

BGS 501, Male sterile genetic 38, *msg38*

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

Previous nomenclature and gene symbolization:

Male sterile *jl* = *msg,,jl* (2).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Selfing - none (2).

Outcrossing - complete female fertility (2).

Stamens - anthers nearly normal in size, but without stomium, filament elongates (2).

Origin of mutant:

A spontaneous mutant in Ingrid (CIho 10083) (2).

Mutational events:

msg38.jl (MSS51, GSHO 2390) in Ingrid (CIho 10083) (1, 2).

Mutant used for description and seed stocks:

msg38.jl (GSHO 2390) in Ingrid; *msg38.jl* in Bowman (PI 483237)*7 (GSHO 2304, BW574, NGB 23437).

References:

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

Prepared:

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

Revised:

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

BGS 502, Male sterile genetic 39, *msg39*

Stock number: BGS 502
Locus name: Male sterile genetic 39
Locus symbol: *msg39*

Previous nomenclature and gene symbolization:

Male sterile dm = *msg*, *dm* (5).

Inheritance:

Monofactorial recessive (1, 5).

Located in chromosome 3H (2); *msg39.dm* is associated with SNP markers from 1_0312 to 1_0044 (positions 173.82 to 190.87 cM) in 3H bins 11 to 12 of a heterozygous plant from the Bowman backcross-derived stock BW575 (2), in 3H bin 11 or 12. Previously associated with chromosome 6H, over 33.9 cM from the *rob1* (orange lemma 1) locus (3).

Description:

Selfing - about 1% in Bozeman, Montana, USA and Elimäki, Finland (1, 5).

Outcrossing - complete female fertility (1).

Stamens - anthers are the same size as fertile sibs, stomium present, and filament elongates (1, 5).

Origin of mutant:

A spontaneous mutant in a Finnish six-rowed barley (P11, CIho 15836) (1, 5).

Mutational events:

msg39.dm (MSS361, GSHO 2391, GSHO 3021) in P11 (CIho 15836) (4, 7); *msg39.dn* (MSS362, GSHO 3022) in a Finnish six-rowed barley (H31, CIho 15837) (1, 4, 7); *msg39.ff* (MSS407) in Sabarlis (CIho 15484) (4, 6).

Mutant used for description and seed stocks:

msg39.dm (GSHO 2391) in P11; *msg39.dm* in Bowman (PI 483237)*7 (GSHO 2080, BW575, NGB 24135).

References:

1. Ahokas, H. 1976. Male sterile mutants of barley. III. Additional inaperturate mutants. *Barley Genet. Newsl.* 6:4-6.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
3. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. *Barley Genet. Newsl.* 20:31-36.
4. Franckowiak, J.D., and E.A. Hockett. 1988. Identification of three new loci which control male sterility of barley. *Barley Genet. Newsl.* 18:11-13.
5. Hockett, E.A. 1977. The genetic male sterile barley collection. *Barley Genet. Newsl.* 7:97-100.
6. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.
7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:106.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:428.

J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:122.

BGS 503, Male sterile genetic 40, *msg40*

Stock number: BGS 503
Locus name: Male sterile genetic 40
Locus symbol: *msg40*

Previous nomenclature and gene symbolization:

Male sterile ac = *msg,,ac* (3, 5).
Male sterile = ms-C (4).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 6H (1); over 27.8 cM from the *rob1* (orange lemma 1) locus (1).

Description:

Selfing - none (3).
Outcrossing - less than 30% in crosses and in the Bowman backcross-derived line.
Stamens - anthers are smaller than those of fertile sibs, no stomium or filament elongation (3).

Origin of mutant:

A spontaneous mutant in Conquest (CIho 11683) (4).

Mutational events:

msg40.ac (MSS095, GSHO 2393) in Conquest (CIho 11683) (2, 3, 5).

Mutant used for description and seed stocks:

msg40.ac (GSHO 2393) in Conquest; *msg40.ac* in Bowman (PI 483237)*6 (GSHO 2081, BW577, NGB 23439).

References:

1. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. *Barley Genet. Newsl.* 20:31-36.
2. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 14:37-40.
3. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) *Barley Genetics II*. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
4. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. *Crop Sci.* 8:754-755.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:107.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:429.

BGS 504, Male sterile genetic 41, *msg41*

Stock number: BGS 504
Locus name: Male sterile genetic 41
Locus symbol: *msg41*

Previous nomenclature and gene symbolization:

Male sterile *aj* = *msg*, *aj* (5).
Male sterile = 65msx166 (6).

Inheritance:

Monofactorial recessive (5).
Location is unknown.

Description:

Selfing - none (3, 5).
Outcrossing - complete female fertility (5), but in the Bowman backcross-derived line seed set is less than 20% after crossing as a female parent.
Stamens - anthers rudimentary, no stomium or filament elongation (3, 5).

Origin of mutant:

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

Mutational events:

msg41.aj (MSS101, GSHO 2394) in Betzes (PI 129430) (4, 6, 7); *msg41.dk* in Betzes (MSS359) (1, 4, 7); *msg41.do* (MSS363) in Maris Baldrac (PI 294512) (2, 4, 7); *msg41.ef* (MSS381) in Hector (Clho 15514), *msg41.el* (MSS387) in Sabarlis (Clho 15484), *msg41.eq* in Sel 12387Co (MSS392), *msg41.fa* (MSS402) in Midas (PI 343078), *msg41.gl* (MSS439) in Maris Mink (PI 467824), *msg41.ij* (MSS489) in Mazurka (PI 410868) (3, 4).

Mutant used for description and seed stocks:

msg41.aj (GSHO 2394) in Betzes; *msg41.aj* in Bowman (PI 483237)*7 (BW976, NGB 23469); *msg41.dk* in Bowman*6 (GSHO 2305, BW578, NGB 23440).

References:

1. Hockett, E.A. 1975. The genetic male sterile barley collection. *Barley Genet. Newsl.* 5:84-86.
2. Hockett, E.A. 1977. The genetic male sterile barley collection. *Barley Genet. Newsl.* 7:97-100.
3. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.
4. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 20:37-40.
5. Hockett, E.A., and R.F. Eslick. 1971. Genetic male sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) *Barley Genetics II*. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
6. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. *Crop Sci.* 8:754-755.
7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:108.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:430.

BGS 505, Male sterile genetic 42, *msg42*

Stock number: BGS 505
Locus name: Male sterile genetic 42
Locus symbol: *msg42*

Previous nomenclature and gene symbolization:

Male sterile db = *msg,,db* (2).
Male sterile = B68-N-109 (2).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 3H (1); over 18.9 cM from the *alm1* (albino lemma 1) locus (1).

Description:

Selfing - none (2, 3).
Outcrossing - complete female fertility (2, 3).
Stamens - anthers rudimentary, no stomium or filament elongation (2, 3).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (2).

Mutational events:

msg42.db (MSS350, GSHO 2395) in Betzes (PI 129430) (1, 4, 5); *msg42.gt* (MSS447) in Berac (PI 355136), *msg42.hw* (MSS476) in Sel 15025Co, *msg42.iy* (MSS504) in Sv73608 (3, 4).

Mutant used for description and seed stocks:

msg42.db (GSHO 2395) in Betzes; *msg42.db* in Bowman (PI 483237)*6 (GSHO 1948, BW579, NGB 23441).

References:

1. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. *Barley Genet. Newsl.* 20:31-36.
2. Hockett, E.A. 1975. The genetic male sterile barley collection. *Barley Genet. Newsl.* 5:84-86.
3. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.
4. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 20:37-40.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:109.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:431.

BGS 506, Male sterile genetic 43, *msg43*

Stock number: BGS 506
Locus name: Male sterile genetic 43
Locus symbol: *msg43*

Previous nomenclature and gene symbolization:

Male sterile br = *msg,,br* (1).
Male sterile = B65msx38 (1).

Inheritance:

Monofactorial recessive (1).
Location is unknown.

Description:

Selfing - none (1).
Outcrossing - complete female fertility (1), but in the Bowman backcross-derived line seed set is less than 30% after crossing as a female parent.
Stamens - anthers rudimentary, no stomium or filament elongation (1).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (1).

Mutational events:

msg43.br (MSS332, GSHO 2396) in Betzes (PI 129430) (1, 2, 3).

Mutant used for description and seed stocks:

msg43.br (GSHO 2396) in Betzes; *msg43.br* in Bowman (PI 483237)*7 (GSHO 2306, BW580, NGB 23442).

References:

1. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. *Barley Genet. Newsl.* 2:139-144.
2. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 20:37-40.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:110.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:432.

BGS 507, Male sterile genetic 44, *msg44*

Stock number: BGS 507
Locus name: Male sterile genetic 44
Locus symbol: *msg44*

Previous nomenclature and gene symbolization:

Male sterile *cx* = *msg,,cx* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Selfing - none (1).

Outcrossing - complete female fertility (1).

Stamens - anthers rudimentary, no stomium or filament elongation (1).

Origin of mutant:

A spontaneous mutant in selection HA6-33-02 (CIho 15835) (1).

Mutational events:

msg44.cx (MSS346, GSHO 2397) in HA6-33-02 (CIho 15835) (1, 2, 3).

Mutant used for description and seed stocks:

msg44.cx (GSHO 2397) in HA6-33-02; *msg44.cx* in Bowman (PI 483237)*7 (GSHO 2307, BW581, NGB 23443).

References:

1. Hockett, E.A. 1975. The genetic male sterile barley collection. *Barley Genet. Newsl.* 5:84-86.
2. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 20:37-40.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:111.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:433.

BGS 508, Male sterile genetic 45, *msg45*

Stock number: BGS 508
Locus name: Male sterile genetic 45
Locus symbol: *msg45*

Previous nomenclature and gene symbolization:

Male sterile *dp* = *msg*, *dp* (1).
Male sterile = 76Y2 (1).

Inheritance:

Monofactorial recessive (1).
Location is unknown.

Description:

Selfing - none (1).
Outcrossing - complete female fertility (1).
Stamens - anthers rudimentary, no stomium or filament elongation (1).

Origin of mutant:

A spontaneous mutant in selection RPB439-71 (CIho 15838) (1).

Mutational events:

msg45.dp (MSS364, GSHO 2398) in RPB439-71 (CIho 15838) (1, 2, 3).

Mutant used for description and seed stocks:

msg45.dp (GSHO 2398) in RPB439-71; *msg45.dp* in Bowman (PI 483237)*4 (GSHO 2308, BW582, NGB 23444).

References:

1. Hockett, E.A. 1979. The genetic male sterile barley collection. *Barley Genet. Newsl.* 9:124-128.
2. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 20:37-40.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. *Crop Sci.* 21:655-659.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:112.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:434.

BGS 509, Male sterile genetic 46, *msg46*

Stock number: BGS 509
Locus name: Male sterile genetic 46
Locus symbol: *msg46*

Previous nomenclature and gene symbolization:

Male sterile ec = *msg,,ec* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Selfing - none (1).

Outcrossing - complete female fertility (1).

Stamens - anthers smaller than those of fertile sibs, no stomium or filament elongation (1).

Origin of mutant:

A spontaneous mutant in Hector (CIho 15514) (1).

Mutational events:

msg46.ec (MSS378, GSHO 2399) in Hector (CIho 15514) (1, 2, 3).

Mutant used for description and seed stocks:

msg46.ec (GSHO 2399) in Hector; *msg46.ec* in Bowman (PI 483237)*4 (GSHO 2309, BW583, NGB 23445).

References:

1. Hockett, E.A. 1979. The genetic male sterile barley collection. Barley Genet. Newsl. 9:124-128.
2. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
3. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. Barley Genet. Newsl. 20:37-40.

Prepared:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:113.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:435.

BGS 510, Male sterile genetic 47, *msg47*

Stock number: BGS 510
Locus name: Male sterile genetic 47
Locus symbol: *msg47*

Previous nomenclature and gene symbolization:

Male sterile ep = *msg,,ep* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Selfing - none (1).

Outcrossing - complete female fertility (1).

Stamens - anthers rudimentary, no stomium or filament elongation (1).

Origin of mutant:

A spontaneous mutant in Sel 12384Co (1).

Mutational events:

msg47.ep (MSS391, GSHO 2400) in Sel 12384Co (1, 2).

Mutant used for description and seed stocks:

msg47.ep (GSHO 2400) in Sel 12384Co; *msg47.ep* in Bowman (PI 483237)*5 (GSHO 2310, BW584, NGB 23446).

References:

1. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.
2. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. *Barley Genet. Newsl.* 20:37-40.

Prepared:

E.A. Hockett. 1991. *Barley Genet. Newsl.* 20:114.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:436.

BGS 511, Reaction to *Puccinia graminis* 1, *Rpg1*

Stock number: BGS 511
Locus name: Reaction to *Puccinia graminis* 1 (wheat stem rust)
Locus symbol: *Rpg1*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia graminis tritici* = *T* (8).

Resistance to *Puccinia graminis* Pers f sp *tritici* Eriks & E Henn = *Rpg1a* (4).

Inheritance:

Monofactorial dominant (8).

Located in chromosome 7HS (2, 3, 8); about 13.2 cM distal to the *brh1* (brachytic 1) locus (3, 12); about 9.2 cM distal from the *Run1* (reaction to *Ustilago nuda* 1) locus (2); about 1.4 cM distal from the *Run1* locus (13); 0.7 cM from RFLP marker ABG077 (5).

Description:

The dominant allele at the *Rpg1* locus confers moderate resistance to most races of *Puccinia graminis* f sp *tritici*. Lesion size and percent stem and leaf sheath infection in adult plants is reduced compared with susceptible plants under field conditions (10, 11). At high temperatures (greater than 20°C), differentiation of seedling reaction types is observed with race 56 (10). These differences correlate with adult plant reactions better than at lower temperatures (9). Differences among cultivars indicate that a modifier of the *Rpg1.e* allele exists (9). Plants with the *Rpg1* gene show a susceptible reaction to pathotype QCC of *Puccinia graminis* f sp *tritici* (6) and to *Puccinia graminis* f sp *secalis* (16). Molecular markers closely linked to the three different sources of the *Rpg1* gene suggest that they originated independently (5). The *Rpg1* region of chromosome 5HS shows synteny to the short arm of rice chromosome 6 (7).

Origin of mutant:

Natural occurrence in Chevron (CIho 1111) and Peatland (CIho 5276) (10); a spontaneous mutant isolated from Wisconsin Pedigree 37 as Kindred (CIho 6969) (1).

Mutational events:

Rpg1.a in Chevron (CIho 1111, GSHO 701) (5, 12); *Rpg1.e* in Peatland (CIho 5276), *Rpg1.f* in Kindred (CIho 6969) (5, 14).

Mutant used for description and seed stocks:

Rpg1.a in Chevron (GSHO 701, CIho 1111); *Rpg1.a* in 80-TT-29 (CIho 16129) (15); *Rpg1.e* from Peatland in Bowman (PI 483237).

References:

1. Åberg, E., and G.A. Wiebe. 1946. Classification of barley varieties grown in the United States and Canada in 1945. USDA Tech. Bull. No. 907. 190 p.
2. Andrews, J.E. 1956. Inheritance of reaction to loose smut, *Ustilago nuda*, and to stem rust, *Puccinia graminis tritici*, in barley. Can. J. Agric. Sci. 36:356-370.
3. Brookins, W.W. 1940. Determination of linkage relationships of factors differentiating reaction to stem rust in barley crosses. Ph.D. Thesis. Univ. of Minnesota, St. Paul.
4. Franckowiak, J.D. 1991. BGS 511, Resistance to *Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn., *Rpg1a*. Barley Genet. Newsl. 20:115.
5. Horvath, D.P., L.S. Dahleen, J.A. Stebbing, and G. Penner. 1995. A co-dominant PCR-based marker for assisted selection of durable stem rust resistance in barley. Crop Sci. 35:1445-1450.
6. Jin, Y., B.J. Steffenson, and T.G. Fetch, Jr. 1994. Sources of resistance to pathotype QCC of *Puccinia graminis* f. sp. *tritici* in barley. Crop Sci. 34:285-288.
7. Kilan, A., D.A. Kudrna, A. Kleinhofs, M. Yano, N. Kurata, B. Steffenson, and T. Sasaki. 1995. Rice-barley synteny and its application to saturation mapping of the barley

Rpg1 region. Nucleic Acids Res. 23:2729-2733.

8. Kramer, H.H., R. Veyl, and W.D. Hanson. 1954. The association of two genetic linkage groups in barley with one chromosome. Genetics 39:159-168.

9. Miller, J.D., and J.W. Lambert. 1955. Variability and inheritance of reaction of barley to race 15B of stem rust. Agron. J. 47:373-377.

10. Patterson, F.L. 1951. Adult plant and seedling reactions of barley varieties and hybrids to 3 races of *Puccinia graminis tritici*. Ph.D. Thesis. Univ. of Wisconsin, Madison.

11. Powers, L., and L. Heines. 1933. Inheritance of reaction to stem rust and barbing of awns in barley crosses. J. Agric. Res. 46:1121-1129.

12. Shands, R.G. 1939. Chevron, a barley variety resistant to stem rust and other diseases. Phytopathology 29:209-211.

13. Shands, R.G. 1964. Inheritance and linkage to stem rust and loose smut resistance and starch type in barley. Phytopathology 54:308-316.

14. Steffenson, B.J. 1992. Analysis of durable resistance to stem rust in barley. Euphytica 63:153-167.

15. Steffenson, B.J., and R.D. Wilcoxson. 1987. Receptivity of barley to *Puccinia graminis* f. sp. *tritici*. Can. J. Plant Path. 9:36-40.

16. Steffenson, B.J., R.D. Wilcoxson, and A.P. Roelfs. 1985. Resistance of barley to *Puccinia graminis* f. sp. *tritici* and *Puccinia graminis* f. sp. *secalis*. Phytopathology 75:1108-1111.

Prepared:

J.D. Franckowiak. 1991. Barley Genet. Newsl. 20:115.

Revised:

J.D. Franckowiak and B.J. Steffenson. 1997. Barley Genet. Newsl. 26:437-438.

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

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

Previous nomenclature and gene symbolization:

Resistance to *Puccinia graminis tritici* = *T2* (2).

Resistance to *Puccinia graminis* Pers. f sp *tritici* Eriks. & E Henn. = *Rpg2b* (1).

Inheritance:

Monofactorial dominant (3, 4).

Location is unknown.

Description:

Moderate resistance to some races of *Puccinia graminis* f sp *tritici* is conferred by the *Rpg2.b* gene. Percent stem and leaf sheath infection and lesion size in adult plants are reduced compared with susceptible plants under field conditions (2, 4, 5). Patterson used linkage data to demonstrate that the *Rpg2* locus differs from the *Rpg1* locus (3).

Origin of mutant:

A spontaneous mutant in Oderbrucker (CIho 4666) isolated in Wisconsin, USA by Mr Hietpas and called Hietpas 5 (CIho 7124) (3, 4).

Mutational events:

Rpg2.b in Hietpas 5 (CIho 7124, GSHO 187, GSHO 1584) (4).

Mutant used for description and seed stocks:

Rpg2.b in Hietpas 5 (GSHO 187, GSHO 1584).

References:

1. Franckowiak, J.D. 1991. BGS 512, Resistance to *Puccinia graminis* Pers. f. sp. *tritici* Eriks. & E. Henn., *Rpg2b*. Barley Genet. Newsl. 20:116.
2. Miller, J.D., and J.W. Lambert. 1955. Variability and inheritance of reaction of barley to race 15B of stem rust. Agron. J. 47:373-377.
3. Patterson, F.L. 1951. Adult plant and seedling reactions of barley varieties and hybrids to 3 races of *Puccinia graminis tritici*. Ph.D. Thesis. Univ. of Wisconsin, Madison.
4. Shands, R.G. 1964. Inheritance and linkage to stem rust and loose smut resistance and starch type in barley. Phytopathology 54:308-316.
5. Steffenson, B.J., R.D. Wilcoxson, and A.P. Roelfs. 1985. Resistance of barley to *Puccinia graminis* f. sp. *tritici* and *Puccinia graminis* f. sp. *secalis*. Phytopathology 75:1108-1111.

