

BGS 601, Proanthocyanidin-free 19, *ant19*

Stock number: BGS 601  
Locus name: Proanthocyanidin-free 19  
Locus symbol: *ant19*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

The mutant plants synthesize a wild type amount of anthocyanins in their vegetative parts, but the testa layers of the grains lack catechins and proanthocyanidins (2). The *ant19* gene is probably the structural gene coding for leucoanthocyanidin reductase, the enzyme catalyzing the conversion of leucoanthocyanidins into catechins (3, 4).

Origin of mutant:

A sodium azide induced mutant in Alf (NGB 13682) (1).

Mutational events:

*ant19.109* (NGB 13703, GSHO 1631) in Alf (NGB 13682) (2).

Mutant used for description and seed stock:

*ant19.109* (NGB 13703, GSHO 1631) in Alf.

References:

1. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
2. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:76-79.
3. Kristiansen, K.N. 1984. Biosynthesis of proanthocyanidins in barley: Genetic control of the conversion of dihydroquercetin to catechin and procyanidins. *Carlsberg Res. Commun.* 49:503-524.
4. Tanner, G.J., K.N. Kristiansen, and B. Jende-Strid. 1992. Biosynthesis of proanthocyanidins (condensed tannins) in barley. *Bulletin de Liaison - Groupe Polyphenols* 16:170-173.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:92.

BGS 602, Anthocyanin-rich 20, *ant20*

Stock number: BGS 602  
Locus name: Anthocyanin-rich 20  
Locus symbol: *ant20*

Previous nomenclature and symbolization:

Rubrum = rub (1).

Inheritance:

Monofactorial recessive ( 3, 5).

Location is unknown.

Description:

Compared to their mother varieties, mutant plants synthesize an increased amount of anthocyanin in their vegetative parts. All mutant alleles develop bright red anthocyanin pigmentation in the awns. (2, 4).

Origin of mutant:

A neutron induced mutant in Foma (Clho 11333) (2).

Mutational events:

*ant20.1104* (NGB 114602, GSHO 1633), *20.1106* (NGB 114604) in Foma (Clho 11333) (3); *ant20.1114* in Gunhild (NGB 13690) (5).

Mutant used for description and seed stock:

*ant20.1104* (NGB 114602, GSHO 1633) in Foma.

References:

1. Gustafsson, ÅÅ., 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.
2. Jende-Strid, B. 1978. Mutations affecting flavonoid synthesis in barley. *Carlsberg Res. Commun.* 43:265-273.
3. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:76-79.
4. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.
5. Jende-Strid, B. 1995. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 24:162-165.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:93.

BGS 603, Proanthocyanidin-free 21, *ant21*

Stock number: BGS 603  
Locus name: Proanthocyanidin-free 21  
Locus symbol: *ant21*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 6H, close to the centromere (1).

Description:

Under normal growing conditions no anthocyanins are observed in the vegetative parts of the mutant plants. The mutant grains lack proanthocyanidins and no precursors of proanthocyanidins are accumulated. The action of the gene *ant21* is unknown, but it might be involved in the regulation of anthocyanin and proanthocyanidin biosynthesis (5, 6).

Origin of mutant:

A sodium azide induced mutant in Georgie (PI 447012, NGB 13683) (2).

Mutational events:

*ant21.194* (NGB 13704) in Georgie (PI 447012, NGB 13683) (3); *ant21.207* in Hege 876 (4); *ant21.271* (NGB 23215) in Secobra 18193 (NGB 13684) (4); *ant21.526* in Advance (CIho 15804) (4); *ant21.1507* in Amagi-Nijo (3); *ant21.1513* (GSHO 1634) in Haruna-Nijo (3); *ant21.1514* in Nirakei 61 (4); *ant21.1516* in Nirakei 61 (3).

Mutant used for description and seed stock:

*ant21.194* (NGB 13704) in Georgie; *ant21.1513* (GSHO 1634) in Haruna-Nijo; *ant21.1513* in Bowman (PI 483237)\*4 (GSHO 1855); *ant21.1513* in Bowman\*7 (BW021, NGB 20429).

References:

1. Falk, D.E. 1994. Coordinator's report: Chromosome 6. Barley Genet. Newsl. 23:154.
2. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. Barley Genet. Newsl. 8:55-57.
3. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. Barley Genet. Newsl. 14:76-79.
4. Jende-Strid, B. 1988. Coordinator's report: Anthocyanin genes. Stock list of ant mutants kept at the Carlsberg Laboratory. Barley Genet. Newsl. 18:74-79.
5. Jende-Strid, B. 1991. Gene-enzyme relations in the pathway of flavonoid biosynthesis in barley. Theor. Appl. Genet. 81:658-674.
6. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. Hereditas 119:187-204.

Prepared:

B. Jende-Strid. 1999. Barley Genet. Newsl. 29:94.

BGS 604, Proanthocyanidin-free 22, *ant22*

Stock number: BGS 604  
Locus name: Proanthocyanidin-free 22  
Locus symbol: *ant22*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 2HL (2); closely linked to the *Zeo2* (Zeocriton 2) locus (2); *ant22.1508* is associated with SNP markers 1\_1340 to 2\_0895 (positions 166.06 to 209.87 cM) in 2H of the Bowman backcross-derived line BW022 (1); likely in 2HL bin 13 based on the lack of recombination with the dense spike trait (*Zeo2*) (3). Previously located in 7H when the dense spike trait was believed to be controlled by the *dsp1* (dense spike 1) gene (1, 3).

Description:

No anthocyanin pigmentation is observed in the vegetative parts of the mutant plants. The testa layers of the grains of the *ant22* mutants lack proanthocyanidins and catechins but accumulate homoeriodictyol and chrysoeriol (7, 8). It is likely that the *ant22* gene codes for one subunit and the *ant17* gene for the other subunit of the dimeric flavanone 3-hydroxylase enzyme, which catalyzes the conversion of flavanones into dihydroflavonols (7, 9). Plants of the Bowman backcross-derived line BW022 were slightly shorter than Bowman and shorter rachis internodes, 3.4 vs. 4.6 mm. The kernels of BW022 plants were 5 to 10% lighter and slightly shorter and thinner. The reduced in grain size appear to be an effect of the *ant 22.1508* allele in BW022 while reductions in culm length and rachis internode length appeared associated with the *Zeo2* allele (3). A close linkage of the *ant22.1508* allele to the short rachis internode trait was observed in BW022 (3). But instead of *dsp1* (dense spike 1) in 7H, the critical dense spike trait was shown to be in 2HL where the *Zeo2* gene is located (2).

Origin of mutant:

A sodium azide induced mutant in Hege 802 (4).

Mutational events:

*ant22.212* in Hege 802 (4); *ant22.603* (CN 37389) in Harrington (6); *ant22.1500*, *22.1501*, *22.1504* in Amagi-Nijo (4); *ant22.1508* (NGB 13705, GSHO 1635) in Haruna-Nijo (5).

Mutant used for description and seed stock:

*ant22.1508* (NGB 13705, GSHO 1635) in Haruna-Nijo; *ant22.1508* in Bowman (PI 483237)\*3 (GSHO 1841); *ant22.1508* in Bowman\*6 (BW022, NGB 20430).

References:

1. Boyd, P.W., and D. E. Falk. 1990. (Personal communications).
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. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
5. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:76-79.
6. Jende-Strid, B. 1991. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 20:87-88.

7. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.

8. Jende-Strid, B., and K. N. Kristiansen. 1987. Genetics of flavonoid biosynthesis in barley. p. 445-453. In: S. Yasuda and T. Konishi (eds.) *Barley Genetics V. Proc. Fifth Int. Barley Genet. Symp.*, Okayama 1986. Sanyo Press Co., Okayama.

9. Meldgaard, M. 1992. Expression of chalcone synthase, dihydroflavonol reductase, and flavanone 3-hydroxylase in mutants in barley deficient in anthocyanin and proanthocyanidin biosynthesis. *Theor. Appl. Genet.* 83:695-706.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:95.

Revised:

J.D. Franckowiak 2011. *Barley Genet. Newsl.* 41:191-192.

BGS 605, Proanthocyanidin-free 25, *ant25*

Stock number: BGS 605  
Locus name: Proanthocyanidin-free 25  
Locus symbol: *ant25*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

Mutant plants do not synthesize anthocyanin in the vegetative parts, but the expression of anthocyanin pigmentation seems to be more dependent on the growing conditions than in the wild type barley. Developing grains of the mutants synthesize variable but always small amounts of catechin and proanthocyanidins, whereas ripe grains lack these compounds when tested by the vullin test (4). The *ant25* gene might be involved in the regulation of anthocyanin and proanthocyanidin biosynthesis (5).

Origin of mutant:

A sodium azide induced mutant in Secobra 18193 (NGB 13684) (1).

Mutational events:

*ant25.264* (NGB 13706), *25.265* in Secobra 18193 (NGB 13684) (2); *ant25.273* (NGB 24307), *25.274* (NGB 24308) in VP 116 (NGB 13691) (2); *ant25.283* (NGB 24309) in Hege 550/75 (NGB 13692) (3); *ant25.368* (NGB 24310) in Gimpel (PI 564720) (2); *ant25.371* (NGB 24311) in Ca 184612 (2); *ant25.420* (NGB 24312) in Kaya (3); *ant25.461* (NGB 24313) in Pamela (3); *ant25.477* (NGB24214) in Zenit (PI 464447, NGB 13686) (3).

Mutant used for description and seed stock:

*ant25.264* (NGB 13706) in Secobra 18193; *ant25.371* (GSHO 1638) in Ca 184612.

References:

1. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
2. Jende-Strid, B. 1988. Coordinator's report: Anthocyanin genes. Stock list of *ant* mutants kept at the Carlsberg Laboratory. *Barley Genet. Newsl.* 18:74-79.
3. Jende-Strid, B. 1991. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 20:87-88.
4. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.
5. Tanner, G.J., K.N. Kristiansen, and B. Jende-Strid. 1992. Biosynthesis of proanthocyanidins (condensed tannins) in barley. *Bulletin de Liaison - Groupe Polyphenols* 16:170-173.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:96.

BGS 606, Proanthocyanidin-free 26, *ant26*

Stock number: BGS 606  
Locus name: Proanthocyanidin-free 26  
Locus symbol: *ant26*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (2, 4, 5).

Location is unknown.

Description:

Mutant plants develop a wild type amount of anthocyanin pigments in the vegetative parts. Developing grains synthesize catechin and trace amounts of proanthocyanidins, whereas mature grains are classified as proanthocyanidin-free (3). The *ant26* gene might control the putative flavanol-condensing enzyme, which catalyzes the condensation of leucoanthocyanidins and catechins to dimeric proanthocyanidins (3, 6).

Origin of mutant:

A sodium azide induced mutant in Grit (PI 548764, NGB 13685) (1).

Mutational events:

*ant26.483* (NGB 13707, NGB 23023, GSHO 1639), *26.485* (NGB 13708, NGB 23024), *26.486* (NGB 23025), *26.487* (NGB 23026) in Grit (PI 548764, NGB 13685) (2); *ant26.2002* (NGB 23027), *26.2004* (NGB 23028), in Grit (4); *ant26.2008* (NGB 23029), *26.2009* (NGB 23030) in Grit (5).

Mutant used for description and seed stock:

*ant26.483* (NGB 13707, GSHO 1639) in Grit; *ant26.485* (NGB 13708) in Grit.

References:

1. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
2. Jende-Strid, B. 1991. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 20:87-88.
3. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204
4. Jende-Strid, B. 1993. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 22:136-137.
5. Jende-Strid, B. 1995. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 24:162-165.
6. Tanner, G.J., K.N. Kristiansen, and B. Jende-Strid. 1992. Biosynthesis of proanthocyanidins (condensed tannins) in barley. *Bulletin de Liaison - Groupe Polyphenols* 16:170-173.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:97.

