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:

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. Kleinhofs, A. (Unpublished).
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.

BGS 624, Opposite spikelets 1, *ops1*

Stock number:	BGS 624
Locus name:	Opposite spikelets 1
Locus symbol:	*ops1*

Previous nomenclature and gene symbolization:

Opposite spikelets-3 = *op-3* (3, 4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 7HS (1); *ops1.3* is associated with SNP markers 2_1419 to 1_0965 (positions 0.00 to 38.08 cM) in 7H bins 01 to 03 of the Bowman backcross-derived line BW641 (1).

Description:

Plants with the *ops1.3* gene have a reduced number of tillers and very few late tillers. Variable lengths of the rachis internodes caused an irregular arrangement of spikelets in the spike. Compared to normal sibs, *ops1.3* plants were slightly shorter and lower yielding (2, 4). Plants of the Bowman backcross-derived line for *ops1.3*, BW641, yielded 1/4 to 1/2 as much grain as Bowman plants. Kernels of BW641 were slightly larger than those of Bowman in low stress environments and slightly smaller in higher stress environments (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763) (4).

Mutational events:

ops1.3 (NGB 115379, GSHO 2427) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

ops1.3 (GSHO 2427, NGB 115379) in Bonus; *ops1.3* in Bowman (PI 483237)*6 (GSHO 2318); *ops1.3* in Bowman*7 (BW641, NGB 22206).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:125.

Revised:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:165.

BGS 635, Necroticans 7 *nec7*

Stock number:	BGS 635
Locus name:	Necroticans 7
Locus symbol:	*nec7*

Previous nomenclature and gene symbolization:

Necroticans 45 = *nec-45* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosomes 1H or 6H or 7H (1); *nec7.45* is associated with SNP markers 1_0186 to 2_0990 (positions 37.21 to 115.07 cM) in 1H bins 04 to 10, with SNP markers 1_0799 to 1_1029 (positions 50.33 to 70.15 cM) in 6H bins 04 to 05, and with SNP markers 1_0971 to 2_0245 (positions 0.00 to 13.19 cM) in 7H bin 01 of the Bowman backcross-derived line BW634 (1), likely in 1H.

Description:

As each tiller of plants homozygous for the *nec7* gene starts to head, dark brown blotches become visible on the leaf blades and sheaths. The blotches are variable in size and irregular in shape. They gradually enlarge and partially coalesce. Blotches range in size from small spots to large ones that may include 1/5 of the leaf blade or more. Some blotches are partially surrounded by a golden or yellowish halo before that region of the leaf dies (2, 4). When *nec7* plants are grown in greenhouses, formation of the dark brown blotches is associated with a distinct musty odor, which persists even after plants ripen (2). Plants of the Bowman backcross-derived line for *nec7.45*, BW634, were about 15% shorter than Bowman plants. The number of kernels per spike for BW634 varied from 2 to 3 more to 2 less. Kernel weights varied from equal to 20% less and grain yields were about 3/4 those of Bowman. The number and size of blotches varied widely across environments (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500) (4).

Mutational events:

nec7.45 (*nec-45*, NGB 115306, GSHO 2420) in Kristina (NGB 1500) (4).

Mutant used for description and seed stocks:

nec7.45 (GSHO 2420, NGB 115306) in Kristina; *nec7.45* in Bowman (PI 483237)*4 (BW634, NGB 22200).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. Barley Genet. Newsl. 32:136.

Revised:

U. Lundqvist and J. D. Franckowiak. 2011. Barley Genet. Newsl. 41:198.

U. Lundqvist and J. D. Franckowiak. 2013. Barley Genet. Newsl. 43:166.

BGS 636, Tip sterile 2, *tst2*

Stock number: BGS 636
Locus name: Tip sterile 2
Locus symbol: *tst2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 4HL (1); *tst2.a* is associated with SNP markers 2_0765 to 2_0732 (positions 127.80 to 134.44 cM) in 4H bins 09 to 10 of the Bowman backcross-derived line BW883 (1).

Description:

Spikes of *tst2.b* plants are 1/4 to 1/2 of normal length because seed set fails in the upper portion of the spike. Slow or poor development of the spike reduces both the number of rachis internodes and number of fertile spikelets (2, 5). Many spikes of the Bowman backcross-derived line for *tst2.b* (BW883) set less than 10 seeds. The BW883 plants are about 5/6 the height of normal sibs caused largely by shorter peduncles. Both rachis internode length and awn length are reduced in *tst2* plants (2). Kernel weights are about 3/4 of normal and seed yields are about 1/5 those of Bowman (2). Heading dates are not delayed for BW883 (2).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (4, 5).

Mutational events:

tst2.b (Mut. 2249, DWS1337, GSHO 1781) in Donaria (PI 161974) 3, 4).

Mutant used for description and seed stocks:

tst2.b (GSHO 1781) in Donaria; *tst2.b* in Bowman (PI 483237)*4 (GSHO 2280); *tst2.b* in Bowman*6 (BW883, NGB 22317).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator’s report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Scholz, F. 1956. Mutationsversuche an Kulturpflanzen. V. Die Vererbung zweier sich variabel manifestierender Übergangsmerkmale von bespelzter zu nackter Gerste bei röntgeninduzierten Mutanten. Kulturpflanze 4:228-246.
5. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l. I. Kulturpflanze 6:123-166.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. Barley Genet. Newsl. 32:137.

Revised:

J.D. Franckowiak. 2005. Barley Genet. Newsl. 35:193. (Locus symbol was changed from *lin2*.)

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:292.

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:167.
BGS 645, Bushy spike 1, *bsp1*

Stock number: BGS 645
Locus name: Bushy spike 1
Locus symbol: *bsp1*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive, homozygotes do not produce anthers or ovaries (1).
Location is unknown.
Description:
The mutant plants appear normal except they form very bushy spikes caused by many awn-like structures. Spikelets of *bsp1.a* mutants lack reproductive tissue and are completely sterile. The mutant must be maintained as a heterozygote (1).
Origin of mutant:
A fast neutron induced mutant in Morex (CIho 15773).
Mutational events:
bsp1.a (FN346, GSHO 3652) in Morex (CIho 15773) (1).
Mutant used for description and seed stocks:
bsp1.a (FN346, GSHO 3652) in Morex.
References:
1. Kleinhofs, A. (Unpublished).
Prepared:
A. Kleinhofs. 2005. Barley Genet. Newsl. 35:203.
Revised:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:168.

BGS 646, Ovaryless 2, *ovl2*

Stock number:	BGS 646
Locus name:	Ovaryless 2
Locus symbol:	*ovl2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants appear normal except carpels are rudimentary and plants are female sterile. Plant development appears normal. Anther development is normal and pollen is viable (1). The *ovl2.b* mutant must be maintained as a heterozygote (1). The ovaryless 1 (*ovl1.a*) mutant (BGS 176, GSHO 610) was not available for allelism tests, but the two mutants are phenotypically very different in plant morphology (1).

Origin of mutant:

A fast neutron induced mutant in Harrington (Agriculture Canada Licence No: 2126) (1).

Mutational events:

ovl2.b (FN347, GSHO 3655) in Harrington (Agriculture Canada Licence No: 2126) (1).

Mutant used for description and seed stocks:

ovl2.b FN347, GSHO 3655) in Harrington.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:204.

Revised:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:169.

BGS 647, Tip sterile 1, *tst1*

Stock number:	BGS 647
Locus name:	Tip sterile 1
Locus symbol:	*tst1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 6HL (likely) (1); *tst1.c* is associated with a large segment of SNP markers 1_0882 to 2_0531 (positions 70.15 to 160.38 cM) in 6H bins 05 to 09, and with smaller group of SNP markers in 7HL, of the Bowman backcross-derived line BW882 (1).

Description:

Mutant plants and spikes appear normal except there is no seed set in the tip of the spike (3). In the Bowman backcross-derived line under greenhouse conditions, seed set is 40 to 60% with no fertile spikelets at the terminal 4 to 6 nodes of the rachis. The *tst1.c* mutant differs from *lin1* (lesser internode number 1) (BGS 99) and *tst2* (BGS 636) plants because *lin1* is not associated with tip sterility and *tst2* produces more sterility and reduces height and vigor (2). Under field conditions, the number of kernels per spike for the *tst1.c* mutant in the Bowman backcross-derived line, BW882, varied from 30% less to near normal. Kernels of BW882 were 10 to 15% wider than those of Bowman and weighed 10 to 15% more. Grain yields of BW882 were about 2/3 those of Bowman. Other morphological traits of BW882 were similar to those of Bowman (2).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (3).

Mutational events:

tst1.c (FN43, GSHO 3644) in Steptoe (CIho 15229) (3).

Mutant used for description and seed stocks:

tst1.c (FN43, GSHO 3644) in Steptoe; *tst1.c* in Bowman (PI 483237)*4 (BW882, NGB 22316).

References:

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

Prepared:

A. Kleinhofs and J.D. Franckowiak. 2005. Barley Genet. Newsl. 35:205.

Revised:

J.D. Franckowiak and A. Kleinhofs. 2013. Barley Genet. Newsl. 43:170.

BGS 648, Multiovary 4, *mov4*

Stock number:	BGS 648
Locus name:	Multiovary 4
Locus symbol:	*mov4*

Previous nomenclature and gene symbolization:

Multiovary 8 = *mo8* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Spikelets of this partial multiovary mutant have two carpels, two anthers, and two lodicules. One of the anthers appears to have been converted to a carpel; however, this conversion does not occur in all spikelets. Spikelets with two carpels often set two seeds. Mutant plants are often difficult to identify (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutational events:

mov4.k (FN315, *mo8*, GSHO 3643) in Steptoe (CIho 15229) (1). Two other very similar mutants have also been isolated, *mov.m* (FN316, GSHO 3672) and *mov.n* (FN487, GSHO 3673), as fast neutron induced mutants in Steptoe (1). The *mov.n* has a higher frequency of multiovary spikelets and these spikelets set two kernels more often (1).