Prepared:

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

Revised:

J.D. Franckowiak and B.J. Steffenson. 1997. Barley Genet. Newsl. 26:439.

BGS 513, Xantha seedling 2, *xnt2*

Stock number: BGS 513
Locus name: Xantha seedling 2
Locus symbol: *xnt2*

Previous nomenclature and gene symbolization:

Xantha seedling b = x_b (1).

Yellow seedling b = x_b (2).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Seedlings are yellow in color and do not develop green pigmentation. Since they do not survive beyond the two leaf stage, the *xnt2.b* gene must be maintained as a heterozygous stock (1).

Origin of mutant:

A spontaneous mutant in Black Hulless (PI 24849) (1).

Mutational events:

xnt2.b (x_b) (Black Hulless II, GSHO 2) in Black Hulless (PI 24849) (1).

Mutant used for description and seed stocks:

xnt2.b in Black Hulless (GSHO 2).

References:

1. Robertson, D.W. 1932. The effect of a lethal in the heterozygous condition on barley development. Colorado Agric. Exp. Stn. Tech. Bull. 1. 12 p.

2. Haus, T.E. 1988. BGS 513, Yellow seedling, x_b . Barley Genet. Newsl. 18:82.

Prepared:

T.E. Haus 1988. Barley Genet. Newsl. 18:82.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:440.

BGS 515, Reaction to *Septoria passerinii* 1, *Rsp1*

Stock number: BGS 515
Locus name: Reaction to *Septoria passerinii* 1
Locus symbol: *Rsp1*

Previous nomenclature and gene symbolization:

Resistance to *Septoria passerinii* Sacc = *Sep* (1, 2).

Inheritance:

Monofactorial incomplete dominant (2).

Location is unknown (2).

Description:

The *Rsp1.a* gene conditions a high level of resistance to a single spore culture of *Septoria passerinii* isolated in Minnesota, USA. Infection occurs on F₁ seedlings, but is limited to a few lesions (2).

Origin of mutant:

Natural occurrence in accession Clho 4249-2 (Clho 14300) (2).

Mutational events:

Rsp1.a in Clho 14300 (GSHO 2510) (2).

Mutant used for description and seed stocks:

Rsp1.a in Clho 14300 (GSHO 2510).

References:

1. Moseman, J.G. 1972. Report on genes for resistance to pests. Barley Genet. Newsl. 2:145-147.
2. Rasmusson, D.C., and W.E. Rogers. 1963. Inheritance of resistance to septoria in barley. Crop Sci. 3:161-163.

Prepared:

D.C. Rasmusson. 1988. Barley Genet. Newsl. 18:84 as BGS 465.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:441.

BGS 516, Reaction to *Septoria passerinii* 2, *Rsp2*

Stock number: BGS 516
Locus name: Reaction to *Septoria passerinii* 2
Locus symbol: *Rsp2*

Previous nomenclature and gene symbolization:

Resistance to *Septoria passerinii* Sacc = *Sep*₂ (1, 2).

Inheritance:

Monofactorial incomplete dominant (2).

Location in chromosome 1HS (3); about 3.9 cM from the *Rsp3* (reaction to *Septoria passerinii* 3) locus (2); cosegregation with SCAR marker E-ACT/M-CAA-170a and close to the *Rsp3* locus (3); about 17.6 cM proximal from marker RFLP Act8 (3).

Description:

The *Rsp2.b* gene conditions a high level of resistance to a single spore culture of *Septoria passerinii* isolated in Minnesota, USA. Pycnidia are observed in some, but not all lesions, on all F₁ plants (2).

Origin of mutant:

Natural occurrence in accession Clho 4780 (PI 70837) (2).

Mutational events:

Rsp2.b in PI 70837 (GSHO 2511) (2).

Mutant used for description and seed stocks:

Rsp2.b in PI 70837 (GSHO 2511).

References:

1. Moseman, J.G. 1972. Report on genes for resistance to pests. Barley Genet. Newsl. 2:145-147.
2. Rasmusson, D.C., and W.E. Rogers. 1963. Inheritance of resistance to septoria in barley. Crop Sci. 3:161-163.
3. Zhong, S., H. Toubia-Rahme, B.J. Steffenson, and K.P. Smith. 2006. Molecular mapping and marker-assisted selection of genes for septoria speckled leaf blotch resistance in barley. Phytopathology 96:993-999.

Prepared:

D.C. Rasmusson. 1988. Barley Genet. Newsl. 18:85 as BGS 466.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:442.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:275.

BGS 517, Reaction to *Septoria passerinii* 3, *Rsp3*

Stock number: BGS 517
Locus name: Reaction to *Septoria passerinii* 3
Locus symbol: *Rsp3*

Previous nomenclature and gene symbolization:

Resistance to *Septoria passerinii* Sacc = *Sep*₃ (1, 2).

Inheritance:

Monofactorial incomplete dominant (2).

Location in chromosome 1HS (3); about 3.9 cM from the *Rsp2* (reaction to *Septoria passerinii* 2) locus (2); cosegregation with SCAR marker E-ACT/M-CAA-170a and close to the *Rsp2* locus (3); about 17.6 cM proximal from marker RFLP Act8 (3).

Description:

The *Rsp3.c* gene conditions a high level of resistance to a single spore culture of *Septoria passerinii* isolated in Minnesota, USA. Infection occurs on F₁ seedlings, but is limited to a few lesions (2).

Origin of mutant:

Natural occurrence in selection II-51-43 from a Feebar/Kindred cross (Clho 10644) (2).

Mutational events:

Rsp3.c in Clho 10644 (GSHO 2512) (2).

Mutant used for description and seed stocks:

Rsp3.c in Clho 10644 (GSHO 2512).

References:

1. Moseman, J.G. 1972. Report on genes for resistance to pests. Barley Genet. Newsl. 2:145-147.
2. Rasmusson, D.C., and W.E. Rogers. 1963. Inheritance of resistance to septoria in barley. Crop Sci. 3:161-163.
3. Zhong, S., H. Toubia-Rahme, B.J. Steffenson, and K.P. Smith. 2006. Molecular mapping and marker-assisted selection of genes for septoria speckled leaf blotch resistance in barley. Phytopathology 96:993-999.

Prepared:

D.C. Rasmusson. 1988. Barley Genet. Newsl. 18:86 as BGS 467.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:443.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:276.

BGS 518, Semidwarf 1, *sdw1*

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

Previous nomenclature and gene symbolization:

Denso dwarf = *denso* (7, 17).

Hordeum vulgare gibberellin 20-oxidase = *Hv20ox2* (9, 10).

Inheritance:

Monofactorial recessive (7, 18); some F₁'s are intermediate in height (1, 12).

Location in chromosome 3HL (2, 13); probably proximal from the *gsh2* (glossy sheath 2) locus and near RFLP marker PSR170 (13); in bin 3H-11 (11); near RFLP marker R1545 (20); *sdw1* is close to SNP marker 1_0867 (14); *sdw1.a* is associated with SNP markers 1_0044 to 2_0650 (positions about 190 to 192.00 cM) in 3H bin 12 of the Bowman backcross-derived line BW827 (4); *sdw1.d* is associated with SNP markers 2_0023 to 1_0821 (positions 169.94 to 190.87 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW828 (4), in 3H bin 12.

Description:

Plants homozygous for the *sdw1.a* gene ranged from 10 to 30 cm shorter than normal sibs, with expression partial dependent on environment (1, 17, 19). Spike length was variable, but fully as long as normal barley. The stock used for description of the *sdw1.a* gene, M21, has the short straw and long spike of the original 'Jotun Mutant' as well as a large culm diameter from its parent 'Vantage' (1, 19). The semidwarf mutants, 'Diamant' and 'Abed Denso', are alleles at the *sdw1* locus (7, 15). Alleles at the *sdw1* locus are associated with semi-prostrate juvenile growth (7, 17), delayed maturity (5, 7, 8, 17, 20), smaller grain size (7), and reduced malt quality (5, 8, 17). The *sdw1* mutants are GA sensitive (3, 21). They are very likely mutants in an orthologue of the rice *sd1* gene (21), which encodes a GA-oxidase that produces lower levels of GA and reduced levels of cause the dwarf phenotype (9, 16). A gibberellin 20-oxidase gene (*Hv20ox2*) was identified as the candidate gene for *sdw1* (9, 10). The reduced expression of *Hv20ox2* increased the number of effective tillers and enhanced grain yield (10). The reduction in *Hv20ox2* levels was 4-fold in the *sdw1.d* mutant and 60-fold in the *sdw1.a* mutant (10). Plants of the Bowman backcross-derived line for *sdw1.a*, BW827, were 15 to 30% shorter than Bowman and heading was delayed 1 to 3 days. Plants of the Bowman backcross-derived line for *sdw1.d*, BW828, were 10 to 20% shorter than Bowman, heading was delayed 1 to 3 days, and spikes had 1 to 2 more kernels in some trials. Kernels of BW827 and BW828 were up to 10% lighter than Bowman kernels in some trials. Grain yields of BW828 were similar to those of Bowman, while those of BW827 were about 85% of the Bowman yields (6).

Origin of mutant:

An X-ray induced mutant in the Norwegian cultivar Jotun (PI 467357) isolated as Jotun 22 by Knut Mikaelson (1, 12).

Mutational events:

sdw1.a (66/86, GSHO 1414) in Jotun (PI 467357) (19); *sdw1.c* (*denso*) in Abed Denso (PI 361639) (7); *sdw1.d* (Diamant, PI 330397, PI 467775) in Valticky (PI 268173) (7); *sdw1.e* (Risø no. 9265) in Bomi (PI 43371) (7). Note that the *denso* name was original assigned to the *sdw1.c* mutant (7), but now cultivars with the *sdw1.d* mutant from Diamant are described as having the *denso* mutant.

Mutant used for description and seed stocks:

sdw1.a in M21 (Clho 15481, GSHO 2513) from the cross Jotun Mutant/Kindred// Vantage (19); *sdw1.d* in Trumpf (Triumph, PI 548762, GSHO 2465) from Diamant; *sdw1.a* from a Jotun derivative in Bowman (PI 483237)*7 (GSHO 1978), in Bowman*8 (BW827, NGB 22264); *sdw1.d* from Trumpf in Bowman*4 (GSHO 1979), in Bowman*5 (BW828, NGB 22265).

References:

1. Ali, M.A.M., O. Okiror, and D.C. Rasmusson. 1978. Performance of semidwarf barley. *Crop Sci.* 18:418-422.
2. Barau, U.M., K.J. Chambers, W.T.B. Thomas, C.A. Hackett, V. Lea, P. Jack, B.P. Forster, R. Waugh, and W. Powell. 1993. Molecular mapping of genes determining height, time to heading, and growth habit in barley (*Hordeum vulgare*). *Genome* 36:1080-1087.
3. Boulger, M.C., R.G. Sears, and W.E. Kronstad. 1982. An investigation of the association between dwarfing sources and gibberellic acid response in barley. p. 550-553. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.) *Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp.*, Edinburgh. Edinburgh Univ. Press, Edinburgh.
4. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
5. Foster, A.E., and A.P. Thompson. 1987. Effects of a semidwarf gene from Jotun on agronomic and quality traits of barley. p. 979-982. *In* S. Yasuda and T. Konishi (eds.) *Barley Genetics V. Proc. Fifth Int. Barley Genet. Symp.*, Okayama, 1986. Sanyo Press Co., Okayama.
6. Franckowiak, J.D. (Unpublished).
7. Haahr, V., and D. von Wettstein. 1976. Studies of an induced, high-yielding dwarf-mutant of spring barley. p. 215-218. *In* H. Gaul (ed.) *Barley Genetics III, Proc. Third Int. Barley Genet. Symp.*, Garching, 1975. Verlag Karl Thiemig, München.
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9. Jia, Q.J., J.J. Zhang, S. Westcott, X.Q. Zhang, M. Bellgard, R. Lance, and C.G. Li. 2009. GA-20 oxidase as a candidate for the semidwarf gene *sdw1/denso* in barley. *Funct. Integr. Genomics* 9:255-262.
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11. Kleinhofs, A. 2006. Integrating molecular and morphological/physiological marker maps. *Barley Genet. Newsl.* 36:66-82.
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16. Murai, M., T. Komazaki, and S. Sato. 2004. Effects of *sd1* and *Ur1* (Undulate rachis - 1) on lodging resistance and related traits in rice. *Breed. Sci.* 54: 333-340.

17. Powell, W., P.D.J. Caligari, W.T.B. Thomas, and J.L. Jinks. 1985. The effects of major genes on quantitatively varying characters in barley. 2. The *denso* and day length response loci. *Heredity* 54:349-352.
18. Powell, W., P.D.J. Caligari, W.T.B. Thomas, and J.L. Jinks. 1991. The effects of major genes on quantitatively varying characters in barley. 4. The *GPert* and *denso* loci and quality characters. *Heredity* 66:381-389.
19. Rasmusson, D.C., E.E. Bantari, and J.W. Lambert. 1973. Registration of M21 and M22 semidwarf barley. *Crop Sci.* 13:777.
20. Yin, X., P.C. Struik, F.A. van Eeuwijk, P. Stam, and J. Tang. 2005. QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley. *J. Exp. Bot.* 56:967-976.
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[http://www.cdesign.com.au/proceedings_abts2005/posters%20\(pdf\)/poster_li.pdf](http://www.cdesign.com.au/proceedings_abts2005/posters%20(pdf)/poster_li.pdf).

Prepared:

D.C. Rasmusson. 1988. *Barley Genet. Newsl.* 18:87 as BGS 468.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:444-445.

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:277-278.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:176-178,

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

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

Previous nomenclature and gene symbolization:

Many noded dwarf = *m* (2, 4).

Inheritance:

Monofactorial recessive (2, 3, 4).

Location is unknown.

Description:

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

Origin of mutant:

A spontaneous mutant in Mesa (Clho 2328) (2).

Mutational events:

mnd1.a (GSHO 253) in Mesa (Clho 2328) (2).

Mutant used for description and seed stocks:

mnd1.a (GSHO 253) in Mesa; *mnd1.a* from R.I. Wolfe's Multiple Recessive Marker Stock for chromosome 2 in Bowman (PI 483237)*9 (GSHO 2038, BW518, NGB 20746).

References:

1. Cooper, J.P. (Unpublished).
2. Harlan, H.V., and M.N. Pope. 1922. Many-noded dwarf barley. J. Hered. 13:269-273.
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4. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.

Prepared:

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

BGS 520, Male sterile genetic 48, *msg48*

Stock number: BGS 520
Locus name: Male sterile genetic 48
Locus symbol: *msg48*

Previous nomenclature and gene symbolization:

Male sterile genetic jt = *msg,,jt* and Msg76-5 (3).

Inheritance:

Monofactorial recessive (2, 3).

Probably located in chromosome 1H (1); *msg48.jt* is associated with SNP markers from 1_0744 to 1_0552 (positions 39.84 to 88.33 cM) in 1H bins 05 to 08 of a heterozygous plant from the Bowman backcross-derived stock BW585, plus small heterozygous regions in 4HL and 7HL, (1).

Description:

Selfing - 5% (2), but it may be near 50% in certain environments.

Outcrossing - Complete female fertility (2).

Stamens - anthers slightly smaller than fertile sib with filament elongation, but no stomium (2).

Origin of mutant:

A spontaneous mutant in Simba (PI 584816, NGB 1505) (2).

Mutational events:

msg48.jt (MSS525, GSHO 2401) in Simba (PI 584816, NGB 1505) (2, 3).

Mutant used for description and seed stocks:

msg48.jt (GSHO 2401) in Simba; *msg48.jt* in Bowman (PI 483237)*4 (GSHO 1925, BW585, NGB 24136).

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., and E.A. Hockett. 1992. Allelism tests for the genetic male sterile *msg,,jt*. *Barley Genet. Newsl.* 21:23-24.
3. Hockett, E. A. 1984. Coordinator's report. The genetic male sterile barley collection. *Barley Genet. Newsl.* 14:70-75.

Prepared:

J.D. Franckowiak and E.A. Hockett. 1997. *Barley Genet. Newsl.* 26:447.

Revised:

J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:123.

BGS 521, Mottled leaf 1, *mtt1*

Stock number: BGS 521
Locus name: Mottled leaf 1
Locus symbol: *mtt1*

Previous nomenclature and gene symbolization:

Mottled leaves = *mt* (5).
Mottled leaves 3 = *mt₃* (4).

Inheritance:

Monofactorial recessive (5).
Located in chromosome 1H (4); based on linkage drag near the *s/s1.a* (small lateral spikelet 1) locus (3); *mtt1.a* is associated with SNP markers 1_0760 to 2_0229 (positions 52.84 to 106.61 cM) in 1H bins 05 to 10 of the Bowman backcross-derived line BW600 (1), likely in 1H bin 08.

Description:

Seedlings have two to four clearly marked white bands across or partially across the leaves. Necrosis of the white region occurs later and the leaf is constricted in these regions. Temperatures at germination over 20°C reduce the extent of mottling. Plant mortality is low at Edmonton, Alberta, Canada, where temperatures are low, but nearly 100% at St. Paul, Minnesota, USA (4). Heading of the Bowman backcross-derived line BW600 was delayed by about 6 days, plants were approximately 10% shorter, and grain yields were 15 to 30% of normal. Compared to Bowman, kernels of BW600 were slightly shorter and narrower and kernel weights were 10 to 30% lower (2).

Origin of mutant:

An induced mutant in Montcalm (CIho 7149) (4).

Mutational events:

mtt1.a (*mt*) (Alb Acc 284, OUM070, GSHO 622) in Montcalm (CIho 7149) (4).

Mutant used for description and seed stocks:

mtt1.a (OUM070, GSHO 622) in Montcalm; *mtt1.a* in Bowman (PI 483237)*4 (GSHO 2036); *mtt1.a* in Bowman*7 (BW600, NGB 22166).

References:

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

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:448.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:179.

BGS 522, Eceriferum-yi, *cer-yi*

Stock number: BGS 522
Locus name: Eceriferum-yi
Locus symbol: *cer-yi*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2H (1); *cer-yi.254* is associated with SNP markers 1_0326 to 1_1533 (positions 16.91 to 141.56 cM) in 2H bins 01 to 10 of the Bowman backcross-derived line BW140 (1).

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (4). Plants of line Bowman backcross-derived line containing *cer-yi.254*, BW140, headed over one day later than Bowman, had 2 or 3 more kernels per spike, and kernels were slightly shorter and lighter. Grain yields were slightly lower than those of Bowman (2). During development of the line BW140, slightly reduced fertility was observed in F1 plants (2). Since the SNP markers retained BW140 involve a large portion of 2HL (1), the *cer-yi.254* mutant may include an inversion (1, 2).

Origin of mutant:

An X-ray induced mutant in Foma (Clho 11333) (3).

Mutational events:

cer-yi.254 (NGB 111141, GSHO 1542) in Foma (Clho 11333), *-yi.956* (NGB 111844) in Bonus (PI 189763) (4); *cer-yi.1213* (NGB 112101) in Kristina (NGB 1500), *-yi.1353* (NGB 112241) in Bonus (5).