BGS 607, Proanthocyanidin-free 27, *ant27*

Stock number: BGS 607  
Locus name: Proanthocyanidin-free 27  
Locus symbol: *ant27*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (2, 4).

Location is unknown.

Description:

Mutant plants produce a wild type amount of anthocyanins in their vegetative parts. The testa layers of the mature grains lack catechins and proanthocyanidins (2). The action of the *ant27* gene is unknown, but it might be involved in the condensation reaction of leucoanthocyanidin and catechin to yield proanthocyanidins or in the regulation of the proanthocyanidin specific branch of the flavonoid pathway (3, 5).

Origin of mutant:

A sodium azide induced mutant in Zenit (PI 564447, NGB 13686) (1).

Mutational events:

*ant27.488* (NGB 13709, GSHO 1640), *27.489*, *27.490* in Zenit (PI 564447, NGB 13686) (2); *ant27.2043* (NGB 13710), *27.2045* in Arena (NGB 13687) (4).

Mutant used for description and seed stock:

*ant27.488* (NGB 13709, GSHO 1640) in Zenit; *ant27.2043* (NGB 13710) in Arena.

References:

1. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
2. Jende-Strid, B. 1991. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 20:87-88.
3. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.
4. Jende-Strid, B. 1993. Coordinator's report: Anthocyanin genes. *BGN* 22:136-137.
5. Tanner, G.J., K.N. Kristiansen, and B. Jende-Strid. 1992. Biosynthesis of proanthocyanidins (condensed tannins) in barley. *Bulletin de Liaison - Groupe Polyphenols* 16:170-173.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:98.

BGS 608, Proanthocyanidin-free 28, *ant28*

Stock number: BGS 608  
Locus name: Proanthocyanidin-free 28  
Locus symbol: *ant28*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL, close to the *Est4* (esterase 4) locus (1).

Description:

Mutant plants synthesize a wild type amount of anthocyanins in their vegetative parts. The testa layers of the mutant grains lack catechins and proanthocyanidins. The *ant28* gene affects the proanthocyanidin specific branch of the flavonoid pathway, but the exact nature of the gene action is not known (3).

Origin of mutant:

A sodium azide induced mutant in Grit (PI 548764, NGB 13685) (2).

Mutational events:

*ant28.484* (NGB 13711) in Grit (PI 548764, NGB 13685 (4); *ant28.493* (NGB 21978), *28.494*, *28.495* (NGB 21979) in Catrin (4); *ant28.2092* (NGB 21980), *28.2093* (NGB 21981), *28.2095* (NGB 22827) in Nairn (4); *ant28.2131* (NGB 12712), *28.2132* (NGB 21982) in Alexis (PI 564487, NGB 13688) (4).

Mutant used for description and seed stock:

*ant28.484* (NGB 13711) in Grit; *ant28.2131* (NGB 13712) in Alexis.

References:

1. Garvin, D.F., J.E. Miller-Garvin, E.A. Viccars, J.V. Jacobsen, and A.H.D. Brown. 1998. Identification of molecular markers linked to *ant28-484*, a mutation that eliminates proanthocyanidin production in barley seeds. *Crop. Sci.* 38:1250-1255.
2. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
3. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.
4. Jende-Strid, B. 1993. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 22:136-137.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:99.

BGS 609, Proanthocyanidin-free 29, *ant29*

Stock number: BGS 609  
Locus name: Proanthocyanidin-free 29  
Locus symbol: *ant29*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Mutant plants synthesize a wild type amount of anthocyanins in the vegetative parts. Under stress conditions the mutant grains can produce a varying but always small amount of proanthocyanidins. Compared to the wild type the proanthocyanidin content is clearly decreased (2).

Origin of mutant:

A sodium azide induced mutant in the breeding line Ca 708912 (Triumph x Tyra) (1).

Mutational events:

*ant29.2110* (NGB 13713) in Ca 708912 (2); *ant29.2014*, *29.2016* in Natasha (PI 592171) (2).

Mutant used for description and seed stock:

*ant29.2110* (NGB 13713) in Ca 708912.

References:

1. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
2. Jende-Strid, B. 1995. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 24:162-165.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:100.

BGS 610, Proanthocyanidin-free 30, *ant30*

Stock number: BGS 610  
Locus name: Proanthocyanidin-free 30  
Locus symbol: *ant30*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

No anthocyanin pigmentation is observed in any vegetative plant parts. The leaves of the mutant plants show drastically reduced amounts of flavonoids, an increased UV-B sensitivity, and the chalcone-glucoside isosalipurposide is accumulated. The mutant plants are extremely sensitive to powdery mildew. The *ant30* gene most likely codes for the chalcone isomerase enzyme, which catalyzes the conversion of chalcones into flavanones (3).

Origin of mutant:

A sodium azide induced mutant in Gunhild (PI 464655, NGB 13690) (1).

Mutational events:

*ant30.245* (NGB 13674) in Gunhild (PI 464655, NGB 13690) (2, 3); *ant30.272* (NGB 13675) in VP 116 (NGB 13691) (2, 3); *ant30.287* (NGB 13676) in Hege 550/75 (NGB 13692) (2, 3); *ant30.310* (NGB 13677) in Ca 33787 (NGB 13693) (2, 3).

Mutant used for description and seed stock:

*ant 30.245* (NGB 13674) in Gunhild; *ant30.287* (NGB 13676) in Hege 550/75.

References:

1. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl* 8:55-57.
2. Jende-Strid, B. 1997. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl* 28:103.
3. Reuber, S., B. Jende-Strid, V. Wray, and G. Weissenböck. 1997. Accumulation of the chalcone isosalipurposide in primary leaves of barley indicates a defective chalcone isomerase. *Phys. Plant.* 101:827-832.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl* 29:101.

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* (2).

Inheritance:

Monofactorial dominant (2).

Location is unknown.

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% (2). Plant height and kernel plumpness are slightly reduced in the Bowman backcross-derived line (1).

Origin of mutant:

A spontaneous mutant in Awnless Atlas (CIho 10965) (2).

Mutational events:

*Nec6.h* (GSHO 977) in Awnless Atlas (CIho 10965) (2).

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

BGS 612, Gigas 2, *gig2*

Stock number: BGS 612  
Locus name: Gigas 2  
Locus symbol: *gig2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1, 2).

Location is unknown.

Description:

Plants with the *gig2* gene are tall and robust. Most plant parts are larger than those of normal sibs and spikes have 4 to 8 more fertile spikelets. In the greenhouse, heading is delayed by two to three weeks and plants are nearly twice as tall as normal sibs. Under field conditions, plants are tall and late and lodge easily. If planted late in North Dakota, *gig2* plants may remain vegetative until the end of the growing season (1).

Origin of mutant:

A spontaneous mutant in the breeding line ND12463 (ND7556/4/ND5835//ND4064/ND2199/3/Bowman/5/ND8879) (1).

Mutational events:

*gig2.b* (ND12463-1, DWS1372, GSHO 1750) in ND12463 (2).

Mutant used for description and seed stocks:

*gig2.b* (GSHO 1750) in ND12463; *gig2.b* in Bowman (PI 483237)\*6 (GSHO 2266);

*gig2.b* in Bowman\*8 (BW382, NGB 20621).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:113.

BGS 613, Branched 1, *brc1*

Stock number: BGS 613  
Locus name: Branched 1  
Locus symbol: *brc1*

Previous nomenclature and gene symbolization:

Branched-5 = *brc-5* (1, 2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HS (2), about 2.5 cM from AFLP marker E3636-2 and proximal from molecular marker CDO665A (2), in bin 2H bin 05.

Description:

A second-order ramification of the barley spike occurs. The basal part of the spike elongate to form rachis-like branches, and thus generating a ramified spike phenotype (1, 2).

Origin of mutant:

Natural occurrence in line BGRC 13145 from the Braunschweig seed collection (*Hordeum vulgare* L. convar. *distichon* (L.) Alef. var. *inerme* Körn.) (3).

Mutational events:

*brc1.5* (G22, SG-H3/5/8-88 from Köln) in BGRC 13145 of Braunschweig seed collection (2, 3).

Mutant used for description and seed stocks:

*brc1.5* in G22 (3); *brc1.5* in Bowman (PI 483237)\*2 (BW071, NGB 20408).

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. Castiglioni, P., C. Pozzi, M. Heun, V. Terzi, K.J. Müller, W. Rohde, and F. Salamini. 1998. An AFLP-based procedure for the efficient mapping of mutations and DNA probes in barley. *Genetics* 149:2039-2056.
3. Salamini, F. (Personal communications).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. *Barley Genet. Newsl.* 32:114.

BGS 614, Zeocriton 2, *Zeo2*

Stock number: BGS 614  
Locus name: Zeocriton 2  
Locus symbol: *Zeo2*

Previous nomenclature and gene symbolization:

Zeocriton with no gene symbol (3, 6).  
Zeocriton 2 = *Zeo2* (5).  
Semidwarf mutant = Mo1 (11).  
Rachis internode length QTL on 2HL = *qSIL.ak-2H* (7).

Inheritance:

Monofactorial dominant (1, 7).  
Located in chromosome 2HL (1, 7, 12); in 2H bin 13 (1); near SRS marker ABG613 (7); near the cleistogamy 1 (*cly1*) locus (7, 9); *Zeo2.c* is associated with SNP markers 1\_0404 to 1\_0072 (positions 186.61 to 239.78 cM) in 2HL bins 12 to 14 of the Bowman backcross-derived line BW939; the dense spike traits in the *dsp1.a* stock (likely *Zeo2.c*) is associated with SNP markers 1\_0376 to 2\_0561 (positions 209.87 to 247.86 cM) in 2HL bins 13 to 14 of the Bowman backcross-derived line BW277; *Zeo2.av* (formerly named *dsp.av*), a *Zeo2* allele with *Pyr1.i* gene, and *Zeo2.d* are associated with SNP markers 2\_1315 to 1\_0315 (positions 193.08 to 224.35 cM) in 2HL bins 12 to 14 of three Bowman backcross-derived lines from Finish cultivars (BW269, BW661, and BW933), respectively; *Zeo2.h* (previously named *Zeo3.h*) is associated with SNP markers 2\_1125 to 2\_0293 (positions 206.17 to 234.63 cM) in 2HL bins 13 to 14 of the Bowman backcross-derived line BW940; *Zeo2.j* is associated with SNP markers 2\_1370 to 1\_1023 (positions 199.54 to 224.35 cM) in 2HL bins 12 to 14 of the Bowman backcross-derived line BW936; a *Zeo2* mutant (with the *eog1.e* gene) is associated with SNP markers 1\_1480 to 2\_0895 (positions 173.50 to 209.91 cM) in 2HL bins 11 to 13 of the Bowman backcross derived line BW302; *Zeo2.ax* (previously named *dsp.ax*) is associated with SNP markers 2\_0064 to 2\_0175 (positions 179.99 to 213.08 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW270; *Zeo2.ax* in the *ant22.1508* stock is associated with SNP markers 1\_1346 to 2\_0895 (positions about 165 to 209.87 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW022 (2), in 2H bin 13. The *Zeo2* locus is very close to the *Zeo1* locus (2).

Description:

The spikes are compact and remain strap-shaped because all rachis internodes are about the same length. Plants are slightly shorter and spikes contain 2 to 4 more fertile spikelets than those of normal sibs (1). Hayes and Harlan (6) named this phenotype zeocriton (little barley), but they reported that three genes controlled this trait in their cross to zeocriton (8). Plants of the Bowman backcross-derived lines with *Zeo2* alleles in the *Zeo2.c* and *Zeo2.ax* group have small anthers (2/3 of normal length) (4) and are associated with small lodicules (closed flowering or cleistogamy) (7, 9). The rachis internode length of plants in Bowman backcross lines for *Zeo2* alleles averaged 3.3 mm compared to 4.5 mm for Bowman. In some test environments, the BW lines for *Zeo2* genes had 1 to 2 more kernels per spike than Bowman and kernel weights were slightly lower. No effects of the *Zeo2* gene on plant height and grain yield were observed (4).

