BGS 10, Short awn 2, lks2

Stock number:	BGS 10
Locus name:	Short awn 2
Locus symbol:	lks2

Previous nomenclature and gene symbolization:

Short awn = a (28, 30).
Short awn = lk (26).
Short awn 2 = lk_1 (12).
Short awn 2 = lk2 (19).
Short awn 4 = lk4 (3, 9).
Unbranched style 4 = u4 (25).
Breviaristatum-15 = ari-15 (8).
Breviaristatum-d = ari-d (5, 6, 8, 13).
Short awn 8 = lk8 (29).

Inheritance:

Monofactorial recessive (11, 12, 13, 22, 25).

Located in chromosome 7HL (11, 13, 14, 24, 25); position estimates for the *lks2* locus ranged from 7.9 to 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (4, 22, 24); *lks2.b* is about 2.8 cM distal from molecular marker WG541 in 7H bin 05 (15); *lks2.b* is 3.6 cM from AFLP marker E4138-3 in subgroup 6 of the Proctor/Nudinka map (16); *lks2.b* is about 8.6 cM proximal from RFLP marker WG380B in 7H bin 08 (1); *lks2.b* is located in the long arm of 7H and flanked by EST-based markers k04151 and k06123 (co-segregation with Bmac64) (27, 31); *lks2.b* is associated with SNP markers 2_0790 to 2_0060 (positions 73.96 to 97.66 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW492 (2); *ubs4.d* is about 8.0 cM distal from the *nud1* (naked caryopsis 1) locus (25); *ubs4.d* is associated with SNP markers 2_0103 to 1_0563 (positions 139.96 to 154.35 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW884 (2); *ari-d.15* is associated with SNP marker 1_0169 (position 142.66 cM) in 7H bin 08 of the Bowman backcross-derived line BW041 (1*); ari-d.44* is associated with SNP markers 1_0056 to 2_0092 (positions 51.93 to 152.29 cM) in 7H bins 04 to 09 of the Bowman backcross-derived line BW035 (2), likely in 7H bin 07. The Lks2 gene has been cloned (31).

Description:

Awns of both central and lateral spikelets of lks2.b spikes are reduced to about 3/5 that of the long awned type. Texture of the short awn is finer and more flexible than that of the long awn, especially in non-uzu genotypes (24, 26, 31). Kernel weights of lks2 plants were slightly reduced and kernels per spike were slightly increased, but other traits remained unchanged (23). The Atlas near-isogenic lines for *lks2* (half awn) were found to respond better to environmental and genetic stress than the normal lines (20, 21). The awn length of heterozygotes in some crosses was shorter that of the normal parent. Awns, as measured from the tip of the last fertile spikelet on the spike to the tip of the awn, of BW492 were about 1/2 as long as Bowman awns, 5 to 6 vs. 11 to 12 cm (5). The number of longitudinal parenchyma cells in the Bowman backcross-derived line BW492 awns was about half that of Bowman awns (31). Kernels of BW492 plants were slightly lighter than those of Bowman and kernel widths averaged slightly less (5). Allelism tests demonstrated that *lks2.b* gene in BW492 is allelic and dominant to *ubs4.d* gene in BW884 and to the *ari-d.15* gene in BW041 (31). All 25 accessions identified as mutants at the lks2 locus had lesions in the Lks2 candidate gene (31). Among accessions with the lks2 phenotype, three variants were found: *lks2.b1* and *lks2.b2* in accessions from China, Japan, and Korea and *lks2.b3* in accessions from Tibet (31). Stigmas of *ari-d* and ubs4 mutants have only a few very short branches, which prevents normal pollen reception and reduces seed set to 13 to 30% in uzu type plants. Both the *uzu1.a* and *srh1.a* (short rachilla hair 1) genes interact with ubs4.d to further reduce in seed set (25). The stigmas have very few stigma hairs (31). Pollen fertility is normal (25). Awn length is about 1/4 normal (4, 31). Seed set for plants of the Bowman backcross-derived lines for *ari-d.15* and *ubs4.d*, BW041 and BW884, respectively, varied from about 10% for plants grown in greenhouses to nearly 50% for plants grown at Aberdeen, Idaho, USA (5). Grain yields of BW041 and BW884 ranged from 1/4 to 1/2 those of Bowman. Compared to Bowman, kernel weights of BW041 and BW884 varied from slightly less to slightly more. Other morphological traits of BW041, BW492, and BW884 were similar to those of Bowman (5).

Origin of mutant:

Spontaneous occurrence in some cultivars and distributed in China, Japan, Korea, and Nepal (9, 18, 22, 26, 31). A spontaneous mutant in Ao Hadaka (OUJ159) (25).

Mutational events:

lks2.b1 and *lks2*.b2 in cultivars of Oriental origin, often associated with the *dsp1.a* (dense spike 1) gene (11, 22, 26, 31); *lks2.b3* in accessions from the Himalayas (including India, Nepal, and Tibet) (31); *lks2.s* (KM7) isolated from Kanto Nijo 29 by N. Kawada (31); *ubs4.d* (Ao Hadaka-hen, GSHO 567) in Ao Hadaka (OUJ159) (25); *ari-d.15* (NGB 115861, GSHO 1652), *-d.35* (NGB 115884), *-d.51* (NGB 115904) in Bonus (PI 189763, NGB 14657) (8); *ari-d.44* (NGB 115896), *-d.57* (NGB 115911) in Bonus (10); *ari-d.105* (NGB 115917), *-d.107* (NGB 115919), *-d.116* (NGB 115928), *-d.129* (NGB 115940), *-d.130 (*NGB 115941), *-d.150* (NGB 115961), *-d.160* (NGB 115970), *-d.186* (NGB 115996*), -d.187* (NGB 115997*), -d.192* (NGB 116002), *-d.193* (NGB 116003), *-d.232* (NGB 116042), *-d.239* (NGB 116048), *-d.240* (NGB 116049), *-d.241* (NGB 116050), *-d.242* (NGB 116051), *-d.243* (NGB 116052), *-d.247* (NGB 116058) in Foma (CIho 11333, NGB 14659), *-d.288* (NGB 116105) in Kristina (NGB 1500, NGB 14661) (8, 10); a possible *lks2* mutant in Morex (CIho 15773) (17, 18).

Mutant used for description and seed stocks:

lks2.b in Honen 6 (OUJ469, PI 307495, GSHO 566) (26); *lks2.b* in Aizu Hadaka 3 (OUJ323) (31); *lks2.b* from Sermo (CIho 7776) in Betzes (PI 129430)*7 (CIho 16558, GP 36) (7); *lks2.b* from Sermo in Compana (CIho 5438)*7 (CIho 16188, GP 40) (7); *lks2.b* from Sermo in Decap (CIho 3351)*7 (CIho 16562, GP 44) (7); *lks2.b* from R.I. Wolfe's Multiple Recessive Stock (GSHO 3451) in Bowman (PI 483237)*9 (GSHO 1850, BW492, NGB 20720); *ubs4.d* (GSHO 567) in Ao Hadaka; *ari-d.15* (GSHO 1652, NGB 115861) in Bonus; *ubs4.d* in Bowman (PI 483237)*6 (GSHO 1849); *ubs4.d* in Bowman*7 (BW884, NGB 22318); *ari-d.15* in Bowman*8 (GSHO 1848, BW041, NGB 20449); *ari-d.44* in Bowman*6 (BW035, NGB 20443).

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BGS 11, Unbranched style 4, ubs4

Stock number:	BGS 11
Locus name:	Unbranched style 4
Locus symbol:	ubs4

Revised locus symbol:

The mutants previously associated with the unbranched style 4 (*ubs4*) or breviaristatum-d (*ari-d*) locus were demonstrated to be alleles at the short awn 2 (*lks2*) locus (10). Mutants previously signed *ari-d* and *ubs4* locus symbols show more pronounced phenotypic effects than variants assigned the lks2 locus symbol (10). See BGS 10 for more information on the alleles at the lks2 locus.

Previous nomenclature and gene symbolization:

Unbranched style 4 = u4 (8).
Breviaristatum-15 = ari-15 (4).
Breviaristatum-d = ari-d (2, 3, 4, 6).
Short awn 8 = lk8 (9).

Inheritance:

Monofactorial recessive (6, 8).

Located in chromosome 7HL (6, 7, 8); *ubs4.d* is about 8.0 cM distal from the *nud1* (naked caryopsis 1) locus (8); *ubs4.d* is associated with SNP markers 2_0103 to 1_0563 (positions 139.96 to 154.35 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW884 (1); *ari-d.15* is associated with SNP marker 1_0169 (position 142.66 cM) in 7H bin 08 of the Bowman backcross-derived line BW041 (1); *ari-d.44* is associated with SNP markers 1_0056 to 2_0092 (positions 51.93 to 152.29 cM) in 7H bins 04 to 09 of the Bowman backcross-derived line BW035 (1), in 7H bin 07.