Mutant used for description and seed stocks:

cer-yi.254 (GSHO 1542, NGB 111141) in Foma; *cer-yi.254* in Bowman (PI 483237)*3 (GSHO 2213); *cer-yi.254* in Bowman*4 (BW140, NGB 20546).

References:

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

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:449.

Revised:

U. Lundqvist and J. D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:180.

BGS 523, Eceriferum-yj, *cer-yj*

Stock number: BGS 523
Locus name: Eceriferum-yj
Locus symbol: *cer-yj*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 1HS (1); *cer-yj.667* is associated with SNP markers 3_0969 to 3_0918 (positions 0.0 to 17.27 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW141 (1).

Description:

Surface wax coating on the leaf blade appears absent on the upper three leaves (wax code ++ ++ -) (4). Plants of the original stock are semidwarf (about 3/4 normal height), but those of the Bowman backcross-derived line are not. Changes in the expression of other morphological trait were not observed in the Bowman backcross-derived line BW141 (2).

Origin of mutant:

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

Mutational events:

cer-yj.667 (NGB 111555, GSHO 1543) in Bonus (PI 189763), *-yj.1217* (NGB 112105) in Kristina (NGB 1500) (3); *cer-yj.937* (NGB 111825) in Bonus (5); *cer-yj.1150* (NGB 112038) in Kristina, *-yj.1811* (NGB 117359) in Bonus (6).

Mutant used for description and seed stocks:

cer-yj.667 (NGB 111555, GSHO 1543) in Bonus; *cer-yj.667* in Bowman (PI 483237)*3 (GSHO 2214); *cer-yj.667* in Bowman*4 (BW141, NGB 20567).

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. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. *Barley Genet. Newsl.* 7:92-96.
5. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. *Barley Genet. Newsl.* 12:169-172.
6. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. *Barley Genet. Newsl.* 15:89-93.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:450.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:124.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike, leaf sheath, and stem appears reduced (wax code + + ++) (2). The original stock has narrow leaves, a lax spike, and extra wax coating on the kernels. Plants of the Bowman backcross-derived line seem to lack surface wax on the nodes (glossy node).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-yk.627 (NGB 111515, GSHO 1544) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

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

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:451.

BGS 525, Eceriferum-yl, *cer-yl*

Stock number: BGS 525
Locus name: Eceriferum-yl
Locus symbol: *cer-yl*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).
Location is unknown.

Description:

Surface wax coating on the spike, the leaf sheath, and the stem appears absent (wax code - - ++). The original mutant stock produces weak plants (about 3/4 normal height) with a high level of sterility (2). Plants in the Bowman backcross-derived line are semidwarf with waxy nodes, coiled peduncles, globose shaped seeds, and poorly attached hull. Reduced seed set can be caused by adverse environmental conditions.

Origin of mutant:

A propane disulfonic acid diethyl ester induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-yl.187 (NGB 111073, GSHO 1545), *-yl.188* (NGB 111074) in Bonus (PI 189763) (2);
cer-yl.407 (NGB 111295) in Foma (CIho 11333), *-yl.821* (NGB 111709) in Bonus (3).

Mutant used for description and seed stocks:

cer-yl.187 (GSHO 1545, NGB 111073) in Bonus; *cer-yl.187* in Bowman (PI 483237)*6 (GSHO 2216); *cer-yl.187* in Bowman*7 (BW143, NGB 20649).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. :92-96.
3. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:452.

BGS 526, Eceriferum-ym, *cer-ym*

Stock number: BGS 526
Locus name: Eceriferum-ym
Locus symbol: *cer-ym*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike, the leaf sheath and stem, and the leaf blade appears absent (wax code - - -) (2). Plants are weak and semidwarf (2/3 normal height) and heading is delayed. In the Bowman backcross-derived line, plants are weak, culms have a kinked peduncle, nodes are wax covered, and seeds are small, globe shaped, and nearly hullless.

Origin of mutant:

An ethylene oxide induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-ym.130, (NGB 111015), *-ym.753* (NGB 111641, GSHO 1546) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

cer-ym.753 (NGB 111641, GSHO 1546) in Bonus; *cer-ym.753* in Bowman (PI 483237)*5 (GSHO 2217); *cer-ym.753* in Bowman*7 (BW144, NGB 20550).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:453.

BGS 527, Eceriferum-yn, *cer-yn*

Stock number: BGS 527
Locus name: Eceriferum-yn
Locus symbol: *cer-yn*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Probably located in chromosome 1H (1); *cer-yn.1112* is associated with SNP markers between 2_0479 to 2_0095 (positions 0.0 to 89.85 cM) in 1H bins 01 to 08 of the Bowman backcross-derived line BW145 and also with SNP markers between 2_1187 and 2_1338 (positions 51.62 and 74.97) in 2H bins 05 to 06 (1).

Description:

Surface wax coating on the spike, leaf sheath, and stem is reduced (wax code + + +) (4). In the Bowman backcross-derived line, the wax coating is only slightly reduced, but nodes are glossy. Grain weight was slightly reduced in Bowman backcross-derived line BW145 and grain yield was 2/3 to 3/4 of normal (2).

Origin of mutant:

An ethylene imine induced mutant in Kristina (NGB 1500) (3).

Mutational events:

cer-yn.1112 (NGB 112000, GSHO 1547) in Kristina (NGB 1500) (4).

Mutant used for description and seed stocks:

cer-yn.1112 (GSHO 1547, NGB112000) in Kristina; *cer-yn.1112* in Bowman (PI 483237)*2 (GSHO 2218); *cer-yn.1112* in Bowman*4 (BW145, NGB 20551).

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:454.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:125.

BGS 528, Eceriferum-yo, *cer-yo*

Stock number: BGS 528
Locus name: Eceriferum-yo
Locus symbol: *cer-yo*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (2). The original stock in Bonus has a high level of sterility. Seedlings of the original stock and the Bowman backcross-derived line have slightly pale green color.

Origin of mutant:

An ethyl methanesulfonate induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-yo.647 (NGB 111535, GSHO 1548) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

cer-yo.647 (GSHO 1548, NGB 111535) in Bonus; *cer-yo.647* in Bowman (PI 483237)*3 (GSHO 2219); *cer-yo.647* in Bowman*4 (BW146, NGB 20552).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:455.

BGS 529, Eceriferum-yp, *cer-yp*

Stock number: BGS 529
Locus name: Eceriferum-yp
Locus symbol: *cer-yp*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (2). Leaves have a pale green color similar that of some chlorina mutants.

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-yp.949 (NGB 111837, GSHO 1549), *-yp.955* (NGB 111843) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

cer-yp.949 (GSHO 1549, NGB 111837) in Bonus; *cer-yp.949* in Bowman (PI 483237)*2 (GSHO 2220); *cer-yp.949* in Bowman*5 (BW147, NGB 20553).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:456.

BGS 530, Eceriferum-yq, *cer-yq*

Stock number: BGS 530
Locus name: Eceriferum-yq
Locus symbol: *cer-yq*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (2). In the Bowman backcross-derived line, the wax coating is reduced only on upper leaf blades (wax code ++ ++ +).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500) (1).

Mutational events:

cer-yq.1246 (NGB 112134, GSHO 1550) in Kristina (NGB 1500) (2).

Mutant used for description and seed stocks:

cer-yq.1246 (GSHO 1550, NGB 112134) in Kristina; *cer-yq.1246* in Bowman (PI 483237)*3 (GSHO 2221); *cer-yq.1246* in Bowman*2 (BW148, NGB 20554).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:457.

BGS 531, Eceriferum-yr, *cer-yr*

Stock number: BGS 531
Locus name: Eceriferum-yr
Locus symbol: *cer-yr*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike appears greatly reduced or absent, and surface wax coating on the leaf sheath and stem is reduced (wax code -/+ +++) (2). Nodes are glossy and appear to lack surface wax.

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333) (1).

Mutational events:

cer-yr.492 (NGB 111380, GSHO 1551) in Foma (CIho 11333), *-yr.1418* (NGB 112306) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

cer-yr.492 (GSHO 1551, NGB 111380) in Foma; *cer-yr.492* in Bowman (PI 483237)*5 (BW149, NGB20555).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:458.

BGS 532, Eceriferum-ys, *cer-ys*

Stock number: BGS 532
Locus name: Eceriferum-ys
Locus symbol: *cer-ys*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the leaf blade appears absent (wax code ++ ++ -) (2). The original stock has a lax spike.

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-ys.680 (NGB 111568, GSHO 1552), *-ys.1352* (NGB 112240) in Bonus (PI 189763) (2); *cer-ys.1182* (NGB 117268), *-ys.1247* (NGB 112135) in Kristina (NGB 1500) (3); *cer-ys.1826* (NGB 117374) in Bonus (4).

Mutant used for description and seed stocks:

cer-ys.680 (GSHO 1552, NGB 111568) in Bonus; *cer-ys.680* in Bowman (PI 483237)*3 (GSHO 2222); *cer-ys.680* in Bowman*5 (BW150, NGB 20556).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. Barley Genet. Newsl. 12:169-172.
3. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.
4. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:459.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

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

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (4). In the Bowman backcrossed-derived line, culm nodes appear to lack surface wax. Most other morphological traits of plants in the Bowman backcross-derived line BW151 were similar to those of Bowman, except for kernel weights were 10 to 15% lower. Grain yields varied from equal to 50% lower (2).

Origin of mutant:

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

Mutational events:

*cer-*yt*.758* (NGB 111646), *-*yt*.938* (NGB 111826, GSHO 1553), *-*yt*.1333* (NGB 112221) in Bonus (PI 189763) (4); *cer-*yt*.1127* (NGB 112015), *-*yt*.1304* (NGB 112192) in Kristina (NGB 1500), *-*yt*.1427* (NGB 112315), *-*yt*.1458* (NGB 112346), *-*yt*.1493* (NGB 112381), *-*yt*.1766* (NGB 112581), *-*yt*.1822* (NGB 117370) in Bonus (5); *cer-*yt*.1379* (NGB 112267) in Bonus (6).

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 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).
4. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. *Barley Genet. Newsl.* 12:169-172.
5. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. *Barley Genet. Newsl.* 15:89-93.
6. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. *Barley Genet. Newsl.* 18:88-91.

Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:126.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Probably located in chromosome 1H (1); *cer-yu.159* is associated with SNP markers between 1_0275 to 2_1126 (positions 63.72 to 110.10 cM) in 1H bins 06 to 10 of the Bowman backcross-derived line BW152 (1), but small donor parent segments in 3HL (SNP markers 2_0523 to 1_0754 at positions 173.82 to 190.87) and in 4HL (SNP markers 2_0765 to 2_0384 at 127.80 to 133.98) are retained in BW152 (1).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 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).
4. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. *Barley Genet. Newsl.* 15:89-93.

Prepared:

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

Revised:

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

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 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).
4. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. *Barley Genet. Newsl.* 15:89-93.
5. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. *Barley Genet. Newsl.* 18:88-91.

Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:128.

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

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

Previous nomenclature and gene symbolization:

Glaucous head = *ge* (10).
Glossy spike 1 = *Gle1* (9).

Inheritance:

Monofactorial dominant (5, 8).
Located in chromosome 1HS (9); about 4.2 cM distal from the *Hor2* (hordein 2, *HorB*) locus (2, 9); *Cer-yy.849* is associated with SNP markers 2_0373 to 1_0419 (positions 0.0 to 6.37 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW154 (1); *Gle1.a* is associated with SNP markers 2_0373 to 2_1226 (positions 0.0 to 13.50 cM) in 1H bins 01 to 02 of the Bowman backcross-derived line BW383 (1), likely in 1H bin 01.

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (6). Concerning the chemical epicuticular wax composition, the *Cer-yy* mutant in Bonus determines waxes lacking β -hydroxy- β -diketones and having relatively increased proportions of primary alcohols. The distribution of the lipid classes is similar to that of wild type plants (8). Other morphological changes were not observed in Bowman backcross-derived lines with *Cer-yy* mutants.

Origin of mutant:

The *Cer-yy* gene or an allele is present in many *Hordeum vulgare* subsp. *spontaneum* accessions and in a few *Hordeum vulgare* subsp. *vulgare* cultivars; an ethyl methanesulfonate induced mutant in Bonus (PI 189763) (3).

Mutational events:

Gle1.a in Cristal (PI 338354) (4, 5, 9, 11); *Cer-yy.437* (NGB 111325) in Foma (CIho 11333), *-yy.649* (NGB 111537), *-yy.650* (NGB 111538), *-yy.849* (NGB 111737, GSHO 1556), *-yy.898* (NGB 111786), *-yy.919* (NGB 111807), *-yy.920* (NGB 111808), *-yy.923* (NGB 111811), *-yy.929* (NGB 111817), *-yy.935* (NGB 111823), *-yy.941* (NGB 111829), *-yy.966* (NGB 111854), *-yy.968* (NGB 111856), *-yy.975* (NGB 111863), *-yy.982* (NGB 111870), *-yy.983* (NGB 111871), *-yy.984* (NGB 111872) in Bonus (PI 189763) (6); *Cer-yy.974* (NGB 111862), *-yy.1717* (NGB 112513) in Bonus (7).

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Jensen, J. 1987. Coordinator's report: Chromosome 5. *Barley Genet. Newsl.* 17:111-113.
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U. 1991. Coordinator's report: *Eceriferum* genes. *Barley Genet. Newsl.* 20:84.
5. Lundqvist, U. 1992. Coordinator's report: *Eceriferum* genes. *Barley Genet. Newsl.* 21:99-101.

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

Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:129-130.

BGS 537, Eceriferum-*yz*, *cer-yz*

Stock number: BGS 537
Locus name: Eceriferum-*yz*
Locus symbol: *cer-yz*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike, leaf sheath, and stem appears slightly reduced (wax code + + ++) (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-yz.1452 (NGB 112340, GSHO 1557), *-yz.1453* (NGB 112341) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

cer-yz.1452 (GSHO 1557, NGB 112340) in Bonus; *cer-yz.1452* in Bowman (PI 483237)*2 (GSHO 2226); *cer-yz.1452* in Bowman*3 (BW155, NGB 21987).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:464.

BGS 538, Eceriferum-xa, *cer-xa*

Stock number: BGS 538
Locus name: Eceriferum-xa
Locus symbol: *cer-xa*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the leaf blade appears absent only on upper leaves (wax code ++ ++ -) (2).

Origin of mutant:

A gamma-ray induced mutant in Foma (Clho 11333) (1).

Mutational events:

cer-xa.585 (NGB 111473, GSHO 1558) in Foma (Clho 11333), *-xa.838* (NGB 111726) in Bonus (PI 189763), *-xa.1113* (NGB 112001) in Kristina (NGB 1500) (2).

Mutant used for description and seed stocks:

cer-xa.585 (GSHO 1558, NGB 111473) in Foma; *cer-xa.585* in Bowman (PI 483237)*2 (GSHO 2227); *cer-xa.585* in Bowman*3 (BW127, NGB 20533).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. Barley Genet. Newsl. 15:89-93.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:465.

BGS 539, Eceriferum-xb, *cer-xb*

Stock number: BGS 539
Locus name: Eceriferum-xb
Locus symbol: *cer-xb*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike appears absent (wax code - ++ ++) (2). In the Bowman backcross-derived line, the peduncle appears to lack surface wax.

Origin of mutant:

An isopropyl methanesulfonate induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-xb.943 (NGB 111831, GSHO 1559) in Bonus (PI 189763), *-xb.1166* (NGB 112054) in Kristina (NGB 1500) (2).

Mutant used for description and seed stocks:

cer-xb.943 (GSHO 1559, NGB 111831) in Bonus; *cer-xb.943* in Bowman (PI 483237)*4 (GSHO 2228); *cer-xb.943* in Bowman*6 (BW128, NGB 20534).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:466.

BGS 540, Eceriferum-xc, *cer-xc*

Stock number: BGS 540
Locus name: Eceriferum-xc
Locus symbol: *cer-xc*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike, leaf sheath, and stem is reduced (wax code + + ++)
(2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-xc.1371 (NGB 112259, GSHO 1560), *-xc.1457* (NGB 112345) in Bonus (PI 189763)
(2).

Mutant used for description and seed stocks:

cer-xc.1371 (GSHO 1560, NGB 112259) in Bonus; *cer-xc.1371* in Bowman (PI 483237)*2 (GSHO 2229); *cer-xc.1371* in Bowman*4 (BW129, NGB 20535).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. Barley Genet. Newsl. 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:467.

BGS 541, Eceriferum-xd, *cer-xd*

Stock number: BGS 541
Locus name: Eceriferum-xd
Locus symbol: *cer-xd*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Surface wax coating on the spike, leaf sheath, and stem is reduced (wax code + + ++)
(2). The Bowman backcross-derived line seems to have extra surface wax on the nodes.

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763) (1).

Mutational events:

cer-xd.1455 (NGB112343, GSHO 1561), *-xd.1492* (NGB 112380) in Bonus (PI 189763)
(2).

Mutant used for description and seed stocks:

cer-xd.1455 (GSHO 1561, NGB 112343) in Bonus; *cer-xd.1455* in Bowman (PI
483237)*2 (GSHO 2230); *cer-xd.1455* in Bowman*4 (BW130, NGB 20536).

References:

1. Lundqvist, U. (Unpublished).
2. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII.
Barley Genet. Newsl. 18:88-91.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:468.

BGS 543, Intermedium spike-f, *int-f*

Stock number: BGS 543
Locus name: Intermedium spike-f
Locus symbol: *int-f*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1, 2).

Location is unknown.

Description:

The spike appears six-rowed, but the lateral spikelets are much smaller, less than half the size of the central spikelets. Lateral spikelets are pointed and often have short awns. Seed set occurs in the lateral spikelets in the upper third of the spike. The base of the spike has shortened rachis internodes and appears erectoides-like (3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (Clho 11333) (3).

Mutational events:

int-f.19 (NGB 115437, GSHO 1767) in Foma (Clho 11333) (2, 3).

Mutant used for description and seed stocks:

int-f.19 (NGB 115437, GSHO 1767) in Foma; *int-f.19* in Bowman (PI 483237)*3 (GSHO 2270); *int-f.19* in Bowman*6 (BW424, NGB 20657).

References:

1. 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. Gustafsson, Å., and U. Lundqvist. 1980. Hexastichon and intermedium mutants in barley. *Hereditas* 92:229-236.
3. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:469.

BGS 544, Intermedium spike-h, *int-h*

Stock number: BGS 544
Locus name: Intermedium spike-h
Locus symbol: *int-h*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Lateral spikelets are enlarged and have an inconspicuously pointed apex, but they do not set seed. Induced mutants show early heading and have an elongated basal rachis internode. The spike appears lax with shortened rachis internodes at the base (1). The Bowman backcross-derived line is slightly shorter (5/6 normal) and produces extra spikelets (up to five fertile ones) at several rachis nodes in the lower half of the spike. Fusion of some spikelets results in double and occasionally triple kernels.

Origin of mutant:

A neutron induced mutant in Kristina (NGB 1500) (1, 2).

Mutational events:

int-h.42 (NGB 115460, GSHO 1768) , *-h.43* (NGB 115461), *-h.44* (NGB 115462) in Kristina (NGB 1500) (1, 2); *int-h.83* (NGB 115501) in Bonus (PI 189763).

Mutant used for description and seed stocks:

int-h.42 (NGB 115460, GSHO 1768) in Kristina; *int-h.42* in Bowman (PI 483237)*5 (GSHO 2271); *int-h.42* in Bowman*6 (BW425, NGB 20658).

References:

1. Gustafsson, Å., and U. Lundqvist. 1980. Hexastichon and intermedium mutants in barley. *Hereditas* 92:229-236.
2. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:470.