Origin of mutant:

A naturally occurring variant in two- and six-rowed barley cultivars (5, 7, 10).

Mutational events:

Based on SNP haplotypes similarity for the retained markers in 2HL, the potential *Zeo2* alleles can be placed in three groups (2, 4). *Zeo2.c* was isolated from line 36Ab51

(GSHO 637), which was called “good zeocriton” (4, 10), can be grouped with *Zeo2.ax* from Clho 6880 and Haruna Nijo; *Zeo2.d* and *Zeo2.av* from Aapo and other Finnish cultivars; *Zeo2.h* and *Zeo2.j* from North American six-rowed cultivars Morex (Clho 15773) and Glenn (Clho 15769), respectively (2, 4); a *Zeo2* allele from Golden Melon (OUJ808, PI 263410) in Kanto Nakato Gold (OUJ 518) (7).

Mutant used for description and seed stocks:

*Zeo2.c* in 36Ab51 (GSHO 637); *Zeo2.c* in Bowman (PI 483237)\*4 (GSHO 3433); *Zeo2.c* in Bowman\*4 (BW939, NGB 22368); *Zeo2.d* from P11 (Clho 15836) in Bowman\*7 (BW933, NGB 22362); *Zeo2.d* from Aapo (PI 467771) via Pokko (PI 467770) in Bowman\*4 (BW269, NGB 22094); *Zeo2.d* with *Pyr1.a* from Aapo (PI 467771) via Pokko (PI 467770) in Bowman\*7 (BW661, NGB 22226); *Zeo2.h* from Morex (Clho 15773) mutant (Mo1, Wa11094-81, GSHO 1611) in Bowman\*8 (BW940, NGB 22369); *Zeo2.j* from Glenn (Clho 15769) mutant SA121-4-5 in Bowman\*7 (BW936, NGB 22365); *Zeo2.ax* from Clho 6880 (Ahang/Twisted Flag//Triple-awn Lemma) in Bowman\*5 (BW270, NGB 22095); *Zeo2.ax* with *ant22.1508* from Haruna Nijo (NGB 13705, GSHO 1635) in Bowman\*6 (BW022, NGB 20430).

References:

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4. Franckowiak, J.D. (Unpublished).
5. Franckowiak, J.D. 1999. Coordinator's report: Semidwarf genes. *Barley Genet. Newsl.* 29:74-79.
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. Agr., Bull. 869. 26 pp.
7. 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. Science* 56:243-252.
8. Smith, L. 1951. Cytology and genetics of barley. *Bot. Rev.* 17:1-51, 133-202, 285-355.
9. Turuspekov, Y., Y. Mano, I. Honda, N. Kawada, Y. Watanabe, and T. Komatsuda, 2004. Identification and mapping of cleistogamy gene in barley. *Theor. Appl. Genet.* 109:480-487.
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12. Yu, G.T., R.D. Horsley, B. Zhang, and J.D. Franckowiak. 2010. A new semi-dwarfing gene identified by molecular mapping of quantitative trait loci in barley. *Theor. Appl. Genet.* 120:853-861.

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:115.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:193-194.

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); based on molecular markers retained in the Bowman backcross-derived line BW917, *wxs1.a* is between SNP markers 1\_0924 to 2\_02472 (positions 107.42 to 159.73 cM) in 7H bins 07 to 09 or between 1\_1118 and 2\_1008 (positions 180.85 to 204.58 cM) in 2H bins 11 to 13 (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 grain has an irregular surface caused by poor adherence of the lemma to the caryopsis. 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 sodium azide induced mutant in Steptoe (Clho 15229) (3).

Mutational events:

*wxs1.a* (FN16) in Steptoe (Clho 15229) (3).

Mutant used for description and seed stocks:

*wxs1.a* (FN16) 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. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
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.

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 (3).

Location is unknown.

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 (3). Grain set is very low in the Bowman backcross-derived line, which causes a problem with maintenance of the line (1).

Origin of mutant:

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

Mutational events:

*cul3.c* (Mut. 3170, DWS 1343, GSHO 2494) in Donaria (PI 161974) (2, 3).

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. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
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Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. *Barley Genet. Newsl.* 32:117.

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* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3HL (5); near AFLP marker E4143-4 in subgroup 32 of the Proctor/Nudinka map (5).

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 (2, 4). 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. The mutant *cul4.15* exhibits the most variation in height over environments (2). Under greenhouse conditions, Bowman line for *cul4.5* developed only two axillary tillers, and it was unicum when combined with the *cul2.b* (uniculm 2) gene (1).

Origin of mutant:

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

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 (4).

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 (BW211, NGB 22038); *cul4.5* in Bowman (PI 483237)\*7 (GSHO 2361, BW212, NGB 22039)

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unicum2 (*cul2*) mutant. *Theor. Appl. Genet.* 106:846–857.
2. Franckowiak, J.D. (Unpublished).
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4. Lundqvist, U. (Unpublished).
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.

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.

BGS 618, Many noded dwarf 3, *mnd3*

Stock number: BGS 618  
Locus name: Many noded dwarf 3  
Locus symbol: *mnd3*

Previous nomenclature and gene symbolization:

Many noded dwarf 3 = *mn3* (5).  
Many noded dwarf = *m3* (4).  
Many noded dwarf 3 = *mnd3* (2).

Inheritance:

Monofactorial recessive (5, 6).  
Located in chromosome 3H (5); over 36.7 cM from the *uzu1* (*uzu 1*) locus (5).

Description:

In plants homozygous for the *mnd3.d* gene, all plant parts are somewhat reduced in size. The number of elongated culm internodes is increased by 1 or 2 compared to normal sibs. Plants are 2/3 to 3/4 normal height. In the Bowman backcross-derived line, spikes are about 1/3 normal length and often show partial fertility. However, the *mnd3.d* gene does not reduce fertility and spike appears normal in R.I. Wolfe's Multiple Marker Stock for chromosome 2H (1).

Origin of mutant:

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

Mutational events:

*mnd3.d* from Montcalm (CIho 7149), but isolated from R.I. Wolfe's Multiple Marker Stock for chromosome 2H (DWS1346) (1, 2).

Mutant used for description and seed stocks:

*mnd3.d* from R.I. Wolfe's 2.1 Multiple Marker Stock crossed to Bowman (GSHO 1797);  
*mnd3.d* in Bowman (PI 483237)\*7 (GSHO 1949, BW519, NGB 20747).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1999. Coordinator's report: Semidwarf genes. Barley Genet. Newsl. 29:74-79.
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
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Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl.32:119.

BGS 619, Bracteatum-a, *bra-a*

Stock number: BGS 619  
Locus name: Bracteatum-a  
Locus symbol: *bra-a*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HS (2); based on linkage drag with the *ant1* (anthocyanin-less 1) locus (2).

Description:

Leaf-like structures or bracts develop from the rachis slightly below the rachis node at which the spikelets are attached (1). The bract associated with the lowest spikelet is always the largest and the bracts become progressively smaller toward the tip of the spike (4). Spikes are about 3/4 normal length and plants are 3/4 normal height in the Bowman backcross-derived line. Peduncles are about 1/3 normal length and the grain is relatively thin. Development of the bracts is poor in the Bowman backcross-derived line (2).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (3, 4).

Mutational events:

*bra-a.001* (NGB 114318), *bra-a.003* (NGB 114320) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

*bra-a.001* (GSHO 1693, NGB 114318) in Bonus; *bra-a.001* in Bowman (PI 483237)\*6 (GSHO 2183); *bra-a.001* in Bowman\*7 (BW067, NGB 20475)

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
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4. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:120.

BGS 620, Calcaroides-b, *cal-b*

Stock number: BGS 620  
Locus name: Calcaroides-b  
Locus symbol: *cal-b*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HL (5); about 4.2 cM proximal from AFLP marker E4040-4 and probably near molecular marker CDO749 in 5H bin 04 (5).

Description:

At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, *cal-b* mutants have a knee-like ectopic structure (1, 5). In mutant *cal-b.2* frequently only an enlargement of the basal third of the awn is evident and the enlargement is expressed more in terminal and subterminal spikelets. Leaf knots and leaf curling occurs also (4). In the Bowman backcross-derived line, plants are slightly shorter and spikes have a more lax arrangement of spikelets (2).

Origin of mutant:

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

Mutational events:

*cal-b.2* (NGB 114282, GSHO 1697), *cal-b.19* (NGB 114298) in Bonus (PI 189763) (4).

Mutant used for description and seed stocks:

*cal-b.2* (GSHO 1697, NGB 114282) in Bonus; *cal-b.2* in Bowman (PI 483237)\*4 (GSHO 2187, BW104, NGB 20510).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
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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. 1993 Coordinator's report: Ear morphology genes. *Barley Genet. Newsl.* 22:137-139.
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Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:121.

BGS 621, *Calcaroides-c*, *Cal-c*

Stock number: BGS 621  
Locus name: *Calcaroides-c*  
Locus symbol: *Cal-c*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (5, 6).

Located in chromosome 5HL (7); very close or allelic to *cal-b* (*calcaroides-b*) locus and near molecular marker WG530 in 5H bin 06 (7); *Cal-c.15* is associated with SNP markers 1\_1198 to 1\_0869 (positions 73.70 to 264.33 cM) in 5H bins 04 to 13 of the Bowman backcrossed-derived line BW105 (2), in 5H bin 06.

Description:

At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, the *Cal-c* mutant bear a well-organized ectopic structure, the sac plus pronounced lemma wings (1, 7). The distal awn is short and develops small wings (7). In contrast to the *Kap1* (hooded lemma 1) phenotype, the sac does not develop into an epiphyllous flower. Leaf knots were observed, but leaf curling was not (7). The awn malformation of *Cal-c* mutants is caused by developmental activation of the phytomeric triad separating the lemma from awn (4). Expression of the *Cal-c* phenotype is stronger in homozygotes and more pronounced in spikelets near the tip of the spike (3). In the Bowman backcrossed-derived line BW105, plants were slightly shorter than Bowman and the awns as measured from the tip of the spike were short, 5 vs. 12 cm. Leaf blade widths were about 2/3 of normal length and the spikes had 3 to 4 fewer kernels. Kernels of BW105 were thinner than those of Bowman and weighed about 20% less. Grain yields approached 1/2 of normal (3).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (5, 6).

Mutational events:

*Cal-c.15* (NGB 114294, GSHO 1567) in Bonus (PI 189763) (6).

Mutant used for description and seed stocks:

*Cal-c.15* (GSHO 1567, NGB 114294) in Bonus; *Cal-c.15* in Bowman (PI 483237)\*4 (GSHO 2188); *Cal-c.15* in Bowman\*6 (BW105, NGB 20511).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992 Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
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7. Pozzi, C., P. Faccioli, V. Terzi, A.M. Stanca, S. Cerioli, P. Castiglioni, R. Fink, R. Capone, K.J. Müller, G. Bossinger, W. Rohde, and F. Salamini. 2000. Genetics of mutations affecting the development of a barley floral bract. *Genetics* 154:1335-1346.

Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:122.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:195-196.

BGS 622, *Calcaroides-e*, *cal-e*

Stock number: BGS 622  
Locus name: Calcaroides-e  
Locus symbol: *cal-e*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HS (3); about 23 cM distal from AFLP marker E3432-2, which is proximal from molecular marker WG889 in 5H bin 06 (3).

Description:

At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, the *cal-e* mutant has a distinctive ectopic structure, which includes a sac, sac appendages, and awn wings (3). The *cal-e* mutant bears a short distal awn. In contrast to the *Kap1* (hooded lemma 1) phenotype, the sac does not develop into an epiphyllous flower (3).