Mutant used for description and seed stocks:

mov4.k (FN315, GSHO 3643) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:206.

Revised:

A. Kleinhofs . 2013. Barley Genet. Newsl. 43:171.

BGS 649, Aborted spike 1, *asp1*

Stock number:	BGS 649
Locus name:	Aborted spike 1
Locus symbol:	*asp1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants appear normal except the spike is rudimentary or missing. The *asp1.a* plants occasionally form spikes with a few spikelets, but the spikelets are mostly sterile. The stock must be maintained as a heterozygote (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutational events:

asp1.a (FN222, GSHO 3654) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

asp1.a (FN222, GSHO 3654) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:207.

Revised:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:172.

BGS 650, Sensitivity to *Ustilago nuda* 1, *sun1*

Stock number:	BGS 650
Locus name:	Sensitivity to *Ustilago nuda* 1
Locus symbol:	*sun1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants appear extremely susceptible to infection by loose smut, *Ustilago nuda* (Jensen) Rostr. Spikes of infected *sun1.a* plants become entirely smutted under field conditions at Pullman, WA, USA, an environment where loose smut infection is rare (1). The occurance of infected plants is much more frequent in seed lots from *sun1.a* plants than in those from other susceptible cultivars (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutational events:

sun1.a (FN395, GSHO 3650) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

sun1.a (FN395, GSHO 3650) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:208.

Revised:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:173.

BGS 651, Late maturity 1, *lam1*

Stock number:	BGS 651
Locus name:	Late maturity 1
Locus symbol:	*lam1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants have a very prostrate growth habit and heading is delayed to very late in the season, and sometimes they do not head. During juvenile stages before the reproductive phase is induced, *lam1.a* plants have very narrow, long leaf blades. Leaves produced during the reproductive phase have wide, short leaf blades (1). The cultivar Steptoe in which the mutant was induced has a winter growth pattern.

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutational events:

lam1.a (FN2, GSHO 3653) in Steptoe (CIho 15229) (1). Several other late heading mutants in Steptoe have been isolated following treatment with mutagenic agents, but allelism tests have not been completed. The mutants and their temporary gene symbols are: *lam.b* (FN197), *lam.c* (FN208), *lam.d* (FN209), *lam.e* (FN212), and *lam.f* (FN229) in Steptoe (1).

Mutant used for description and seed stocks:

lam1.a (FN2, GSHO 3653) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:209.

Revised:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:174.

BGS 652, Yellow leaf 1, *ylf1*

Stock number:	BGS 652
Locus name:	Yellow leaf 1
Locus symbol:	*ylf1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS (1); *ylf1.a* is associated with SNP markers 1_0576 to 2_0790 (positions 54.30 to 73.96 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW922 (1).

Description:

Mutant plants show a gradual yellowing or loss of chlorophyll starting with the margins of leaf blades. Dying or necrosis of the leaf blade or its margins is not observed. The leaves gradually become a yellowish or golden in color with midrib region remaining green. Expression of *ylf1.a* gene is variable and is dependent on light intensity, temperature, moisture stress, and the age of the leaf blade (2). Mutant expression is often better under low light conditions in the greenhouse. High temperatures can induce yellowing of the leaf blade margins in seedlings; however, yellowing is often not expressed until after heading (2). The Bowman backcross-derived line for the *ylf1.a*, BW922, was slightly shorter and had slightly lighter kernels than Bowman. Grain yields were occasionally slightly lower than those of Bowman (2).

Origin of mutant:

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

Mutational events:

ylf1.a (6002) in Villa (PI 399506) (2, 3).

Mutant used for description and seed stocks:

ylf1.a in Villa; *ylf1.a* in Bowman (PI 483237)*8 (BW922, NGB 22351).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gaul, H. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2005. Barley Genet. Newsl. 35:210.

Revised:

J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:175.

BGS 660, Narrow leafed dwarf 2, *nld2*

Stock number:	BGS 660
Locus name:	Narrow leafed dwarf 2
Locus symbol:	*nld2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosomes 5H, 6H, or 7H (1); *nld2.b* is associated with SNP markers 1_0580 to 2_1121 (positions 54.27 to 105.91 cM) in 5H bins 03 to 06, with SNP markers 2_0743 to 2_0036 (positions 73.90 to 169.88 cM) in 6H bins 06 to 11, and with SNP markers 2_0242 to 2_1437 (positions 6.89 to 20.56 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW636 (1).

Description:

The *nld2.b* plants have narrow, dark green leaf blades, which are erect with well-developed midribs. Auricles degenerate to tiny projections, but ligules are normal. Stem internodes are short, and the upper ones are curved. Spikelets are relatively narrow and small, and seed set may be low (2). Kernels of the Bowman backcross-derived line for *nld2.b,* BW636 were thinner (3.2 vs. 3.8 mm) and about 35% lighter than those of Bowman (2). BW 636 plants were 1/3 to 1/2 of normal height, and spikes commonly emerged from the side of the sheath before anthesis. Awns of BW636 plants are similar in length to those of Bowman. BW636 plants are more vigorous than those of the Bowman backcross-derived line for *nld1.a* (narrow leafed dwarf 1), BW635, in Christchurch, New Zealand and in North Dakota greenhouse nurseries, but *nld1.a* was more vigor in the field nursery at Dundee, Scotland. Grain yields of BW636 were often less than 20% of those of Bowman (2).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (3).

Mutational events:

nld2.b (FN45, GSHO 3645) in Steptoe (CIho 15229) (3).

Mutant used for description and seed stocks:

nld2.b (FN45, GSHO 3645) in Steptoe; *nld2.b* in Bowman (PI 483237)*6 (BW636, NGB 22202).

References:

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

Prepared:

J.D. Franckowiak and A. Kleinhofs. 2007. Barley Genet. Newsl. 37:300.

Revised:

J.D. Franckowiak and A. Kleinhofs. 2013. Barley Genet. Newsl. 43:176.

BGS 667, Reaction to *Pyrenophora teres* 1, *Rpt1*

Stock number:	BGS 667
Locus name:	Reaction to *Pyrenophora teres* 1 (*P. teres* f. *teres*, net form of net blotch, NFNB)
Locus symbol:	*Rpt1*

Previous nomenclature and gene symbolization:

Resistance to *Pyrenophora teres* = *Pt* in Tifang (12)
Resistance to *Pyrenophora teres* 1 = Pt_1 in Tifang (9, 12).
Resistance to *Pyrenophora teres* 1a = *Rpt1a* in Tifang (3).
Resistance to *Pyrenophora teres* a = *Pt,,a* (5).
QTL for resistance to *Pyrenophora teres* f. *teres* seedling 3HL = *QRpts3L* (11).
QTL for resistance to NFNB seedling Alexis/Sloop 3H = *QNFNBSLR.Al/S-3H* (7).

Inheritance:

Monofactorial incomplete dominant (3, 6, 9, 12); two complementary genes in Harbin to some isolates (2).

Located in chromosome 3HL (3); *Rpt1.a* is associated with chromosome 3H based on trisomic analysis (3); *Pt,,a* from Igri mapped in 3HL about 0.8 cM distal from RFLP marker cMWG680 (5); several QTL from other cultivars mapped in the proximal region of 3HL (7, 11); near microsatellite marker Bmag606 (7); near microsatellite marker Bmag225 (11).

Description:

Moseman (10) recommended the assignment of a three letter code to disease reaction loci in barley with R as the first letter and the genus and species name of the causal organism as the second and three letters. The seedling reactions of cultivars with the *Rpt1.a* (Pt_1) gene to *Pyrenophora teres* f. *teres* (*Ptt*) isolates were measured as 1 on a scale where 0 = very resistant and 4 = susceptible; however, some *Ptt* isolates produced susceptible reactions in the accessions tested (3). Heterozygous individuals showed intermediate reactions ranging from 1 to 3 (2, 3, 6, 11). Based on a low frequency of susceptible plants in crosses among resistant accessions, Mode and Schaller (9) reported Tifang as having Pt_1, but a closely linked gene (Pt_2) was present in Manchurian, Ming, Harbin Canadian Lake Shore and CIho 4922. An unlinked gene (Pt_3) was also present in CIho 4922 (9). Khan and Boyd (6) concluded that CIho 5791 and CIho 9819 have one the resistance gene of (Pt_a), which is not Pt_1, Pt_2, *or* Pt_3 as described by Mode and Schaller (9). The Pt_1 and Pt_2 genes were assumed to be alleles (6). Bockelman et al. (3) could not differentiate the linked genes in chromosome 3H using trisomic stocks of Betzes and associated only one resistance factor with chromosome 3H, *Rpt1a*. Genes for resistance to various isolates of *Ptt* from several cultivars have been mapped in chromosome 3HL (5, 7, 11). The differences among these reports have not been resolved (8), but Tifang is still classified as having the *Rpt1.a* gene. The presence of additional *Rpt* genes in Tifang is possible because it conferred a resistant response to a large number of California isolates of *Ptt* (13). When testing *Ptt* isolates from around the world, Tifang and Harbin were demonstrated effective to confer effective resistance to many *Ptt* isolates in many countries (1, 4).