BGS 545, Intermedium spike-i, *int-i*

Stock number: BGS 545
Locus name: Intermedium spike-i
Locus symbol: *int-i*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location is chromosome 2HS (1); *int-i.39* is associated with SNP markers 1_1110 to 2_1304 (positions to 34.31 to 58.56 cM) in 2H bins 04 and 05 of the Bowman backcross-derived line BW426) (1), likely in 2H bin 04 or 05.

Description:

Lateral spikelets are enlarged and slightly pointed at the apex, but they fail to set seed. The tip of the spike may have very short rachis internodes and appears very dense or fasciated (4). Plants of the Bowman backcross-derived line BW426 exhibited elongation of the basal rachis internode. BW426 plants were about 3/4 the height of Bowman plants and the spikes had slightly long rachis internodes. Although kernels per spike and seed weights were variable over nurseries, BW426 plants had in general fewer kernels/spike and kernel weights were 10 to 15% below those of Bowman. Grain yields of BW426 were 1/2 to 3/4 of normal (2).

Origin of mutant:

An ethylene imine induced mutant in Kristina (NGB 1500) (4).

Mutational events:

int-i.39 (NGB 115457, GSHO 1769) in Kristina (NGB 1500) (3, 4).

Mutant used for description and seed stocks:

int-i.39 (GSHO 1769, NGB 115457) in Kristina; *int-i.39* in Bowman (PI 483237)*4 (GSHO 2272); *int-i.39* in Bowman*6 (BW426, NGB 20659).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., and U. Lundqvist. 1980. Hexastichon and intermedium mutants in barley. *Hereditas* 92:229-236.
4. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:471.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:181.

BGS 546, Intermedium spike-k, *int-k*

Stock number: BGS 546
Locus name: Intermedium spike-k
Locus symbol: *int-k*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7H (2); *int-k.47* is in the centromeric region closely linked to markers Bmag0217 and Bmac0162 in 7H bins 6 to 7 (2).

Description:

The spike is short and dense in the original mutant. Lateral spikelets are enlarged and the apex is pointed, and they occasionally have a short awn. Seed set does not occur in lateral spikelets and the central spikelets are semi-sterile (3). Plants of the original stock have a dense coating of surface waxes. In the Bowman backcross-derived line, plants are small and weak (about 1/2 normal height) and have short spikes (1/2 normal), reduced awn length (3/4 normal), and very poor seed set. Awns of plants in the derived line are semi-rough, but F1 hybrids with Bowman have semi-smooth awns (1).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500) (3).

Mutational events:

int-k.47 (NGB 115465, GSHO 1770) in Kristina (NGB 1500) (3).

Mutant used for description and seed stocks:

in-k.47 (GSHO 1770, NGB 115465) in Kristina; *int-k.47* in Bowman (PI 483237)*7 (BW427, NGB 20660).

References:

1. Franckowiak, J.D. (Unpublished).
2. Dahleen, L.S., and J.D. Franckowiak. 2006. SSR Linkages to eight additional morphological marker traits. *Barley Genet. Newsl.* 36:12-16.
3. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:472.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:279.

BGS 547, Intermedium spike-m, *int-m*

Stock number: BGS 547
Locus name: Intermedium spike-m
Locus symbol: *int-m*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).
Location is unknown.

Description:

The spike is very short and has irregular rachis internode lengths. Lateral spikelets are enlarged and pointed, but they do not set seed. Spikelet density at the base of the spike is increased. Rachis internodes at the tip of the spike are very short, and the spike appears to have two or three fused or fasciated terminal spikelets. Tillering of *int-m* plants is increased (1, 4) and heading is slightly earlier (4).

Origin of mutant:

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

Mutational events:

int-m.85 (NGB 115503, GSHO 1772) in Bonus (PI 189763) (3); *int-m.la* (GSHO 1773) in Lamont (PI 512036) (2).

Mutant used for description and seed stocks:

int-m.85 (GSHO 1772, NGB 115503) in Bonus; *int-m.85* in Bowman (PI 483237)*7 (GSHO 2273, BW429, NGB 20661); *int-m.la* from Lamont in Bowman (PI 483237)*5 (GSHO 2274, BW430, NGB 20662).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unculm 2 (*cul2*) mutant. *Theor. Appl. Genet.* 106:846-857.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:473.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:280.

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

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

Previous nomenclature and gene symbolization:

Angustifolia = *Ang* (4).

Inheritance:

Monofactorial incomplete dominant (3).

Location in chromosome 1HS (1); associated with 1H based on trisomic analysis (3);

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

Description:

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

Origin of mutant:

A spontaneous mutant in an unknown six-rowed cultivar (3).

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 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. Tsuchiya, T., and R.L. Haines. 1975. Trisomic analysis of nine mutant genes in barley. *Barley Genet. Newsl.* 5:67-69.
4. Tsuchiya, T., S.D. Tanksley, and R. Ward. 1976. Trisomic analysis of three mutant genes in barley. *Barley Genet. Newsl.* 6:95.

Prepared:

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

Revised:

J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:131.

BGS 549, Long glume awn 1, *Lga1*

Stock number: BGS 549
Locus name: Long glume awn 1
Locus symbol: *Lga1*

Previous nomenclature and gene symbolization:

Long glume awn = *L* (2, 3).

Long outer glume = *Log* (1); this gene symbol was recommended by Helgason (1), but the symbol was already used for the *eog1* (elongated outer glume 1) gene (4).

Inheritance:

Monofactorial dominant (1, 2).

Location is unknown.

Description:

In spikelets of plants with the dominant allele (*Lga1.a*), the glume (outer) plus its awn is much longer than the kernel. Heterozygotes have a glume awn of intermediate length. In the short glume awn phenotype (*lga1.b*), the glume length and width are unaltered, but the glume plus its awn are about the same length as the kernel. Tsuchiya (4) reports that the glume awn length is 4 to 6 mm for the short type and 11 to 13 mm for the long type. Recessive alleles at the *eog1* locus (see BGS 57) produce an array of glume sizes, some of which have glumes phenotypically similar to those associated with the dominant allele at the *Lga1* locus. However, large glumes controlled by *eog* alleles are wider than normal and show a recessive inheritance pattern.

Origin of mutant:

The short glume awn appears to be the mutant phenotype and occurs commonly in two-rowed cultivars of Occidental origin.

Mutational events:

Lga1.a in Guy Mayle (Clho 620, GSHO 835) (2, 3); *lga1.b* in Canadian Thorpe (PI 2710) (2, 3).

Mutant used for description and seed stocks:

Lga1.a in Guy Mayle (Clho 620, GSHO 835); *lga1.b* in Canadian Thorpe (GSHO 834); *lga1.b* from Hector (Clho 15514) in Bowman (PI 483237); *Lga1.a* from Akashinriki (OUJ659, PI 467400) mutant OUM113 in Bowman (PI 483237)*8 (GSHO 2147, BW479, NGB 20707).

References:

1. Helgason, S.B. 1964. Inheritance of glume characteristics in some barley crosses. p. 181-185. *In* S. Broekhuizen, G. Dantuma, H. Lamberts, and W. Lange (eds.) Barley Genetics I. Proc. First Int. Barley Genet. Symp., Wageningen, 1963. Centre for Agricultural Publications and Documentation, Wageningen.
2. Neatby, K.W. 1926. Inheritance of quantitative and other characters in a barley cross. *Sci. Agric.* 7:77-84.
3. Neatby, K.W. 1929. An analysis of the inheritances of quantitative characters and linkage in barley. *Sci. Agric.* 9:701-718.
4. Tsuchiya, T. 1974. Preliminary results on genetic studies of outer glume characters in barley. *Barley Genet. Newsl.* 4:76-78.

Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:475.

BGS 550, Breviaristatum-b, *ari-b*

Stock number: BGS 550
Locus name: Breviaristatum-b
Locus symbol: *ari-b*

Previous nomenclature and gene symbolization:

Breviaristatum-11 = *ari-11* (1, 2).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Plants are semidwarf with reduced viability and fertility; leaves are broad, but shortened and lighter green in color; and awns are about 3/4 normal length. Growth is markedly retarded during warm seasons and relatively good during cool seasons (2).

Development of reproductive organs is delayed and sterility causes a stock maintenance problem.

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ari-b.11 (NGB 115856, GSHO 1649), *-b.13* (NGB 115859), *-b.17* (NGB 115863), *-b.19* (115886), *-b.29* (115877) in Bonus (PI 189763), *-b.175* (NGB 115985), *-b.226* (NGB 116035), *-b.238* in Foma (Clho 11333) (2).

Mutant used for description and seed stocks:

ari-b.11 (NGB 115856, GSHO 1649) in Bonus; *ari-b.11* in Bowman (PI 483237)*3 (GSHO 2157, BW039, NGB 20447).

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

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley. Genet. Newsl. 26:476.

BGS 551, Breviaristatum-f, *ari-f*

Stock number: BGS 551
Locus name: Breviaristatum-f
Locus symbol: *ari-f*

Previous nomenclature and gene symbolization:

Breviaristatum-21 = *ari-21* (3, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7H (1); *ari-f.21* is associated with SNP markers 1_0721 to 1_1343 (positions 82.82 to 134.43 cM) in 7H bins 06 to 08 of the Bowman backcross-derived line BW044 (1).

Description:

Awns are thin and often 1/2 to 3/4 normal length, and awn length decreases toward the top of the spike. Spikes are more lax and have fewer rachis internodes than those of parental cultivars. Deformation of the lemma apex causes apical kernels to be naked (4). Plants of the Bowman backcross-derived line for *ari-f.21*, BW044, were 15 to 25% shorter than Bowman and had awns that extended 4 cm beyond the tip of the spike vs. 11 to 12 cm for Bowman. Kernels of BW044 were shorter, 8.6 vs. 9.6 mm, and thinner, 3.3 vs. 3.8 mm, than those of Bowman and weighed 40% less, 3.5 vs. 5.8 mg. The grain yields of BW044 ranged from very little to 20% those of Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ari-f.21 (NGB 115869, GSHO 1654) in Bonus (PI 189763) (5); *ari-f.42* (NGB 115893), -*f.47* (NGB 115899) in Bonus (4); *ari-f.52* (NGB 115905), -*f.54* (NGB 115907), -*f.55a* (NGB 115908) in Bonus (5); *ari-f.113* (NGB 115925) in Foma (Clho 11333) (4); *ari-f.115* (NGB 115927) in Foma (5); *ari-f.123* (NGB 115935), -*f.136* (NGB 115946) in Foma (4); *ari-f.155* (NGB 115964) in Foma (5); *ari-f.168* (NGB 115978), -*f.169* (NGB 115979), -*f.170* (NGB 115980), -*f.224* (NGB 116033), -*f.225* (NGB 116034), -*f.233* (NGB 116043), -*f.235* (NGB 116045) in Foma, -*f.253* (NGB 116064), -*f.254* (NGB 116062), -*f.260* (NGB 116069), -*f.266* (NGB 116076) in Kristina (NGB 1500) (4); *ari-f.268* (NGB 116079), -*f.275* (NGB 116087), -*f.294* (NGB 116114), -*f.295* (NGB 116115), -*f.300* (NGB 116123) in Kristina (5).

Mutant used for description and seed stocks:

ari-f.21 (GSHO 1654, NGB 115869) in Bonus; *ari-f.21* in Bowman (PI 483237)*5 (GSHO 2158); *ari-f.21* in Bowman*7 (BW044, NGB 20452).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:477.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:182-183.

BGS 552, Breviaristatum-j, *ari-j*

Stock number: BGS 552
Locus name: Breviaristatum-j
Locus symbol: *ari-j*

Previous nomenclature and gene symbolization:

Breviaristatum-32 = *ari-32* (1, 2).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Plants are semidwarf (3/4 of normal culm length) and awns are about 5/6 normal length. The peduncle is short and coiled or kinked, and as a result the spike rarely emerges above the flag leaf (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763) (2).

Mutational events:

ari-j.32 (NGB 115881, GSHO 1658) in Bonus (PI 189763) (2); *ari-j.101* (NGB 115914) in Foma (CIho 11333) (3); *ari-j.167* (NGB 115977) in Foma (2).

Mutant used for description and seed stocks:

ari-j.32 (NGB 115881, GSHO 1658) in Bonus; *ari-j.32* in Bowman (PI 483237)*5 (GSHO 2159); *ari-j.32* in Bowman*8 (BW048 NGB 20456).

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:478.

BGS 553, Breviaristatum-k, *ari-k*

Stock number: BGS 553
Locus name: Breviaristatum-k
Locus symbol: *ari-k*

Previous nomenclature and gene symbolization:

Breviaristatum-504 = *ari-504* (1, 2).

Dearistatum-k = *ari-k* (1, 4).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Awns often are normal in length, but they are dehiscent (dearistatum) at maturity.

Variability in awn length is observed over environments and awns seem thinner than normal (2). Awns of plants grown in fall greenhouse nurseries at Fargo, North Dakota, USA, are very short and thread-like.

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

ari-k.501 (NGB 116330, GSHO 1659), *-k.502* (NGB 116331), *-k.503* (NGB 116332), *-k.504* (NGB 116333) in Bonus (PI 189763) (3).

Mutant used for description and seed stocks:

ari-k.504 (NGB 116330, GSHO 1659) in Bonus; *ari-k.504* in Bowman (PI 483237)*3 (GSHO 2160); *ari-k.504* in Bowman*5 (BW049, NGB 20457).

References:

1. 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. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.
3. Lundqvist, U. (Unpublished).
4. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley I. *Hereditas* 62:25-96.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:479.

BGS 554, Breviaristatum-m, *ari-m*

Stock number: BGS 554
Locus name: Breviaristatum-m
Locus symbol: *ari-m*

Previous nomenclature and gene symbolization:

Breviaristatum-28 = *ari-28* (4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 7HS (1); *ari-m.28* is associated with SNP markers 2_0710 to 2_0307 (positions 4.74 to 9.55 cM) in 7H bin 01 of the Bowman backcrossed-derived line BW051 (1), in 7H bin 01.

Description:

Plants are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (3). Kernels are globe-shaped and awns are about 1/2 normal length (4). Spikes are slightly more lax than normal. Based on the chromosomal position of retained SNP markers and morphological characteristics of Bowman backcross-derived line BW051, the *ari-m.28* may be an allele at the *brh1* (brachytic 1) locus (1, 2).

Origin of mutant:

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

Mutational events:

ari-m.12 (NGB 115858, GSHO 1661), *-m.28* (NGB 115876) in Bonus (PI 189763), *-m.141* (NGB 115951), *-m.177* (NGB 115987) in Foma (Clho 11333), *-m.251* (NGB 116095) in (NGB 1500) (4); *ari-m.269* (NGB 116081) in Kristina (NGB 1500) (4, 5).

Mutant used for description and seed stocks:

ari-m.28 (GSHO 1661, NGB 115876) in Bonus; *ari-m.28* in Bowman (PI 483237)*6 (GSHO 2161); *ari-m.28* in Bowman*8 (BW051, NGB 20459).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:480.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:184.

BGS 555, Breviaristatum-n, *ari-n*

Stock number: BGS 555
Locus name: Breviaristatum-n
Locus symbol: *ari-n*

Previous nomenclature and gene symbolization:

Breviaristatum-45 = *ari-45* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7H (1); *ari-n.45* is associated with SNP markers 1_0721 to 1_0700 (positions 82.82 to 144.00 cM) in 7H bins 06 to 08 of the Bowman backcrossed-derived line BW052 (1).

Description:

Awns are 3/4 normal length and arise at an oblique angle, and they are drastically shortened towards the top of the spike (3). Plant height is normal, but spikes are short due to a reduced number of rachis internodes and apical abortion (3). Plants of the Bowman backcross-derived line for *ari-n.45*, BW052, varied in height over environments from 20% shorter to equal to Bowman. Awns extended in specific environments from 2 to 6 cm beyond the tip of the spike while those of Bowman extended about 11 cm. The kernels of BW052 were thinner, 3.5 vs. 3.8 mm, than those of Bowman, slightly shorter and about 25% less, 4.4 vs. 5.9 mg. Grain yields of BW052 varied from 2/3 to 3/4 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (3).

Mutational events:

ari-n.45 (NGB 115897, GSHO 1662), *-n.46* (NGB 115898) in Bonus (PI 189763), *-n.147* (NGB 115958), *-n.163* (NGB 115973), *-n.164* (NGB 115974), *-n.181* (NGB 115991), *-n.219* (NGB 116028), *-n.220* (NGB 116029), *-n.231* (NGB 11601) in Foma (CIho 11333), *-n.258* (NGB 116067), *-n.292* (NGB 116112) in Kristina (NGB 1500) (3, 4).

Mutant used for description and seed stocks:

ari-n.45 (GSHO 1662, NGB 115897) in Bonus; *ari-n.45* in Bowman*6 (BW052, NGB 20406).

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. 1997. *Barley Genet. Newsl.* 26:481.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:185.

BGS 556, Breviaristatum-o, *ari-o*

Stock number: BGS 556
Locus name: Breviaristatum-o
Locus symbol: *ari-o*

Previous nomenclature and gene symbolization:

Breviaristatum-40 = *ari-40* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HL (1); *ari-o.40* is associated with SNP markers 1_0547 and 3_0166 (about position 232 cM) in 7H bin 14 of the Bowman backcross-derived line BW053 (1).

Description:

Plants are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (3). The culm may have a short or extra internode and a leafy bract below the spike. The peduncle is often slightly coiled, and the basal rachis internode is elongated. Kernels are globe-shaped, and awns are about 3/4 normal length (4). Plants of BW053, the Bowman backcross-derived line for mutant *ari-o.40*, were about 25% shorter than Bowman, 65 vs. 90 cm, and awns were about 3 cm shorter. Rachis internode lengths and kernels were slightly shorter for BW053, but spikes had 2 to 3 more kernels. Kernels of BW053 were slightly shorter than those of Bowman. Kernel weights varied from slightly more to 20% less. Grain yields for BW053 varied from 20 to 50% of the Bowman yields (2).

Origin of mutant:

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

Mutational events:

ari-o.40 (NGB 115890, GSHO 1663), *-o.43* (NGB 115894) in Bonus (PI 189763) (4); *ari-o.143* (NGB 115953) in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

ari-o.40 (GSHO 1663, NGB 115890) in Bonus; *ari-o.40* in Bowman (PI 483237)*6 (GSHO 2162); *ari-o.40* in Bowman*7 (BW053, NGB 20461).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:482.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:186.

BGS 557, Breviaristatum-p, *ari-p*

Stock number: BGS 557
Locus name: Breviaristatum-p
Locus symbol: *ari-p*

Previous nomenclature and gene symbolization:

Breviaristatum-27 = *ari-27* (3).

Inheritance:

Monofactorial recessive (3).

Location is unknown, no SNP markers were retained in the Bowman backcross-derived line BW054 for *ari-p.27* (1).

Description:

Awns are about 3/4 normal length, and sterile spikelets occur at random in the original stocks (3). Initially during backcrossing to Bowman, short awned plants headed later than Bowman. In the Bowman backcross-derived line BW054, plants head about one day later than Bowman and have awn length from the tip of the spike of 6 vs. 11 cm. No other morphological differences were observed (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ari-p.27 (NGB 115875, GSHO 1664) in Bonus (PI 189763) (4); *ari-p.108* (NGB 115928), *-p.172* (NGB 115982), *-p.208* (NGB 116016), *-p.209* (NGB 116017), *-p.223* (NGB 116302) in Foma (Clho 11333) (3); *ari-p.278* (NGB 116091) in Kristina (NGB 1500) (4).