Origin of mutant:

A sodium azide induced mutant in Semira (NGB 10716) (1, 2).

Mutational events:

*cal-e.23* (NGB 119382) in Semira (NGB 10716) (2).

Mutant used for description and seed stocks:

*cal-e.23* (NGB 119382) in Semira.

References:

1. 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.
2. Lundqvist, U. 1993 Coordinator's report: Ear morphology genes. *Barley Genet. Newsl.* 22:137-139.
3. Pozzi, C., P. Faccioli, V. Terzi, A.M. Stanca, S. Cerioli, P. Castiglioni, R. Fink, R. Capone, K.J. Müller, G. Bossinger, W. Rohde, and F. Salamini. 2000. Genetics of mutations affecting the development of a barley floral bract. *Genetics* 154:1335-1346.

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:123.

BGS623, Eligulum-a, *eli-a*

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

Previous nomenclature and gene symbolization:

Eligulum-a = *lig-a* (2).  
Eligulum-3 = *eli-3* (4).

Inheritance:

Monofactorial recessive (2).  
Location is unknown.

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 (3, 4). 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 (1, 3). 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 (1).

Origin of mutant:

An ethylene imine induced mutant in Foma (Clho 11333) (2, 3).

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 (Clho 11333) (3); *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) (4), *-a.216* (FN216) in Steptoe (Clho 15229) (1, 3).

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.216* from Steptoe in Bowman\*3 (BW293, NGB20577).

References:

1. Franckowiak, J.D. (Unpublished).
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
3. Kleinhofs, A. (Unpublished).
4. 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.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:290.

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* (2, 3).

Inheritance:

Monofactorial recessive (3).

Location is unknown.

Description:

Plants with the *ops1* gene have a reduced number of tillers and very few late tillers. Variable lengths of the rachis internodes causes an irregular arrangement of spikelets in the spike. Compared to normal sibs, *ops1* plants are slightly shorter and lower yielding (1, 3).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763) (3).

Mutational events:

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

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. Franckowiak, J.D. 2000. (Unpublished).
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
3. Lundqvist, U. 2000. (Unpublished).

Prepared:

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

BGS 625, Scirpoides-a, *sci-a*

Stock number: BGS 625  
Locus name: Scirpoides-a  
Locus symbol: *sci-a*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (1).  
Location is unknown.

Description:

Plants expressing the *sci-a* gene have very narrow leaves and inward folded leaf blades. The tip of emerging leaf blade is sometimes trapped inside the previous one. Folding of the leaf blade persists until maturity. Premature yellowing of leaf blade tips may occur shortly after heading. Spikes are 1/2 to 2/3 normal length and plant height is reduced slightly (1, 3).

Origin of mutant:

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

Mutational events:

*sci-a.3* (NGB 117097) in Bonus (PI 189763) (3); *sci-a.1* (NGB 117095) in Gull (CIho 1145, GSHO 466) (3).

Mutant used for description and seed stocks:

*sci-a.3* (NGB 117097) in Bonus; *sci-a.1* (NGB 117095) in Gull; *sci-a.3* in Bowman (PI 483237)\*4 (GSHO 3430; BW773, NGB 22241); *sci-a.1* in Bowman\*4 (BW772, NGB 22240).

References:

1. Franckowiak, J.D. (Unpublished).
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
3. Lundqvist, U. (Unpublished).

Prepared:

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

BGS 626, Scirpoides leaf-a, *scl-a*

Stock number: BGS 626  
Locus name: Scirpoides leaf-a  
Locus symbol: *scl-a*

Previous nomenclature and gene symbolization:

Scirpoides leaf-6 = *scl.6* (3).  
Scirpoides leaf-1 = *scl.1* (3).  
Scirpoides leaf-2 = *scl.2* (3).  
Scirpoides leaf-4 = *scl.4* (3).

Inheritance:

Monofactorial recessive (2).  
Located in chromosome 1HL (1); *scl-a.6* is associated with SNP markers 1\_0433 to 1\_0396 (positions 139.25 to 143.47 cM) in 1HL bin 11 of Bowman backcross-derived line BW778 (1); *scl-a.2* is associated with SNP marker 2\_0780 (position 154.89 cM) in 1H bin 12 of the Bowman backcross-derived line BW775 (1); *scl-a.4* is associated with SNP markers 1\_0006 and 2\_1126 (position 110.10 cM) in 1HL bin 10 of the Bowman backcross-derived line BW776 (1), likely in 1H bin 11.

Description:

Leaf blades of *scl-a* plants are folded inward and are narrow compared to those of normal sibs. Folding of the leaf blade persists until maturity (2, 3). Plants of Bowman backcross-derived line BW778 were slightly shorter than Bowman, kernels were slightly thinner and lighter, and grain yields were about 20% lower. Plants of BW778 have inward folded leaf blades that are about 2/3 as wide as those of Bowman (2). The mutant stocks *scl.1*, *scl.2*, and *scl.4* are alleles based on allelism tests (2). Their phenotypic similarities to the *scl-a.6* mutant and SNP markers retained in the same region of 1HL suggesting they are alleles at the *scl-a* locus (1, 2).

Origin of mutant:

A neutron induced mutant in Foma (Clho 11333) (3).

Mutational events:

*scl-a.6* (NGB 117105) in Foma (Clho 11333) (3); *scl-a.1* (NGB 117100), *scl-a.2* (NGB 117101), *scl-a.4* (NGB 117102) in Bonus (PI 189763) (1, 2, 3).

Mutant used for description and seed stocks:

*scl-a.6* (NGB 117105) in Foma; *scl-a.6* in Bowman (PI 483237)\*5 (GSHO 3431); *scl-a.6* in Bowman\*6 (BW778, NGB 20755); *scl-a.1* (NGB 117100) in Bonus; *scl-a.1* in Bowman\*4 (BW774, NGB 22242); *scl-a.2* (NGB 117101) in Bonus; *scl-a.2* in Bowman\*5 (BW775, NGB 22243); *scl-a.4* (NGB 117102) in Bonus; *scl-a.4* in Bowman\*5 (BW776, NGB 20753).

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 Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:127.  
U. Lundqvist and J. D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:142.

BGS 627, *Viviparoides-a*, *viv-a*

Stock number: BGS 627  
Locus name: *Viviparoides-a*  
Locus symbol: *viv-a*

Previous nomenclature and gene symbolization:

*Viviparoides-5* = *viv-5* (3, 4).

Inheritance:

Monofactorial recessive (2, 4).

Location is unknown.

Description:

Tillers of *viv-a* plants may remain vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as the culm elongates. Occasionally a short, malformed spike is formed in a lateral position (1, 4). In the Bowman backcross-derived line, only a few tiller exhibit the typical *viviparoides* phenotype. However, plants are shorter, lodge easily, and produce much less grain. Also, awns are slightly shorter, the grain is thinner, and hull adherence is poorer (2).

Origin of mutant:

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

Mutational events:

*viv-a.5* (NGB 115364, GSHO 2498) in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

*viv-a.5* (GSHO 2498, NGB 115364) in Foma; *viv-a.5* in Bowman (PI 483237)\*3 (GSHO 2364); *viv-a.5* in Bowman\*4 (BW896, NGB 22329).

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. 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.* 32:128.

BGS 628, Shrunken endosperm xenia 7, *sex7*

Stock number: BGS 628  
Locus name: Shrunken endosperm xenia 7  
Locus symbol: *sex7*

Previous nomenclature and gene symbolization:

Shrunken endosperm xenia-i = *sex.i* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (2); based on linkage drag with the *raw2* (smooth awn 2) locus (2).

Description:

Starting at the hard dough stage, the grain develops a depression in the dorsal or lemma side. This depression is very distinct at maturity. In plants heterozygous at the *sex7* locus, a xenia pattern of expression is observed. The expression of *sex7* is much stronger than that of *lys1* (high lysine 1), the only other shrunken endosperm xenia mutant located near the *raw1* (smooth awn 1) locus (1).

Origin of mutant:

A spontaneous mutant in a selection from cross I90-374 (Bowman\*5/Mut. 2612) (1).

Mutational events:

*sex7.i* (GSHO 2470) in I90-374-1 (1).

Mutant used for description and seed stocks:

*sex7.i* (GSHO 2470) in I90-374-1; *sex7.i* in Bowman (PI 483237)\*7 (GSHO 2133, BW847, NGB 22284).

References:

1. Franckowiak, J.D. (Unpublished).
2. 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. 32:129.

BGS 629, Mottled leaf 6, *mtt6*

Stock number: BGS 629  
Locus name: Mottled leaf 6  
Locus symbol: *mtt6*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Seedlings are slightly pale green in color and develop a necrotic region partially across the blade of the first. Occasionally necrotic blotches or region develop in subsequent leaf blades. Plants are taller than normal sibs and remain a slightly pale shade of green until maturity. Plant vigor appears normal, but grain yields are slightly lower than those of normal sibs (1).

Origin of mutant:

A spontaneous mutant in selection ND6809 from a ND2654-31/Karl cross (1).

Mutational events:

*mtt6.g* (GSHO 2411) in ND6809-1 (1).

Mutant used for description and seed stocks:

*mtt6.g* (GSHO 2411) in ND6809; *mtt6.g* in Bowman (PI 483237)\*8 (GSHO 2311, BW604, NGB 22170).

References:

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

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:130.

BGS 630, Breviaristatum-s, *Ari-s*

Stock number: BGS 630  
Locus name: Breviaristatum-s  
Locus symbol: *Ari-s*

Previous nomenclature and gene symbolization:

Breviaristatum-265 = *ari-265* (3).

Inheritance:

Monofactorial incomplete dominant (2).

Located in chromosomes 5H or 7H (1); *Ari-s.265* is associated with SNP markers 2\_1177 (position 203.85 cM) in 5H bin 11 and with SNP marker 1\_1291 (position 107.44 cM) in 7H bin 07 of the Bowman backcross-derived line BW057 (1). Note that the expression of marker 1\_1291 was variable among BW lines.

Description:

Awns of plants homozygous for the *Ari-s.265* allele are about 1/3 normal length and slightly wider than those of normal sibs. The grain is wide and short and has a globose shape. Sterile lateral spikelets and glumes are about half normal length. Rachis internodes are shortened slightly, plants are 3/4 to 5/6 of normal height, and plant vigor is reduced (2). Awns of plants heterozygous for the *Ari-s.265* allele were 3/4 normal length. A slight shortening of other parts of the spike was observed in heterozygotes (2). Compared to Bowman, plants of the Bowman backcross-derived line for *Ari-s.265*, BW057, were 10 to 15% shorter, their awns were about half as long, and rachis internodes were shorter, 3.7 vs. 4.5 mm. Kernel were short, 6.3 vs. 9.7 mm and about 40% lighter, 3.5 vs. 5.8 mg. Grain yields of BW057 were about 1/3 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Kristina (NGB 1500) (3, 4).

Mutational events:

*Ari-s.265* (NGB 116074) in Kristina (NGB 1500) (4).

Mutant used for description and seed stocks:

*Ari-s.265* (NGB 116074) in Kristina; *Ari-s.265* in Bowman (PI 483237)\*6 (GSHO 3426); *Ari-s.265* in Bowman\*7 (BW057, NGB 20405).

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. 2002. *Barley Genet. Newsl.* 32:131.  
J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:197.

BGS 631, Brachytic 3, *brh3*

Stock number: BGS 631  
Locus name: Brachytic 3  
Locus symbol: *brh3*

Previous nomenclature and gene symbolization:

Brachytic-g = *brh.g* (2).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

The seedling leaf of *brh3* plants is shorter than that of normal sibs. Plants are 2/3 to 3/4 of normal height and the number of tillers per plant is reduced. Awns are fine with slightly curly tips and are about 1/2 normal length. Spikes of *brh3* plants have a slightly elongated first rachis internode. Seed set may be reduced when plants are grown under greenhouse conditions. (1).