Origin of mutant:

Natural occurrence in Tifang (PI 69426, CIho 14373, CIho 4407-1) collected from Heilongjiang Province in China (3); the same resistance gene may be present in

Canadian Lake Shore (CIho 2758, PI 20819), CIho 4922 (PI 73737), Harbin (CIho 4929, PI 72745), Manchuria (CIho 2330), and Ming (CIho 4797, PI 70854) (6, 9).

Mutational events:

Rpt1.a in Tifang (PI 69426, CIho 14373) collected from Heilongjiang Province in China (3, 10, 12); *Rpt1.a* in Harbin (CIho 4929, PI 72745) (6, 9); *Rpt1.b* in CIho 9819 (PI 195985) from Ethiopia (3); possible alleles are present in Igri (PI 428488) (6), Alexis (PI 564487) (7, 11), and Arapiles (PI 591926) (11).

Mutant used for description and seed stocks:

Rpt1.a in Tifang (PI 69426, CIho 14373), *Rpt1.a* in Harbin (CIho 4929, PI 72745).

References:

1. Afanasenko, O.S., M. Jalli, H.O. Pinnschmidt, O. Filatova, and G.J. Platz. 2009. Development of an international standard set of barley differential genotypes for *Pyrenophora teres* f. *teres*. Plant Pathol. 58:665-676.
2. Afanasenko, O., N. Mironenko, O. Filatova, D. Kopahnke, I. Krämer, and F Ordon. 2007. Genetics of host-pathogen interactions in the *Pyrenophora teres* f. t*eres* (net form) – barley (*Hordeum vulgare*) pathosystem.117:267-280.
3. Bockelman, H.E., E.L. Sharp, and R.F. Eslick. 1977. Trisomic analysis of genes for resistance to scald and net blotch in several barley cultivars. Can. J. Bot. 55:2142-2148.
4. Boungab, K., L. Belabid, Z. Fortas, and B. Bayaa. 2012. Pathotype diversity among Algerian isolates of *Pyrenophora teres* f. *teres*. Phytopathologia Mediterranea 51:577-586.
5. Graner, A., B. Foroughi-Wehr, and A. Tekauz. 1996. RFLP mapping of a gene in barley conferring resistance to net blotch (*Pyrenophora teres*). Euphytica 91:229-234.
6. Khan, T.N., and W.J.R. Boyd. 1969. Inheritance of resistance to net blotch in barley II. Genes conditioning resistance against race W.A.-2. Can. J. Genet. Cytol. 11:592-597.
7. Lehmensiek, A., G.J. Platz, E. Mace, D. Poulsen, and M.W. Sutherland. 2007. Mapping of adult plant resistance to net form of net blotch in three Australian barley populations. Aust. J. Agric. Res. 58:1191-1197.
8. Liu, Z., S.R. Ellwood, R.P. Oliver, and T.L. Friesen. 2011. *Pyrenophora teres*: profile of an increasingly damaging barley pathogen. Mol. Plant Pathol. 12:1-19.
9. Mode, C.J., and C.S. Schaller. 1958. Two additional factors for resistance to net blotch in barley. Agron. J. 50:15-18.
10. Moseman, J.G. 1972. Report on genes for resistance to pests. Barley Genet. Newsl. 2:145-147.
11. Raman, H., G.J. Platz, K.J. Chalmers, R. Raman, B.J. Read, A.R. Barr, and D.B. Moody. 2003. Mapping of genomic regions associated with net form of net blotch resistance in barley. Aust. J. Agric. Res. 54:1359-1367.
12. Schaller, C.W. 1955. Inheritance of resistance to net blotch of barley. Phytopathology 48:477-480.
13. Steffenson, B.J., and R.K. Webster. 1992. Pathotype diversity of *Pyrenophora teres* f. *teres* on barley. Phytopathology 82: 170-177.

Prepared:

J.D. Franckowiak 2012. Barley Genet. Newsl. 42:750.

Revised:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:177-178.

BGS 671, Necrotic leaf spot 8, *nec8*

Stock number: BGS 671
Locus name: Necrotic leaf spot 8
Locus symbol: *nec8*

Previous nomenclature and gene symbolization:

Mutant 3550 (4, 5).
Bipolaris sorokiniana tolerant mutant 1 = *bst1* (2, 3)
Necrotic leaf spot w = *nec.w* (1).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 5HL (2, 4); linked to AFLP markers E40M38-7, E36M36-5, E42M36-14, E42M40-2 and E41M32-5, with E40M38-7 being the closest (2, 4); the closest AFLP markers were P26M65 and P26M77 (2), in 5H bin 11 (2). The Bowman line for *nec8.3550* (BW626) differs from Bowman only for SNP markers near the *Rph3* (reaction to *Puccinia hordei* 3) locus (1).

Description:

Plants of the *nec8.3550* mutant exhibit conspicuous black or brown spots on the leaf blades. The spots usually do not coalesce. The spots appear on all above-ground parts of the plant including the awns. The *nec8.3550* plants showed delayed maturity with seeds being ready for harvest about four weeks later than in the Bowman *Rph3c* (4). Short day conditions lead to a slightly less pronounced phenotypic expression. The phenotype of *nec8.3550* plants is similar to that of the *nec1* (necrotic leaf spot 1) mutant, but allelism can be ruled out due to different mapping positions (4). The *nec8.3550* mutant was classified as a lesion mimic mutant and was demonstrated to be more resistant to spot blotch (*Bipolaris sorokiniana*) isolates than its parent and ND B112 (CIho 11531) (2, 3). Resistance was associated with low hydrogen peroxide level in leaf tissue (2). The *nec8.3550* mutant belongs to the initiation class of lesion mimic mutants. Lower infection levels with leaf rust (*Puccinia hordei*) and increased autofluorescence were reported for *nec8.3550* plants (5). The expression level of *Hvhir3* (*Hordeum vulgare* hypersensitive induced reaction 3) was about 200-fold higher than that found in Bowman *Rph3.c* (5).

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) (4, 5).

Mutational events:

nec8.3550 (GSHO 3600, NGB 20834, NGB 23526) in Bowman *Rph3.*c (Bowman*11//Estate/3.2 uz als MM) (PI 643152, NGB 22452) (4, 5).

Mutant used for description and seed stocks:

nec8.3550 (GSHO 3600, NGB 20834, NGB 23526) in Bowman *Rph3.*c (BW746, PI 643152, NGB 22452); *nec8.3550* from Bowman *Rph3.*c in Bowman (PI 483237) (BW626, NGB 22192).

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. Persson, M., A. Falk, and C. Dixelius. 2009. Studies on the mechanism of resistance

to *Bipolaris sorokiniana* in the barley lesion mimic mutant *bst1*. Mol. Plant Path. 10:587-598.

3. Persson, M., M. Rasmussen, A. Falk, and C. Dixelius. 2008. Barley mutants with enhanced level of resistance to Swedish isolates of *Bipolaris sorokiniana*, casual agent of spot blotch. Plant Breed. 127:639-643.
4. Wright, S.A.I., M. Azarang, and A.B. Falk. 2007. Four new barley mutants. Barley Genet. Newsl. 37:34-36.
5. Wright, S.A.I., M. Azarang, and A.B. Falk. 2013. Barley lesion mimics, supersusceptible or highly resistant to leaf rust and net blotch. Plant Path. 62:982-992.

Prepared:

S.A.I. Wright, A.B. Falk, J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:179-180.

BGS 672, Necrotic leaf spot 9, *nec9*

Stock number: BGS 672
Locus name: Necrotic leaf spot 9
Locus symbol: *nec9*

Previous nomenclature and gene symbolization:
Mutant 3091 (1, 2).
Inheritance:
Monofactorial recessive (1, 2).
Located in chromosome 3HL (1, 2); linked to AFLP marker E37M33-6 in 3H (1, 2).
Description:
Plants with the *nec9.3091* mutation produce brown spots towards the leaf tips and leaf edges, particularly on the first leaf (1). The leaf spot phenotype of the *nec9.3091* mutant resembles those of mutants *nec4.f* (necrotic leaf spot 4) and *nec5.g* (necrotic leaf spot 5), but it is not allelic to them (1, 2). The *Hv-hir3* (*Hordeum vulgare* hypersensitive induced reaction 3) and *Hv-hir4* (*Hordeum vulgare* hypersensitive induced reaction 4) genes are expressed significantly more in mutant *nec9.3091* than in the Bowman *Rph3.c* line (2).
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) (1, 2).
Mutational events:
nec9.3091 (GSHO 3599, NGB 23525) in Bowman *Rph3.*c (Bowman*11//Estate/3.2 uz als MM) (PI 643152, NGB 22452) (1, 2).
Mutant used for description and seed stocks:
nec9.3091 (GSHO 3599, NGB 23525) in Bowman *Rph3.*c (BW746, PI 643152, NGB 22452).
References:
1. Wright, S.A.I., M. Azarang, and A.B. Falk. 2007. Four new barley mutants. Barley Genet. Newsl. 37:34-36.
2. Wright, S.A.I., M. Azarang, and A.B. Falk. 2013. Barley lesion mimics, supersusceptible or highly resistant to leaf rust and net blotch. Plant Path. 62:982-992.
Prepared:
S.A.I. Wright, A.B. Falk, J.D. Franckowiak and U. Lundqvist. 2013. Barley Genet. Newsl. 43:181.

BGS 674, Mottled leaf 8, *mtt8*

Stock number: BGS 674
Locus name: Mottled leaf 8
Locus symbol: *mtt8*

Previous nomenclature and gene symbolization:

Mutant 1661 (2).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown (3). The Bowman line for *mtt8.1661* (BW598) differs from Bowman only for SNP markers near the *Rph3* (reaction to *Puccinia hordei* 3) locus (1).