Description:

The stigma has only a few very short branches, which prevents normal pollen reception and reduces seed set to 13 to 30% in uzu type plants. Both the *uzu1.a* and *srh1.a* (short rachilla hair 1) genes interact with *ubs4.d* to further reduce in seed set. Pollen fertility is normal (8). Awn length is about 1/4 normal (4). Seed set on plants of the Bowman backcross-derived lines for *ari-d.15* and *ubs4.d*, BW041 and BW884, respectively, varied from about 10% for plants grown in greenhouses to nearly 50% for plants grown at Aberdeen, Idaho, USA (2). Awns of BW884 and BW041 extended about 3 cm beyond the tip of the tip while those of Bowman extended about 11 cm (2). Grain yields of BW041 and BW884 ranged from 1/4 to 1/2 those of Bowman. Compared to Bowman, kernel weights varied from slightly less to slightly more. Other morphological traits of BW041 and BW884 were similar to those of Bowman (2).

Origin of mutant:

A spontaneous mutant in Ao Hadaka (OUJ159) (8).

Mutational events:

ubs4.d (Ao Hadaka-hen , GSHO 567) in Ao Hadaka (OUJ159) (8); *ari-d.15 (*NGB 115861, GSHO 1652), *-d.35* (NGB 115884), *-d.51* (NGB 115904) in Bonus (PI 189763, NGB 14657) (4); *ari-d.44* (NGB 115896), *-d.57* (NGB 115911) in Bonus (5); *ari-d.105* (NGB 115917), *-d.107* (NGB 115919), *-d.116* (NGB 115928), *-d.129* (NGB 115940), *-d.130* (NGB 115941), *-d.150* (NGB 115961), *-d.160* (NGB 115970), *-d.186* (NGB 115996), *-d.187* (NGB 115997), *-d.192* (NGB 116002), *-d.193* (NGB 116003), *-d.232* (NGB 116042), *-d.239* (NGB 116048*), -d.240* (NGB 116049), *-d.241* (NGB 116050), *-d.242* (NGB 116051), *-d.243* (NGB 116052), *-d.247* (NGB 116058) in Foma (CIho 11333, NGB 14659), *-d.288* (NGB 116105) in Kristina (NGB 1500, NGB 14661) (4, 5).

Mutant used for description and seed stocks:

ubs4.d (GSHO 567) in Ao Hadaka; *ari-d.15* (GSHO 1652, NGB 115861) in Bonus;

ubs4.d in Bowman (PI 483237)*6 (GSHO 1849), *ubs4.d* in Bowman*7 (BW884, NGB 22318*); ari-d.15* in Bowman*8 (GSHO 1848, BW041, NGB 20449); *ari-d.44* in Bowman*6 (BW035, NGB 20443).

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BGS 31, Shrunken endosperm xenia 6, sex6

Stock number:	BGS 31
Locus name:	Shrunken endosperm xenia 6
Locus symbol:	sex6

Previous nomenclature and gene symbolization:

starch synthase IIa = ssIIa (6).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 7HS (8); *sex6.h* is located about 2.8 cM distal from the *seg2* (shrunken endosperm genetic 2) locus (7); *sex6.h* is about 3.1 cM from the centromere (8); *sex6.h* is over 45.8 cM proximal from the *Est5* (esterase 5) locus (8); sex6.h is about 4.4 cM from the breakpoint in translocation stock T1-5a (9); *sex6.h* is associated with SNP markers 1_1028 to 2_0485 (positions 72.84 to 84.79 cM) in 7H bin 07 of the Bowman backcrossed-derived line BW846 (2), in 7H bin 07.

Description:

After the soft dough stage, kernels develop a central depression in the lemma side, which becomes progressively more distinct with maturity. The depression is similar in size to that produced by *sex1* (shrunken endosperm xenia 1) mutants. The mutant has a xenia expression that permitting classification of kernels from heterozygous plants as normal or shrunken with an expected 3:1 ratio (3). Kernels of allelic mutants, M292 and M342, had a high amylose starch phenotype, 60 to 70% compared to 25% in normal barley (6). The starch synthase IIa (*ssIIa*) gene is a candidate gene altered by these mutations (6). Compared to Bowman, plants of the Bowman backcross-derived line for *sex6.h*, BW846, were about 10% shorter and headed about three days later. Kernel weights for BW846 were 2/3 to 3/4 of those for Bowman, 3.8 vs.5.6 mg. Grain yields of BW846 were about 1/2 those recorded for Bowman (3). On a per kernel basis, grain from lines containing both the high amylose 1 (*amo1, ssIIIa*) mutant and the *sex6* (*ssIIa*) mutant from the M292 synthesize significantly more amylose than wild- than wild type lines and the *sex6* mutants (5).

Origin of mutant:

A spontaneous mutant in K6827 (an introduction from Turkey) (1).

Mutational events:

sex6.h (GSHO 2476) in K6827 (MK6827) (1); M292 (Himalaya292) and M342 (Himalaya342) in Himalaya (CIho 1312) (5, 6).

Mutant used for description and seed stocks:

sex6.h (GSHO 2476) in K6827, *sex6.h* in Bowman (PI 483237)*6 (GSHO 3425); *sex6.h* in Bowman*7 (BW846, NGB 22283); *sex6.h* in NFC Tipple (Syngenta Seeds Ltd., Market Rasen, UK)*3 (4).

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Revised:

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BGS 34, Male sterile genetic 50, *msg50*

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

Previous nomenclature and gene symbolization:

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

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 7HL (2); *msg50.gh* is about 18.9 cM from the *lks2* (short awn 2) locus (2); *msg50.hm* is about 8.7 cM from the *lks2* locus (2); *msg50.hm* is associated with SNP markers 2_1270 to 2_1229 (positions 93.97 to 176.37 cM) in 7H bins 06 to 10 in a heterozygous plant from Bowman backcross-derived line BW588 (1); *msg50.gh* is associated with SNP markers 2_1270 to 1_1440 (positions 93.97 to 198.70 cM) in 7H bins 06 to 12 in a heterozygous plant from Bowman backcross-derived line BW972 (1).

Description:

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

Outcrossing - complete female fertility (4).

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

Origin of mutant:

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

Mutational events:

msg50.gh (MSS435) in Maris Mink (PI 467824) (2, 4; *msg50.hm* (MSS466, GSHO 2404) in Berac (PI 355136) (2, 4).

Mutant used for description and seed stocks:

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

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Prepared:

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Revised:

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

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:88.

BGS 44, Brachytic 16, *brh16*

Stock number: BGS 44
Locus name: Brachytic 16
Locus symbol: *brh16*

Revised locus symbol:

The *brh16.v* mutant is one of the allele at the *ari-o.40* (Breviaristatum-o) locus (2). Other alleles at previously named loci include *ert-u.56* (Erectoides-u, BGS 92), *ert-zd.159* (Erectoides-zd, BGS 93), and *brh14.q* (Brachytic 14, BGS 148) (1). See BGS 556 for more information on the alleles at the *ari-o* locus.

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 7HL (1, 2); *brh16.v* is approximately 7.4 cM proximal from SSR marker Bmag0135 in 7H bin 13 (1); no heterogeneous SNP markers were retained in the Bowman backcross-derived line for *brh16.v,* BW087 (3); *brh16.v* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (2) in the barley genome map (7).

Description:

Plants are less than 2/3 of normal height and awns are about 3/4 of normal length in the Bowman backcross-derived line. The peduncle is about 2/3 normal length. The rachis internodes are slightly shorter than normal. The tip of the spike has a fascinated appearance because spikelets are very close together (1, 6). Since kernels per spikes and kernel size were not reduced, much of the yield loss was probably associated with reduced tillering (1, 6). The original introduction (HE 2816) contained two dwarf mutants, but only *brh16.v* gene was isolated in the Bowman backcross-derived line (5, 8). Compared to Bowman, plants of the Bowman backcross-derived line for *brh16.v*, BW087, were 30 to 40% shorter and had short peduncles, 17 vs. 31 cm. Awns and rachis internodes were slightly shorter. Leaf blades were shorter and slightly narrower. Kernels of BW087 were slightly shorter and varied in weight from equal to 10% lighter than those of Bowman. Grain yields of BW087 were about 1/4 those of Bowman (1, 5). As with other mutants at the *ari-o* locus*, brh16.v* shows a brassinosteroid-deficient phenotype that includes a short culm, about 70% of normal, caused largely by an extreme shortening of the second culm internode (2). Other common traits include shorter rachis internodes, short awns, acute leaf angles, slightly undulating leaf margins, and a slightly elongated basal rachis internode (2). The six Bowman backcross-derived lines with a mutation at the *ari-o* or *HvDIM* locus, *ari-o.40*, *brh14.af*, *brh14.q*, *brh16.v*, *ert-u.56*, and *ert-zd.159*, have retained a small, common genetic donor parent interval (2). The sequence of *HvDIM*, encoding the barley Δ^5-sterol-Δ^{24}-reductase DIMINUTO, corresponds directly to single-nucleotide polymorphism (SNP) marker 1_0547 located in the telomere on the long arm of chromosome 7H (2).