Mutant used for description and seed stocks:

ari-p.27 (GSHO 1664, NGB 115875) in Bonus; *ari-p.27* in Bowman (PI 483237)*3 (GSHO 2163), in Bowman*7 (BW054, NGB 20462).

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. 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. 1997. *Barley Genet. Newsl.* 26:483.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:132.

BGS 558, Breviaristatum-q, *ari-q*

Stock number: BGS 558
Locus name: Breviaristatum-q
Locus symbol: *ari-q*

Previous nomenclature and gene symbolization:

Breviaristatum-271 = *ari-271* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The spike is short with irregular placement of spikelets. Awns are about 3/4 normal length. Lateral spikelets are missing from a few basal rachis nodes and two awns occur occasionally on the terminal spikelet (1). Plants are about 3/4 normal height.

Origin of mutant:

An ethyl methanesulfonate induced mutant in Kristina (NGB 1500) (1).

Mutational events:

ari-q.271 (NGB 119347), *-q.280* (NGB 118094, GSHO 1665), *-q.281* (NGB 116096, 116097) in Kristina (NGB 1500) (1).

Mutant used for description and seed stocks:

ari-q.280 (NGB 118094, GSHO 1665) in Kristina; *ari-q.280* in Bowman (PI 483237)*4 (GSHO 2164); *ari-q.280* in Bowman*7 (BW055, NGB 20463).

References:

1. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. *Hereditas* 80:263-278.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl* 26:484.

BGS 559, *Breviaristatum-r*, *ari-r*

Stock number: BGS 559
Locus name: *Breviaristatum-r*
Locus symbol: *ari-r*

Previous nomenclature and gene symbolization:

Breviaristatum-14 = *ari-14* (4).

Inheritance:

Monofactorial recessive (4).

Location in chromosome 5H (1); *ari-r.14* is associated with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73 cM) in 5H bins 04 to 06 of the Bowman backcross-derived line BW056 (1).

Description:

Plants are semidwarf (less than 1/2 normal height) with compact spikes and globe-shaped kernels. Awns are stiff and less than 1/3 normal length (4). Plants are vigorous, but heading is delayed. This mutant can be placed in the brachytic class of semidwarfs based on growth pattern (3). The growth habit of *ari-r.14* is semi-prostrate. Plants of the Bowman backcross-derived line for *ari-r.14* (BW056) were 1/3 to 1/2 the height of Bowman with peduncles about 1/2 normal length. Leaf blades were short, about half normal, but width was near normal. Awns were 1/2 to 3/4 normal length, the number of fertile spikelets per spike was reduced by about 20%, and spikes had shortened rachis internodes, 3.3 vs. 4.5 mm. Kernels of BW056 were 25% shorter than those of Bowman and kernel weights were nearly 40% less, 3.3 vs. 5.6 mg. Grain yield of BW056 were about 1/3 those of Bowman (2).

Origin of mutant:

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

Mutational events:

ari-r.14 (GSHO 1666, NGB 115860) in Bonus (PI 189763), *-r.202* (NGB 116011) in Foma (CIho 11333) (4); *ari-r.236* (NGB 116046) in Foma (5); *ari-r.282* (NGB 116098) in Kristina (NGB 1500) (4); *ari-r.314* (NGB 116145), *-r.318* (NGB 116151) in Kristina (5).

Mutant used for description and seed stocks:

ari-r.14 (GSHO 1666, NGB 115860) in Bonus; *ari-r.14* in Bowman (PI 483237)*6 (GSHO 2165, BW056, NGB 20464).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of *breviaristatum* mutants in barley. *Hereditas* 80:263-278.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:485.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:187.

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

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

Previous nomenclature and gene symbolization:

Erectoides-18 = *ert-18* (3).

Inheritance:

Monofactorial recessive, but some partial dominance is expressed (3, 6).

Located in chromosome 1H (1); *ert-f.18* is associated with SNP markers 2_0617 to 2_1361 (positions 50.96 to 82.35 cM) in 1H bins 05 to 08 of the Bowman backcross-derived line BW308 (1).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

ert-f.18 (GSHO 478, NGB 112620) in Bonus; *ert-f.18* in Bowman (PI 483237)*6 (GSHO 2004, BW308, NGB 22104).

References:

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

Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 2010. *Barley Genet. Newsl.* 40:133.

BGS 561, Erectoides-h, *ert-h*

Stock number: BGS 561
Locus name: Erectoides-h
Locus symbol: *ert-h*

Previous nomenclature and gene symbolization:

Erectoides-25 = *ert-25* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Plants are semidwarf (about 3/4 normal height), and spike density is increased only slightly (3). Maturity may be somewhat delayed. Because selection of *ert-h* plants is difficult in crosses to Bowman, and the identity of the gene in the Bowman backcross-derived line needs to be rechecked.

Origin of mutant:

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

Mutational events:

ert-h.25 (NGB 112626, GSHO 481) in Bonus (PI 189763) (1); *ert-h.68* (NGB 112667) in Bonus (2).

Mutant used for description and seed stocks:

ert-h.25 (GSHO 481, NGB 112626) in Bonus; *ert-h.25* in Bowman (PI 483237)*3 (GSHO 2252, BW310, NGB 22106).

References:

1. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
2. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) *Recent Plant Breeding Research*. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
3. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:487.

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

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

Previous nomenclature and gene symbolization:

Erectoides-32 = *ert-32* (2).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Spikes are semicompact with rachis internode length values from 2.4 to 2.8 mm. Culm length is 3/4 to 5/6 of normal (5). The improved straw strength of this mutant has potential agronomic value as indicated by the release of the *ert-k.32* stock as the cultivar Pallas (1, 3).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ert-k.32 (NGB 112633, GSHO 485) in Bonus (PI 189763) (2); *ert-k.76* (NGB 112675) in Bonus (3); *ert-k.93* (NGB 112692) in Bonus, *-k.309* (NGB 112825) in Foma (CIho 11333) (5); *ert-k.302* (NGB 112819), *-k.435* (NGB 112951), *-k.459* (NGB 112974), *-k.477* (NGB 112993) in Foma (4).

Mutant used for description and seed stocks:

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

References:

1. Borg, G., K. Fröier, and Å. Gustafsson. 1958. Pallas barley, a variety produced by ionizing radiation: its significance for plant breeding and evolution. p. 1-17. Proc. 2nd Int. Conf. Peaceful Uses Atomic Energy Geneva, 1958, (A/CONF. 15/P/2468).
2. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
3. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
4. Lundqvist, U. (Unpublished).
5. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:488.

BGS 563, Erectoides-I, *ert-I*

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

Previous nomenclature and gene symbolization:

Erectoides-12 = *ert-12* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Spikes are slightly denser with rachis internode length values from 2.7 to 3.0 mm. Plant height is about 5/6 of normal (4).

Origin of mutant:

An X-ray induced mutant in Maja (PI 184884) (1).

Mutational events:

ert-I.12 (NGB 112613, GSHO 486) in Maja (PI 184884) (1); *ert-I.45* (NGB 112645), *-I.72* (NGB 112671) in Bonus (PI 189763) (2); *ert-I.114* (NGB 112713), *-I.155* (NGB 112754), *-I.156* (NGB 112755), *-I.162* (NGB 112762) in Bonus, *-I.304* (NGB 112821), *-I.324* (NGB 112839), *-I.371* (NGB 112887) in Foma (CIho 11333) (3); *ert-I.450* (NGB 112965) in Foma (4).

Mutant used for description and seed stocks:

ert-I.12 (NGB 112613, GSHO 486) in Maja; *ert-I.12* in Bowman (PI 483237)*4 (GSHO 2254); *ert-I.12* in Bowman*5 (BW315, NGB 22110).

References:

1. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
2. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) *Recent Plant Breeding Research*. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
3. Lundqvist, U. (Unpublished).
4. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:489.

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

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

Previous nomenclature and gene symbolization:

Erectoides-44 = *ert-44* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Spikes are semicompact with an estimated rachis internode length of 2.7 mm, and the culm length is 3/4 of normal (3).

Origin of mutant:

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

Mutational events:

ert-p.44 (NGB 112644, GSHO 490) in Bonus (PI 189763) (1); *ert-p.116* (NGB 112715), -*p.117* (NGB 112716) in Bonus, -*p.301* (NGB 112818), -*p.370* (NGB 112886), -*p.501* (NGB 113017) in Foma (CIho 11333) (2).

Mutant used for description and seed stocks:

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

References:

1. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
2. Lundqvist, U. (Unpublished).
3. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

Prepared:

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

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

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

Previous nomenclature and gene symbolization:

Erectoides-50 = *ert-50* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Rachis internode length is reduced slightly to about 3.0 mm in the original mutant, and culm length is about 5/6 of normal (2). The mutant is represented by very late segregates from F₂ progenies of crosses to Bowman. Awn length is reduced slightly.

Origin of mutant:

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

Mutational events:

ert-s.50 (NGB 112649, GSHO 493) in Bonus (PI 189763) (1).

Mutant used for description and seed stocks:

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

References:

1. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
2. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

Prepared:

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

BGS 566, Erectoides-t, *ert-t*

Stock number: BGS 566
Locus name: Erectoides-t
Locus symbol: *ert-t*

Previous nomenclature and gene symbolization:

Erectoides-55 = *ert-55* (7).
Brachytic 4 = *br4* (10).
Brachytic-g = *brh.g* (2, 4).
Brachytic-h = *brh.h* (2, 4).
Brachytic-i = *brh.i* (2, 4).
Brachytic-y = *brh.y* (2, 4).
Brachytic 3 = *brh3* (2, 5).

Inheritance:

Monofactorial recessive (4, 7, 9).
Located in chromosome 2HS (2); approximately 11.4 cM distal from SSR marker Bmac0134 (2), near the boundary between 2H bins 01 and 02 (2); *ert-t.55* is associated SNP markers 1_0326 to 2_0563 (positions 16.91 to 21.19) in 2H bin 02 of the Bowman backcross-derived line BW324 (3); *brh3.g* is associated SNP markers 2_0609 to 1_1059 (positions unmapped to 17.96) in 2H bin 02 of the Bowman backcross-derived line BW091 (3); *brh3.y* is associated SNP markers 1_0326 to 1_0180 (positions 16.91 to 40.06) in 2H bins 02 to 04 of the Bowman backcross-derived line BW094 (3); no SNP markers were retained in 2HS of the Bowman backcross-derived line BW093 for *brh3.i* (3), likely in 2H bin 02.

Description:

Spikes are semi-compact, rachis internode length is about 2.7 mm in the original mutant, and culm length is about 2/3 of normal. These phenotypic traits plus short awns are inherited together (9). Based on general appearance of the plants, *ert-t* can be placed in the brachytic class of semidwarf mutants (4, 10). Awns are about 2/3 normal length and curled or coiled near their tips. The *ert-t.55* mutant has short seedling leaves and is sensitive to gibberellic acid treatment (1). When Bowman was compared to the Bowman backcross-derived lines BW091, BW093, BW094, and BW324, peduncles and plants were about 2/3 of normal length, rachis internodes were slightly short, and lodging was reduced. Kernels are shorter and slightly lighter and yields were about 1/2 normal (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (7).

Mutational events:

ert-t.55 (NGB 112654, GSHO 494) in Bonus (PI 189763) (7); *brh3.g* (17:10:1, GSHO 1672), *brh3.h* (17:11:3, GSHO 1673), *brh3.i* (17:12:1, GSHO 1674) in Birgitta (NGB 1494 and 14667) (2, 4, 5, 8); *brh3.y* (10001, GSHO 1688) in Bido (PI 399485) (2, 4, 6).

Mutant used for description and seed stocks:

ert-t.55 (GSHO 494, NGB 112654) in Bonus; *ert-t.55* in Bowman (PI 483237)*7 (GSHO 2257, BW324, NGB 22119); *brh3.g* in Birgitta (GSHO 1672); *brh3.g* in Bowman*7 (GSHO 2167, BW091, NGB 20496); *brh3.i* in Birgitta (GSHO 1674); *brh3.i* in Bowman*7 (GSHO 2169, BW093, NGB 20499); *brh3.y* in Bido (GSHO 1688); *brh3.y* in Bowman*6 (GSHO 2178, BW094, NGB 20500).

References:

1. Börner, A. 1996. GA response in semidwarf barley. Barley Genet. Newsl. 25:24-26.
2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.

3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology*. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
5. Franckowiak, J.D. 2002. BGS 631, Brachytic 3, *brh3*. *Barley Genet. Newsl.* 32:132.
6. Gaul, H. 1986. (Personal communications).
7. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. *Hereditas* 44:523-530.
8. Lehmann, L.C. 1985. (Personal communications).
9. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.
10. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and erectoides mutants. *Barley Genet. Newsl.* 6:79-81.

Prepared:

- U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:492.
J.D. Franckowiak. 2002. BGS 631, Brachytic 3, *brh3*. *Barley Genet. Newsl.* 32:132.

Revised:

- J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:281-282.
J.D. Franckowiak and U. Lundqvist. 2010. *Barley Genet. Newsl.* 40:134-135.

BGS 567, Erectoides, *ert-v*

Stock number: BGS 567
Locus name: Erectoides-v
Locus symbol: *ert-v*

Previous nomenclature and gene symbolization:

Erectoides-57 = *ert-57* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6H (1); *ert-v.57* is associated with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 of the Bowman backcross-derived line BW326 (1).

Description:

Spikes appear abnormal with irregular placement of kernels. Rachis internode length is reduced with average values from 1.7 to 3.1 mm. Plants are weak and semi-sterile, anthers are often whitish, and culm length is about 3/4 of normal (4). Phenotypically the *ert-v.57* mutant could be classified as an opposite spikelet type. Plants of the Bowman backcross-derived line for *ert-v.57*, BW326, have relatively low vigor with grain yield about 1/3 those of Bowman. BW326 headed 3 days later than Bowman, was 15 to 20% shorter, and had 3 to 6 fewer kernels per spike. Rachis internode lengths averaged 3.2 vs. 4.6 mm for Bowman. Kernel weights for BW326 were 20 to 25% lower and test weights were very low (2).

Origin of mutant:

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

Mutational events:

ert-v.57 (NGB 112656, GSHO 497) in Bonus (3); *ert-v.172* (NGB 112772) in Bonus, -*v.313* in Foma (CIho 11333) (4).

Mutant used for description and seed stocks:

ert-v.57 (GSHO 497, NGB 112856) in Bonus; *ert-v.57* in Bowman (PI 483237)*6 (GSHO 2258); *ert-v.57* in Bowman*7 (BW326, NGB 22121).

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:493.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:188.

BGS 568, Erectoides-x, *ert-x*

Stock number: BGS 568
Locus name: Erectoides-x
Locus symbol: *ert-x*

Previous nomenclature and gene symbolization:

Erectoides-58 = *ert-58* (3).

Inheritance:

Monofactorial recessive (3).

Location in chromosomes 1H or 7H (1); *ert-x.58* is associated with SNP markers 2_0617 to 2_1126 (positions 50.96 to 110.10 cM) in 1H bins 05 to 10 and markers 1_1028 to 2_0230 (positions 97.66 to 118.80 cM) in 7H bin 07 of the Bowman backcrossed-derived line BW327 (1).

Description:

Spikes are semi-compact with a rachis internode length value of 2.7 mm. Culm length is about 3/4 of normal (4). Compared to Bowman, the backcross-derived line BW327 had internode lengths of 3.5 vs. 4.6 mm, awn lengths were 7 vs. 11 cm, and plants headed 3 to 4 days later. Other morphological traits and yields of BW327 were similar to those of Bowman (2).

Origin of mutant:

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

Mutational events:

ert-x.58 (NGB 112657, GSHO 498) in Bonus (PI 189763) (3, 4).

Mutant used for description and seed stocks:

ert-x.58 (GSHO 498, NGB 112657) in Bonus; *ert-x.58* in Bowman (PI 483237)*5 (GSHO 2259); *ert-x.58* in Bowman*7 (BW327, NGB 22122).

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:494.

Revised:

U. Lundqvist and J.D. Franckowiak. 2010. *Barley Genet. Newsl.* 40:136.

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

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

Previous nomenclature and gene symbolization:

Erectoides-69 = *ert-69* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Plants have slightly denser spikes than the parent with an average rachis internode length value of 2.8 mm. Culm length is about 5/6 of normal (2). The mutant phenotype has not been observed in crosses to Bowman.

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (1).

Mutational events:

ert-y.69 (NGB 112668, GSHO 499) in Bonus (PI 189763) (1).

Mutant used for description and seed stocks:

ert-y.69 (NGB 112668, GSHO 499) in Bonus; *ert-y.69* in Bowman (PI 483237)'1 (BW328, NGB 22123).

References:

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

Prepared:

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

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

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

Previous nomenclature and gene symbolization:

Erectoides-71 = *ert-71* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Plants have slightly denser spikes than their parent; with a rachis internode length value of 2.8 mm. Culm length is about 3/4 of normal (2). Variability within the spike in rachis internode length occurs in the Bowman backcross-derived line. Also, mutant plants have leaf blades that are slightly narrower than those of normal sibs.

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (1).

Mutational events:

ert-z.71 (NGB 112670, GSHO 500) in Bonus (PI 189763) (1).

Mutant used for description and seed stocks:

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

References:

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

Prepared:

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

BGS 571, Erectoides-za, *ert-za*

Stock number: BGS 571
Locus name: Erectoides-za
Locus symbol: *ert-za*

Previous nomenclature and gene symbolization:

Erectoides-102 = *ert-102* (2).
Brachytic 7 = *br7* (3).

Inheritance:

Monofactorial recessive (1, 2).
Location is unknown.

Description:

Plants are semidwarf (3/4 normal height) and can be placed in the brachytic class of semidwarfs (1, 3). Peduncles are relatively short, the leaf blade attachment appears more erect than normal, and kernels are slightly rounded or globe-shaped.

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (2).

Mutational events:

ert-za.102 (NGB 112701, GSHO 501), *-za.146* (NGB 112745) in Bonus (PI 189763) (2).

Mutant used for description and seed stocks:

ert-za.102 (NGB 112701, GSHO 501) in Bonus; *ert-za.102* in Bowman (PI 483237)*6 (GSHO 2261); *ert-za.102* in Bowman*7 (BW330, NGB 22125).

References:

1. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
2. Lundqvist, U. (Unpublished).
3. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and erectoides mutants. *Barley Genet. Newsl.* 6:79-81.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:497.

BGS 572, Erectoides-zb, *ert-zb*

Stock number: BGS 572
Locus name: Erectoides-zb
Locus symbol: *ert-zb*

Previous nomenclature and gene symbolization:

Erectoides-132 = *ert-132* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Plants are 3/4 normal height and spikes tend to emerge prematurely (1).

Origin of mutant:

A diepoxybutane induced mutant in Bonus (PI 189763) (1).

Mutational events:

ert-zb.132 (NGB 112731, GSHO 502) in Bonus (PI 189763) (1).

Mutant used for description and seed stocks:

ert-zb.132 (NGB 112731, GSHO 502) in Bonus; *ert-zb.132* in Bowman (PI 483237)*5
(GSHO 2262, BW331, NGB 22126)

References:

1. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:498.

BGS 573, Erectoides-zc, *ert-zc*

Stock number: BGS 573
Locus name: Erectoides-zc
Locus symbol: *ert-zc*

Previous nomenclature and gene symbolization:

Erectoides-149 = *ert-149* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Spikes are semicompact and plants are semidwarf (3/4 normal height). The basal rachis internode is slightly elongated.

Origin of mutant:

An ethylene oxide induced mutant in Bonus (PI 189763) (1).

Mutational events:

ert-zc.149 (NGB 112748, GSHO 503) in Bonus (PI 189763) (1).