Description:

The *mtt8.1661* seedlings display chlorotic bands, which are more pronounced on the first leaf. Under long day conditions, the bands do not appear on the later emerging leaves and the plants eventually seem to recover normal phenotype. Under short day conditions, the mutation is semi-lethal since all leaves develop the characteristic chlorotic bands and the plants fail to reach maturity and produce seeds. However, the phenotype was initially more severe under long day conditions (2, 3). The cell walls of leaf blade tissues that display the bleached phenotype in *mtt8.1661* plants are highly autofluorescent and the fluorescence is more pronounced in the vascular tissues. The green tissues of the same mutant show little or no autofluorescence. The cell walls are clearly thickened in lesioned tissue (3). The *mtt8.1661* mutant showed enhanced resistance to the *P. hordei* isolate that was virulent on *Rph3.c*, with no pustules on bleached tissues and very few on surrounding green tissue of the first leaf (3). The *mtt8.1661* 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:

mtt8.1661 (GSHO 3597, NGB 23523) 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:

mtt8.1661 (GSHO 3597, NGB 23523) in Bowman *Rph3.*c (BW746, PI 643152, NGB 22452); *mtt8.1661* from Bowman *Rph3.*c in Bowman (PI 483237) (BW598, NGB 22164).

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. Wright, S.A.I., M. Azarang, and A.B. Falk. 2007. Four new barley mutants. Barley Genet. Newsl. 37:34-36.
3. Wright, S.A.I., M. Azarang, and A.B. Falk. 2013. Barley lesion mimics, supersusceptible or highly resistant to leaf rust and net blotch. Plant Path. 62:982-992.

Prepared:

S.A.I. Wright, A.B. Falk, J.D. Franckowiak, and U. Lundqvist. 2013. Barley Genet. Newsl. 43:182.

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 *mtt8.1661* (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).

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. Wright, S.A.I., M. Azarang, and A.B. Falk. 2007. Four new barley mutants. Barley Genet. Newsl. 37:34-36.
3. Wright, S.A.I., M. Azarang, and A.B. Falk. 2013. Barley lesion mimics, supersusceptible or highly resistant to leaf rust and net blotch. Plant Path. 62:982-992.

Prepared:

S.A.I. Wright, A.B. Falk, J.D. Franckowiak, and U. Lundqvist. 2013. Barley Genet. Newsl. 43:183.

BGS 681, Necroticans 10, *nec10*

Stock number: BGS 681
Locus name: Necroticans 10
Locus symbol: *nec10*

Previous nomenclature and gene symbolization:

Necroticans S1-1, S1-2, S1-3 = *necS1-1, necS1-2, necS1-3* (2, 3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 3H (3); co-segregation with Contig4211_at, Contig4212_s_at, and Contig10850_s_, which co-segregate with marker ABG399 in 3H bin 06 (3); *nec10.o* is associated with SNP markers 2_1145 to 2_0597 (positions 65.96 to 119.10 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW611 (1), in 3H bin 06 (3).

Description:

The necrotic phenotype is expressed as extensive small brown to black spots extending down the leaf and subsequently dying leaf tips. Black spots are present on awns. Plant vigor is poor. All alleles exhibit enhanced resistance to *Puccinia graminis* f. sp. *tritici* races MCC and QCC and *P. graminis* f. sp. *secalis* isolate 92-MN-90, but not to stripe rust (*Puccinia striiformis* f. sp. *hordei*). Probable candidate gene encodes a cation/proton-exchanging protein and may be Contig4211_at (3).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 1529) (2, 3).

Mutation events:

nec10.o (FN044, *necS1-1*, GSHO 3607), *nec10.ab* (FN211, *necS1-2*, GSHO 3608), *nec10.ac* (FN303, *necS1-3*, GSHO 3609) in Steptoe (CIho 1529) (2).

Mutant used for description and seed stocks:

nec10.o (FN044, GSHO 3607), *nec10.ab* (FN211, GSHO 3608) and *nec10.ac* (FN303, GSHO 3609) in Steptoe; *nec10.o* in Bowman (PI 483237)*4 (BW611, NGB 22177).

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. Kleinhofs, A. (Unpublished).
3. Zhang, L., L. Lavery, U. Gill, K. Gill, B. Steffenson, G. Yan, X. Chen and A. Kleinhofs. 2009. A cation/proton-exchanging protein is a candidate for the barley *NecS1* gene controlling necrosis and enhanced defense response to stem rust. Theor. Appl. Genet. 118:385-397.

Prepared:

A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:184.

BGS 682, Necroticans 11, *nec11*

Stock number:	BGS 682
Locus name:	Necroticans 11
Locus symbol:	*nec11*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1H (1); *nec11.ad* is in 1H bin 09 (1).

Description:

Necrotic phenotype is expressed as blotchy light brown to bleached necrosis progressing until the leaf blade turns yellow and dies starting at the tip. Vigor of *nec11.ad* plants is good to fair in Steptoe and very good in Morex (2). All three alleles are defective in the barley disease response gene *pti1* (serine/threonine kinase Pto-interacting 1) (1). The necrotic phenotype behaves as if controlled by a typical monofactorial recessive gene in crosses with Steptoe; however, when crossed to Morex the segregation ratio in the F2 progeny is closer to 15 normal to 1 necrotic, suggesting that Morex has a dominant gene that suppresses the necrotic phenotype or whose recessive or non-functional allele is required for the expression of the necrotic phenotype. This putative gene has not been characterized (2).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (2).

Mutation events:

nec11.ad (FN227, GSHO 3610), *nec11.ae* (FN364, GSHO 3611), *nec11.af* (FN450, GSHO 3612) in Steptoe (CIho 15229) (2).

Mutant used for description and seed stocks:

nec11.ad (FN227, GSHO 3610), *nec11.ae* (FN364, GSHO 3611), *nec11.af* (FN450, GSHO 3612) in Steptoe.

References:

1. Nirmala, J., and A. Kleinhofs (Unpublished).
2. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:185.

BGS 683, Necroticans 12, *nec12*

Stock number: BGS 683
Locus name: Necroticans 12
Locus symbol: *nec12*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Location is unknown.
Description:
The phenotype is expressed as a few very distinct small to medium brown spots on young leaf blades. On older leaves of *nec12* plants, the spots turn to a uniform whitish necrotic bleaching occurring primarily on the underside of the leaf blade (1). This whitish color is very noticeable and distinctive and is observed more toward the base of the leaf blade. Very few spots, if any, are present on the awns. Plant vigor is good (1).
Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) (1).
Mutation events:
nec12.ag (FN225, GSHO 3613), *nec12.ah* (FN248, GSHO 3614), *nec12.ai* (FN250, GSHO 3615) in Steptoe (CIho 15229) (1).
Mutant used for description and seed stocks:
*nec12.ag (*FN225, 3613), *nec12.ah* (FN248, GSHO 3614), *nec12.ai* (FN250, GSHO 3615) in Steptoe.
References:
Kleinhofs, A. (Unpublished).
Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:186.

BGS 684, Necroticans 13, *nec13*

Stock number: BGS 684
Locus name: Necroticans 13
Locus symbol: *nec13*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Location is unknown.
Description:
The necrotic phenotype produces infrequent small to medium sized dark brown spots on the leaf blades, but it is not expressed on awns (1). Little chlorosis is observed around the necrotic lesions. Plants with the *nec13.ak* (FN361, GSHO 3617) or *nec13.al* (FN365, GSHO 3618) mutant sometimes show streaking necrotic spots on the leaf blades. The vigor of mutant plants is excellent (1).
Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) (1).
Mutation events:
nec13.aj (FN360, GSHO 3616), *nec13.ak* (FN361, GSH 3617), and *nec13.al* (FN365, GSHO 3618) in Steptoe (CIho 15229) (1).
Mutant used for description and seed stocks:
nec13.aj (FN360, GSHO 3616), *nec13.ak* (FN361, GSHO 3617), and *nec13.al* (FN365, GSHO 3618) in Steptoe.
References:
1. Kleinhofs, A. (Unpublished).
Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:187.

BGS 685, Necroticans 14, *nec14*

Stock number:	BGS 685
Locus name:	Necroticans 14
Locus symbol:	*nec14*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Large black spots develop on young leaf blades of *nec14.am* plants and become fairly numerous on older leaves and awns. The *nec14.am* plants have good vigor (1).

Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 1529) (1).

Mutation events:
nec14.am (FN065, GSHO 3619) in Steptoe (CIho 1529) (1).

Mutant used for description and seed stocks:
nec14.am (FN065, GSHO 3619) in Steptoe.

References:
1. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:188.

BGS 686, Necroticans 15, *nec15*

Stock number: BGS 686
Locus name: Necroticans 15
Locus symbol: *nec15*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Location is unknown.
Description:
Large dark brown spots develop primarily on older leaf blades. The spots may be surrounded by chlorosis and their gradual spreading results in death of older leaves. Mutant plants have good vigor (1). The *nec15.an* mutant may be allelic to *nec15.az* (FN452, GSHO 3632), but this needs to be confirm. It is not allelic to the necrotic leaf spot 1 (*nec1.a*) gene (GSHO 989), necrotic leaf spot 3 (*nec3.d*) gene (GSHO 1330), necroticans 10 (*nec10.o*) mutant (FN044, GSHO 3607), necroticans 11 (*nec11.ad*) mutant (FN227, GSHO 3610), necroticans 12 (*nec12.ag*) mutant (FN225, GSHO 3613), necroticans 13 (*nec13.aj*) mutant (FN360, GSHO 3616), necroticans 16 (*nec16.ao*) mutant (FN201, GSHO 3621), necroticans 17 (*nec17.ap*) mutant (FN242, GSHO 3622), and necroticans 19 (*nec19.ar*) mutant (FN327, GSHO 3624) (1).
Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) (1).
Mutation events:
nec15.an (FN093, GSHO 3620) in Steptoe (CIho 15229); *nec15.az* (FN452, GSHO 3632) in Steptoe (1).
Mutant used for description and seed stocks:
nec15.an (FN093, GSHO 3620) and *nec15.az* (FN452, GSHO 3632) in Steptoe.
References:
1. Kleinhofs, A. (Unpublished).
Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:189.