Origin of mutant:

Probably an ethyl methanesulphonate induced mutant in Korál (PI 467778) (8).

Mutational events:

brh16.v in HE 2816 (DWS1176, GSHO 1686) from a cross between two semidwarf mutants (6, 8).

Mutant used for description and seed stocks:

brh16.v in HE 2816/Bowman (GSHO 1686); *brh16.v* in Bowman (PI 483237)*7 (GSHO 2177, BW087, NGB 20494).

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Prepared:

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Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:89-90.

BGS 59, Grandpa 1, *gpa1*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3).

Located in chromosome 2HL (6, 7); *gp a1.a* is about 24.5 cM distal from the *lig1* (liguleless 1) locus (5); *gpa1.a* is associated with SNP markers 2_0069 to 10085 (positions 179.99 to 247.86 cM) in 2H bins 11 to 14 of the Bowman backcross-derived line BW397 (1).

Description:

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

Origin of mutant:

A spontaneous mutant in Lyallpur (PI 57954) isolated by GA Wiebe (4).

Mutational events:

gpa1.a (CIho 6027, GSHO 519) in Lyallpur (PI 57954) (4); *gpa1.b* (*gp2*) (GSHO 1379) in Montcalm (CIho 7149) (5, 7, 8).

Mutant used for description and seed stocks:

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

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Prepared:

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Revised:

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J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:95.
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BGS 60, Liguleless 1, *lig1*

Stock number: BGS 60
Locus name: Liguleless 1
Locus symbol: *lig1*

Previous nomenclature and gene symbolization:
Ligule and auricle less = *al* (9).
Liguleless = *li* (8).
Exauriculum = *aur-a* (1).

Inheritance:
Monofactorial recessive (9).
Located in chromosome 2HL (6, 9, 10); *lig1.my* is about 25.1 cM distal from the *mtt4* (mottled leaf 4) locus (2); *lig1.my* is near AFLP marker E3633-1 in subgroup 21 of the Proctor/Nudinka map (7); *lig1.my* is associated with SNP markers 1_0383 to 2_0994 (positions 207.22 to 233.44 cM) in 2H bins 13 to 14 of the Bowman backcross-derived line BW483 (1); *lig1.2* is associated with SNP markers 1_0446 to 2_0994 (positions 199.54 to 233.44 cM) in 2H bins 12 to 14 of the Bowman backcross-derived line BW482 (1), likely in 2H bin 13.

Description:
The ligule and auricle of all leaves are absent, and the leaf blades are erect along the stem. Liguleless plants can be identified visually at all stages of growth (9). Reverse mutation of some mutants is possible (4). The fine structure analysis of the *lig1* locus conducted by Konishi (5) showed that some mutants can recombine. The Bowman backcross-derived lines with the *lig1* gene, BW482 and 483, are similar in maturity, agronomic traits, and yield to Bowman (2).

Origin of mutant:
A spontaneous mutant in an unknown cultivar, Muyoji (liguleless) (OUL007) (8).

Mutational events:
lig1.my as Muyoji (OUL007, GSHO 6) (9); *lig1.ky* in Koyo (PI 190819)*, lig1.a1* (OUM001), *lig1.a2* in Akashinriki (PI 467400, OUJ659); *lig1.c1, lig1.c2, lig1.c3, lig1.c4* in Chikurin Ibaraki 1 (OUJ030, CIho 7370) (5); *aur-a.1* (*lig1.b1*) (NGB 114359), *aur-a.*2 (*lig1.b2*) (NGB 114360), *aur-a.7* (*lig1.b7*) (NGB 114365), *aur-a.8* (*lig1.b8*) (NGB 114366), *aur-a.9* (*lig1.b9*) (NGB 114367) in Bonus (NGB 14657, PI 189763;), *aur-a.3* (*lig1.b3*) (NGB 114361), *aur-a.4* (*lig1.b4*) (NGB 114362)*, aur-a.5* (*lig1.b5*) (NGB 114363), *aur-a.6* (*lig1.b6*) (NGB 114364), *aur-a.10* (*lig1.b10*) (NGB 114368) in Foma (NGB 14659, CIho 11333) (5); *aur-a.11* (*lig1.b11*) (NGB 114369)*, aur-a.12* (*lig1.b12*) (NGB 114370) in Kristina (NGB 1500, NGB 14667), *aur-a.13* (*lig1.b13*) (NGB 114372)*, aur-a.14* (*lig1.b14*) (NGB 114373) in Bonus, *aur-a.15* (*lig1.b15*) (NGB 119377) in Golf (PI 488529, NGB 1520) (6); *lig1.2* in Bonus from the stock *eli-a.2* (eligulum-a.2) (NGB 115389) as the second mutant (1, 2).

Mutant used for description and seed stocks:
lig1.my (GSHO 6) as Muyoji; *lig1.my* in Bowman (PI 483237)*8 (GSHO 1930, BW483, NGB 20711); *lig1.2* from a Bonus mutant (NGB 115389) in Bowman*5 (BW482, NGB 20710).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:120.

Revised:

J.D. Franckowiak, U. Lundqvist, T. Konishi. 1997. Barley Genet. Newsl. 26:96.
U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:205-206.
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BGS 71, Compositum 2, *com2*

Stock number:	BGS 71
Locus name:	Compositum 2
Locus symbol:	*com2*

Previous nomenclature and gene symbolization:

Branching inflorescent, rachilla 2 = *bir2* (4, 5).
Branched-5 = *brc-5* (1, 2, 9, 10).

Inheritance:

Monofactorial recessive (4, 12).

Located in chromosome 2HS (2, 4, 5); *com2.g* is linked to *Eam1* (early maturity 1) (4); *brc1.5* maps in 2H subgroup 17 at about 55 cM, near markers MWG2067 and CDO665 (2); BLASTn association of *brh1.5* with rice gene *FUZZY PANICLE* (*FZP*) (10); *com2.g* is associated with SNP markers 1_0525 to 1_0325 (positions 65.03 to 90.54 cM) in 2H bins 04 to 06 of the Bowman backcross-derived line BW192 (3); *com2.k* is associated with markers 1_0943 to 1_1015 (positions 34.31 to 91.62 cM) in 2H bins 04 to 07 of the Bowman backcross-derived line BW187 (3); the Bowman backcross-derived line BW191 for *com2.f*, BW191, did not contain any donor parent SNP markers (3), likely in 2H bin 06.

Description:

The spike is malformed because spike branches fail to abort and spike branches form from rachis nodes in the basal half of the spike (1). Spike branches form at more rachis nodes under favorable conditions for vigor growth (6, 7). Plants of the Bowman backcross-derived line for *com2.f* and *com2.g*, BW191 and BW192, were slightly shorter than Bowman and often had slightly shorter awns. Kernel sizes were variable for BW191 and BW192 and average weights were lower than those of Bowman. Kernels were on average shorter and thinner, but BW191 plants had smaller grains than those of BW192. Grain yields of BW191 and BW192 were commonly lower than those of Bowman (6). The degree of spike branching is in part dependent on environment (9). The *com2* mutant disrupts production of COM2 containing an AP2/ERF (an ethylene-responsive element DNA binding factor) domain that represses inflorescence branch formation (9).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (12).

Mutational events:

com2.f (Mut 2201, GSHO 1700) in Donaria (PI 161974) (12); *com2.g* (GSHO 1703) from the ICARDA-CIMMYT collection of barley freaks (5); *com2.k* in Davis 1153 (GSHO 79) (3); *brc1.5* (G22, SG-H3/5/8-88 from Köln) in BGRC 13145 of Braunschweig seed collection (2, 11); *com2.25* (L228H*, Irregular spike 25*, NGB 113475) in Foma (CIho 11333, NGB 14659) (8, 9); *com2.m* (TILLMore48), *com2.n* (TILLMore5865) in Barke (HOR 13170) in Gatersleben (IPK) Gene bank (9). The variants *com2.g*, *com2.k*, and *brh1.5* may have arisen from the same mutational event (S221R) (3, 9).

Mutant used for description and seed stocks:

com2.f (GSHO 1700) in Donaria; *com2.f* in Bowman (PI 483237)*7 (GSHO 2233, BW191, NGB 22023); *com2.g* in a freak stock from CIMMYT (GSHO 1703); *com2.g* in Bowman (PI 483237)*8 (GSHO 1878, BW192, NGB 22024); *com2.k* in Davis 1153 (GSHO 79); *com2.k* in Bowman*3 (BW187, NGB 22019); *brc1.5* from BGRC 13145 in Bowman*2 (BW071, NGB 20408).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:108.

Revised:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:53-54.

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:95-96.