Origin of mutant:

Probably a sodium azide induced mutant in Birgitta (NSGC 1870) (5).

Mutational events:

*brh3.g* (17:10:1, DWS1002, GSHO 1672) in Birgitta (NSGC 1870) (2, 3, 5); *brh3.y* (10001, DWS1230, GSHO 1688) in Bido (PI 399485) (2, 4).

Mutant used for description and seed stocks:

*brh3.g* (GSHO 1672) in Birgitta; *brh3.g* in Bowman (PI 483237)\*7 (GSHO 2167);  
*brh3.g* in Bowman (PI 483237)\*7 (GSHO 2167, BW091, NGB 20497).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
4. Gaul, H. 1986. (Personal communications).
5. Lehmann, L. 1985. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:134.

BGS 632, Many noded dwarf 5, *mnd5*

Stock number: BGS 632  
Locus name: Many noded dwarf 5  
Locus symbol: *mnd5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

When grown in the field, plants are about 1/2 normal height with numerous tillers. Each tiller has numerous small leaves and a spike of about 1/3 normal size. Plants head late under field conditions. Culm branches with 4 to 7 leaves each may develop at the uppermost culm node, but these branches develop late and have very small spikes.

When grown in the greenhouse, plants are tall and late compared with normal sibs. Each culm may have 15 to 20 elongated internodes (1).

Origin of mutant:

A spontaneous mutant in cross C2-95-199 [Logan (PI 592784)/ND15053] (1).

Mutational events:

*mnd5.g* in C2-95-199-1 (1).

Mutant used for description and seed stocks:

*mnd5.g* in C2-95-199-1; *mnd5.g* in Bowman (PI483237)\*4 (BW521, NGB 20749).

References:

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

Prepared:

J.D. Franckowiak, 2002. Barley Genet. Newsl. 32:133.

BGS 633, Many noded dwarf 6, *mnd6*

Stock number: BGS 633  
Locus name: Many noded dwarf 6  
Locus symbol: *mnd6*

Previous nomenclature and gene symbolization:

Densinodosum-6 = *den-6* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL (5); near AFLP marker E3743-3 in subgroup 65 of the Proctor/Nudinka map (5).

Description:

Plants with the *mnd6.6* gene are about 2/3 normal height and have many elongated internodes in each culm (1, 4). The number of elongated internodes can be up to 20 in the original stock when grown in Sweden. Kernels are thin and small (4). The number of tillers per plant is increased compared to normal sibs. Peduncles are very short, about 1/3 normal length, and awns are about 1/2 normal length. Spikes are shorter with slightly over half the kernel number of Bowman. The Bowman backcross-derived line has 9 to 10 elongated internodes per tiller. Kernels of the Bowman *mnd6* line are thinner and about 2/3 of normal weight (2). The grain yields of the *mnd6* line are about 3/4 normal (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (4).

Mutational events:

*mnd6.6* (NGB 114514, GSHO 1713) in Bonus (PI 189763) (4); *mnd6.8* (NGB 114516) in Bonus (4, 5).

Mutant used for description and seed stocks:

*mnd6.6* (GSHO 1713, NGB 114514) in Bonus; *mnd6.6* in Bowman (PI 483237)\*7 (GSHO 2235, BW522, NGB 20750).

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. 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).
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.

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:134.

Revised:

U. Lundqvist and J. D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:291.

BGS 634, Premature ripe 2, *pmr2*

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

Previous nomenclature and gene symbolization:

Necroticans 50 = *nec-50* (2, 3).

Inheritance:

Monofactorial recessive (3).

Location is unknown.

Description:

Plants appear normal until shortly before heading. Prior to heading, tan to light brown blotches start to develop on the leaf blades. The blotches enlarge rapidly and coalesce and the leaf blades gradually die (1, 3). Peduncle elongation is poor, and plants are shorter than normal sibs. Although leaf sheaths and spikes remain green, plants ripen prematurely. After the plants ripen, the straw collapses easily. The grain is small and thin (1).

Origin of mutant:

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

Mutational events:

*pmr2.b* (*nec-50*) (NGB 115311, GSHO 2421), *pmr2.c* (*nec-54*) (NGB 115316, GSHO 2422) in Bonus (PI 189763) (3).

Mutant used for description and seed stocks:

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

References:

1. Franckowiak, J.D. (Unpublished).
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
3. Lundqvist, U. (Unpublished).

Prepared:

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

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 varies 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.

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 (4).  
Location is unknown.

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 (1, 4). Most spikes of the Bowman backcross-derived line set less than 10 seeds. Plants are shorter than are normal sibs because peduncles fail to elongate normally. Both rachis internode length and awn length are reduced in *tst2* plants (1).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (3, 4).

Mutational events:

*tst2.b* (Mut. 2249, DWS1337, GSHO 1781) in Donaria (PI 161974) (2, 3).

Mutant used for description and seed stocks:

*tst2.b* (GSHO 1781) in Donaria; *tst2.b* in Bowman (PI 483237)\*5 (GSHO 2280); *tst2.b* in Bowman\*6 (BW883, NGB 22317).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
3. 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.
4. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l.l. 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.

BGS 637, NADH nitrate reductase-deficient 1, *nar1*

Stock number: BGS 637  
Locus name: NADH nitrate reductase-deficient 1 (EC1.6.6.1; Acc. No. X57844 and X57845)  
Locus symbol: *nar1*

Previous nomenclature and gene symbolization:  
None.

Inheritance:  
Monofactorial co-dominant based on enzyme assay (4).  
Located in chromosome 6HS (2) in bin 6H-01 (3), about 0.8 cM proximal from molecular marker ABG466 (3).

Description:  
Mutants are characterized by low in vivo nitrate reductase activity and low in vitro NADH nitrate activity. FMNH<sub>2</sub> and cytochrome c reductase activity is variable among the different alleles. All mutants have elevated nitrite reductase activity and accumulate nitrate to variable degrees (1, 8). All *nar1* mutants have normal xanthine dehydrogenase activity. All *nar1* mutants are viable and morphologically normal except some alleles are slightly light green. Yields are slightly depressed (6). The mutant Xno29 (*nar1.j*) does not grow well in field plots probably due to other associated mutations (1).

Origin of mutant:  
A sodium azide induced mutant in Steptoe (CIho 15229) (4).

Mutational events:  
*nar1.a* (Az12, GSHO 2413), *nar1.b* (Az13, GSHO 2414), *nar1.c* (Az23), *nar1.d* (Az28), *nar1.e* (Az29), *nar1.f* (Az30), *nar1.g* (Az31), *nar1.h* (Az32), *nar1.i* (Az33) in Steptoe (CIho 15229) (5); *nar1.j* (Xno29) in Winer (7); *nar1.k* (EMS29), *nar1.l* (EMS31) in Steptoe (5); *nar1.m* (Az56), *nar1.n* (Az57), *nar1.p* (Az63), *nar1.q* (Az64); *nar1.r* (Az65), *nar1.t* (Az67), *nar1.ab* (Az76), *nar1.ac* (Az77), *nar1.ai* (Az79), *nar1.aj* (Az80) in Steptoe (5); *nar1.ao* (BSMV1) in Vantage (CIho 7324) (1).

Mutant used for description and seed stocks:  
*nar1.a* (Az12, GSHO 2413) in Steptoe

References:

1. Kleinhofs, A. (Unpublished).
2. Kleinhofs, A., S. Chao, and P.J. Sharp. 1988. Mapping of nitrate reductase genes in barley and wheat. p. 541-546. *In* T.E. Miller and R.M.D. Koebner (eds.) Seventh Int. Wheat Genetics Symposium.
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 86:705-712.
4. Kleinhofs, A., T. Kuo, and R.L. Warner. 1980. Characterization of nitrate reductase-deficient barley mutants. *Molec. Gen. Genet.* 177:421-425.
5. Kleinhofs, A., R.L. Warner, J.M. Lawrence, J.M. Melzer, J.M. Jeter, and D.A. Kudrna. 1989. Molecular genetics of nitrate reductase in barley. p. 197-211. *In* J.L. Wray and J.R. Kinghorn (eds.) *Molecular and Genetic Aspects of Nitrate Assimilation*, Chapter 13. Proc. 2nd Int. Symp. on Nitrate Assimilation - Molecular and Genetic Aspects, St. Andrews, July, 1987. Oxford Univ. Press, New York.
6. Oh, J.Y., R.L. Warner, and A. Kleinhofs. 1980. Effects of nitrate reductase deficiency upon growth, yield, and protein in barley. *Crop Sci.* 20:487-490.

7. Tokarev, B.I., and V.K. Shumny. 1977. Detection of barley mutants with low level of nitrate reductase activity after seed treatment with ethylmethane sulphonate. *Genetika (Moskva)* 13:2097-2103.

8. Warner, R.L., C.J. Lin, and A. Kleinhofs. 1977. Nitrate reductase-deficient mutants in barley. *Nature* 269:406-407.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:194-195.

BGS 638, NADH nitrate reductase-deficient 2, *nar2*

Stock number: BGS 638  
Locus name: NADH nitrate reductase-deficient 2 (molybdenum cofactor)  
Locus symbol: *nar2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Location in chromosome 5HL (2); near molecular marker ABC324 in 5H bin 06 (2); morphological marker data placed *nar2* about 8.4 cM proximal from the *nld1* (narrow leafed dwarf 1) locus (5); about 23 cM distal from the *mtt2* (mottled leaf 2) locus (5).

Description:

The *nar2* mutants are characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity due to defective molybdenum cofactor synthesis or insertion (4). Some alleles are viable (*nar2.a2*), but they have a definite light green color and loss of vigor (3). The *nar2.ad* and *nar2.ag* homozygotes are not viable and they must be maintained as heterozygotes (1).

Origin of mutant:

A sodium azide induced mutant in Steptoe (Clho 15229) (4).

Mutational events:

*nar2.a2* (Az34, GSHO 2415) in Steptoe (Clho 15229) (4); *nar2.ad* (R9401), *nar2.ag* (R9201) in Maris Mink (PI 467824) (1).

Mutant used for description and seed stocks:

*nar2.a2* (GSHO 2415) in Steptoe.

References:

1. Bright, S.W.J. P.B. Norbury, J. Franklin, D.W. Kirk, and J.L. Wray. 1983. A conditional lethal *cnx*-type nitrate reductase-deficient barley mutant. *Mol. Gen. Genet.* 189:240-244.
2. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. *Barley Genet. Newsl.* 27:105-112.
3. Kleinhofs, A. (Unpublished).
4. Kleinhofs, A., T. Kuo, and R.L. Warner. 1980. Characterization of nitrate reductase-deficient barley mutants. *Molec. Gen. Genet.* 177:421-425.
5. Melzer, J.M., A. Kleinhofs, D.A. Kudrna, R.L. Warner, and T.K. Blake. 1988. Genetic mapping of barley nitrate reductase-deficient *nar1* and *nar2* loci. *Theor. Appl. Genet.* 75:767-771.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:196.

BGS 639, NADH nitrate reductase-deficient 3, *nar3*

Stock number: BGS 639  
Locus name: NADH nitrate reductase-deficient 3 (molybdenum cofactor)  
Locus symbol: *nar3*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Location in chromosome 7HS (1); near molecular marker MWG836 in 7H bin 05 (1).

Description:

The *nar3* mutants are characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity due to defective molybdenum cofactor synthesis or insertion (3). The *nar3* mutants are lethal and must be maintained as heterozygotes (2).

Origin of mutant:

An ethyl methanesulphonate induced mutant in Winer (4).