BGS 687, Necroticans 16, *nec16*

Stock number: BGS 687
Locus name: Necroticans 16
Locus symbol: *nec16*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located unknown.

Description:

The phenotype is expressed as large dark black spots that are fairly numerous on the leaf blades. The necrotic spots seem more common near the margins of the leaf blade. The vigor of mutant plants is good. The *nec16.ao* mutant is not allelic to *nec15.an* (FN093, GSHO 3620, BGS 686) (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec16.ao (FN201, GSHO 3621) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

nec16.ao (FN201, GSHO 3621) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:190.

BGS 688, Necroticans 17, *nec17*

Stock number:	BGS 688
Locus name:	Necroticans 17
Locus symbol:	*nec17*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Numerous brown spots of various sizes develop on older leaf blades of mutant plants. The vigor of *nec17.ap* plants is poor. The *nec17.ap* mutant is not allelic to the necrotic leaf spot 1 gene (*nec1.a*, GSHO 989, BGS 222) and necroticans 15 (*nec15.an* (GSHO 3620, BGS 686). It is phenotypically very different from other named necroticans (*nec*) genes (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec17.ap (FN242, GSHO 3622) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

nec17.ap (FN242, GSHO 3622) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A.Kleinhofs. 2013. Barley Genet. Newsl. 43:191.

BGS 689, Necroticans18, *nec18*

Stock number:	BGS 689
Locus name:	Necroticans 18
Locus symbol:	*nec18*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Expression of the *nec18.aq* mutant is first observed as a few small dark brown flecks on the leaf blades. Streaking of the numerous light brown to brown necrotic lesions occurs on older leaf blades of *nec18.aq* plants. The lesions spread resulting in death of leaf blades. The vigor of *nec18.aq* plants is fair (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec18.aq (FN275, GSHO 3623) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

nec18.aq (FN275, GSHO 3623) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:192.

BGS 690, Necroticans 19, *nec19*

Stock number:	BGS 690
Locus name:	Necroticans 19
Locus symbol:	*nec19*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants show extensive medium brown necrosis of leaf blades with lesions spreading and resulting in death of older leaf blades. The *nec19.ar* plants showed fair to good plant vigor. The *nec19.ar* mutant is phenotypically similar to later stages of symptom expression caused by the *nec18.aq* (necroticans 18) mutant (FN275, GSHO 3623, BGS 689), but lesions appear slightly darker. The *nec19.ar* mutant is not allelic to the *nec15.an* (necroticans 15) mutant (FN023, GSHO 3620, BGS 686) (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec19.ar (FN327, GSHO 3624) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

nec19.ar (FN327, GSHO 3624) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:193.

BGS 691, Necroticans 20, *nec20*

Stock number:	BGS 691
Locus name:	Necroticans 20
Locus symbol:	*nec20*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Initial expression of the *nec20.as* mutant is widely scattered small medium brown necrotic spots on the leaf blades. Later mutant plants show extensive brown necrosis of leaf blades with lesions spreading and resulting in death of older leaf blades. The phenotype of *nec20.as* plants is similar to that of the *nec18.aq* (necroticans 18) mutant (FN275, GSHO 3623) and the *nec19.ar* (necroticans 19) mutant (FN327, GSHO 3624) plants (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec20.as (FN366, GSHO 3625) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

nec20.as (FN366, GSHO 3625) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:194.

BGS 692, Necroticans 21, *nec21*

Stock number: BGS 692
Locus name: Necroticans 21
Locus symbol: *nec21*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The mutant phenotype for *nec21.at* appears as small light brown, elongated spots on the leaf blades. Older leaf blades show a gradually developing necrosis at the base as spots enlarge and become more numerous. The vigor of mutant plants is fair (1). The *nec21.at* stock (FN367, GSHO 3626) also exhibited a light green color, which may be an associated mutation; however, it was not separated from the necrotic phenotype in a small population (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec21.at (FN367, GSHO 3626) in Steptoe(CIho 15229) (1).

Mutant used for description and seed stocks:

nec21.at (FN367, GSHO 3626) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:195.

BGS 693, Necroticans 22, *Nec22*

Stock number:	BGS 693
Locus name:	Necroticans 22
Locus symbol:	*Nec22*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Location is unknown.

Description:

Small to large brown irregularly shaped spots develop on the leaf blades of *Nec22.au* plants. The spots show a little spreading as the leaves mature. The *Nec22.au* mutant is not allelic with the only previously reported dominant necrotic leaf mutant, necrotic leaf spot 6, (*Nec6.h*) (GSHO 2424, BGS 611). The *Nec22.au* mutant is possibly allelic with *Nec26.ay* (FN451, GSHO 3631, BGS 697); however, the conclusion was based on a small number of F2 plants (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

Nec22.au (FN368, GSHO 3627) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

Nec22.au (FN368, GSHO 3627) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:196.

BGS 694, Necroticans 23, *nec23*

Stock number:	BGS 694
Locus name:	Necroticans 23
Locus symbol:	*nec23*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Leaf blades of *nec23.av* plants produce small to medium sized dark brown spots. Chlorosis of the leaf blade occurs first in regions where the spots are numerous. The mutant plants have good vigor. The *nec23.av* mutant is not allelic to the mutant *nec15.az* (necroticans 15) mutant (FN452, GSHO 3632) (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec23.av (FN369, GSHO 3628) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

Nec23.av (FN369, GSHO 3628) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:197.

BGS 695, Necroticans 24, *Nec24*

Stock number:	BGS 695
Locus name:	Necroticans 24
Locus symbol:	*Nec24*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Location is unknown.

Description:

The *Nec24.aw* plants produce large dark brown spots on the leaf blades. The necrotic spots are not surrounded by chlorosis, but do show a little spreading. The phenotypic expression is similar to that of *Nec22.au* (necroticans 22) (FN368, GSHO 3627), but the spots tends to fade more on older leaves (1). Allelism between *Nec22.au* and *Nec24.aw* mutants has not been checked. The *Nec24.aw* mutant is not allelic to the *Nec26.ay* (necroticans 26) mutant (FN451, GSHO 3631) (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

Nec24.aw (FN371, GSHO 3629) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

Nec24.aw (FN371, GSHO 3629) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:198.

BGS 696, Necroticans 25, *nec25*

Stock number: BGS 696
Locus name: Necroticans 25
Locus symbol: *nec25*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Leaf blades of *nec25.ax* plants gradually form dark brown necrotic spots that gradually enlarge. Older leaves have scattered spots of various sizes. The spots may be associated with a slight chlorosis of the surrounding leaf tissue. (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

nec25.ax (FN396, GSHO 3630) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

nec25.ax (FN396, GSHO 3630) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:199.

BGS 697, Necroticans 26, *Nec26*

Stock number:	BGS 697
Locus name:	Necroticans 26
Locus symbol:	*Nec26*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Location is unknown.

Description:

The leaf blades of mutant plants develop extensive dark rust colored, spotty necrosis, which often covers older leaf blades completely leading to death. Little or no chlorosis around the necrotic lesions was observed. The *Nec26.ay* mutant is possibly allelic to *Nec22.au* (necroticans 22) (FN368, GSHO 3627), but it is not allelic to *Nec24.aw* (necroticans 24) (FN371, GSHO 3629). Plants of the *Nec26.ay* stock have fair vigor (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (1).

Mutation events:

Nec26.ay (FN451, GSHO 3631) in Steptoe (CIho 15229) (1).

Mutant used for description and seed stocks:

Nec26.ay (FN451, GSHO 3631) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:200.

BGS 698, Necroticans 27, *nec27*

Stock number:	BGS 698
Locus name:	Necroticans 27
Locus symbol:	*nec27*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Large black spots develop on the leaf blades of *nec27.ba* plants and exhibit a slight increase in size as leaves mature. Older leaf blades showed more necrosis and gradually they become yellow and die (1). The *nec27.bb* mutant (γ08-125, GSHO 3634) is phenotypically similar to the *nec27.ba* mutant (1).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (1).

Mutation events:

nec27.ba (γ06-05, GSHO 3633) and *nec27.bb* (γ08-125, GSHO 3634) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

nec27.ba (γ06-05, GSHO 3633) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:201.

BGS 699, Necroticans 28, *nec28*

Stock number: BGS 699
Locus name: Necroticans 28
Locus symbol: *nec28*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Location is unknown.
Description:
Large black spots develop on the leaf blades of *nec28.bc* plants and exhibit a slight increase in size as leaves mature. Older leaf blades showed more chlorosis around lesions and they gradually became yellow and died (1). Phenotypic expression of *nec28.bc* is similar to that of the *nec27.ba* mutant (GSHO 3633, BGS 698) (1).
Origin of mutant:
A gamma ray induced mutant in Morex (CIho 15773) (1).
Mutation events:
nec28.bc (*γ*08-126, GSHO 3635) in Morex (CIho 15773) (1).
Mutant used for description and seed stocks:
nec28.bc (*γ*08-126, GSHO 3635) in Morex.
References:
1. Kleinhofs, A. (Unpublished).
Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:202.