Mutant used for description and seed stocks:

ert-zc.149 (NGB 112748, GSHO 503) in Bonus; *ert-zc.149* in Bowman (PI 483237)*3 (GSHO 2263); *ert-zc.149* in Bowman*4 (BW332, NGB 22127).

References:

1. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:499.

BGS 574, Erectoides-ze, *ert-ze*

Stock number: BGS 574
Locus name: Erectoides-ze
Locus symbol: *ert-ze*

Previous nomenclature and gene symbolization:

Erectoides-105 = *ert-105* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Spikes are semicompact, but other phenotypic traits appear normal.

Origin of mutant:

A spontaneous mutant in Bonus (PI 189763) (1).

Mutational events:

ert-ze.105 (NGB 112704, GSHO 505) in Bonus (PI 189763) (1).

Mutant used for description and seed stocks:

ert-ze.105 (NGB 112704, GSHO 505) in Bonus; *ert-ze.105* in Bowman (PI 483237)*5 (GSHO 2264); *ert-ze.105* in Bowman*6 (BW334, NGB 22129).

References:

1. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:500.

BGS 575, Reaction to *Puccinia hordei* 6, *Rph6*

Stock number: BGS 575
Locus name: Reaction to *Puccinia hordei* 6 (barley leaf rust)
Locus symbol: *Rph6*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth = X (3, 4).
Resistance to *Puccinia hordei* Otth = Pa_x (4).

Inheritance:

Monofactorial dominant, but an allele at the *Rph2* (reaction to *Puccinia hordei* 2) locus is present in the original cultivar (3, 4, 5).
Location is unknown.

Description:

The seedling reaction type is 0;ⁿ - 1^c with race 4 culture 57-19. Heterozygotes frequently show an intermediate response (type 2 or 3 reaction) to inoculation with pathogen races (3).

Origin of mutant:

Natural occurrence in Bolivia (PI 36360) (2, 3).

Mutational events:

Rph6.f in Bolivia (PI 36360, GSHO 1598) (3, 4).

Mutant used for description and seed stocks:

Rph6.f in Bolivia (PI 36360, GSHO 1598); *Rph6.f* (without an *Rph2* allele) in Bowman (PI 483237)*4 (GSHO 2323) (1); *Rph6.f* (without an *Rph2* allele) in Bowman*8 (PI643155, BW756, NGB 22461).

References:

1. Chicaiza, O., J.D. Franckowiak, and B.J. Steffenson. 1996. Backcross-derived lines of barley differing for leaf rust resistance genes. pp. 198-200. In G.H.J. Kema, R.E. Niks, and R.A. Daamen (eds.) Proc. 9th Eur. & Medit. Cereal Rusts & Mildews Conf. Drukkerij Ponsen en Looijen B.V., Wageningen.
2. Henderson, M.T. 1945. Studies of the sources of resistance and inheritance of reaction to leaf rust, *Puccinia anomala* Rostr., in barley. Ph.D. Thesis. Univ. of Minnesota, St. Paul.
3. Roane, C.W. 1962. Inheritance of reaction to *Puccinia hordei* in barley. I. Genes for resistance among North American race differentiating varieties. *Phytopathology* 52:1288-1295.
4. Roane, C.W., and T.M. Starling. 1967. Inheritance of reaction to *Puccinia hordei* in barley. II. Gene symbols for loci in differential cultivars. *Phytopathology* 57:66-68.
5. Starling, T.M. 1955. Sources, inheritance, and linkage relationships of resistance to race 4 of leaf rust (*Puccinia hordei* Otth), race 9 of powdery mildew (*Erysiphe graminis hordei* El. Marchal), and certain agronomic characters in barley. *Iowa State Coll. J. Sci.* 30:438-439.

Prepared:

J.D. Franckowiak and Y. Jin. 1997. *Barley Genet. Newsl.* 26:501.

BGS 576, Reaction to *Puccinia hordei* 8, *Rph8*

Stock number: BGS 576
Locus name: Reaction to *Puccinia hordei* 8 (barley leaf rust)
Locus symbol: *Rph8*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 8 = *Pa8* (3, 4).

Inheritance:

Monofactorial dominant (3).

Location is unknown.

Description:

The seedling reaction type is 1-2 to 2^{CN} with race 8 culture ND8702, depending on environmental conditions. Egypt 4 is susceptible to most isolates of *Puccinia hordei* (2, 3, 4), but a resistant reaction to a few isolates is reported (1, 3, 4). Resistance is expressed better at 15EC than at 20EC, and the infection type observed in heterozygotes is often intermediate between those of the parents.

Origin of mutant:

Natural occurrence in Egypt 4 (CIho 6481) (3, 4).

Mutational events:

Rph8.h in Egypt 4 (CIho 6481, GSHO 1600) (3, 4).

Mutant used for description and seed stocks:

Rph8.h in Egypt 4 (CIho 6481, GSHO 1600); *Rph8.h* in Bowman (PI 483237)*2 (GSHO 2324); *Rph8.h* in Bowman*8 (PI 643157, BW760, NGB 22466).

References:

1. Levine, M.N., and W.J. Cherewick. 1952. Studies on dwarf leaf rust of barley. U.S. Dep. Agric. Tech. Bull. 1056. 17 p.
2. Reinhold, M., and E.L. Sharp. 1982. Virulence types of *Puccinia hordei* from North America, North Africa and the Middle East. Plant Dis. 66:1009-1011.
3. Roane, C.W. 1962. Inheritance of reaction to *Puccinia hordei* in barley. I. Genes for resistance among North American race differentiating varieties. Phytopathology 52:1288-1295.
4. Tan, B.H. 1977. A new gene for resistance to *Puccinia hordei* in certain Ethiopian barleys. Cereal Rust Bull. 5:39-43.

Prepared:

J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:502.

BGS 577, Reaction to *Schizaphis graminum* 2, *Rsg2*

Stock number: BGS 577
Locus name: Reaction to *Schizaphis graminum* 2 (greenbug)
Locus symbol: *Rsg2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Location is unknown.

Description:

Resistant seedlings infested with greenbugs (aphids) are not killed or severely stunted by a buildup of the greenbug population, but susceptible seedlings are killed or severely stunted (1, 4). The resistance provided by PI 426756 (4 to 5 readings on a 1 to 9 scale) to most *S. graminum* biotypes was less effective than that provided the *Rsg1.a* gene in Post 90 (PI 549081) (2 to 3 readings) (3). PI 426756 was confirmed to provide resistance (2 to 3 readings) to the TX1 isolate of *S. graminum*, which produces a susceptible reaction (9 reading) on Post 90 (2).

Origin of mutant:

Natural occurrence in Joa (PI 426756) (1, 4).

Mutational events:

Rsg2.b in PI 426756 (1).

Mutant used for description and seed stocks:

Rsg2.b in PI 426756 (GSHO 2513).

References:

1. Merkle, O.G., J.A. Webster, and G.H. Mogen. 1987. Inheritance of a second source of greenbug resistance in barley. *Crop Sci.* 27:241-243.
2. Porter, D.R., J.D. Burd, and D.W. Mornhinweg. 2007. Differentiating greenbug resistance genes in barley. *Euphytica* 153:11-14.
3. Porter, D.R., and D.W. Mornhinweg. 2004. Characterization of greenbug resistance in barley. *Plant Breed.* 123:493-494.
4. Webster, J.A., and K.J. Starks. 1984. Sources of resistance in barley to two biotypes of greenbug *Schizaphis graminum* (Rondani), Homoptera: Aphididae. *Protect. Ecol.* 6:51-55.

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:503.

Revised:

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:283.

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

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

Previous nomenclature and gene symbolization:

Early 7 = *ea-b7* (3).
Early maturity-b = *ea-b* (9).

Inheritance:

Monofactorial recessive (3, 4).
Location is unknown.

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

mat-b.7 (NGB 110007, GSHO 1788) in Bonus; *mat-b.7* in Bowman (PI 483237)*3 (GSHO 2282); *mat-b.7* in Bowman*7 (BW507, NGB 20735). (This stock has only a *mat-c* mutant.)

References:

1. Dormling, I., and Å. Gustafsson. 1969. Phytotron cultivation of early barley mutants. Theor. Appl. Genet. 39:51-61.
2. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley

climatology. Biol. Zent. Bl. 101:763-782.

3. Gustafsson, Å., A. Hagberg, and U. Lundqvist. 1960. The induction of early mutants in Bonus barley. *Hereditas* 46:675-699.

4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.

5. Gustafsson, Å., and U. Lundqvist 1976. Controlled environment and short-day tolerance in barley mutants. p. 45-53. *In* Induced Mutants in Cross-breeding. Proc. Advisory Group, Vienna, 1975. Int. Atomic Energy Agency, Vienna.

6. Lundqvist, U. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.

7. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.

8. Lundqvist, U. (Unpublished).

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

Prepared:

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

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

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

Previous nomenclature and gene symbolization:

Early 16 = *ea-c16* (3).
Early maturity-c = *ea-c* (9).

Inheritance:

Monofactorial recessive (3, 4).
Location is unknown.

Description:

Early heading mutants at the *mat-c* locus show a rather drastic increase in earliness (heading 7 days earlier than the parents) under field cultivation in Sweden (3). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (1, 2, 5). Slightly later heading of some *mat-c* alleles is reported (5, 8). Early heading is also associated with decreased culm length, kernels per spike, and grain yield. Mutants have reduced culm length, caused by the reduction in internode number, and the length of the peduncle is increased. Spike length and spikelet number are markedly reduced (1, 3).

Origin of mutant:

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

Mutational events:

mat-c.16 (NGB 110016) in Bonus (3); *mat-c.19* (NGB 110019, GSHO 1789), -c.32 (NGB 110032), -c.93 (NGB 110093), -c.94 (NGB 110094) in Bonus (PI 189763), -c.101 (NGB 110101), -c.122 (NGB 110122), -c.400 (NGB 110400) in Foma (CIho 11333), -c.745 (NGB 110745) in Kristina (NGB 1500), -c.758 (NGB 110758), -c.760 (NGB 110760), -c.770 (NGB 110770), -c.865 (NGB 110865), -c.881 (NGB 110881), -c.907116862), -c.910 (NGB 117441), -c.913 (NGB 117444), -c.926 (NGB 117457), -c.943 (NGB 117474) in Bonus, -c.966 (NGB 117497) in Sv 79353, -c.1091 (NGB 117622) in Sv Vg74233, -c.1096 (NGB 117627) in Sv Frida (NGB 1519), -c.1102 (NGB 117633) in Sv Semira (NSL 206731), -c.1107 (NGB 119555), -c.1108 (NGB 119556), -c.1109 (NGB 119557), -c.1111 (NGB 119559), -c.1114 (NGB 119562), -c.1115 (NGB 119563) in Sv Frida, -c.1118 (NGB 119566), -c.1120 (NGB 119568) in Sv Semira (6, 7, 8).

Mutant used for description and seed stocks:

mat-c.19 (NGB 110019, GSHO 1789) in Bonus; *mat-c.19* in Bowman (PI 483237)*2 (GSHO 2283); *mat-c.19* in Bowman*6 (BW508, NGB 20736)

References:

1. Dormling, I., and Å. Gustafsson. 1969. Phytotron cultivation of early barley mutants. *Theor. Appl. Genet.* 39:51-61.
2. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-782.
3. Gustafsson, Å., A. Hagberg, and U. Lundqvist. 1960. The induction of early mutants in Bonus barley. *Hereditas* 46:675-699.
4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
5. Gustafsson, Å., and U. Lundqvist 1976. Controlled environment and short-day tolerance in barley mutants. p. 45-53. *In* Induced Mutants in Cross-breeding. Proc. Advisory Group, Vienna, 1975. Int. Atomic Energy Agency, Vienna.
6. Lundqvist, U. 1991. Swedish mutation research in barley with plant breeding aspects.

A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.

7. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.

8. Lundqvist, U. (Unpublished).

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:506.

BGS 580, Praematurum-d, *mat-d*

Stock number: BGS 580
Locus name: Praematurum-d
Locus symbol: *mat-d*

Previous nomenclature and gene symbolization:

Early 14 = *ea-d14* (3).
Early maturity-d = *ea-d* (8).

Inheritance:

Monofactorial incomplete dominant (3).
Location is unknown.

Description:

Early heading mutants at the *mat-d* locus (4) have a moderate increase in earliness (heading 3 days earlier than the parents) under field cultivation in Sweden (5, 6). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (2). Early heading is also associated with increased culm length and grain yield. The length of the peduncle is increased and mutants have longer spikes. Compared with the drastic maturity mutants at *eam8* (*mat-a*), *mat-b*, and *mat-c* loci, mutants at the *mat-d* locus have a normal number of the culm internodes (1, 3). Plants with narrow leaves are observed in progenies from crosses to Bowman.

Origin of mutant:

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

Mutational events:

mat-d.14 (NGB 110014) in Bonus (PI 189763) (3); *mat-d.124* (NGB 110124) in Foma (CIho 11333) (5, 6, 7).

Mutant used for description and seed stocks:

mat-d.14 (NGB 110124, GSHO 1790) in Bonus; *mat-d.14* in Bowman (PI 483237)*6 (BW509, NGB 20737).

References:

1. Dormling, I., and Å. Gustafsson. 1969. Phytotron cultivation of early barley mutants. *Theor. Appl. Genet.* 39:51-61.
2. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-782.
3. Gustafsson, Å., A. Hagberg, and U. Lundqvist. 1960. The induction of early mutants in Bonus barley. *Hereditas* 46:675-699.
4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
5. Lundqvist, U. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.*
6. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.
7. Lundqvist, U. (Unpublished).
8. Søggaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. *Carlsberg Res. Commun.* 52:123-196.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:507.

BGS 581, Praematurum-e, *mat-e*

Stock number: BGS 581
Locus name: Praematurum-e
Locus symbol: *mat-e*

Previous nomenclature and gene symbolization:

Praematurum-18 = *mat-18* (3).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Early heading mutants at the *mat-e* locus show a rather drastic increase in earliness (heading 6 days earlier than the parents) under field cultivation in Sweden (1, 4, 5). When grown under controlled environmental conditions, the mutant *mat-e.18* is photo- and thermoperiod insensitive (1). Mutants have a pronounced short-day type of photoperiod response (1, 3, 6). A slight delay in heading and less photoperiod neutrality is associated with other alleles at this locus (4).

Origin of mutant:

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

Mutational events

mat-e.18 (NGB 110018, GSHO 1791) in Bonus (PI 189763) (3); *mat-e.55* (NGB 110055), *-e.69* (NGB 110069), *-e.98* (NGB 110098) in Bonus, *-e.655* (NGB 110655) in Kristina (NGB 1500), *-e.854* (NGB 110854), *-e.883* (NGB 110883), *-e.890* (NGB 116845) in Bonus, *-e.1093* (NGB 117624) in Sv Ög74233 (4, 5, 6).

Mutant used for description and seed stocks:

mat-e.18 (NGB 110018, GSHO 1791) in Bonus; *mat-e.18* in Bowman (PI 483237)*5 (BW510, NGB 20738).

References:

1. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-78.
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. Gustafsson, Å., and U. Lundqvist 1976. Controlled environment and short-day tolerance in barley mutants. p. 45-53. *In* Induced Mutants in Cross-breeding. Proc. advisory Group, Vienna, 1975. Int. Atomic Energy Agency, Vienna.
4. Lundqvist, U. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.
5. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.
6. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:508.

BGS 582, Praematurum-f, *mat-f*

Stock number: BGS 582
Locus name: Praematurum-f
Locus symbol: *mat-f*

Previous nomenclature and gene symbolization:

Praematurum-23 = *mat-23* (7).

Inheritance:

Monofactorial recessive (4).

Likely located in chromosome 1H (1); SNP markers retained in the Bowman backcross-derived line BW511 for *mat-f.23* showing showing continuous markers from Bonus are 1_0764 to 1_1326 (positions 61.55 to 82.35 cM) in 1H bins 06 to 08 and 1_0310 to 2_0152 (positions 285.74 to 298.99) in 5HL bin 15 (1).

Description:

Early heading mutants at the *mat-f* locus have a moderate increase in earliness (heading 3 to 4 days earlier than the parents) under field cultivation in Sweden (6, 7). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (3). Early heading of *mat-f.23* segregates was observed in fall greenhouse nurseries in Fargo, North Dakota. The Bowman backcross-derived line BW511 was similar in maturity to Bowman and other agronomic traits when grown in Scotland. In New Zealand, it was slightly shorter than Bowman, while in Idaho grain yields were lower than those of Bowman. When grown under short-day conditions in Queensland, *mat-f.23* plants headed about 7 days earlier than Bowman (2).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (7).

Mutational events

mat-f.23 (NGB 110023, GSHO 1792), *-f.780* (NGB 110780), *-f.875* (NGB 110875), *-f.891* (NGB 116846), *-f.908* (NGB 1117439), *-f.932* (NGB 117463) in Bonus (PI 189763), *-f.983* (NGB 117514) in Sv 79353 (5, 6, 7).

Mutant used for description and seed stocks:

mat-f.23 (GSHO 1792, NGB 110023) in Bonus; *mat-f.23* in Bowman (PI 483237)*2 (GSHO 2284); *mat-f.23* in Bowman*5 (BW511, NGB 20739).

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. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-782.
4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
5. Lundqvist, U. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.
6. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.
7. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26: 509.
Revised:
J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:137.

BGS 583, Praematurum-g, *mat-g*

Stock number: BGS 583
Locus name: Praematurum-g
Locus symbol: *mat-g*

Previous nomenclature and gene symbolization:

Praematurum-30 = *mat-30* (5).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Early heading mutants at the *mat-g* locus have a moderate increase in earliness (heading 3 to 4 days earlier than the parents) under field cultivation in Sweden (3, 4).

When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (1).

Origin of mutant:

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

Mutational events

mat-g.30 (NGB 110030, GSHO 1793), *-g.873* (NGB 110873), *-g.877* (NGB 110877) in Bonus (PI 189763), *-g.985* (NGB 117516) in Sv 79353 (3, 4, 5).

Mutant used for description and seed stocks:

mat-g.30 (NGB 110030, GSHO 1793) in Bonus; *mat-g.30* in Bowman (PI 483237)*2 (GSHO 2285); *mat-g.30* in Bowman*5 (BW512, NGB 20740).

References:

1. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-782.
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. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.
4. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:510.

BGS 584, Praematurum-h, *mat-h*

Stock number: BGS 584
Locus name: Praematurum-h
Locus symbol: *mat-h*

Previous nomenclature and gene symbolization:

Praematurum-36 = *mat-36* (5).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 4HL(1); *mat-h.36* is associated with SNP markers 2_1130 to 1_1019 (positions 175.48 to 183.54 cM) in 4H bins 12 to 13 of the Bowman backcross-derived line BW513 (1).

Description:

Early heading mutants at the *mat-h* locus show a drastic increase in earliness (heading 6 days earlier than the parents) under field cultivation in Sweden (4, 5). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (1). The BW513 line with the *mat-h.36* mutant is similar to BW115 line with the *cer-k.39* mutant in terms of both chromosomal SNP markers retained and phenotype attributes (2). Plants with narrow leaves were found in progeny from the cross of the *mat-h.36* stock to Bowman.

Origin of mutant:

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

Mutational events

mat-h.36 (NGB 110036, GSHO 1794), *-h.935* (NGB 117466) in Bonus (PI 189763) (3, 4).

Mutant used for description and seed stocks:

mat-h.36 (NGB 110036, GSHO 1794) in Bonus; *mat-h.36* in Bowman (PI 483237)*2 (GSHO 2286); *mat-h.36* in Bowman*7 (BW513, NGB 20741).

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. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-782.
4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
5. Lundqvist, U. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.
6. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.
7. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:511.