Mutational events:

*nar3.a3* (Xno18) in Winer (3); *nar3.b2* (Xno19) in Winer (4); *nar3.x* (Az71) in Steptoe (Clho 15229) (2).

Mutant used for description and seed stocks:

*nar3.x* (Az71) in Steptoe.

References:

1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. *Barley Genet. Newsl.* 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., R.L. Warner, J.M. Lawrence, J.M. Melzer, J.M. Jeter, and D.A. Kudrna. 1989. Molecular genetics of nitrate reductase in barley. p. 197-211. *In* J.L. Wray and J.R. Kinghorn (eds.) *Molecular and Genetic Aspects of Nitrate Assimilation*, Chapter 13. Proc. 2nd Int. Symp. on Nitrate Assimilation - Molecular and Genetic Aspects, St. Andrews, July, 1987. Oxford Univ. Press, New York.
4. Tokarev, B.I., and V.K. Shumny. 1977. Detection of barley mutants with low level of nitrate reductase activity after seed treatment with ethylmethane sulphonate. *Genetika (Moskva)* 13:2097-2103.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:197.

BGS 640, NADH nitrate reductase-deficient 4, *nar4*

Stock number: BGS 640  
Locus name: NADH nitrate reductase-deficient 4 (molybdenum cofactor)  
Locus symbol: *nar4*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location in chromosome 2HL (1); co-segregating with *Gln2* (glutamine synthetase 2) in 2H bin 13 (1).

Description:

The *nar4* mutant is characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). It is lethal under field conditions, but can be grown to maturity in the greenhouse with a reduced nitrogen source (2).

Origin of mutant:

A sodium azide induced mutant in Steptoe (CIho 15229) (2).

Mutational events:

*nar4.y* (Az72) in Steptoe (CIho 15229) (2).

Mutant used for description and seed stocks:

*nar4.y* (Az72) in Steptoe.

References:

1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. *Barley Genet. Newsl.* 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 86:705-712.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:198.

BGS 641, NADH nitrate reductase-deficient 5, *nar5*

Stock number: BGS 641  
Locus name: NADH nitrate reductase-deficient 5 (molybdenum cofactor)  
Locus symbol: *nar5*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location in chromosome 5HL (1); near molecular marker ABC324 in bin 5H-06 (1).

Description:

The *nar5* mutants are characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). All alleles are somewhat light green and viable as homozygotes (1).

Origin of mutant:

A sodium azide induced mutant in Steptoe (Clho 15229) (2).

Mutational events:

*nar5.o* (Az62), *nar5.s* (Az66), *nar5.u* (Az68, GSHO 2417) in Steptoe (Clho 15229) (2).

Mutant used for description and seed stocks:

*nar5.o* (Az62) in Steptoe.

References:

1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. Barley Genet. Newsl. 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:199.

BGS 642, NADH nitrate reductase-deficient 6, *nar6*

Stock number: BGS 642  
Locus name: NADH nitrate reductase-deficient 6 (molybdenum cofactor)  
Locus symbol: *nar6*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location in chromosome 2HL (1), co-segregating with *nar4* and *Gln2* (glutamine synthetase 2) in 2H bin 13 (1).

Description:

The *nar6* mutant is characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). Homozygotes are not viable and the *nar6* gene must be maintained as a heterozygote (2).

Origin of mutant:

A sodium azide induced mutant in Steptoe (CIho 15229) (2).

Mutational events:

*nar6.v* (Az69) in Steptoe (CIho 15229) (2).

Mutant used for description and seed stocks:

*nar6.v* (Az69) in Steptoe.

References:

1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. *Barley Genet. Newsl.* 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 86:705-712.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:200.

BGS 643, NADH nitrate reductase-deficient 7, *nar7*

Stock number: BGS 643  
Locus name: NADH nitrate reductase-deficient 7 [NAD(P)H nitrate reductase-deficient EC1.6.6.2, Acc. No. X60173]  
Locus symbol: *nar7*

Previous nomenclature and gene symbolization:  
None.

Inheritance:  
Monofactorial recessive (4).  
Location in chromosome 6HL (2, 3); approximately 4.2 cM proximal from the *Amy1* (alpha-amylase 1) locus in 6H bin 09 (2, 3).

Description:  
The *nar7* mutant lacks root NAD(P)H-bispecific nitrate reductase activity (4). All other reductase associated activities, xanthine dehydrogenase and nitrate reductase are normal. The mutant is viable and appears morphologically normal in all respects (1). The *nar7.w* mutant was selected for very low nitrate reductase activity in a *nar1.a* stock. This double mutant was crossed to Steptoe and the two mutants were separated by enzyme analysis of the progeny (1).

Origin of mutant:  
A sodium azide induced mutant in Steptoe (CIho 15229) mutant *nar1.a* (Az12) (3, 4).

Mutational events:  
*nar7.w* (Az70, GSHO 2418) in Steptoe (CIho 15229) (3).

Mutant used for description and seed stocks:  
*nar7.w* (GSHO 1418) in Steptoe.

References:  
1. Kleinhofs, A. (Unpublished).  
2. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 86:705-712.  
3. Warner, R.L., D.A. Kudrna, and A. Kleinhofs. 1995. Association of the NAD(P)H-bispecific nitrate reductase structural gene with the *Nar7* locus in barley. *Genome* 38:743-746.  
4. Warner, R.L., K.R. Narayanan, and A. Kleinhofs. 1987. Inheritance and expression of NAD(P)H nitrate reductase in barley. *Theor. Appl. Genet.* 74:714-717.

Prepared:  
A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:201.

BGS 644, NADH nitrate reductase-deficient 8, *nar8*

Stock number: BGS 644  
Locus name: NADH nitrate reductase-deficient 8 (molybdenum cofactor)  
Locus symbol: *nar8*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location in chromosome 6HS (1); close to molecular marker ABG378 in 6H bin 01 (1).

Description:

The *nar8* mutant is characterized by a pleiotropic loss of nitrate reductase and xanthine dehydrogenase activity (3). The homozygote is not viable and mutant must be maintained as a heterozygote (2).

Origin of mutant:

A sodium azide induced mutant in Steptoe (CIho 15229) (2).

Mutational events:

*nar8.z* (Az73) in Steptoe (CIho 15229) (2).

Mutant used for description and seed stocks:

*nar8.z* (Az73) in Steptoe.

References:

1. Kleinhofs, A. 1997. Integrated barley RFLP and classical marker maps. *Barley Genet. Newsl.* 27:105-112.
2. Kleinhofs, A. (Unpublished).
3. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 86:705-712.

Prepared:

A. Kleinhofs. 2005. *Barley Genet. Newsl.* 35:202.

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 appears normal except for a very bushy spike caused by many awn-like structures. Spikelets 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* (FN 346) in Morex (CIho 15773) (1).

Mutant used for description and seed stocks:

*bsp1.a* (FN 346) in Morex.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

A. Kleinhofs. 2005. Barley Genet. Newsl. 35:203.

BGS 646, Ovaryless 2, *ov12*

Stock number: BGS 646  
Locus name: Ovaryless 2  
Locus symbol: *ov12*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Mutant plants appear normal except carpels are rudimentary and female sterile. Plant development appears normal. Anther development is normal and pollen is viable (1).

The *ov11.a* (BGS 176, GSHO 610) mutant was not available for allelism tests.

Origin of mutant:

A fast neutron induced mutant in Harrington (1).

Mutational events:

*ov12.b* (FN 347) in Harrington (1).

Mutant used for description and seed stocks:

*ov12.b* FN 347) in Harrington.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

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

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 (1, 2).

Location is unknown.

Description:

Mutant plants and spikes appear normal except there is no seed set in the tip of the spike (2). In the Bowman backcross-derived line, seed set is 40 to 60% with no fertile spikelets at the terminal 4 to 6 nodes of the rachis. The *tst1* mutant differs from *lin1* (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 (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (2).

Mutational events:

*tst1.c* (FN 43) in Steptoe (CIho 15229) (2).

Mutant used for description and seed stocks:

*tst1.c* (FN 43) in Steptoe; *tst1.c* in Bowman (PI 483237)\*4.(BW882, NGB 22316).

References:

1. Franckowiak, J.D. (Unpublished).
2. Kleinhofs, A. (Unpublished).

Prepared:

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

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:

The mutant spikelet has 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 (Clho 15229) (1).

Mutational events:

*mov4.k* (FN 315, *mo8*) in Steptoe (Clho 15229) (1).

Mutant used for description and seed stocks:

*mov4.k* (FN 315) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

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

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. A few spikelets are formed occasionally, but they are mostly sterile. The stock must be maintained as a heterozygote (1).

Origin of mutant:

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

Mutational events:

*asp1.a* (FN 222) in Steptoe (Clho 15229) (1).

Mutant used for description and seed stocks:

*asp1.a* (FN 222) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

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

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 loose smut, *Ustilago nuda* (Jensen) Rostr. Spikes become entirely smutted under field conditions at Pullman, WA, USA where loose smut is rare and confined to one or a few florets (1).

Origin of mutant:

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

Mutational events:

*sun1.a* (FN 395) in Steptoe (Clho 15229) (1).

Mutant used for description and seed stocks:

*sun1.a* (FN 395) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

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

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, 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. Several other late heading mutants in Steptoe have been isolated following treatment with mutagenic agents, but allelism test 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 cv. Steptoe (1).

Origin of mutant:

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

Mutational events:

*lam1.a* (FN 2) in Steptoe (Clho 15229) (1).

Mutant used for description and seed stocks:

*lam1.a* (FN 2) in Steptoe.

References:

1. Kleinhofs, A. (Unpublished).

Prepared:

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

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 (1).

Location is unknown.

Description:

Mutant plants show a gradual yellowing or loss of chlorophyll starting in 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* gene is variable and is dependent on light intensity, temperature, moisture stress, and the age of the leaf blade. 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 (1). The Bowman backcross-derived line with the *ylf1* gene can have slightly smaller kernels and lower grain yields than normal Bowman (1).

Origin of mutant:

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

Mutational events:

*ylf1.a* (6002) in Villa (PI 399506) (1, 2).

Mutant used for description and seed stocks:

*ylf1.a* (6002) in Villa; *ylf1.a* in Bowman (PI 483237)\*8 (BW922, NGB 22351).

References:

1. Franckowiak, J.D. (Unpublished).
2. Gaul, H. (Personal communications).

Prepared:

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

BGS 653, Brachytic 10, *brh10*

Stock number: BGS 653  
Locus name: Brachytic 10  
Locus symbol: *brh10*

Previous nomenclature and gene symbolization:

Brachytic-I = *brh.1* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 2HS (1); approximately 12.9 cM distal from SSR marker Bmac0850 in 2H bin 08 (1).

Description:

Plants are about 3/4 normal height and peduncles are over 3/4 normal length. Awns are about 3/4 of normal length. Rachis internodes are slightly shorter than those of normal sibs, but the number of fertile rachis nodes is increased by over 2. Seedling leaves of *brh10* plants are relatively short. Kernels of the Bowman *brh10* line are shorter (7.3 vs. 9.6 mm) and about 20% lighter than those of Bowman. Plants have an erect growth habit and grain yields averaged 20% less than those of Bowman (1, 2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).

Mutational events:

*brh10.1* (17:15:2, DWS1007, GSHO 1677) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (4, 5).

Mutant used for description and seed stocks:

*brh10.1* (GSHO 1677) in Birgitta; *brh10.1* in Bowman (PI 483237)\*7 (GSHO 2171); *brh10.1* in Bowman\*8 (BW081, NGB 20488).

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:293.

BGS 654, Brachytic 11, *brh11*

Stock number: BGS 654  
Locus name: Brachytic 11  
Locus symbol: *brh11*

Previous nomenclature and gene symbolization:

Brachytic-n = *brh.n* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS (1); about 6.7 cM proximal from SSR marker Bmac0113 in 5H bin 04 (1).