BGS 700, Necroticans 29, *nec29*

Stock number:	BGS 700
Locus name:	Necroticans 29
Locus symbol:	*nec29*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Large black spots develop on the leaf blades of *nec29.bd* plants and exhibit a slight increase in size as leaves mature. Older leaf blades showed more necrosis and gradually they become yellow and died (1). The *nec29.bd* mutant is phenotypically similar to the *nec27.ba* (necroticans 27) mutant, but it is not allelic (1).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (1).

Mutation events:

nec29.bd (*γ*08-127, GSHO 3636) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

nec29.bd (*γ*08-127, GSHO 3636) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:203.

BGS 701, Necroticans 30, *nec30*

Stock number: BGS 701
Locus name: Necroticans 30
Locus symbol: *nec30*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Location is unknown.

Description:
Large black spots develop on the leaf blades of *nec30.be* plants and exhibit a slight increase in size as leaves mature. Older leaf blades showed more chlorosis around lesions and they gradually became yellow and died (1). Phenotypic expression of the *nec30.be* mutant is similar to that of the *nec27.ba* mutant (GSHO 3633, BGS 698) mutant (1).

Origin of mutant:
A gamma ray induced mutant in Morex (CIho 15773) (1).

Mutation events:
nec30.be (γ08-128, GSHO 3637) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:
nec30.be (γ08-128, GSHO 3637) in Morex.

References:
1. Kleinhofs, A. (Unpublished).

Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:204.

BGS 702, Necroticans 31, *nec31*

Stock number:	BGS 702
Locus name:	Necroticans 31
Locus symbol:	*nec31*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Large black spots develop on the leaf blades of *nec31.bf* plants and exhibit a slight increase in size as leaves mature. Older leaf blades showed more chlorosis around lesions and they gradually became yellow and died (1). Phenotypic expression of *nec31.bf* is similar to that of the *nec27.ba* (GSHO 3633, BGS 698) mutant (1).

Origin of mutant:

A gamma ray induced mutant in Morex (CIho 15773) (1).

Mutation events:

nec31.bf (γ08-129, GSHO 3638) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

nec31.bf (γ08-129, GSHO 3638) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:205.

BGS 703, Necroticans 32, *nec32*

Stock number:	BGS 703
Locus name:	Necroticans 32
Locus symbol:	*nec32*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Large black spots develop on the leaf blades of *nec32.bg* plants and exhibit a slight increase in size as leaves mature. Older leaf blades showed more chlorosis around lesions and gradually they become yellow and died. The *nec32.bg* mutant is phenotypically similar to the *nec27.ba* (GSHO 3633, BGS 698) mutant, but it is not allelic (1).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (1).

Mutation events:

nec32.bg (*γ*08-130, GSHO 3639) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

nec32.bg (*γ*08-130, GSHO 3639) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:206.

BGS 704, Necroticans 33, *nec33*

Stock number:	BGS 704
Locus name:	Necroticans 33
Locus symbol:	*nec33*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Small black spots appear on the leaf blades, leaf sheaths, and awns of mutant plants. The spots are similar to those produced by mutants at the *nec1* (necrotic leaf spot 1) locus, but spots of the *nec33.bh* mutants appear in distinct linear rows and leaf blades show tip necrosis (1). The *nec33.bh* mutant is not allelic at the *nec1* locus. The *nec33.bh* plants headed very late when grown at the Washington State University Agronomy Farm near Pullman, WA, USA (1).

Origin of mutant:

A gamma ray induced mutant in CIho 4196 (1).

Mutation events:

nec33.bh (*γ*07-093, GSHO 3640) in CIho 4196 (1).

Mutant used for description and seed stocks:

nec33.bh (*γ*07-093, GSHO 3640) in CIho 4196.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:207.

BGS 711, Reaction to *Pyrenophora teres* 3, *Rpt3*

Stock number:	BGS 711
Locus name:	Reaction to *Pyrenophora teres* 3 (*P. teres* f. *teres*, net form of net blotch, NFNB)
Locus symbol:	*Rpt3*

Previous nomenclature and gene symbolization:

QTL for resistance to *Pyrenophora teres f. teres* seedling 2H = *QRptts2* (5).

QTL for resistance to NFNB seedling Alexis/Sloop 2H = *QNFNBSLR.Al/S-2H* (7).

Inheritance:

Monofactorial incomplete dominant (1); recessive resistance in CIho 9831 (6).

Located in chromosome 2HS (1, 6, 10); *Rpt3* from CIho 9831 is linked to the *vrs1* (six rowed spike 1) locus (6); a QTL is proximal from SSR marker HVM36 (7, 9); a QTL is near DArT marker bPb-4877 in 2H bin 04 (5).

Description:

The seedling reactions of cultivars with the *Rpt3* gene for resistance to *Pyrenophora teres* f. *teres* (*Ptt*) isolates were often scored 1 on a scale where 0 = very resistant and 4 = susceptible (1). Heterozygous individuals showed intermediate reactions of 1 to 3 (1). A QTL for resistance to some *Ptt* isolates in Kaputar was mapped to chromosome 2H (2). QTL for resistance to *Ptt* in Franklin (10) and Sloop (7, 10) were mapped to chromosome 2HS. A minor effect QTL in 2HS was detected in CIho 9819 by Manninen et al. (9), but not by Bockelman et al. (1). Other QTL for *Ptt* resistance reported to be associated with chromosome 2H were summarized by Liu et al. (8).

Origin of mutant:

Natural occurrence in Tennessee Awnless D22-5 (CIho 7584) (1).

Mutational events:

Rpt3.d in Tennessee Awnless D22-5 (CIho 7584) (1); possible allelic QTL are present in CIho 9831 (PI 197102) from Japan (6), Steptoe (CIho 15229) from Washington (11), Kaputar (PI 591928) from Mexico (2), Franklin (PI 573729) from Australia (10), Sloop (Norbert/Schooner) from Australia (7, 10), ND11231-12 (Logan sib, PI 643261) from North Dakota (3), TR251 (TR229//AC Oxbow/ND7556) from Canada (5).

Mutant used for description and seed stocks:

Rpt3.d in Tennessee Awnless D22-5 (CIho 7584).

References:

1. Bockelman, H.E., E.L. Sharp, and R.F. Eslick. 1977. Trisomic analysis of genes for resistance to scald and net blotch in several barley cultivars. Can. J. Bot. 55:2142-2148.
2. Cakir, M., S. Gupta, G.J. Platz, G.A. Ablett, R. Loughman, L.C. Emebiri, D. Poulsen, C.D. Li, R.C.M. Lance, N.W. Galeway, M.G.K. Jones, and R. Appels. 2003. Mapping and validation of the genes for resistance to *Pyrenophora teres* f. *teres* in barley (*Hordeum vulgare* L.). Aust. J. Agric. Res. 54:1369-1377.
3. Emebiri, L.C., G. Platz, and D.B. Moody. 2005. Disease resistance genes in a doubled haploid population of two-rowed barley segregating for malting quality attributes. Aust. J. Agric. Res. 56:49-56.
4. Friesen T.L., J.D. Faris, Z. Lai, and B.J. Steffenson. 2006. Identification and chromosomal location of major genes for resistance to *Pyrenophora teres* in a doubled-haploid barley population Genome 49: 855-859.
5. Grewal, T.S., B.G. Rossnagel, C.J. Ponzniak, and G.J. Scoles. 2008. Mapping

quantitative trait loci associated with barley net blotch resistance. Theor. Appl. Genet. 116: 529-539.

6. Ho, K.M., A. Tekauz, T.M. Choo, and R.A. Martin. 1996. Genetic studies on net blotch resistance in a barley cross. Can. J. Pl. Sci. 56:715-719.

7. Lehmensiek, A., G.J. Platz, E. Mace, D. Poulsen, and M.W. Sutherland. 2007. Mapping of adult plant resistance to net form of net blotch in three Australian barley populations. Aust. J. Agric. Res. 58:1191-1197.

8. Liu, Z., S.R. Ellwood, R.P. Oliver, and T.L. Friesen. 2011. *Pyrenophora teres***:** profile of an increasingly damaging barley pathogen. Mol. Plant Pathol. 12:1-19.

9. Manninen, O.M., M. Jalli, R. Kalendar, A. Schulman, O. Afanasenko, and J. Robinson. 2006. Mapping of major spot-type and net-type net-blotch resistance genes in Ethiopian barley line CI 9819. Genome 49: 1564-1571.

10. Raman, H., G.J. Platz, K.J. Chalmers, R. Raman, B.J. Read, A.R. Barr, and D.B. Moody. 2003. Mapping of genomic regions associated with net form of net blotch resistance in barley. Australian J. Agric. Res. 54: 1359-1367.

11. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:208-209.

BGS 713, Reaction to *Pyrenophora teres* 6, *Rpt6*

Stock number:	BGS 713
Locus name:	Reaction to *Pyrenophora teres* 6 (*P. teres* f. *maculata*, spot form of net blotch, SFNB)
Locus symbol:	*Rpt6*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Located in chromosome 5HL (1), *Rpt6.g* is located within 1.5 cM of microsatellite marker HVLUE, which located in the proximal region of the long arm (1).