Revised:

U. Lundqvist and J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:662.

BGS 585, Praematurum-i, *mat-i*

Stock number: BGS 585
Locus name: Praematurum-i
Locus symbol: *mat-i*

Previous nomenclature and gene symbolization:

Praematurum-37 = *mat-37* (5).

Inheritance:

Monofactorial recessive (2).

Location is unknown.

Description:

Early heading mutants at the *mat-i* locus have a drastic increase in earliness (heading 6 days earlier than the parents) under field cultivation in Sweden (4, 5). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (1). Spikes of mutants are relatively short (5), and the expression of earliness is relatively strong in the Bowman backcross-derived line.

Origin of mutant:

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

Mutational events

mat-i.37 (NGB 110037, GSHO 1795), *-i.76* (NGB 110076) in Bonus (PI 189763), *-i.303* (NGB 110303) in Foma (CIho 11333), *-i.742* (NGB 110742) in Kristina (NGB 1500), *-i.901* (NGB 116856), *-i.914* (NGB 117445) in Bonus (3, 4, 5).

Mutant used for description and seed stocks:

mat-i.37 (NGB 110037, GSHO 1795) in Bonus; *mat-i.37* in Bowman (PI 483237)*3 (GSHO 2287); *mat-i.37* in Bowman*7 (BW514, NGB 20742).

References:

1. Gustafsson, Å., I. Dormling, and U. Lundqvist. 1982. Gene, genotype and barley climatology. *Biol. Zent. Bl.* 101:763-782.
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. 1991. Swedish mutation research in barley with plant breeding aspects. A historical review. p. 135-148. *In* Plant Mutation Breeding for Crop Improvement. Proc. Int. Symp. Vienna, 1990. Int. Atomic Energy Agency, Vienna.
4. Lundqvist, U. 1992. Coordinator's report: Earliness genes. *Barley Genet. Newsl.* 21:127-129.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:512.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
4. Kleinhofs, A. 2006. Integrating molecular and morphological/physiological marker maps. *Barley Genet. Newsl.* 36:66-82.
5. Lundqvist, U. (Unpublished).
6. Nybom, N. 1954. Mutation types in barley. *Acta Agric. Scand.* 4:430-456.
7. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.

Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:284.

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:139-140.

BGS 587, Albino seedling 3, *abo3*

Stock number: BGS 587
Locus name: Albino seedling 3
Locus symbol: *abo3*

Previous nomenclature and gene symbolization:

Albino 2 = *a2* (2).
Albino seedling 2 = *a2* (3).
Albino seedling-za = *alb-za* (5).

Inheritance:

Monofactorial recessive (1, 2).
Location is unknown.

Description:

Seedlings lack normal pigmentation; they are white and die at a two or three leaf stage (1, 2). The *abo3.c* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in an unknown cultivar (1).

Mutational events:

abo3.c (*a2*, GSHO 165) in an unknown cultivar (3); *alb-za.111* (NGB 14781) in Bonus (PI 189763) (4, 5, 6).

Mutant used for description and seed stocks:

abo3.c (GSHO 165) in an unknown cultivar; *alb-za.111* (NGB 14781) in Bonus.

References:

1. Hallqvist, C. 1926. Koppelungen und synthetische Lethalität bei den Chlorophyllfaktoren der Gerste. *Hereditas* 8:229-254.
2. Nilsson-Ehle, H. 1922. Über freie Kombination und Koppelung verschiedener Chlorophyllerbinheiten bei Gerste. *Hereditas* 3:191-199.
3. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. *J. Am. Soc. Agron.* 33:47-64.
4. Simpson, D.J., and D. von Wettstein. 1992. Coordinator's report: Nuclear genes affecting the chloroplast. Stock list of mutants kept at the Carlsberg Laboratory. *Barley Genet. Newsl.* 21:102-108.
5. Wettstein, D. von, and K. Kristiansen. 1973. Stock list for nuclear gene mutants affecting the chloroplast. *Barley Genet. Newsl.* 3:113-117.
6. Wettstein, D. von, and K. Kristiansen. 1982. Chloroplast genes: Progress report II on diallelic tests between mapped chloroplast genes and chloroplast genes in stock collection at Copenhagen. *Barley Genet. Newsl.* 12:93-94.

Prepared:

J.D. Franckowiak and A. Hang. 1997. *Barley Genet. Newsl.* 26:514.

BGS 588, Albino seedling 10, *abo10*

Stock number: BGS 588
Locus name: Albino seedling 10
Locus symbol: *abo10*

Previous nomenclature and gene symbolization:

White seedling t2 = a_{t2} (1).

Albino seedling t2 = a_{t2} (2).

Inheritance:

Monofactorial recessive and expressed in the endosperm as a xenia effect (1).

Location is unknown.

Description:

Seedlings are very weak and white in color (1). A xenia effect of the *abo10.j* gene on seed size is described in Robertson (1). Seeds, which are homozygous for this seedling lethal gene, are shriveled with a 1000-kernel weight of 23.4 g compared with 46.5 g for normal kernels. After germination, the endosperm turns watery instead of pasty as found with normal seeds (1). Plants with this phenotype are classified as albino mutants (2).

The *abo10.j* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Canadian Thorpe (PI 2710) (1).

Mutational events:

abo10.j (Canadian Thorpe I, GSHO 57) in Canadian Thorpe (PI 2710) (1).

Mutant used for description and seed stocks:

abo10.j (GSHO 57) in Canadian Thorpe.

References:

1. Robertson, D.W. 1932. The effect of a lethal in the heterozygous condition on barley development. Colorado Agric. Exp. Stn. Tech. Bull. 1. 12 p.
2. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:515.

BGS 589, Albino seedling 11, *abo11*

Stock number: BGS 589
Locus name: Albino seedling 11
Locus symbol: *abo11*

Previous nomenclature and gene symbolization:

Albino seedling t = *alb^t* (1).

Albino seedling t3 = *a_{t3}* (3).

Inheritance:

Monofactorial recessive (1, 2).

Location is unknown.

Description:

Seedlings are albino when grown under low temperature conditions (below 7.5°C), but normal green under high temperature conditions (above 18.5°C). Failure to produce chlorophyll seems confined to early seedling stages (2).

Origin of mutant:

A spontaneous mutant in Trebi (PI 537442) (2, 3).

Mutational events:

abo11.k (Trebi II, GSHO 233) in Trebi (PI 537442) (3).

Mutant used for description and seed stocks:

abo11.k (GSHO 233) in Trebi.

References:

1. Buckley, G.F.H. 1930. Inheritance in barley with special reference to the color of caryopsis and lemma. *Sci. Agric.* 10:460-492.
2. Collins, J.L. 1927. A low temperature type of albinism in barley. *J. Hered.* 18:331-334.
3. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. *J. Am. Soc. Agron.* 33:47-64.

Prepared:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:516.

BGS 590, Reaction to *Puccinia hordei* 13, *Rph13*

Stock number: BGS 590
Locus name: Reaction to *Puccinia hordei* 13 (barley leaf rust)
Locus symbol: *Rph13*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (2, 3).

Location is unknown (2).

Description:

The seedling reaction to most isolates of *Puccinia hordei* is a small necrotic fleck (2).

The seedling reaction of heterozygotes is indistinguishable from that of homozygous resistant seedlings (2).

Origin of mutant:

Observed in line BS 99-2-1 (PI 531849) from the Cambridge Plant Breeding Institute (2, 3), which was selected from a cross having a *Hordeum vulgare* subsp. *spontaneum* accession from Israel as the donor parent (3).

Mutational events:

Rph13.x in *Hordeum vulgare* subsp. *spontaneum* (HS 2986) and transferred to Berac (PI 355136) by backcrossing [BS 99-2-1 (Berac*3/HS 2986), PI 531849, GSHO 1591] (1, 2, 3).

Mutant used for description and seed stocks:

Rph13.x from HS 2986 in Berac (PI 355136)*3 (PI 531849, GSHO 1591); *Rph13.x* in Bowman (PI 483237)*3 (GSHO 2325); *Rph13.x* in Bowman*7 (PI 643162, BW685, NGB 22391).

References:

1. Franckowiak, J.D., Y. Jin, and B.J. Steffenson. 1997. Recommended allele symbols for leaf rust resistance genes in barley. *Barley Genet. Newsl.* 27:36-44.
2. Jin, Y., G.H. Cui, B.J. Steffenson, and J.D. Franckowiak. 1996. New leaf rust resistance genes in barley and their allelic and linkage relationships with other *Rph* genes. *Phytopathology* 86:887-890.
3. Jin, Y., and B.J. Steffenson. 1994. Inheritance of resistance to *Puccinia hordei* in cultivated and wild barley. *J. Hered.* 85:451-454.

Prepared:

J.D. Franckowiak and Y. Jin. 1998. *Barley Genet. Newsl.* 28:31.

BGS 591, Reaction to *Puccinia hordei* 14, *Rph14*

Stock number: BGS 591
Locus name: Reaction to *Puccinia hordei* 14 (barley leaf rust)
Locus symbol: *Rph14*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial incomplete dominant (2, 3).

Location is unknown.

Description:

The seedling reaction to most isolates of *Puccinia hordei* ranges from chlorotic flecks to small lesions (2). Variability in seedling test conditions may alter the size and type of lesion observed. The seedling reaction of heterozygotes is frequently intermediate between that of resistant and susceptible seedlings (3).

Origin of mutant:

Natural occurrence in PI 531901-1 (PI 584760) from Egypt (3).

Mutational events:

Rph14.ab in PI 584760 (GSHO 1592) (1, 2).

Mutant used for description and seed stocks:

Rph14.ab in PI 584760 (GSHO 1592); *Rph14.ab* in Bowman (PI 483237)*2 (GSHO 2325); *Rph14.ab* in Bowman*5 (PI 643163, BW686, NGB 22392).

References:

1. Franckowiak, J.D., Y. Jin, and B.J. Steffenson. 1997. Recommended allele symbols for leaf rust resistance genes in barley. *Barley Genet. Newsl.* 27:36-44.
2. Jin, Y., G.H. Cui, B.J. Steffenson, and J.D. Franckowiak. 1996. New leaf rust resistance genes in barley and their allelic and linkage relationships with other *Rph* genes. *Phytopathology* 86:887-890.
3. Jin, Y., and B.J. Steffenson. 1994. Inheritance of resistance to *Puccinia hordei* in cultivated and wild barley. *J. Hered.* 85:451-454.

Prepared:

J.D. Franckowiak and Y. Jin. 1998. *Barley Genet. Newsl.* 28:32.

BGS 592, Yellow head 2, *yhd2*

Stock number: BGS 592
Locus name: Yellow head 2
Locus symbol: *yhd2*

Previous nomenclature and gene symbolization:

Yellow head 2 = *yh2* (1).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

Seedlings are slightly yellow-green compared to normal sibs. The lighter green color persists until after heading. The phenotype is similar to that expressed by some chlorina mutants.

Origin of mutant:

A spontaneous mutant in Compana (PI 539111).

Mutational events:

yhd2.b (Golden Compana, GSHO 757) in Compana (PI 539111).

Mutant used for description and seed stocks:

yhd2.b (GSHO 757) in Compana; *yhd2.b* in Bowman (PI 483237)*6 (GSHO 2037);

yhd2.b in Bowman*7 (BW921, NGB 22350).

References:

1. Eslick, R.F. (Unpublished).

Prepared:

J.D. Franckowiak. 1998. Barley Genet. Newsl. 28:33.

BGS 593, Awned palea 1, *adp1*

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

Previous nomenclature and gene symbolization:

Awned palea = *adp* (1).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 3HL (2); about 5.8 cM distal from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (2).

Description:

This mutant was isolated as a partially female sterile plant with abnormal spikes. The palea is elongated to form two awns (2), which are derived from two fused bracts that form the palea (3). Pistils are often transformed into leafy buds and result in low female fertility and greatly reduced seed set. Two of the anthers appear normal and the third is deformed to some extent (1). Pollen fertility is good (1).

Origin of mutant:

A spontaneous mutant in an inbred line (1).

Mutational events:

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

Mutant used for description and seed stocks:

adp1.a in a selection, with the *eog1.a* (elongated outer glume 1) gene from Svalöfs Gullkorn 91 [AHOR 226, a mutant of Gull (Clho 1145, GSHO 466)] (1), crossed to the unknown line (GSHO 1618); *adp1.a* in Bowman*5 (GSHO 1950, BW010, NGB 20416).

References:

1. Ahokas, H. 1977. A mutant of barley: Awned palea. Barley Genet. Newsl. 7:8-10.
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.
3. Williams, R.F. 1975. The Shoot Apex and Leaf Growth. Cambridge University Press, Cambridge.

Prepared:

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

Revised:

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

BGS 594, Anthocyanin-deficient 3, *ant3*

Stock number: BGS 594
Locus name: Anthocyanin-deficient 3
Locus symbol: *ant3*

Previous nomenclature and symbolization:

Exrubrum = rub (1).

Inheritance:

Monofactorial recessive (3).

Location is unknown.

Description:

There is no anthocyanin pigmentation in the vegetative parts of the mutant plants except for the lemmas. Slight anthocyanin pigmentation has been observed in the lemmas of the mutant grains. All three mutant alleles have short stems and are late in development compared to the mother varieties (2, 4).

Origin of mutant:

A neutron induced mutant in Bonus (PI 189763) (2).

Mutational events:

ant3.5, *ant3.8* (NGB 114557, GSHO 1641) in Bonus (PI 189763) (2, 4); *ant3.39* (NGB 114594) in Kristina (NGB 1500) (2, 4).

Mutant used for description and seed stock:

ant3.5 (NGB 114556, GSHO 1641) in Bonus.

References:

1. Gustafsson Å.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. 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., and U. Lundqvist. 1978. Diallelic tests of anthocyanin-deficient mutants. *Barley Genet. Newsl.* 8:57-59.

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:82.

BGS 595, Anthocyanin-deficient 4, *ant4*

Stock number: BGS 595
Locus name: Anthocyanin-deficient 4
Locus symbol: *ant4*

Previous nomenclature and symbolization:

Exrubrum = rub (4).

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 4H (1); *ant4.16* is associated with SNP markers 2_1122 to 1_1500 (positions 47.7 to 115.92 cM) in 4H bins 05 to 08 of the Bowman backcross-derived line BW024 and also SNP markers 2_0972 to 1_0139 (positions 156.09 to 160.38 cM) in 6H bin 09 of BW024 (1).

Description:

Depending on the growing conditions, a slight pigmentation can be observed in the auricles, awns and lemmas of the mutant plants. The amount of anthocyanin pigmentation was clearly decreased compared to the mother varieties (5, 8). The original mutant alleles, *ant4.16* and *ant4.17*, were taller and later maturing than their mother cultivar Foma (5, 7). The Bowman backcrossed derived line for *ant4.16* (BW024) was 10 to 20% taller than Bowman in both field and greenhouse tests, partially because its peduncles were longer (2). Slightly earlier heading of BW024 was observed under glasshouse conditions. BW024 plants lodged more than Bowman in field tests. The spikes of BW024 had one to three fewer kernels and rachis internodes were slightly shorter. Kernels were 10 to 15% lighter and grain yields were slightly lower than those of Bowman (2).

Origin of mutant:

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

Mutational events:

ant4.11 (NGB 114560), *4.16* (NGB 114565, GSHO 1642), *4.17* (NGB 114566), *4.28* (NGB 114583), *4.31* (NGB 114586) in Foma (Clho 11333) (7); *ant4.32* (NGB 114587) in Foma (5); *ant4.37* (NGB 114592) in Foma (7); *ant4.40* (NGB 114595) in Bonus (PI 189763) (7); *ant4.44* (NGB 119349) in Bonus (6); *ant4.53* (NGB 111870) in Bonus (5); *ant4.124* in Nordal (NGB 13680) (5).

Mutant used for description and seed stock:

ant4.11 (NGB 114560) in Foma; *ant 4.16* (NGB 114565, GSHO 1642) in Foma; *ant4.16* in Bowman (PI 483237)*3 (GSHO 2267); *ant4.16* in Bowman*7 (BW024, NGB 20432).

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. Jende-Strid, B. 1978. Mutations affecting flavonoid synthesis in barley. *Carlsberg Res. Commun.* 43:265-273.
5. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:57-59.
6. 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.
7. Jende-Strid, B., and U. Lundqvist. 1978. Diallelic tests of anthocyanin-deficient

mutants. Barley Genet. Newsl. 8:57-59.

Prepared:

B. Jende-Strid. 1999. Barley Genet. Newsl. 29:83.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:189-190.

BGS 596, Anthocyanin-deficient 5, *ant5*

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

Previous nomenclature and symbolization:

Green stem = rs2 (1).
Exrubrum = rub (2).

Inheritance:

Monofactorial recessive (3, 4).
Location is unknown.

Description:

The mutant plants do not synthesize anthocyanins in their vegetative parts under normal growing conditions (4, 5). The stem does not develop a purple pigmentation as it approaches maturity (1).

Origin of mutant:

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

Mutational events:

ant5.9 (NGB 114558, GSHO 1643) in Bonus (PI 189763) (6); *ant5.18* (NGB 114567) in Foma (CIho11333) (4); *ant5.24* (NGB 114573) in Foma (6); *ant5.a* (BGM 122) (4).

Mutant used for description and seed stock:

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

References:

1. Finch, R.A., and E. Simpson. 1978. New colours and complementary colour genes in barley. *Z. Pflanzenzücht.* 81:40-53.
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. Jende-Strid, B. 1978. Mutations affecting flavonoid synthesis in barley. *Carlsberg Res. Commun.* 43:265-273.
4. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:76-79.
5. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.
6. Jende-Strid, B., and U. Lundqvist. 1978. Diallelic tests of anthocyanin-deficient mutants. *Barley Genet. Newsl.* 8:57-59.

Prepared:

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

BGS 597, Anthocyanin-deficient 6, *ant6*

Stock number: BGS 597
Locus name: Anthocyanin-deficient 6
Locus symbol: *ant6*

Previous nomenclature and symbolization:

Exrubrum = rub (1).

Inheritance:

Monofactorial recessive (3).

Location is unknown.

Description:

Compared to the mother cultivars, the anthocyanin pigmentation is clearly decreased in the vegetative parts of the mutant plants (2, 4).

Origin of mutant:

A N-ethyl-N-nitrosourethane induced mutant in Foma (Clho 11333) (2).

Mutational events:

ant6.33 (NGB 114588), GSHO 1644) in Foma (Clho 11333) (4); *ant6.38* (NGB 114593) in Kristina (4).

Mutant used for description and seed stock:

ant6.33 (NGB 114588, GSHO 1644) in Foma.

References:

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Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:85.

BGS 598, Proanthocyanidin-free 13, *ant13*

Stock number: BGS 598
Locus name: Proanthocyanidin-free 13
Locus symbol: *ant13*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 6HL (1); near the centromere and the *sex1* (shrunken endosperm xenia1) locus (1).

Description:

Under normal growing conditions no anthocyanin pigmentation is observed in any of the vegetative plant parts (10). Under stress conditions anthocyanin pigmentation can occur in the mutant plants, but it is never as strong as in the wild type. The testa layers of the grains of the *ant13* mutants are totally lacking proanthocyanidins and precursors of proanthocyanidins. The *ant13* locus is coding for a transcription factor involved in the expression of the structural genes in the flavonoid pathway (7, 11). Almost all mutant alleles are induced with sodium azide (3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (Clho 11333) (2).