BGS 74, Extra floret-c, *flo-c*

Stock number: BGS 74
Locus name: Extra floret-c
Locus symbol: *flo-c*

Revised locus symbol:

The *flo-c.5* mutant is likely an allele at the *flo-a* (Extra floret-a) locus based similar phenotypic expression (2) and retained SNP markers in 6H of the Bowman backcross-derived line (BW369) (1). It is recommended that the mutant be renamed *flo-a.5*. See BGS 182 for more information on the alleles at the *flo-a* locus.

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 6HL (1); *flo-c.5* is associated with SNP markers 1_0427 to 1_1246 (positions 56.64 to 134.55 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW369 (1); likely in 6H bins 07 or 08.

Description:

Extra floral bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra floral bracts is most common in the central portion of the spike, but rarely will the floral bracts develop into another spikelet (2, 4). Except for the occasional development of a floral bract below the central spikelet, the Bowman backcross-derived lines for presumed mutants at the *flo-a* locus, BW367, BW368, and BW369, were phenotypically similar to Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333, NGB 14659) (4).

Mutational events:

flo-c.5 (*flo-a.5*) (NGB 114275) in Foma (CIho 11333, NGB 14659) (4).

Mutant used for description and seed stocks:

flo-c.5 (*flo-a.5*) (GSHO 1743, NGB 114275) in Foma; *flo-c.5* in Bowman (PI 483237)*7 (GSHO 1877, BW369, NGB 20608). [The *flo-c.5* mutant is likely an allele at the *flo-a* locus in 6HL (1, 2)].

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:111.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:97.

BGS 80, Anthocyanin-less 2, *ant2*

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

Previous nomenclature and gene symbolization:

Non-purple straw = p_r or *pr* (8).
Anthocyanin-less = *ant-2* (2, 6).
Exrubrum = *rub* (4).
Colorless leaf tip 2 = clt_2 (5), c_2 (5).

Inheritance:

Monofactorial recessive (2, 7).

Located in chromosome 2HL (2, 7); *ant2* is about 15.1 cM distal from the *vrs1* (six-rowed spike 1) locus (8, 9, 10*); ant2.20* has no SNP markers in the Bowman backcross-derived line, BW019, that are deviant from those of Bowman (1); *ant2.h* is associated with SNP markers 1_0247 to 2_0182 (positions 150.96 to 185.53 cM) in 2H bins 10 to 12 in Bowman backcross-derived line BW020 (1).

Description:

Anthocyanin pigments are not observed in any vegetative plant parts, including the stem, auricles, lemma, and awn (2, 5, 6). The straw does not develop a purple pigmentation as it approaches maturity (8). The recommended symbol for the dominant allele is *Ant2.c* (formerly *Pr*).

Origin of mutant:

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

Mutational events:

ant2.d (*pr1.b*) in Alva (NSGC1866), *ant2.e* (*pr1.c*) in Balder (NGB 14668, PI 195481), *ant2.f* (*pr1.d*) in Cambrinus (PI 321779), *ant2.g* (*pr1.e*) in Sultan (PI 339814) (7); *ant2.15* (NGB 114564)*, 2.20* (NGB 114569, GSHO 1632)*, 2.23* (NGB 114572)*, 2.25* (NGB 114575)*, 2.26* (NGB 114576)*, 2.27* (NGB 114278) in Foma (CIho 11333, NGB 14659) (4); *ant2.41* (NGB 114596) in Mari (PI 428407, NGB 14656) (7), *ant2.46* (NGB 111505) in Foma, *2.47* (NGB 111823)*, 2.48* (NGB 111782)*, 2.49* (NGB 111808)*, 2.50* (NGB 111811)*, 2.51* (NGB 111817)*, 2.54* (NGB 111872)*, 2.55* (NGB 111787) in Bonus (PI 189763, NGB 14657) (7); *2.112, 2.113, 2.114, 2.115, 2.116, 2.117, 2.118, 2.120, 2.121, 2.122, 2.130* in Nordal (7); *ant2.h (pr1.f*) in Shyri (GSHO 2430) (3).

Mutant used for description and seed stocks:

ant2.20 (NGB 114569, GSHO 1632) in Foma; *ant2.h* (GSHO 2430) in Shyri; *ant2.h* from Shyri in Bowman (PI 483237)*5 (GSHO 1919); *ant2.h* in Bowman*7 (BW020, NGB 20428); *ant2.20* (NGB 114569, GSHO 1632) from Mari in Bowman*2 (GSHO 1920); *ant2.20* in Bowman*6 (BW019, NGB 20427).

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Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:118.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:98-99.

BGS 92, Erectoides-u, *ert-u*

Stock number: BGS 92
Locus name: Erectoides-u
Locus symbol: *ert-u*

Revised locus symbol:

The *ert-u.56* mutant is one of the alleles at the *ari-o* (Breviaristatum-o) locus (1). Other alleles at previously named loci include *ert-zd.159* (Erectoides-zd, BGS 93), *brh14.q* (Brachytic 14, BGS 148), and *brh16.v* (Brachytic 16, BGS 44) (1). See BGS 556 for more information on the alleles at the *ari-o* locus.

Previous nomenclature and gene symbolization:

Erectoides-56 = *ert-56* (6).
Brachytic 5 = *br5* (10).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 7HL (1, 2); *ert-u.56* is associated with SNP marker 1_0547 (about position 228 cM) in 7H bin 13 of the Bowman backcross-derived line BW325 (2); *ert-u.56* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (1) in the barley genome map (9). The *ert-u.56* mutant was previously associated with chromosome 2H based on linkage drag with the *Gth1* (toothed lemma 1) locus (4).

Description:

Spikes are slightly denser than those of the parent with a rachis internode length estimate of 2.7 mm, and culms are about 3/4 normal length (7). Plants have a brachytic-like pattern of growth (3, 10). Spike density is decreased by GA_3 treatment of plants as the flag leaf emerges (8). Compared to Bowman, plants of the Bowman backcross-derived line for *ert-u.56*, BW325, were 10 to 20% shorter; and had shorter peduncles, approximately 23 vs. 31 cm and shorter awns, 8 vs. 11 cm beyond the tip of the last spikelet. Rachis internodes of BW325 averaged 4.1 vs. 4.6 mm for Bowman. Also, leaf blades and kernels were slightly shorter. The kernel weights for BW325 were nearly equal to those of Bowman, but grain yields were 25 to 50% lower (5). As with other mutants at the *ari-o* locus, *ert-u.56* shows a brassinosteroid-deficient phenotype that includes a short culm, about 70% of normal, caused largely by an extreme shortening of the second culm internode (1). Other common traits include shorter rachis internodes, short awns, acute leaf angles, slightly undulating leaf margins, and a slightly elongated basal rachis internode (1). The six Bowman backcross-derived lines with a mutation at the *ari-o* or *HvDIM* locus, *ari-o.40*, *brh14.af*, *brh14.q*, *brh16.v*, *ert-u.56*, and *ert-zd.159*, have retained a small, common genetic donor parent interval (1). The sequence of *HvDIM*, encoding the barley Δ^5-sterol-Δ^{24}-reductase DIMINUTO, corresponds directly to single-nucleotide polymorphism (SNP) marker 1_0547 located in the telomere on the long arm of chromosome 7H (1).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB 14657) (6).

Mutational events:

ert-u.56 (NGB 112655, GSHO 496) in Bonus (PI 189763, NGB 14657) (6).

Mutant used for description and seed stocks:

ert-u.56 in Bonus (NGB 112655, GSHO 496); *ert-u.56* in Bowman (PI 483237)*8 (GSHO 1904, BW325, NGB 22120).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:131.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:100-101.

BGS 93, Erectoides-zd, *ert-zd*

Stock number: BGS 93
Locus name: Erectoides-zd
Locus symbol: *ert-zd*

Revised locus symbol:

The *ert-zd.159* mutant is one of the alleles at the *ari-o.40* (Breviaristatum-o) (1). Other alleles at previously named loci include *ert-u.56* (Erectoides-u, BGS 92), *brh14.q* (Brachytic 14, BGS 148), and *brh16.v* (Brachytic 16, BGS 44) (1). See BGS 556 for more information on the alleles at the *ari-o* locus.

Previous nomenclature and gene symbolization:

Erectoides-159 = *ert-159* (6).
Brachytic 7 = *br7* (8).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 7HL (1, 2); *ert-zd.159* is associated with SNP marker 1_0547 (about position 228 cM) in 7H bin 13 of the Bowman backcross-derived line BW333 (2). *ert-u.56* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (1) in the barley genome map (7). Previously located in chromosome 2H, based on linkage drag with the *Gth1* (toothed lemma 1) locus (4).