Description:

The seedling reactions of CIho 9819 to *Pyrenophora teres* f. *maculata* (*Ptm*) isolates ranged from 2 to 6 on a scale where 1 = very resistant and 10 = very susceptible (1). The *Rpt6.g* gene of CIho 9819 from Ethiopia confers isolate specific resistance to *Ptm* (1). CIho 9819 was resistant to two *Ptm* isolates from Finland, but not to the isolate from the Czech Republic (1). A QTL for adult plant resistance to *Ptm* from Galleon and VB 9104 was mapped in the short arm of 5H (2), and is probably independent of the *Rpt6* locus.

Origin of mutant:

Natural occurrence in CIho 9819 (PI 195985) collected from Welo, Ethiopia (1).

Mutational events:

Rpt6.g from CIho 9819 (PI 195985) collected from Welo, Ethiopia (1).

Mutant used for description and seed stocks:

Rpt6.g in CIho 9819.

References:

1. Manninen, O.M., M. Jalli, R. Kalendar, A. Schulman, O. Afanasenko, and J. Robinson. 2006. Mapping of major spot-type and net-type net-blotch resistance genes in Ethiopian barley line CI 9819. Genome 49:1564-1571.

2. Williams, K.J., G.J. Platz, A.R. Barr, J. Cheong, K. Willsmore, M. Cakir, and H. Wallwork**.** 2003. A comparison of the genetics of seedling and adult plant resistance to the spot form of net blotch (*Pyrenophora teres* f. *maculata*). Aust. J. Agric. Res. 54:1387-1394.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:210.

BGS 714, Reaction to *Pyrenophora teres* 7, *Rpt7*

Stock number:	BGS 714
Locus name:	Reaction to *Pyrenophora teres* 7 (*P. teres* f. teres, net form of net blotch, NFNB)
Locus symbol:	*Rpt7*

Previous nomenclature and gene symbolization:

QTL for resistance to *Pyrenophora teres* seedling 4H = *Qrpts4* (4).

QTL for resistance to NFNB seedling Alexis/Sloop 4Ha = *QNFNBAPR.Al/S-4Ha* (2).

QTL for resistance to *Pyrenophora teres* 4H bins 5 to 7 = *Rpt-4H-5-7* (8).

Inheritance:

Monofactorial dominant (2, 4).

Located in chromosome 4HL (1, 2, 4, 5); *Rpt7.h* from Halcyon is near SSR markers Bmac906 and Bmac181 (4, 5); *Rpt7.h* from OUH602 is near SSR maker Bmag808 and Bmag353 (8); *Rpt7.h* from TR251 is between SSR marker HVM3 and DArT maker bPb-0098 in bin 06 (1); *Rpt7.h* from Sloop is near markers HVM3 and Bmag344 (2).

Description:

Halcyon exhibited a 3 seedling reaction to isolate NNB50 of *Pyrenophora teres* f. *teres* (*Ptt*) on a 1 to 10 scale (4), while the susceptible parent Sloop had a 9 reading (4). Steptoe had a reading of 4 while Morex had 8 on a 1 to 10 scale (7). TR251 had seedling responses to two *Ptt* isolates ranging from 2.0 to 2.8 on a 1 to 10 scale, but only with isolate WR858 was a QTL from TR251 detected in 4H (1), Based on adult plant reactions, Sloop was the resistant parent (readings 1 to 4 on a 0 to 9 scale) in the cross to Alexis (readings 6 to 8) (2). However, four other QTL for adult plant resistance were mapped in the Alexis/Sloop cross (2). The QTL for *Ptt* resistance reported to be associated with chromosome 4H were summarized by Liu et al. (3).

Origin of mutant:

Natural occurrence of in Halcyon (PI 531062, Warboys/Maris Otter) (4), possibly present in Steptoe (CIho 15229) (6, 7), and in TR251 (TR229//AC Oxbow/ND7556) (1). The adult plant resistance from Sloop (Norbert/Schooner) may be at a different locus in the same chromosomal region (2),

Mutational events:

Rpt7.h in Halcyon (PI 531062, Warboys/Maris Otter) (4, 5). Other possible alleles are present in Steptoe (CIho 15229, WA 3564/Unitan) (6, 7), Sloop (Norbert/Schooner) (2), TR251 (TR229//AC Oxbow/ND7556) (1), and OUH602 (*Hordeum vulgare* ssp. *spontaneum*) (8).

Mutant used for description and seed stocks:

Rpt7.h in Halcyon; *Rpt7.h* in Steptoe; *Rpt7.h* in TR251; adult plant resistance in Sloop (2),

References:

1. Grewal, T.S., B.G. Rossnagel, C.J. Ponzniak, and G.J. Scoles. 2008. Mapping quantitative trait loci associated with barley net blotch resistance. Theor. Appl. Genet. 116: 529-539.

2. Lehmensiek, A., G.J. Platz, E. Mace, D. Poulsen, and M.W. Sutherland. 2007. Mapping of adult plant resistance to net type of net blotch in three Australian barley populations. Aust. J. Agric. Res. 58:1191-1197.

3. Liu, Z., S.R. Ellwood, R.P. Oliver, and T.L. Friesen. 2011. *Pyrenophora teres*: profile

of an increasingly damaging barley pathogen. Molecular Plant Pathology, 12:1-19.
4. Raman, H., G.J. Platz, K.J. Chalmers, R. Raman, B.J. Read, A.R. Barr, and D.B. Moody. 2003. Mapping of genomic regions associated with net form of net blotch resistance in barley. Aust. J. Agric. Res. 54: 1359-1367.
5. Read, B.J., H. Raman, G. McMichael, K.J. Chalmers, G.A. Ablett G.J. Platz, R. Raman, R.K. Genger, W.J.R. Boyd, C.D. Li, C.R. Grime, R.F. Park, H. Wallwork, R. Prangnell, R.C.M. Lance. 2003. Mapping of QTL analysis of the barley population Sloop×Halcyon. Aust. J. Agric. Res. 54:1145-1153.
6. Sato, K., K. Takeda, and P.M. Hayes. 1996. QTL analysis for net blotch resistance in barley. Vol 1 p. 298-300. *In* A.E. Slinkard, G.J. Scoles, and B.G. Rossnagel (eds.). Barley Genetics VII. Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp. Proceed., Saskatoon. Univ. Ext. Press, Univ. of Saskatchewan, Saskatoon, Canada.
7. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs, 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.
8. Yun, S.J., L. Gyenis, P.M. Hayes, I. Matus, K.P. Smith, B.J. Steffenson, and G.J. Muehlbauer. 2005. Quantitative trait loci for multiple disease resistance in wild barley. Crop Sci. 45:2563-2572.

Prepared:

J.D. Franckowiak and G.J. Platz. 2013. Barley Genet. Newsl. 43:211-212.

BGS 718, Opposite spikelets 2, *ops2*

Stock number: BGS 718
Locus name: Opposite spikelets 2
Locus symbol: *ops2*

Previous nomenclature and gene symbolization:

Opposite spikelets-2 = *op-2* (3, 4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 5HL (1); *ops2.2* is associated with SNP markers 1_0217 to 1_0869 (positions 234.98 to 264.33 cM) in 5H bins 12 to 13 of the Bowman backcross-derived line BW640 (1).

Description:

The *ops2.2* plants have variable rachis internode lengths, which causes an irregular arrangement of spikelets in the spike (3, 4). Compared to Bowman, *ops2.2* plants of the Bowman backcross-derived line, BW640, were about 2/3 normal height and had shorter peduncles, 2/3 to 3/4 of normal. Average rachis internode lengths were 4.1 vs. 4.8 cm for Bowman. The awns of BW640 were slightly shorter and kernels were 10% smaller and lighter. Grain yields of BW640 were 1/2 to 2/3 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Foma (CIho 11333) (4).

Mutational events:

ops2.2 (NGB 115378, GSHO 2426) in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

ops2.2 (GSHO 2426, NGB 115378) in Bonus; *ops2.2* in Bowman (PI 483237)*2 (GSHO 2317); *ops2.2* in Bowman*5 (BW640, NGB 22205).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:213.

BGS 719, Opposite spikelets 3, *ops3*

Stock number:	BGS 719
Locus name:	Opposite spikelets 3
Locus symbol:	*ops3*

Previous nomenclature and gene symbolization:

Opposite spikelets-1 = *op-1* (3, 4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 5HS (1); *ops3.1* is associated with SNP markers 1_1048 to 1_0688 (positions 46.35 to 52.12 cM) in 5H bin 03 and with SNP markers 2_0722 and 2_0495 (positions 23.45 and 32.35 cM) in 7H bin 02 of the Bowman backcross-derived line BW639 (1), likely in 5H bin 03.

Description:

The opposite spike like arrangement of spikelets in the spike of *ops3.1* plants is caused variable rachis internode lengths (3, 4). Compared to normal sibs, plants of the Bowman backcross-derived line for *ops3.1*, BW639, were slightly later and taller and had slightly longer peduncles (2). Plants of the BW639 had 2 to 4 more kernels per spike and yielded about 3/4 as much grain as Bowman plants (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (4).

Mutational events:

ops3.1 (NGB 115377, GSHO 2425) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

ops3.1 (GSHO 2425, NGB 115377) in Bonus; *ops3.1* in Bowman (PI 483237)*2 (GSHO 2316); *ops3.1*in Bowman*5 (BW639, NGB 22204).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:214.

BGS 720, Viviparoides-c, *viv-c*

Stock number:	BGS 720
Locus name:	Viviparoides-c
Locus symbol:	*viv-c*

Previous nomenclature and gene symbolization:

Viviparoides-1 = *viv-1* (4, 5).

Inheritance:

Monofactorial recessive (5).

Location in chromosome 5H (2); *viv-c.1* is associated with SNP markers 2_0761 to 2_1239 (positions 43.06 to 107.53 cM) in 5H bins 02 to 06 of the Bowman backcross-derived line BW890 (2).