Mutational events:

ant13.13 (NGB 114562) in Foma (Clho 11333) (10); *ant13.101* in Nordal (NGB 13680) (4); *ant13.110*, *13.155*, *13.156*, *13.157*, *13.158* in Alf (NGB 13682) (4); *ant13.149*, *13.152* (NGB 13694) in Triumph (PI 268180, NGB 13678) (4); *ant13.350*, *13.351*, *13.353* in Triumph (5); *ant13.172* in Ark Royal (PI 447006) (4); *ant13.173* in Ark Royal (5); *ant13.201*, *13.202*, *13.203* in Secobra 4681 (4); *ant13.205* in Hege 876 (4); *ant13.213*, *13.214* in Hege 802 (4); *ant13.218*, *13.219*, *13.223* (NGB 13696), *13.225* in Secobra 4743 (NGB 13679) (4); *13.222* (NGB 13695) in Secobra 4743 (5); *ant13.228*, *13.229*, *13.230* in Ca 9930 (5); *ant13.232*, *13.233* in Tron (4); *ant13.238* in Gunhild (PI 464655, NGB 13690) (4); *ant13.266* in Secobra 18193 (NGB 13684) (4); *ant13.277*, *13.278* in VP 116 (NGB 13691) (4); *ant13.282*, *13.284*, *13.285* in Hege 550/75 (NGB 13692) (5); *ant13.305*, *13.308* in Ca 41507 (5); *ant13.311*, *13.312*, *13.313*, *13.314*, *13.315*, *13.317* in Ca 33787 (NGB 13693) (5); *ant13.320*, *13.327*, *13.328*, *13.329* in Harry (PI 491575) (5); *ant13.333* in Koral (PI 46778) (5); *ant13.334* in Helena (5); *ant13.343* in NZ 716.01 (5); *ant13.345*, *13.346*, *13.347*, *13.348*, *13.349* in Grimmet (PI 483048) (5); *ant13.354*, *13.355* in Hege 841/80 (5); *ant13.358* in Hege 15/74A (5); *ant13.360* in Hege 12473 (5); *ant13.361*, *13.362*, *13.363*, *13.364* in Ca 36167 (5); *ant13.369* in Ackermann 72/440 (5); *ant13.373*, *13.416*, *13.443* in Kaya (5); *ant13.381*, *13.385*, *13.393*, *13.466* in Irene (5); *ant13.394*, *13.395* in Hege 1644 (5); *ant13.397*, *13.398*, *13.399*, *13.400* in Camir (5); *ant13.401*, *13.403*, *13.404* in Odin (5); *ant13.406* in Odin (9); *ant13.409*, *13.446* in Catrin (5); *ant13.411*, *13.412* in Ca 710516 (5); *ant13.430*, *13.434* in NZ 1836-3 (5); *ant13.437* in NZ 1836-3 (9); *ant13.449* in Ca 601427 (5); *ant13.472* in Hege 1012/81 (5); *ant13.479* in Zenit (PI 564447, NGB 13686) (5); *ant13.482* in Secobra 9709 (5); *ant13.503*, *13.521*, *13.522*, *13.523* in Advance (Clho 15804) (5); *ant13.524*, *13.525* in Advance (4); *ant13.527*, *13.536*, *13.593*, *13.594*, *13.616* in Advance (5); *ant13.510*, *13.513* in 72AB3484 (4); *ant13.514*, *13.517* in WA9037-75 (5); *ant13.529*, *13.531* in Morex (Clho 15773) (4); *ant13.548* in Cree (Clho 15256) (5); *ant13.564*, *13.566* in Manker (Clho 15549) (5); *ant13.581*, *13.582* in Dickson (Clho 10968) (5); *ant13.583* in Dickson (12); *ant13.587*, *13.608*, *13.609*, *13.614* in Andr., (PI 469107) (5); *ant13.605* in Moravian 111

(CIho 15812) (5); ant13.626 in Morex (5); ant13.631, 13.634 in Clark (CIho 15857) (12); ant13.635 in Hazen (PI 483238) (12); ant13.639 in 8892-78 (12); ant13.646 in 10016-83 (12); ant13.656 in 12809-83 (12); ant13.1523 in Nirakei 60 (4); ant13.2010 (NGB 23016), 13.2011 (NGB 23017) in Grit (PI 548764, NGB 13685) (6); ant13.2019 in Natasha (PI 592171) (8); ant13.2024 in Natasha (6); ant13.2037, 13.2040 in Natasha (8); ant13.2068 in Natasha (6); ant13.2103, 13.2114 in Carula (8); ant13.5006, 13.5007 in Igri (PI 428488) (8); ant13.5011, 13.5012, 13.5013, 13.5014 in Monix (PI 584859) (5); ant13.5015 in Monix (6); ant13.5016 in SP 185 (6); ant13.5017 in Bollo (PI 378531) (9); ant13.5020, 13.5031 in Sonja (PI 392047) (5); ant13.5032 in Sonja (6); ant 13.5029 in Trigger (PI 473541) (5); ant13.5033 in Kaskade (6); *ant13.5047* in Lucia (6).

Mutant used for description and seed stock:

ant13.13 (NGB 114562) in Foma; *ant13.152* (NGB 13694, GSHO 1624) in Triumph; *ant13.152* in Bowman (PI 483237)*3 (GSHO 2076); *ant13.152* in Bowman*5 (BW015, NGB 20423).

References:

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2. Jende-Strid, B. 1978. Mutations affecting flavonoid synthesis in barley. *Carlsberg Res. Commun.* 43:265-273.
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7. Jende-Strid, B. 1991. Gene-enzyme relations in the pathway of flavonoid biosynthesis in barley. *Theor. Appl. Genet.* 81:668-674.
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9. Jende-Strid, B. 1995. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 24:162-165.
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11. Meldgaard, M. 1992. Expression of chalcone synthase, dihydroflavonol reductase, and flavanone 3-hydroxylase in mutants of barley deficient in anthocyanin and proanthocyanidin biosynthesis. *Theor. Appl. Genet.* 83:695-706.
12. Ullrich, S., and J. Cochran. 1998. (Personal communications).

Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:86-87.

BGS 599, Proanthocyanidin-free 17, *ant17*

Stock number: BGS 599
Locus name: Proanthocyanidin-free 17
Locus symbol: *ant17*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 3HS (1); it has been shown that *ant17.148* is an allele at the *seg3* (shrunken endosperm genetic 3, see BGS 379) locus (2).

Description:

Under normal growing conditions no anthocyanin pigmentation is observed in the mutant plants. The testa layers of the grain of the *ant17* mutants lack proanthocyanidins and catechins, but accumulate homoeriodictyol and chrysoeriol (7, 10). A full length cDNA clone from barley, coding for a protein consisting of 377 amino acids (42 kDa), has been isolated. It shows a homology of 71% to the flavanone-3-hydroxylase enzyme protein from *Antirrhinum majus* (12). It is likely that the *ant17* gene codes for one subunit and the *ant22* gene for the other subunit of the dimeric flavanone 3-hydroxylase enzyme, which catalyzes the conversion of flavanones into dihydroflavanols (7, 12). The mutant stock *ant17.148* was released as cultivar Galant (11). Alleles at the *ant17* locus that have been examined in the Bowman genetic background showed a variable reduction in kernel weight: *ant17.148* and *seg3.c* about 1/3 normal and *ant17.567* about 3/4 normal (2).

Origin of mutant:

A sodium azide induced mutant in Nordal (NGB 13680) (3).

Mutational events:

ant17.103, *17.104*, *17.105*, *17.139* (NGB 13697), *17.140*, *17.142*, *17.143*, *17.145* in Nordal (NGB 13680) (4); *ant17.107* in Alf (NGB13682) (4); *ant17.147*, *17.148* (Galant) (NGB 13698), *17.150*, *17.151*, *17.153*, *17.154*, *17.180*, *17.185* in Triumph (PI 268180, NGB 13678) (4); *ant17.352* in Triumph (5); *ant17.160* in Gula Abed (NGB 13681) (4); *ant17.165*, *17.167*, *17.169*, *17.171*, *17.174*, *17.182* in Ark Royal (PI 447006) (4); *ant17.192*, *17.193* in Georgie (PI 447012, NGB 13683) (4); *ant17.199* in Secobra 4681 (4); *ant17.200* in Secobra 4681 (5); *ant17.208* in Hege 876 (4); *ant17.210*, *17.211*, *17.217* in Hege 802 (4); *ant 17.216* in Hege 802 (5); *ant17.220*, *17.221*, *17.224*, in Secobra 4743 (NGB 13679) (4); *ant17.227* in Ca 59995 (5); *ant17.231* in Tron (4); *ant17.237*, *17.239*, *17.241*, *17.242*, *17.247*, *17.249* in Gunhild (PI 464655, NGB 13690) (4); *ant17.243*, *17.246* in Gunhild (5); *ant17.250*, *17.251*, *17.252*, *17.253*, *17.255* in Tokak (PI 264251) (4); *ant17.267*, *17.268*, *17.269* in Secobra 18193 (NGB 13684) (4); *ant17.270* in Secobra 18193 (5); *ant17.280* in Hege 550/75 (NGB 13692) (9); *ant17.288*, *17.289*, *17.290* in Hege 550/75 (4); *ant17.293*, *17.294*, *17.295*, *17.296* in Bonus (PI 189763) (4); *ant17.297*, *17.298*, *17.300*, *17.301*, *17.307* in Ca 41507 (4); *ant17.306*, *17.340* in Ca 41507 (5); *ant17.316* in Ca 33787 (NGB 13693) (5); *ant17.318*, *17.321*, *17.326* in Harry (PI 491575) (5); *ant17.331* in Hege A2/A4 (5); *ant17.335*, *17.336*, *17.338* in Ackermann 724/5/7 (5); *ant17.359* in Hege15/74-1A (5); *ant17.370* in Ackermann 72/440 (5); *ant17.372*, *17.413*, *17.414*, *17.417*, *17.418*, *17.419*, *17.444* in Kaya (5); *ant17.375* in Fanette (6); *ant17.379*, *17.382*, *17.383*, *17.386*, *17.387*, *17.388*, *17.389*, *17.390*, *17.391*, *17.464*, *17.465* in Irene (5); *ant17.405* in Odin (6); *ant17.408* in KMJ 326 (5); *ant17.410*, *17.447* in Catrin (5); *ant17.421* in VBS 18707 (5); *ant17.422*, *17.423*, *17.424*, *17.426* in NZ 3789 (5); *ant17.432* in NZ 1836-3 (5); *ant17.438*, *17.439* in

NZ 732.01 (5); *ant17.440* in Nordal (5); *ant17.450* in Ca 601427 (5); *ant17.453*, *17.455*, *17.457*, *17.458* in Ackermann 1734/5 (5); *ant17.462* in Pamela (5); *ant17.469* (NGB 23018), *17.470* (NGB 23019) in Grit (PI 548764, NGB 13685) (5); *ant17.475* in Zenit (PI 564447, NGB 13686) (5); *ant17.476* in Zenit (6); *ant17.480* in Secobra 9709 (5); *ant17.501* in Advance (Clho 15804) (4); *ant17.504* in Karla (Clho 15860) (4); *ant17.506*, *17.507*, *17.508*, *17.509* in OR 9114 (4); *ant17.515*, *17.516*, *17.518* in WA9037-75 (4); *ant17.520* in WA9044-75 (4); *ant17.530* in Morex (Clho15773) (4); *ant17.537*, *17.595*, *17.619*, *17.620* in Advance (5); *ant17.560*, *17.561*, *17.563*, *17.565*, *17.567* in Manker (Clho 15549) (5); *ant17.597* in Morex (6); *ant17.598* in Morex (5); *ant17.600* in S 80351 (5); *ant17.601* in Moravian 111 (Clho 15812) (5); *ant17.604* in Harrington (6); *ant17.612* in Andre, (PI 469107) (5); *ant17.624* in Klages (Clho 15478) (5); *ant17.625* in Robust (M36, PI 476976) (5); *ant17.630* in Azure (Clho 15865) (13); *ant17.636*, *17.658* in Cougbar (PI 496400) (13); *ant17.637* in 8892-78 (13); *ant17.661* in Crest (PI 561409) (13); *ant17.1502*, *17.1505*, *17.1519* in Amagi-Nijo (4); *ant17.1510*, *17.1511* in Haruna-Nijo (4); *ant17.1515* in Nirakei 61 (4); *ant17.1537* in Nirakei 62 (5); *ant17.1544* in Nirakei 63 (5); *ant17.1534* in Nirasaki-Nijo 14 (5); *ant17.2022*, *17.2067* in Natasha (PI 592171) (6); *ant17.2084* in Hege 694/82 (9); *ant17.2106* in Ca 708912 (8); *ant17.5019* in Sonja (PI 302047) (9); *ant17.5024* in Ackermann 72/27/4 (6); *ant17.5028* in Trigger (PI 473541) (9); *ant17.5034* in Kaskade (9); *ant17.5035*, *17.5036*, *17.5037* in Video (6); *ant17.5038*, *17.5039*, *17.5040*, *17.5042* in Sonja (6); *ant17.5044* in Ackermann 27/220/8 (6).

Mutant used for description and seed stock:

ant17.139 (NGB 13697) in Nordal; *ant17.148* (Galant, NGB 13698, GSHO 1628) in Triumph; *ant17.148* in Bowman (PI 483237)*4 (GSHO 1973, BW016, NGB 20424); *ant17.567* in Manker (GSHO 1629); *ant17.567* in Bowman*5 (GSHO 1974); *ant17.567* in Bowman*7 (BW017, NGB 20425); *seg3.c* from Compana in Bowman (PI 483237)*7 (GSHO 1957, BW836, NGB 22273).

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2. Franckowiak, J.D. (Personal communications).
3. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
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Prepared:

B. Jende-Strid. 1999. *Barley Genet. Newsl.* 29:88-89.

Revised:

B. Jende-Strid and U. Lundqvist. 2007. *Barley Genet. Newsl.* 37:286-288.

BGS 600, Proanthocyanidin-free 18, *ant18*

Stock number: BGS 600
Locus name: Proanthocyanidin-free18
Locus symbol: *ant18*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).
Located in chromosome 7HL (1).

Description:

No anthocyanin pigmentation is observed in the mutant plants. The ripe grains of the *ant18* mutants have a shrunken appearance (4). The testa layers of the grains of the *ant18* mutants lack proanthocyanidins and catechins but accumulate small amounts of dihydroquercetin (8, 9). The *ant18* gene has been isolated and sequenced. It codes for a protein with a deduced amino acid sequence of 354 residues and a molecular weight of 38.4 kDa (10). It has been proved that the *ant18* gene is the structural gene coding for the dihydroflavonol reductase enzyme, which catalyzes the conversion of dihydroflavonols into leucoanthocyanidins (8, 10, 13). The nucleotide sequences of the *ant18* genes from four *ant18* mutants have been analyzed in detail and the nature of the sodium azide induced mutations in the four mutants has been revealed (11).

Origin of mutant:

A sodium azide induced mutant in Nordal (NGB 13680) (2).

Mutational events:

ant18.102 (GSHO 1630), *18.141*, *18.144* in Nordal (NGB 13680) (3); *ant18.106*, *18.111* in Alf (NGB 13682) (3); *ant18.146*, *18.186* in Triumph (PI 268180, NGB 13678) (3); *ant18.159* (NGB 13699), *18.161* (NGB 13700), *18.162* (NGB 13701), *18.164* (NGB 13702), *18.183* in Gula Abed (NGB 13681) (3); *ant18.166*, *18.170*, *18.175*, *18.176*, *18.177*, *18.178*, *18.179* in Ark Royal (PI 447006) (3); *ant18.168* in Triumph (4); *ant18.195*, *18.196*, *18.197* in Georgie (PI 447012, NGB 13683) (3); *ant18.198*, *18.204* in Secobra 4681 (3); *ant18.206* in Hege 876 (3); *ant18.209* in Hege 802 (3); *ant18.215*, *18.226* in Hege 802 (4); *ant18.234*, *18.235* in Tron (3); *ant18.236*, *18.240*, *18.244*, *18.248* in Gunhild (PI 464655, NGB 13690) (3); *ant18.254* in Tokak (PI 264251) (4); *ant18.256*, *18.257*, *18.258*, *18.259*, *18.260*, *18.261*, *18.262*, *18.263* in Tokak (3); *ant18.275*, *18.276*, *18.279* in VP116 (NGB 13691) (3); *ant18.281*, *18.286*, *18.291* in Hege 550/75 (NGB 13692) (3); *ant18.292* in Bonus (PI 189763) (3); *ant18.299*, *18.302*, *18.303*, *18.304*, *18.309*, *18.339*, *18.341* in Ca 41507 (3); *ant18.319*, *18.323*, *18.324*, *18.325* in Harry (PI 491575) (4); *ant18.332* in Ca 603801 (4); *ant18.337* in Ackermann 724/5/7 (4); *ant18.342* in Secobra 18193 (NGB 13684) (3); *ant18.344* in NZ 716.01 (4); *ant18.356*, *18.357* in Hege 841/80 (4); *ant18.365*, *18.366* in Ca 36167 (4); *ant18.367* in Gimpel (PI 564720) (4); *ant18.374*, *18.376*, *18.377* in Fanette (4); *ant18.378* in Ca 33787 (NGB 13693) (4); *ant18.380*, *18.392*, *18.463* in Irene (4); *ant18.402* in Odin (4); *ant18.415* in Kaya (4); *ant18.425* in NZ 3789 (4); *ant18.427* in NZ 3789 (5); *ant18.428*, *18.429*, *18.431*, *18.433*, *18.435*, *18.436* in NZ 1836-3 (4); *ant18.442* in Ca 710516 (4); *ant18.448* in Catrin (4); *ant18.451* in Ca 601427 (4); *ant18.454*, *18.456*, *18.459* in Ackermann 1734/5 (4); *ant18.460* in Pamela (4); *ant18.467* (NGB 23020), *18.468* (NGB 23021), *18.471* (NGB 23022) in Grit (PI 548764, NGB 13685) (4); *ant18.473*, *18.474* in Almudena (5); *ant18.478* in Zenit (PI 574447, NGB 13686) (4); *ant18.481* in Secobra 9709 (4); *ant18.505* in WA 8953-75 (3); *ant18.512* in 72AB3484 (3); *ant18.519* in WA9044-75 (3); *ant18.532*, *18.533*, *18.591*, *18.592*, *18.617*, *18.618*, *18.621* in Advance

(Clho 15804) (4); *ant18.610*, *18.611*, *18.613* in Andre, (PI 469107) (4); *ant18.623* in Klages (Clho 15478) (4); *ant18.638* in 8892-78 (12); *ant18.659*, *18.660* in Coughbar (PI 496400) (12); *ant18.1503*, *18.1506*, *18.1517*, *18.1518* in Amagi-Nijo (3); *ant18.1509* in Haruna-Nijo (3); *18.1531*, *18.1532* in Nirasaki-Nijo 14 (4); *ant18.1536* in Nirakei 62 (4); *ant18.1539* in Nirakei 63 (4); *ant18.5001*, *18.5002*, *18.5003*, *18.5004*, *18.5005*, *18.5008*, *18.5009*, *18.5010* in Igri (PI 428488) (6); *ant18.5018*, *18.5022*, *18.5023*, *18.5030*, *18.5041* in Sonja (PI 392047) (7); *ant18.5027* in Video (7); *ant18.5043* in Ackermann 27/4/98 (7); *ant18.5046*, *18.5048* in Lucia (7); *ant18.5049* in Marinka.

Mutant used for description and seed stock:

ant18.102 (GSHO 1630) in Nordal; *ant18.161* (NGB 13700) in Gula Abed; *ant18.162* (NGB 13701) in Gula Abed; *ant18.102* in Bowman (PI 483237)*3 (GSHO 1856); *ant18.102* in Bowman*7 (BW018, NGB 20426).

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