Description:

Plants have a brachytic-like pattern of growth and are about 3/4 normal height (3, 8) Plants of Bowman backcross-derived line for mutant *ert-zd.159*, BW333, were 10 to 20% shorter than Bowman and the awns were about 3 cm shorter. Rachis internode lengths were slightly shorter and kernels were slightly wider compared to those of Bowman. Kernel weights for BW333 varied from slightly more to 15% less. Grain yields varied from 1/3 to 1/2 those for Bowman (5). As with other mutants at the *ari-o* locus*, ert-zd.159* shows a brassinosteroid-deficient phenotype that includes a short culm, about 70% of normal, caused largely by an extreme shortening of the second culm internode (1). Other common traits include shorter rachis internodes, short awns, acute leaf angles, slightly undulating leaf margins, and a slightly elongated basal rachis internode (1). The six Bowman backcross-derived lines with a mutation at the *ari-o* or *HvDIM* locus, *ari-o.40*, *brh14.af*, *brh14.q*, *brh16.v*, *ert-u.56*, and *ert-zd.159*, have retained a small, common genetic donor parent interval (1). The sequence of *HvDIM*, encoding the barley Δ^5-sterol-Δ^{24}-reductase DIMINUTO, corresponds directly to single-nucleotide polymorphism (SNP) marker 1_0547 located in the telomere on the long arm of chromosome 7H (1).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB 14657) (6).

Mutational events:

ert-zd.159 (NGB 112758, GSHO 504) in Bonus (PI 189763, NGB 14657) (6).

Mutant used for description and seed stocks:

ert-zd.159 in Bonus (GSHO 504, NGB 112758); *ert-zd.159* in Bowman (PI 483237)*7 (GSHO 1901, BW333, NGB 22128).

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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:132.

Revised:
U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:91.
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:102-103.

BGS 102, Uzu 1, *uzu1*

Stock number: BGS 102
Locus name: Uzu 1 (semi-brachytic)
Locus symbol: *uzu1*

Previous nomenclature and gene symbolization:

Normal vs uzu = *h* (25).
Uzu = *u* (12).
Uzu (semi-brachytic) = *uz* (24).
Uzu 2 = *uz2* (10, 27, 29).
Uzu 3 = *uz3* (10, 27, 29).
Hordeum vulgare BR-insensitive 1 = *HvBRI1* (3).
Erectoides-79 = *ert-79* (9).
Breviaristatum-256 = *ari-256* (11).

Inheritance:

Monofactorial recessive (12, 20, 22, 24).

Located in chromosome 3HL (18, 19, 24); *uzu1.a* is about 17.6 cM proximal from the *alm1* (albino lemma 1) locus (23); *uzu1.a* is in bin 3H 06 near cDNA marker C1271 (3); *uzu1.a* is about 10.1 cM from AFLP marker E3733-6 in subgroup 27 of the Proctor/Nudinka map (16); *uzu1.a* is associated with SNP markers 1_0373 to 1_1314 (positions 92.55 to 107.40 cM) in 3H bins 06 to 07 of the Bowman backcross-derived line BW885 (5); *uzu1.a* with *sld1.a* (slender dwarf 1) is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman line BW860 (5); *uzu1.a* with *wst1.c* (white streak 1) is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman line BW912 (5); *ert-ii.79* is associated with SNP markers 2_0686 to 2_0931 (positions 67.01 to 104.39 cM) in 3H bins 05 to 06 of the Bowman line BW312 (5); *uzu1.256* (formerly *ari.256*) is associated with SNP markers 1_0728 to 2_1405 (positions 96.75 to 187.28 cM) in 3H bins 06 to 12 of Bowman line BW033 (5); the *ert-ii.79* allele at the *uzu1* (*HvBRI1*) locus is positioned at 57.1 cM (4) on the barley genome map (26), in 3H bin 06.

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (21, 22, 24). These organs are often reduced in length and increased in width. Changes in organ length are temperature sensitive, but heading date and maturity are unaltered. The coleoptile of uzu plants shows a prominent projection or hook near the apex. Sometimes the coleoptile of the mutant shows a V-shaped notch on the side opposite from the projection. Thus, the apex of the coleoptile has two notches, one on each side (22, 27, 28). The temperature sensitive reduction in culm length of *uzu1.a* plants ranged from less than 15% in cool environments to over 75% in warm ones (6). The Bowman backcross-derived line for *uzu1.a*, BW885, produced plants that were 20 to 40% shorter than Bowman, awns were about 1/3 of normal length, rachis internodes were shorter, 3.0 vs.4.7 mm, and leaf blades were shorter and wider. Kernels of BW885 were shorter, 7.9 vs. 9.5 mm, and lighter, averaged 4.7 vs. 5.7 mg. Spikes of BW885 often had 2 more kernels than those of Bowman. Grain yields of BW885 ranged from 1/3 to 3/4 those of Bowman (6). Chono et al. (3) reported that the *uzu1.a* variant is caused by a mutation that changed a highly conserved residue of the kinase domain of the *HvBRI1* protein [*BRI1* (brassinosteroid insensitive 1) of *Arabidopsis*] from His-857 to Arg-857. When grown at low temperatures, the *uzu1.a* mutant was a semidwarf with 80% of wild-type culm length. The overall plant architecture is more erect, with acute leaf blade angles. Short-awned spikes are compact with dense basal spikelets, and frequently with opposite spikelets in the tip caused by irregular elongation of rachis internodes. Leaf blade margins and auricles of *uzu1.a* plants have a slightly undulating appearance (4). When grown at 26°C, *uzu1.a* plants (BW885) showed extreme dwarfing, less than 1/3 the height of Bowman plants. This extreme dwarfing caused by temperature was not observed with other mutants at the *uzu1* locus (4). In progeny from crosses to the BW885 line, tillering was reduced (1). The *uzu1.a* variant was associated with decreased incidence of crown root, *Fusarium pseudograminearum* (2).

Origin of mutant:

Natural occurrence in some cultivars of Japanese origin (21, 22).

Mutational events:

uzu1.a (OUJ371, PI 182624, GSHO 1300) in East Asian cultivars with a winter growth habit (17, 22, 29); *uzu1.b* (092AR) in Aramir (PI 467781) (7, 8); *uzu1.c* 36 (Katovice, Poland 32-1-1) in the doubled-haploid line H930 (4); *ert-ii.79* (NGB 112678, GSHO 483) in Bonus (PI 189763, NGB 14657) (4, 8); *uzu1.256* (formerly *ari.256*) (NGB 116065) in Kristina (NGB 1500, NGB 14661) (4, 11).

Mutant used for description and seed stocks:

uzu1.a (OUJ371, PI 182624, GSHO 1300) in Baitori 11 (OUJ 043); *uzu1.a* in Bowman (PI 483237)*7 (GSHO 1963, BW885, NGB 20787); *uzu1.a* with *wst1.*c (OUL074, GSHO 569) from Akashinriki (PI 467400, OUJ659) in Bowman*8 (GSHO 1967, BW912, NGB 22343); *uzu1.a* with *sld1.a* (OUM148, GSHO 2489) from Akashinriki in Bowman*8 (GSHO 1971, BW860, NGB 22297); *ert-ii.79* in Bowman (PI 483237)*7 (GSHO 1982, BW312, NGB 22108); *uzu1.256* (formerly *ari.256*) from Kristina in Bowman*6 (BW033, NGB20441).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:124.

Revised:

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J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:136-137.

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BGS 133, Semidwarf 2, *sdw2*

Stock number:	BGS 133
Locus name:	Semidwarf 2
Locus symbol:	*sdw2*

Previous nomenclature and gene symbolization:

Semidwarf-b = *sdw-b* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3HL (3); *sdw2.b* is over 34.5 cM distal from the *sld1* (slender dwarf 1) locus (3); *sdw2.b* is associated with SNP markers 2_0650 to 2_0612 (positions 192.0 to 198.33 cM) in 3H bins 12 to 13 of the Bowman backcross-derived line BW829 (1).

Description:

Plants are about 3/4 normal height; culms are thin with narrow, short, erect leaves. The flag leaf is narrow and short. The peduncle is short, the collar has a small leaf-like bract, and the basal rachis internode is elongated (3). Compared to Bowman, plants of the Bowman backcross-derived line for *sdw2.b*, BW829, were shorter 10 to 20% shorter, peduncles were 1/2 to 2/3 as long, rachis internodes were 10 to 20% shorter, and leaf blades were about 2/3 normal length and width. BW829 plants headed 1 to 3 days earlier than Bowman and they yielded about 2/3 as much. Kernels were shorter and thinner and weighed about 20% less, 4.6 vs 5.6 mg (2).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Mg4170 (3).

Mutational events:

sdw2.b (267MK, later called 437MK, GSHO 2466) in Mg4170 (3).

Mutant used for description and seed stocks:

sdw2.b (GSHO 2466) in Mg4170; *sdw2.b* in Bowman (PI 483237)*7 (GSHO 1965, BW829, NGB 22266).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:169.

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:108.