Description:

Plants are 2/3 to 3/4 normal height and peduncles are 3/4 to 5/6 normal length. The length of the rachis internodes is about 3/4 as long as those of normal sibs. Seedling leaves of *brh11* plants are relatively short. Kernels of the Bowman *brh11* line are shorter (7.2 vs. 9.6 mm) and about 25% lighter than those of Bowman. Plants have an erect growth habit and grain yields of the *brh11* line averaged less than 1/2 of those for Bowman (1, 2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).

Mutational events:

*brh11.n* (17:19:2, DWS1011, GSHO 1679) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (4, 5).

Mutant used for description and seed stocks:

*brh11.n* (GSHO 1679) in Birgitta; *brh11.n* in Bowman (PI 483237)\*6 (GSHO 2172, BW082, NGB 20489).

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:294.

BGS 655, Brachytic 12, *brh12*

Stock number: BGS 655  
Locus name: Brachytic 12  
Locus symbol: *brh12*

Previous nomenclature and gene symbolization:

Brachytic-o = *brh.o* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS (1); approximately 13.5 cM distal from SSR marker Bmag0387 in 5H bin 03 (1).

Description:

Plants are 2/3 to 3/4 of normal height. Awns and peduncles are about 3/4 normal length. The length of the rachis internodes is about 3/4 of normal sibs. Seedling leaves of *brh12* plants are relatively short. Kernels of the Bowman *brh12* line are shorter (7.9 vs. 9.6 mm) and about 20% lighter than those of Bowman. Grain yields of the *brh12* line averaged slightly more than 1/2 of those for Bowman (1, 2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).

Mutational events:

*brh12.o* (17:20:2, DWS1012, GSHO 1680) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (4, 5).

Mutant used for description and seed stocks:

*brh12.o* (GSHO 1680) in Birgitta; *brh12.o* in Bowman (PI 483237)\*7 (GSHO 2173, BW083, NGB 20490).

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:295.

BGS 656, Brachytic 13, *brh13*

Stock number: BGS 656  
Locus name: Brachytic 13  
Locus symbol: *brh13*

Previous nomenclature and gene symbolization:

Brachytic-p = *brh.p* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS (1); approximately 8.7 cM distal from SSR marker Bmag0387 in 5H bin 03 (1).

Description:

Plants are about 2/3 normal height and awns are about 1/2 normal length. Peduncles and leaf blades are about 2/3 and 3/4 normal length, respectively. The length of the rachis internodes is about 3/4 of that of Bowman. The spikelets at the tip of the spike are close together giving a fasciated appearance. Seedling leaves of *brh13* plants are relatively short. Plants lodge relatively easily. Kernels of the Bowman *brh13* line are about the same size as those of Bowman, but kernel weights are about 20% less. The *brh13* plants have an erect growth habit and their grain yields are about 1/2 of those of Bowman (1, 2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).

Mutational events:

*brh13.p* (18:02:4, DWS1013, GSHO 1681) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (4, 5).

Mutant used for description and seed stocks:

*brh13.p* (GSHO 1681) in Birgitta; *brh13.p* in Bowman (PI 483237)\*6 (GSHO 2174, BW084, NGB 20491).

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:296.

BGS 657, Brachytic 15, *brh15*

Stock number: BGS 657  
Locus name: Brachytic 15  
Locus symbol: *brh15*

Previous nomenclature and gene symbolization:

Brachytic-u = *brh.u* (3).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown (1).

Description:

Plants have numerous tillers with small leaves, spikes, and kernels. Prior to heading plants appear to be grassy culms similar to those produced by the *slw2* (slender dwarf 2) and *slw4* (slender dwarf 4) mutants, but heading is not drastically delayed. Culms and peduncles are about 1/2 normal length. Awns and rachis internodes are slightly shorter than those of normal sibs. Leaf blades are narrow and about 1/2 normal length. Mutant plants headed 2 to 3 days later than normal sibs. No lodging was observed. Spikes of *brh15* plants had nearly 4 fewer kernels than those of Bowman. Kernels of the Bowman *brh15* line are slightly shorter (8.6 vs. 9.6 mm), thinner (3.4 vs. 3.8 mm), and about 30% lighter than those of Bowman. The grain yield of the *brh15* line averaged about 2/3 of that recorded for Bowman (1, 2).

Origin of mutant:

A N-methyl-N-nitrosourea induced mutant in Julia (PI 339811) (5, 6).

Mutational events:

*brh15.u* (409 JK, DWS1156, GSHO 1685) in Julia (PI 339811) (4, 6).

Mutant used for description and seed stocks:

*brh15.u* (GSHO 1685) in 409 JK/Bowman; *brh15.u* in Bowman (PI 483237)\*5 (GSHO 2176, BW086, NGB 20493).

References:

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Micke, A., and M. Maluszynski, M. 1984. List of semi-dwarf cereal stocks. *In Semi-dwarf Cereal Mutants and Their Use in Cross-breeding II.* IAEA-TECDOC-307. IAEA, Vienna.
6. Szarejko, I., M. Maluszynski, M. Nawrot, and B. Skawinska-Zydron. 1988. Semi-dwarf mutants and heterosis in barley. II. Interaction between several mutant genes responsible for dwarfism in barley. p. 241-246. *In Semi-dwarf Cereal Mutants and their Use in Cross-breeding III.* IAEA-TECDOC-455, IAEA, Vienna.

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:297.

BGS 658, Brachytic 17, *brh17*

Stock number: BGS 658  
Locus name: Brachytic 17  
Locus symbol: *brh17*

Previous nomenclature and gene symbolization:

Semidwarf mutant = Mo4 (5).  
Brachytic-ab = *brh.ab* (3).

Inheritance:

Monofactorial recessive (3, 4).  
Located in chromosome 5HS (1); approximately 11.6 cM proximal from SSR marker Bmag0387 in 5H bin 03 (1).

Description:

Plants are about 3/4 normal height and awns are 5/6 of normal length. Peduncles are slightly shortened. Rachis internodes are about 20% shorter than those of normal sibs. Seedling leaves of *brh17* plants are relatively short. Kernels of the Bowman *brh17* line are shorter (7.7 vs. 9.6 mm) and about 20% lighter than those of Bowman. Lodging is reduced in the backcross-derived line and grain yields averaged slightly less than those of Bowman (1, 2).

Origin of mutant:

A sodium azide induced mutant in Morex (Clho 15773) (6).

Mutational events:

*brh17.ab* (Wa14355-83, Mo4, DWS1260, GSHO 1669) in Morex (Clho 15773) (4, 5).

Mutant used for description and seed stocks:

*brh17.ab* (GSHO 1669) in Morex; *brh17.ab* in Bowman (PI 483237)\*6 (GSHO 2181, BW088, NGB 20495).

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Nedel, J.L., S.E. Ullrich, J.A. Clancy, and W.L. Pan. 1993. Barley semidwarf and standard isotype yield and malting quality response to nitrogen. *Crop Sci.* 33:258-263.
6. Ullrich, S.E., and Aydin, A. 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:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:298.

BGS 659, Brachytic 18, *brh18*

Stock number: BGS 659  
Locus name: Brachytic 18  
Locus symbol: *brh18*

Previous nomenclature and gene symbolization:

Brachytic-ac = *brh.ac* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS (1); approximately 9.2 cM distal from SSR marker Bmac0163 in 5H bin 01 (1).

Description:

Plants are about 2/3 normal height and awns are less than 2/3 of normal length. Peduncles are slightly coiled and about 5/6 the length of those of normal sibs. Rachis internodes are about 20% shorter than those of Bowman. Seedling leaves of *brh18* plants are relatively short. Kernels of *brh18* plants are similar in weight to those of Bowman, but slightly shorter. Lodging is reduced, but grain yields averaged slight more than 1/2 of those for Bowman (1, 2).

Origin of mutant:

An induced mutant backcrossed into Triumph (CIho 11612, GSHO 2465) (5).

Mutational events:

*brh18.ac* (402B, DWS1277, GSHO 1670) in mo6/4\*Triumph (CIho 11612, GSHO 2465) (4, 5).

Mutant used for description and seed stocks:

*brh18.ac* (GSHO 1670) in Mo6/4\*Triumph; *brh18.ac* in Bowman (PI 483237)\*6 (GSHO 2182, BW089, NGB 22474).

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. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
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. Falk, D. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:299.

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 (1, 2).

Location is unknown.

Description:

Mutant plants have narrow, dark green leaves, 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. Kernels of the Bowman *nld2* line are thinner (3.2 vs. 3.8 mm) and about 35% lighter than those of Bowman (1). Plants are 1/2 to 1/3 of normal height, the spike commonly emerges from the side of the sheath before anthesis. Awns of the *nld2.b* line are similar in length to those of Bowman. The *nld2.b* Bowman line is more vigorous than *nld1.a* in Christchurch, New Zealand and in North Dakota greenhouse nurseries, but *nld1.a* was more vigor in the Dundee, Scotland nursery. Seed yields are generally less than 20% of those of Bowman (1).

Origin of mutant:

A fast neutron induced mutant in Steptoe (CIho 15229) (2).

Mutational events:

*nld2.b* in Steptoe (CIho 15229) (2).

Mutant used for description and seed stocks:

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

References:

1. Franckowiak, J.D. (Unpublished).
2. Kleinhofs, A. (Unpublished).

Prepared:

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

BGS 661, Double seed 1, *dub1*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (2); near AFLP marker E4038-4 in subgroups 66 to 67 of the Proctor/Nudinka map (2).

Description:

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

Origin of mutant:

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

Mutational events:

*dub1.1* (NGB 114331), *dub1.2* (NGB 114332) in Bonus (PI 189763) (1); *dub1.3* (NGB 114333), *dub1.7* (NGB 114337), *dub1.8* (NGB 114338), *dub1.9* (NGB 114339), *dub1.10* (NGB114340), *dub1.11* (NGB 114341), *dub1.12* (NGB 114342) in Foma (CIho 11333) (1); *dub1.18a* (NGB 114345), *dub1.18b* (NGB 114346, 114347) in Kristina (NGB 1500) (1); *dub1.19* (NGB 114348), *dub1.20* (NGB 114349, 114350) in Bonus (1).

Mutant used for description and seed stocks:

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

References:

1. Lundqvist, U. (Unpublished).
2. 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.

Prepared:

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

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

Stock number: BGS 667  
Locus name: Reaction to *Pyrenophora teres* 1  
Locus symbol: *Rpt1*

Previous nomenclature and gene symbolization:

Resistance to *Pyrenophora teres* = *Pt* (5)  
Resistance to *Pyrenophora teres* 1 = *Pt1* (4) and *Pt2* (3, 4).  
Resistance to *Pyrenophora teres* 1a = *Rpt1a* (1).

Inheritance:

Monofactorial incomplete dominant (1, 3, 5).  
Located on chromosome 3H (1).

Description:

The reaction of cultivars with the *Rpt1* gene to *Pyrenophora teres* f. *teres* isolates is often 1 on a scale where 0 = very resistant and 4 = susceptible; however, some isolates produced susceptible reactions (1). Heterozygous individuals showed intermediate reactions ranging from 1 to 3 (1, 3, 5). Based on a low frequency of susceptible plant in crosses among resistant accessions, Mode and Schaller (4) classified Tifang as having different, but closely linked genes (*Pt<sub>1</sub>* and *Pt<sub>2</sub>*), compared to Manchurian, Ming, and Canadian Lake Shore. Bockelman et al. (1) could not differentiate the linked genes on chromosome 3H. Khan and Boyd (3) concluded from their study that the resistance gene of Tifang was not *Rpt1*, *Rpt2*, or *Rpt3*. This difference of opinion has not been resolved, but Tifang is still classified as having *Rpt1* (1).

Origin of mutant:

Natural occurrence in Tifang (PI 69426, CIho 14373) collected from Heilongjiang Province in China (1).