Description:

Tillers of the *viv-c.1* plants in the original mutant stock often remained vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as new phytomers are added, but occasionally a short, malformed spike develops. In these spikes, many spikelets are replaced by plantlets. In the spikes that produce kernels, arrangement of spikelets is irregular (1, 5). In the Bowman backcross-derived line for *viv-1.c* (BW890), spikes were compact and multiflorous. Compared to Bowman at Leeston, New Zealand, BW890 plants headed four days later and had slightly shorter peduncles and stature. Kernels were about 2/3 normal weight and grain yields were about 1/3 those of Bowman (3). At Aberdeen, Idaho, USA, expression of the vivpariodes phenotype in BW890 plants are much stronger. Grain yields were nearly none to 1/4 those of Bowman and kernels were about 1/2 normal weight. The number of kernels per spike was reduced to 3/4 of normal or less and rachis internodes were 20% shorter (3), In the glasshouse at Lund, Sweden, the spikes of BW890 plants were short, irregular six-rowed with some calcaroides-like hoods and kernels were semi-naked (5).

Origin of mutant:

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

Mutational events:

viv-c.1 (NGB 115360, GSHO 2497) in Foma (CIho 11333) (5).

Mutant used for description and seed stocks:

viv-c.1 (GSHO 2497, NGB 115360 in Foma; *viv-c.1* in Bowman (PI 483237)*2 (GSHO 2365); *viv-c.1* in Bowman*4 (BW890, NGB 22323).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. 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. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:215.

BGS 721, Breviaristatum-w, *ari-w*

Stock number:	BGS 721
Locus name:	Breviaristatum-w
Locus symbol:	*ari-w*

Previous nomenclature and gene symbolization:

Breviaristatum-153 = *ari-153* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7H (1); ar*i-w.153* is associated with SNP markers 1_0721 to 1_0563 (positions 82.82 to 154.35 cM) in 7H bins 06 to 09 of the Bowman backcross-derived line BW027 (1).

Description:

Awns of *ari-w.153* plants about 1/2 normal length (3) and mature late (4). Compared to Bowman, plants of the Bowman backcross-derived line for *ari-w.153*, BW027, were slightly taller and had awns that were thin and 1/3 to 1/2 normal length. Kernels of BW027 were slightly longer and thinner than those of Bowman and weighted slightly more. Grain yields and test weights of BW027 were equal to or slightly higher than those of Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (CIho 11333) (3, 4).

Mutational events:

ari-w.153 (NGB 115962) in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

ari-w.153 (NGB 115962) in Foma; *ari-w.153* in Bowman (PI 483237)*6 (BW027, NGB 20435).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:216.

BGS 722, Breviaristatum-y, *ari-y*

Stock number:	BGS 721
Locus name:	Breviaristatum-y
Locus symbol:	*ari-y*

Previous nomenclature and gene symbolization:

Breviaristatum-9 = *ari-9* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5H (1, 2); linked to the *raw1* (smooth awn 1) locus based on linkage drag (2); *ari-y.9* is associated with SNP markers 1_1456 to 2_1177 (positions 195.82 to 203.85 cM) in 5H bins 10 to 11 of the Bowman backcross-derived line BW037 (1).

Description:

Plants of the *ari-y.9* are smaller than Bonus in all vegetative organs and stature (3, 4). The size reduction of *ari-y.9* plants was maintained in the Bowman backcross-derived line, BW037. The awn length of BW037 varied over environments, but averaged about 1/2 that of Bowman. The leaves were about 2/3 normal width and 3/4 normal length. Compared to Bowman, BW037 plants were 15 to 20% shorter, peduncles were 20 to 25% shorter, rachis internodes were slightly shorter, kernels per spike were 3 to 5 fewer, kernels were narrower, and kernel weights were low averaging 4.2 vs. 5.5 mg. Test weights of BW037 grain were lower and grain yields were 1/4 to 1/2 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (3, 4).

Mutational events:

ari-y.9 (NGB 115854) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

ari-y.9 (NGB 115854) in Bonus; *ari-y.9* in Bowman (PI 483237)*6 (BW037, NGB 20445).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:217.

BGS 723, Multiovary 5, *mov5*

Stock number:	BGS 723
Locus name:	Multiovary 5
Locus symbol:	*mov5*

Previous nomenclature and gene symbolization:

Multiovary o = *mov.o* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Spikelets of the *mov5.o* (FN532) mutant have three carpels with the lodicules being somewhat abnormal. The lodicules do not form clear sepal-like structures as occurs in *mov1.f* (multiovary 1) mutant (BGS 043). Stamens are absent. The *mov5.o* plants appear nearly normal although they are somewhat shorter than normal segregates (1). The mutant does not set seed and needs to be maintained as a heterozygote (1). Based on the distinct morphological features of the *mov5.o* spikelets, this mutant is unlikely to be allelic to previous named multiovary loci (1).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) (1).

Mutational events:

mov5.o (FN532, GSHO 3671) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

mov5.o (FN532, GSHO 3671) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:218.

BGS 724, Short awn 6, *lks6*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2, 3).

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

Description:

Awns of *lks6.q* plants are about one half normal length compared to the control. Otherwise the plants appear fairly normal (3). Under greenhouse conditions plants of the Bowman backcross-derived line for *lks6.q*, BW489, had reduced plant vigor, slightly reduced seed set, and awns that were about 1/3 normal length (2). Based on phenotypic expression and chromosome segments retained, the *lks6.q* mutant is unlikely to be allelic at previously described short awn (*lks*) loci or the breviaristatum (*ari*) loci.

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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

Prepared:

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

BGS 725, Ovaryless 3, *ovl3*

Stock number: BGS 725
Locus name: Ovaryless 3
Locus symbol: *ovl3*

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Location is unknown.
Description:
The *ovl3.c* plants are later and much shorter than normal sibs. Plants are female sterile, but male fertile (1). The *ovl3.c* mutant must be maintained as a heterozygote (1). Allelism testing with (Ovaryless 1) *ovl1.a* (GSHO 610, BGS 176) and (Ovaryless 3) *ovl2.b* (GSHO 3655, BGS 646) mutants were not conducted, but the three mutants are phenotypically very different morphologically (1).
Origin of mutant:
A fast neutron induced mutant in Harrington. (Agriculture Canada Licence No: 2126) (1).
Mutational events:
ovl3.c (FN510, GSHO 3687) in Harrington (Agriculture Canada Licence No: 2126) (1).
Mutant used for description and seed stocks:
ovl3.c (FN510, GSHO 3687) in Harrington.
References:
1. Kleinhofs, A. (Unpublished).
Prepared:
A. Kleinhofs. 2013. Barley Genet. Newsl. 43:220.

BGS 726, Many-noded dwarf 7, *mnd7*

Stock number:	BGS 726
Locus name:	Many-noded dwarf 7
Locus symbol:	*mnd7*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location is unknown; *mnd7.h* is associated with retained SNP markers in large segments of chromosomes 1H, 3H, 4H, and 5H of Bowman backcross-derived line BW517 (1).

Description:

The *mnd7.h* plants are short (1/2 normal height) with many elongated culm internodes, small thin leaves, and very short spikes. Phenotypically the *mnd7.h* plants appear similar to Many noded dwarf 1 (*mnd1.a*) (BGS 519) plants (3); however branching of the culm at the peduncle node was not observed (2). SNP markers in the region of chromosome 2H associated with presence of *mnd1.a* were not retained in BW517 (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (3).

Mutational events:

mnd7.h (FN233, GSHO 3686) in Steptoe (CIho 15229) (3).

Mutant used for description and seed stocks:

mnd7.h (FN233, GSHO 3686) in Steptoe; *mnd7.h* in Bowman (PI 483237)*3 (BW517, NGB 20745).

References:

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

Prepared:

A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:221.

BGS 727, Unbranched style 5, *ubs5*

Stock number:	BGS 727
Locus name:	Unbranched style 5
Locus symbol:	*ubs5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The *ubs5.e* plants have stigmas that are nearly devoid of stigma hairs. Seed set is somewhat reduced, but other morphological traits of *ubs5.e* plants are unaltered (1). Plants are female sterile, but male fertile (1). When compared to mutants at other loci associated with few stigma hairs and reduced seed set, the *ubs5* mutants do not have the short awns of (Unbranched style 4), *ubs4* (BGS 11) mutants or glossy spikes (reduced surface wax coating of the spike) of eceriferum-yd (*cer-yd*, BGS 447) and eceriferum-yh (*cer-yh*, BGS 451) mutants.

Origin of mutant:

A fast neutron induced mutant in Harrington (1).

Mutational events:

ubs5.e (FN348, GSHO 3675) and *ubs5.f* (FN521, GSHO 3676) in Harrington with allelism based on phenotypic similarity (1).

Mutant used for description and seed stocks:

ubs5.e (FN348, GSHO 3675) in Harrington.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:222.

BGS 728, Fenoxaprop-p-ethyl reaction 1, *fxp1*

Stock number:	BGS 728
Locus name:	Fenoxaprop-p-ethyl reaction 1
Locus symbol:	*fxp1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Exposure *fxp1.a* plants to the grass specific herbicide fenoxaprop-p-ethyl results in yellowing and dying of the plants. The *fxp1.a* plants are normal in the absence of the herbicide (1).

Origin of mutant:

A fast neutron induced mutant in Morex (CIho 15773) (1).

Mutational events:

fxp1.a (FN561, GSHO 3684) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

fxp1.a (FN561, GSHO 3684) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2013. Barley Genet. Newsl. 43:223.