BGS 135, Erectoides-ii, *ert-ii*

Stock number:	BGS 135
Locus name:	Erectoides-ii
Locus symbol:	*ert-ii*

Revised locus symbol:

The *ert-ii.79* mutant is an allele at the *uzu1* (uzu1) or *HvBRI1* (*Hordeum vulgare* brassinosteroid insensitive 1) locus (1, 2). See BGS 102 for more information on the alleles at the *uzu1* or *HvBRI1* locus.

Previous nomenclature and gene symbolization:

Erectoides-79 = *ert-79* (1, 5).

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 3HL (5, 6); *ert-ii.79* is over 6.6 cM distal from the centromere (5, 6); *ert-ii.79* is associated with SNP markers 2_1533 to 2_0931 (positions 67.01 to 104.39 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW312 (3); the *ert-ii.79* allele at the *uzu1* (*HvBRI1*) locus is positioned at 57.1 cM (2) on the barley genome map (9), in 3H bin 06.

Description:

Plants are about 1/2 normal height and the spike has an elongated basal rachis internode. Spikes are relatively short and show a slight reduction in rachis internode length with a range of values from 2.7 to 3.0 mm (8). Compared to Bowman, culms of the Bowman backcross-derived line for *ert-ii.79*, BW312, and their peduncles were about 2/3 normal length. Heading of BW312 was delayed by 1 to 3 days. Kernels were slightly shorter and wider, but kernels weights were similar. Grain yields of BW312 were about half those of Bowman (4). BW312 with *ert-ii.79* and BW885 with *uzu1.a* showed a brassinosteroid signaling-deficient phenotype in a leaf-unrolling test (2). In contrast to its allele *uzu1.a*, a drastic reduction in culm length was not caused in the *ert-ii.79* mutant when grown under high temperatures (2).

Origin of mutant:

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

Mutational events:

ert-ii.79 (NGB 112678, GSHO 483) in Bonus (PI 189763, NGB 14657) (5, 8).

Mutant used for description and seed stocks:

ert-ii.79 (NGB 112678, GSHO 483) in Bonus; *ert-ii.79* in Bowman (PI 483237)*7 (GSHO 1982, BW312, NGB 22108).

References:

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9. The International Barley Genome Sequencing Consortium. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature 491:711-716.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:172.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:109-110.

BGS 148, Brachytic 14, *brh14*

Stock number: BGS 148
Locus name: Brachytic 14
Locus symbol: *brh14*

Revised locus symbol:

The *brh14.q* and *brh14.af* mutants are alleles at the *ari-o.40* (Breviaristatum-o) locus (3). Other alleles at previously named loci include *ert-u.56* (Erectoides-u, BGS 92), *ert-zd.159* (Erectoides-zd, BGS 93), and *brh16.v* (Brachytic 16, BGS 44) (3). See BGS 556 for more information on the alleles at the *ari-o* locus.

Previous nomenclature and gene symbolization:

Brachytic-q = *brh.q* (5).
Brachytic-af = *brh.af* (3, 8).

Inheritance:

Monofactorial recessive (5, 9).

Located in chromosome 7HL (3, 4); *brh14.q* is associated with SNP marker 1_0387 (position 229.65 cM) in 7H bin 13 of the Bowman backcross-derived line BW085 (4); *brh14.af* is associated SNP markers 1_0174 to 1_0378 (position 229.66 cM) in 7H bin 13 of Bowman backcross-derived line BW072 (4); *brh14.q* and *brh14.af* are alleles at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (3) in the barley genome map (11). Previously located approximately 24.9 cM proximal from SSR marker Bmac0029 in 3H bin 15 (2).

Description:

Plants are about 2/3 normal height, awns are 1/3 to 3/4 normal, peduncles are about 2//3 normal length, and rachis internodes are about 7/8 normal length (2, 9, 10). Seedling leaves of *brh14.q* plants are relatively short, but they do respond to gibberellic acid treatment (1). Failure of the internode below the peduncle to elongate was observed in double dwarfs involving *brh14.q* in the Akashinriki genetic background (10). Compared to Bowman, the backcross-derived line for *brh14.q*, BW085, showed reduced elongation of many tissues and an erect growth habit. Leaf blades were smaller and narrower, about 3/4 normal length. Average peduncle length was 20 vs. 30 cm, rachis internodes were slightly shorter, 4.0 vs. 4.4 mm, and awns varied from 1/4 to 3/4 normal length over field environments. The kernels of BW085 were visually shorter, 8.4 vs. 9.7 mm, and weighed less, 5.0 vs. 5.7 mg. BW085 plants headed about 3 days later than Bowman and had 2 to 3 more kernels per spike. However, the grain yields of BW085 average 1/4 to 13 of those for Bowman and grain test weights were reduced (2, 6). The *brh14.af* mutant is very dwarf, with leaf blades, culms, and awns being about 50% of wild type. Seed set is OK, but kernels are also much smaller than those of normal Steptoe (8). As with other mutants at the *ari-o* locus, *brh14.q* and *brh14.af* plants of their respective backcross-derived lines exhibit a brassinosteroid-deficient phenotype that includes a short culm, about 70% of normal, caused largely by an extreme shortening of the second culm internode (3). Other common traits include shorter rachis internodes, short awns, acute leaf angles, slightly undulating leaf margins, and a slightly elongated basal rachis internode (3). The six Bowman backcross-derived lines with a mutation at the *ari-o* or *HvDIM* locus, *ari-o.40*, *brh14.af*, *brh14.q*, *brh16.v*, *ert-u.56*, and *ert-zd.159*, have retained a small, common DNA interval from their donor parents (3). This segment contains the sequence of *HvDIM*, encoding the barley Δ^5-sterol-Δ^{24}-reductase DIMINUTO, and corresponds directly to single-nucleotide polymorphism (SNP) marker 1_0547 located in the telomere on the long arm of chromosome 7H (3).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (9, 10).

Mutational events:

brh14.q (OUM131, dw-d, DWS1035, GSHO 1682) in Akashinriki (OUJ659, PI 467400) (5, 7, 9, 10); *brh14.af* (FN46) in Steptoe (CIho 15229) (3, 8).

Mutant used for description and seed stocks:

brh14.q (GSHO 1682) in Akashinriki; *brh14.q* in Bowman (PI 483237)*6 (GSHO 2175, BW085, NGB 20492); *brh14.af* from Steptoe in Bowman*7 (BW072, NGB 20479).

References

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11. The International Barley Genome Sequencing Consortium. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature 491:711-716.

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:231.

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:111-112.

BGS 166, Male sterile genetic 25, *msg25*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 8).

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

Description:

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

Outcrossing - complete female fertility (7).

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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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Univ., Bozeman.

Prepared:

E.A. Hockett. 1974. Barley Genet. Newsl. 4:135 as BGS 386.
E.A. Hockett. 1975. Barley Genet. Newsl. 5:112.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:192.
J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:101-102.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:113-114.

BGS 168, Globosum-a, *glo-a*

Stock number:	BGS 168
Locus name:	Globosum-a
Locus symbol:	*glo-a*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 4H (2, 5); *glo-a.1003* is associated with chromosome 4H based on crosses to a translocation set (2, 5); *glo-a.1003* is associated with SNP markers 3_0554 and 1_0510 (positions 140.93 and 149.26 cM) in 4H bin 10 of Bowman backcross-derived line BW392 (1).

Description:

Fertile spikelets are shortened and the resulting kernels are nearly round or globe-shaped. Sterile lateral spikelets are 1/2 normal length and twisted (3). In the Bowman backcross-derived line for *glo-a.1003*, BW392, kernel length was much reduced and other spike tissues were reduced in length. Kernel weights were very low, 4.2 vs. 5.6 mg, and so were test weights. Compared to Bowman, BW392 plants were 10% shorter and peduncles were about 20% shorter. Awn length varied 1/3 to 2/3 of that for Bowman. The grain yield of BW392 averaged about 15% lower than that of Bowman (3).

Origin of mutant:

An X-ray induced mutant in Proctor (PI 280420) (1, 3).

Mutational events:

glo-a.1003 (1343/63, GSHO 1328) in Proctor (PI 280420) (1, 2, 3).

Mutant used for description and seed stocks:

glo-a.1003 (GSHO 1328) in Proctor; *glo-a.1003* in Bowman (PI 483237)*7 (GSHO 2006, BW392, NGB 20630).

References:

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Prepared:

G. Fischbeck. 1978. Barley Genet. Newsl. 8:152.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:194.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:115.

BGS 182, Extra floret-a, *flo-a*

Stock number:	BGS 182
Locus name:	Extra floret-a
Locus symbol:	*flo-a*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Location in chromosome 6HL (1); *flo-a.1* is associated with SNP markers 1_0539 to 1_0040 (positions 76.05 to 107.26 cM) in 6H bins 06 to 07 of the Bowman backcross-derived line BW367 (1); *flo-a.3* is associated with SNP markers 2_0746 to 1_1246 (positions 125.86 to 134.55 cM) in 6H bin 08 of the Bowman backcross-derived line BW368 (1); *flo-a.5* is associated with SNP markers 1_0061 to 1_1246 (positions 70.15 to 134.55 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW369 (1), likely in 6H bin 07.