Mutational events:

*Rpt1.a* in Tifang (PI 69426, CIho 14373) (1); *Rpt1.b* in CIho 9819 (PI 195985) (1); the same gene or a possible allele may be present in Manchurian (CIho 739), Ming (PI 70854), and Canadian Lake Shore (PI 20819) (1, 4); *Rpt1.a* in CIho 9820 (PI 195986) (2).

Mutant used for description and seed stocks:

*Rpt1.a* in Tifang (PI 69426, CIho 14373) collected from Heilongjiang Province in China (1).

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. Cromey, M.G., and R.A. Parks. 2003. Pathogenic variation in *Drechslera teres* in New Zealand. *New Zealand Plant Protection* 56:251-256.
3. Khan, T.N., and W.J.R. Boyd. 1969. Inheritance of resistance to net blotch in barley II. Gene conditioning resistance against race W.A.-2. *Can. J. Genet. Cytol.* 11:592-597.
4. Mode, C.J., and C.S. Schaller. 1958. Two additional factors for resistance to net blotch in barley. *Agron. J.* 50:15-18.
5. Schaller, C.W. 1955. Inheritance of resistance to net blotch of barley. *Phytopathology* 48:477-480.

Prepared:

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

BGS 673, Corn stalk 1, *cst1*

Stock number: BGS 673  
Locus name: Corn stalk 1  
Locus symbol: *cst1*

Previous nomenclature and gene symbolization:

Corn stalk = *cs* (2).

Inheritance:

Monofactorial recessive (2, 4).

Location in chromosome 5HL (1, 2); associated with the T2-7b and T6-7c translocation breakpoints (2); *cst1.a* is associated with SNP markers 2\_0653 to 2\_1452 (positions 199.0 to 244.39 cM) in 5HL bins 11 to 13 of the Bowman backcross-derived line BW197 (1).

Description:

The *cst1.a* mutant produces a semidwarf unicum plants with thick culms in six rowed barley, which have moderate to very low seed set (4). As *cst1.a* gene was backcrossed into two-rowed barley Bowman, an increase in tillering and improved seed set were observed. Plants of the Bowman backcross-derived line BW197 were about 3/4 normal height and had very compact spikes, 2.8 vs. 4.5 mm. Awns, peduncles, and leaf blades of BW197 were about 3/4 the length of those of Bowman. Kernels of BW197 were slightly shorter than those of Bowman and the average seed weight was 4.5 vs. 5.7 mg. Grain yields of BW197 were very low (3).

Origin of mutant:

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

Mutational events:

*cst1.a* in Husky (CIho 9537) (2).

Mutant used for description and seed stocks:

*cst1.a* in LACZ95469, a six-rowed genetic stock from Lacombe, Alberta (4); *cst1.a* from LACZ95469 in Bowman (PI 483237)\*5 (BW197, NGB 22029).

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. 1961. Inheritance and linkage studies in barley using chromosomal interchange and marker stocks. Ph.D. Thesis, Univ. of Saskatchewan, pp 70.
3. Franckowiak, J.D. (Unpublished).
4. Wolfe, R.I. (Personal communications).

Prepared:

J.D. Franckowiak 2011. *Barley Genet. Newsl.* 41:199.

BGS 676, Chlorina seedling 16, *fch16*

Stock number: BGS 676  
Locus name: Chlorina seedling 16  
Locus symbol: *fch16*

Previous nomenclature and gene symbolization:

Chlorina seedling 117 = *clo.117* (3, 4).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 2HS (1); *fch16.117* is associated with SNP markers 2\_1187 to 2\_1338 (positions 51.52 to 74.97 cM) in 2H bin 05 to 06 of the Bowman backcross-derived line BW185 (1).

Description:

Seedling and immature leaves are pale yellow-green (chlorophyll deficient) in color and gradually become darker. A slight yellow green color may be observed prior to heading (2, 3). Leaf blades of the Bowman backcross-derived line BW185 are slightly wider than those of Bowman. The spikes of BW185 plants were observed to have slightly few kernels than Bowman in some trials. The *fch16.117* plants are 10 to 20% shorter than Bowman and show about a four day delay in anthesis. Kernel weights and grain yields were about normal (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763) (3, 5).

Mutational events:

*fch16.117* (NGB 22623) in Bonus (PI 189763) (3, 4, 5).

Mutant used for description and seed stocks:

*fch16.117* (NGB 22623) in Bonus; *fch16.117* in Bowman (PI 483237)\*5 (BW185, NGB 22017).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epub. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Simpson, D.J., O. Machold, G. Høyer-Hansen, and D. von Wettstein. 1985. *Chlorina* mutants of barley (*Hordeum vulgare* L.). *Carlsberg Res. Commun.* 50:223-238.
5. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at Carlsberg Laboratory. *Barley Genet. Newsl.* 21:102-108.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2010. *Barley Genet. Newsl.* 40:144.

BGS 677, Mottled leaf 7, *mtt7*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2).

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

Description:

Seedlings are weak and leaf blades have vertical chlorotic to necrotic streaks where chlorophyll development is poor. Plants are very weak, but can be grown to maturity under greenhouse conditions. Mutant plants have few tillers, short spikes and are 1/2 to 2/3 of normal height (2). The new gene symbol *mtt7.h* is suggested for the mutant because no other mottled mutant has a similar phenotype or is located in chromosome 2HS (1, 2).

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Zhang, L., T. Fetch, J. Nirmala, D. Schmierer, R. Brueggeman, B. Steffenson, and A. Kleinhofs. 2006. *Rpr1*, a gene required for *Rpg1*-dependent resistance to stem rust in barley. *Theor. Appl. Genet.* 113:847-855.

Prepared:

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

BGS 678, *Breviaristatum-u*, *ari-u*

Stock number: BGS 678  
Locus name: *Breviaristatum-u*  
Locus symbol: *ari-u*

Previous nomenclature and gene symbolization:

*Breviaristatum-245* = *ari.245* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HS (1); *ari-u.245* is associated with SNP markers 2\_0609 to 2\_1377 (positions about 13.0 to 20.11 cM) from Foma in 2H bin 02 of the Bowman backcrossed-derived line BW031 (1), in 2H bin 02.

Description:

Plants have reduced awn length, about 2/3 of normal with an undulated awn tip and an erect or brachytic growth habit (3). In the Bowman backcross-derived line for *ari-u.245*, BW031, a brachytic-like growth habit was observed, but expression of morphological traits was variable among nurseries with plant growth more reduced in moisture stressed nurseries. BW031 plants were 10 to 40% shorter and peduncles were 20 to 40% shorter compared to Bowman plants. Awn lengths of BW031 were 2/3 to 3/4 those for Bowman and rachis internode length varied from 2.9 to 4.3 mm compared to about 4.5 mm for Bowman. Kernels of BW031 were slightly smaller and 20% lighter. Grain yields varied from less than 1/3 to 3/4 of the Bowman yields (2). The variability in trait expression over environments observed in BW031 could be described as phenotypic plasticity, see Lacaze et al. (4).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Foma (CIho 11333) (3, 5).

Mutational events:

*ari-u.245* (NGB 116054) in Foma (CIho 11333) (2, 3).

Mutant used for description and seed stocks:

*ari-u.245* (NGB 116054) in Foma; *ari-u.245* via ND14701 in Bowman (PI 483237)\*5 (BW031, NGB 20439).

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. Lacaze, X., P. M. Hayes, and A. Korol. 2009. Genetics of phenotypic plasticity: QTL analysis in barley, *Hordeum vulgare*. *Heredity* 102:163-173.
5. Lundqvist, U. (Unpublished).

Prepared:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:200.

BGS 679, Accordion rachis 4, *acr4*

Stock number: BGS 679  
Locus name: Accordion rachis 4  
Locus symbol: *acr4*

Previous nomenclature and gene symbolization:

Accordion rachis 3 = *acr-3* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 2H or/and 6HL(1); *acr4.3* is associated with SNP markers 1\_0891 to 2\_1533 (positions 54.47 to 141.56 cM) in 2H bins 05 to 10 of the Bowman backcrossed-derived line BW004 and associated with SNP markers 1\_0015 to 2\_0733 (positions 160.38 to 180.69 cM) in 6HL bins 10 to 11 of BW004 (1).

Description:

The *acr4.3* mutant plants have multiple changes from normal besides elongated rachis internodes (3). Plant height is reduced, maturity is delayed, awns are short, the basal rachis internode is elongated, and partial fertility occurs (3). Plants of the Bowman backcross-derived line for *acr4.3*, BW004, showed similar alterations in plant morphology. The two largest DNA segments of BW004 in which donor parent SNP markers are retained overlap regions where lax spike loci have been mapped: 2HL (*acr1*, accordion rachis 1) and 6HL (*lax-c*, *laxatum-c*) (1, 2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (3).

Mutational events:

*acr4.3* (NGB 115043) in Bonus (PI 189763) (2, 3).

Mutant used for description and seed stocks:

*acr4.3* (NGB 115043) Bonus; *acr4.3* in Bowman (PI 483237)\*3 (BW004, NGB 20412).

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:201.

BGS 680, Breviaristatum-v, *ari-v*

Stock number: BGS 680  
Locus name: Breviaristatum-v  
Locus symbol: *ari-v*

Previous nomenclature and gene symbolization:

Breviaristatum-137 = *ari.137* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HS (1); *ari-v.137* is associated with SNP markers 2\_1065 to 2\_0265 (positions about 40.91 to 94.02 cM) in 5H bins 02 to 04 of Bowman backcrossed-derived line BW026 (1).

Description:

The mutant was selected as having slight shorter awns with weak calcariodes expression compared to the parental line Foma and a slight increase in plant height (3). The Bowman backcross-derived line for *ari-v.137*, BW026, was about 15% taller than Bowman, approximately 99 vs. 87 cm (2). The awns were 1 to 3 cm shorter than those of Bowman. Kernels of BW026 were 15% longer than those of Bowman and weighed 5 to 10% more. Grain yields of BW026 were similar to those of Bowman, but their test weights were slightly lower (2).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Foma (Clho 11333) (3, 4).

Mutational events:

*ari-v.137* (NGB 115947) in Foma (Clho 11333) (3, 4).

Mutant used for description and seed stocks:

*ari-v.137* (NGB 115947) in Foma; *ari-v.137* via ND15006 in Bowman (PI 483237)\*5 (BW026, NGB 20412).

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:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:202.

BGS 707, Required for *Puccinia graminis* resistance 1, *rpr1*

Stock number: BGS707  
Locus name: Required for *Puccinia graminis* resistance 1  
Locus symbol: *rpr1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 4H (1); *rpr1.a* is between the markers Adh4 and ABA003 and co-segregating with markers Contig4901\_s\_at, Contig7061\_s\_at, and HU03D17U\_s\_at (1), in 4H bin 05.

Description:

Susceptible mutant plants of Morex, when challenged with *Puccinia graminis* f. sp. *tritici* race MCCF, exhibited infection types 3 to 3+ similar to the highly susceptible cv. Steptoe as compared with infection types 0;1 to 10 for the resistant parent cv. Morex (1). The *rpr1.a* mutant line still has a functional *Rpg1* gene as demonstrated by expression of an *Rpg1* speciWc mRNA and Rpg1 protein, but it has a deletion that removed the markers Contig4901\_s\_at, Contig7061\_s\_at, and HU03D17U\_s\_at (1). These are candidate for the *Rpr1* gene (1).

Origin of mutant:

A fast neutron induced mutant in Morex (Clho 15773) (1).

Mutation events:

*rpr1.a* (FN559a) in Morex (Clho 15773) (1).

Mutant used for description and seed stocks:

*rpr1.a* (FN559a) in Morex.

References:

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

Prepared:

A. Kleinhofs 2012. Barley Genet. Newsl. 42:757.