Description:

Extra floral bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra floral bracts is most common in the central portion of the spike, but rarely will the floral bracts form another spikelet (2, 4). Except for the occasional development of a floral bract below the central spikelet, the Bowman backcross-derived lines for mutants at the *flo-a* locus, BW367, BW368, and BW369 were similar to Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333, NGB 14659) (4).

Mutational events:

flo-a.1 (NGB 114271, GSHO 1741) in Foma (CIho 11333, NGB 14659) (4); *flo-a.3* (NGB 114273, GSHO 1742), previously named *flo-b.3*, in Foma (4); *flo-a.5* (NGB 114275, GSHO 1743), previously named *flo-c.5*, in Foma (4).

Mutant used for description and seed stocks:

flo-a.1 (GSHO 1741, NGB 114271) in Foma; *flo-a.3* (GSHO 1742, NGB 114273) in Foma; *flo-a.5* (GSHO 1743, NGB 114275) in Foma; *flo-a.1* in Bowman (PI 483237)*5 (GSHO 2005), in Bowman*7 (BW367, NGB 20606); *flo-a.3* in Bowman (PI 483237)*6 (GSHO 2128, BW368, NGB 20607); *flo-a.5* in Bowman (PI 483237)*7 (GSHO 1877, BW369, NGB 20608).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:205.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:112.

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:116.

BGS 230, Globosum-e, *glo-e*

Stock number:	BGS 230
Locus name:	Globosum-e
Locus symbol:	*glo-e*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 3HL or 1HS (1); *glo-e.15* is associated with SNP markers 1_0646 to 1_0694 (positions 239.73 to 248.51 cM) in 3H bin 15 and with SNP markers 2_0373 to 2_1067 (positions 0.10 to 3.18 cM) in 1H bin 01 in Bowman backcross-derived line BW396 (1).

Description:

Plants appear normal, but kernels are larger and more rounded than those of normal sibs (3). No morphological differences were noted between Bowman and the Bowman backcross-derived line for *glo-e.15*, BW396, except kernels seemed a little wider (2).

Origin of mutant:

A neutron induced mutant in Foma (CIho 11333, NGB 14659) (4).

Mutational events:

glo-e.15 (*glo-e.1010,* NGB 115633, GSHO 1755) in Foma (CIho 11333, NGB 14659) (3, 4).

Mutant used for description and seed stocks:

glo-e.15 (NGB 115633, GSHO 1755) in Foma; *glo-e.15* in Bowman (PI 483237)*7 (GSHO 2050, BW396, NGB 20634).

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Prepared:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:228.

Revised:

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:117.

BGS 252, Early maturity 7, *eam7*

Stock number: BGS 252
Locus name: Early maturity 7
Locus symbol: *eam7*

Previous nomenclature and gene symbolization:

Early heading = *ec* (9).
Early maturity 7 = *ea7* (8).

Inheritance:

Monofactorial recessive (5, 8).

Located in chromosome 6HS (9); *eam7.g* is about 0.5 cM from the *rob1* (orange lemma 1) locus (8); *eam7.g* is about 3.0 cM from the centromere (7); *eam7.g* is near the centromere and between markers mwg2264 and mwg916 (10); *eam7.g* is associated with SNP markers 2_0886 to 1_0978 (positions 3.28 to 156.09 cM) in 6H bins 01 to 06 of the Bowman backcross-derived line BW288 (1); *eam7.g* is associated with homozygous SNP markers 2_0886 to 2_0291 (positions 3.28 to 81.35 cM) in 6H bins 01 to 06 of the Bowman backcross-derived line BW287 (1), likely in 6H bin 05.

Description:

Under short-day conditions in California, USA, plants with the *eam7.g* mutant bloomed about 4 weeks before California Mariout, produced relatively few tillers, and were fine stemmed and relatively short. Differences were less pronounced under long-day conditions (8). Mutants were partially insensitive to photoperiod and have a vernalization requirement (9). Under long-day conditions, segregates expressing the *eam7.g* gene were difficult to identify (6). The differences in heading dates for Atsel [*Eam1.a* (Early maturity 1) plus *eam7.g*] and Betzes (*eam1* and *Eam7*) were 55 and 18 days under short and long days, respectively (10). When the *Eam1.a* gene is not present, *eam7.g* plants headed 10 to 14 days earlier than Bowman in nurseries at Yuma, Arizona, USA, but only 3 to 5 days earlier at Fargo, North Dakota, USA (2). The *Eam1.a* gene present in California Mariout apparently interacts with the *eam7.g* allele under short-day conditions to cause extreme earliness (2). The Bowman backcross lines for *eam7.g*, BW287 and BW288, were 4 to 10 days earlier than Bowman under short days, but no differences were observed under long days (2). The *HvCO7* (*Hordeum vulgare CONSTANS 7*) gene was located on the same chromosome arm as *eam7 gene (5).*

Origin of mutant:

A spontaneous mutant in Atlas (PI 539108) identified as Atsel (CIho 6250) (3); present in male sterile Club Mariout/6*California Mariout (PI 527380) (3, 9).

Mutational events:

eam7.g in BC$_6$ California Mariout (GBC326, GSHO 579) (4, 8); *eam7.n* (Ea1), *eam7.o* (Ea2), *eam7.p* (Ea3) in Chikurin Ibaraki 1 (OUJ069, CIho 7370) (11).

Mutant used for description and seed stocks:

eam7.g in BC$_6$ California Mariout (GSHO 579); *eam7.g* in Bowman (PI 483237)*3 (GSHO 2068, BW288, NGB 20572), *eam7.g* in Bowman*2 (BW287, NGB 20571).

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Prepared:

C.R. Burnham. 1971. Barley Genet. Newsl. 1:155. Early heading, *ea7*.

Revised:

J.D. Franckowiak and L.W. Gallagher. 1997. Barley Genet. Newsl. 26:233.
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:123-124.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:118-119.

BGS 260, Chlorina seedling 11, *fch11*

Stock number:	BGS 260
Locus name:	Chlorina seedling 11
Locus symbol:	*fch11*

Previous nomenclature and gene symbolization:

Pale green = *pg* 3).

Chlorina seedling 11 = *f11* (1).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 6HL (5); *fch11.t* is about 6.1 cM distal from the *rob1* (orange lemma 1) locus (3, 5); *fch11.t* is associated with SNP markers 2_0651 to 1_0377 (positions 89.78 to 91.91 cM) in 6H bin 07 in Bowman backcross-derived line BW353 (2).

Description:

Seedlings are pale yellow-green and often have white blotches on the seedling leaves. Plants remain light green until maturity (3). Compared to Bowman, plants of the Bowman backcross-derived line for *fch11.t*, BW353, headed 2 to 4 days later and were slightly taller. Kernels of BW353 were 10% lighter only in drought stressed environments. Grain yields of BW353 were 1/2 to 3/4 of those for Bowman (4).

Origin of mutant:

An X-ray induced mutant in Himalaya (CIho 1312) obtained by Caldecott and North at the University of Minnesota (1).

Mutational events:

fch11.t (GBC357 and GBC359, GSHO 1738) in Himalaya (CIho 1312) (1).

Mutant used for description and seed stocks:

fch11.t (GSHO 1738) in Himalaya; *fch11.t* in Bowman (PI 483237)*6 (GSHO 2082); *fch11.t* in Bowman*7 (BW353, NGB 20592).

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Prepared:

C.R. Burnham and K.J. Kasha. 1979. Barley Genet. Newsl. 9:133.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:240.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:120.

BGS 327, Extra floret-b, *flo-b*

Stock number:	BGS 327
Locus name:	Extra floret-b
Locus symbol:	*flo-b*

Revised locus symbol:

The *flo-b.3* mutant is likely an allele at the *flo-a* (Extra floret-a) locus based similar phenotypic expression (2) and retained SNP markers in 6H of the Bowman backcross-derived line (BW368) (1). It is recommended that the mutant be renamed *flo-a.3*. See BGS 182 for more information on the alleles at the *flo-a* locus.

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 6HL (1); *flo-b.3* is associated with SNP markers 2_0746 to 1-1246 (positions 125.86 to 134.55 cM) in 6H bin 08 of the Bowman backcross-derived line BW368 (1); likely in 6H bins 07 or 08.

Description:

Extra floral bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra floral bracts is most common in the central portion of the spike, but rarely will the floral bracts form another spikelet (2, 4). Except for the occasional development of a floral bract below the central spikelet, the Bowman backcross-derived lines for presumed mutants at the *flo-a* locus, BW367, BW368, and BW369, were phenotypically similar to Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333, NGB 14659) (4).

Mutational events:

flo-b.3 (NGB 114273, GSHO 1742) in Foma (CIho 11333, NGB 14659) (4).

Mutant used for description and seed stocks:

flo-b.3 (GSHO 1742, NGB 114273) in Foma; *flo-b.3* in Bowman (PI 483237)*6 (GSHO 2128, BW368, NGB 20607). [The *flo-b.3* mutant is likely an allele at the *flo-a* locus in 6HL (1, 2)].

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:275.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:121.

BGS 335, Male sterile genetic 49, *msg49*

Stock number:	BGS 335
Locus name:	Male sterile genetic 49
Locus symbol:	*msg49*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2, 3, 4).

Located in chromosome 5HL (2); *msg49.jw* is about 10.4 cM from the *raw1* (smooth awn 1) locus (2); *msg49.jw* is associated with SNP markers 2_1150 to 2_0629 (positions 145.57 to 187.37 cM) in 5H bins 09 to 10 in a homozygous male sterile plant from Bowman backcross-derived line BW586 (1).

Description:

Selfing - none (4).

Outcrossing - Complete female fertility (4).

Stamens - anthers rudimentary, no stomium or filament elongation (4).

Origin of mutant:

A spontaneous mutant in ND7369, a six-rowed selection from North Dakota State University, Fargo, North Dakota, USA (4).

Mutational events:

msg49.jw (MSS528, GSHO 2402) in ND7369 (3, 4).

Mutant used for description and seed stocks:

msg49.jw (GSHO 2402) in ND7369; *msg49.jw* in Bowman (PI 483237)*8 (GSHO 2141, BW586, NGB 24137).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:283.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:122.

BGS 348, Early maturity 5, *Eam5*

Stock number:	BGS 348
Locus name:	Early maturity 5
Locus symbol:	*Eam5*

Previous nomenclature and gene symbolization:

Early maturity = *Ea* (11, 17).
Early maturity 3 = *Ea3* (4, 5).
Early maturity 5 = *Ea5* (7).
Early maturity 8 = *Ea8* (12).
Hordeum vulgare phytochrome C early = *HvPhyC-e* (8, 9).

Inheritance:

Monofactorial dominant (16, 18), semi-dominant (9).

Located in chromosome 5HL (4, 8, 9, 16); very close to the *raw1* (smooth awn 1) locus (16, 17, 18); a QTL for earliness associated with the *Sgh2* locus among spring type segregates from the winter parent (1, 10, 13, 14, 16); *Eam5.x* is associated with SNP markers 1_0094 to 1_0589 (positions 187.39 to 234.98 cM) in 5H bins 10 to 14 of Bowman backcross-derived line BW286 (2), *Eam5.x* is associated with SNP markers 1_0094 to 1_0589 (positions 187.39 to 247.08 cM) in 5H bins 10 to 13 of Bowman backcross-derived line BW285 (2); *Eam5.x* is associated with SNP markers 1_1507 to1_0870 (positions 192.80 to 274.24 cM) in 5H bins 10 to 14 of Bowman backcross-derived line BW291 (2). BW285, BW286 and BW291 have identical SNP markers from 1-1090 to1_0095 (positions 203-.85 to 210.59 in 5H bin 11 (2); the *Eam5* locus is linked to *Sgh2* (*Vrn-H1*) (spring growth habit 2) locus at a distance of 1.5 cM and to *HvCK2α* (Casein Kinase II alpha) by 3.1 cM (8), in 5H bin 11.

Description:

An earliness factor closely linked to the rough awn gene was identified in spring barley (17). Plants with the *Eam5* gene head 3 to 10 days earlier than normal sibs under short-day conditions (3, 11). Early heading is commonly associated a shorter stature compared to normal sibs. The slight reduction in plant height is also observed under long-day conditions. Peduncles and rachis internodes are slightly shortened (3). The *Eam5.x* gene appears to be the common early maturity gene present in winter sown spring barley cultivars used in China and Japan; and it is present in the ICARDA/CIMMYT barley lines developed in Mexico. Complex interactions with other genes conditioning photoperiod response have been observed (3, 18). Takahashi and Yasuda (16) classified plants that were about 10 days earlier than normal spring barley under short days as having the *Sgh2.I* (spring growth of habit 2, grade 1) gene. The earliness gene from Indian Barley showed a dominant inheritance pattern (16). Early heading caused by a QTL in 5HL was associated with decreased sensitivity to frost injury (1, 10). The *Sgh2* (*Vrn-H1*) locus is closely linked to the candidate gene for photoperiod sensitivity, the red/far-red light photoreceptor *Phytochrome C* (*HvPhyC*) (5, 15), which was later demonstrated to cosegregate with early flowering (8, 9). BW285 with the *Eam5.x* gene has the linked recessive allele, *sgh2.b*, for winter growth habit at the *Sgh2* (*Vrn-H1*) locus while Bowman has the recessive allele at the *Eam5* locus and the dominant spring growth habit allele *Sgh2.I* (9). *Eam5.x* (*HvPhyC*) interacts with long-day response gene *Eam1* (*Ppd-H1*) to accelerate flowering under short-day conditions (9, 18). This is the response reported by Takahashi and Yasuda (16). BW285 and several Japanese cultivars have specific mutation named haplotype 7 in the first exon of *HvPhyC* (9). The difference in responses associated with the *Eam5.x* gene reported by Nishida et al. (8) and Pankin et al. (9) may be caused by the presence of the *Eam6.h* (early maturity 6) or *eps-2S* (earliness per se 2S) allele in the Bowman backcross-derived lines (3).

Origin of mutant:

Natural occurrence in Indian cultivars (4, 6); present in Japanese winter barleys (8, 10, 13, 16); isolated from ICARDA/CIMMYT selection CMB85-533-H-1Y-1B-0Y-5B (Higuerilla*2/Gobernadora) (3).

Mutational events:

Eam5.x in CMB85-533 (3); *Eam5.x* in fall planted Chinese and Japanese cultivars (13, 14, 16).

Mutant used for description and seed stocks:

Eam5.x in CMB85-533; *Eam5.x* from CMB85-533 in Bowman (PI 483237)*6 (GSHO 3424); *Eam5.x* from CM85-533 in Bowman*7 (BW285 and BW286, NGB 20569 and NGB 20570); *Eam5.x* from Japanese breeding line (DH6) in Bowman*5 (BW291, NGB 20575).

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Prepared:
J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:109.

Revised:
J.D. Franckowiak and G. Yu. 2007. Barley Genet. Newsl. 37:260-261.
J.D. Franckowiak and G. Yu. 2015. Barley Genet. Newsl. 45:123-125.

BGS 357, Male sterile genetic 1, *msg1*

Stock number:	BGS 357
Locus name:	Male sterile genetic 1
Locus symbol:	*msg1*

Previous nomenclature and gene symbolization:

Male sterile = *ms* (14).

Male sterile 1 = *ms1* (5).

Inheritance:

Monofactorial recessive (16).

Located in chromosome 1HL (13); *msg1.ca* is near the centromere (8); *msg1.ca* is about 10.0 cM proximal from the *nec1* (necrotic leaf spot 1) locus (11, 14); probably proximal from the small lateral spikelet 1 (*sls1*) gene which also originated from MSS005 (2); *msg1.ca* is associated with SNP markers 1_0933 to 1_0324 (positions 82.35 to 87.19 cM) in 1H bin 08 of a heterozygous plant from the Bowman backcross-derived line BW545 (1), in 1H bin 08.

Description:

Selfing - none (7).

Outcrossing - complete female fertility (7).

Stamens - anthers smaller than fertile sib, no stromium or filament elongation (15).

Pollen - microspores degenerate at or before the free microspore stage (12); non-staining, shrunken, and devoid of cytoplasm (15).

Cytology - normal development and differentiation of anthers until completion of meiosis (12). SNP markers in the plant studied as *msg1.ca* of Bowman backcross-derived line BW145 were identical to those of Bowman (1).

Origin of mutant:

A spontaneous mutant in the Composite Cross line CIho 5368 (16).

Mutational events:

msg1.ca (GSHO 1810) from CIho 5368 in Betzes (PI 129430)*11 (MSS005) (12, 16); *msg1.i* (MSS077) in 80TT25 (CIho 13638), *msg1.t* (MSS042) in Trophy (CIho 10647), *msg1.ai* (MSS100) in Betzes (PI 129430) (9, 10); *msg1.ar* (MSS310) in Glossy Brachytic (CIho 15246), *msg1.bp* (MSS330) in Betzes (3, 10); *msg1.cz* (MSS348) in Betzes (4, 10); *msg1.gb* (MSS429) in Maris Mink (5); *msg1.jv* (MSS527) in a Harrington outcross (6).

Mutant used for description and seed stocks:

msg1.ca in Betzes*11 (GSHO 1810); *msg1.ca* in Bowman (PI 483237)*8 (GSHO 2042, BW545, NGB 24128).

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:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:175.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:304-305.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:98-99.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:126-127.

BGS 358, Male sterile genetic 2, *msg2*

Stock number:	BGS 358
Locus name:	Male sterile genetic 2
Locus symbol:	*msg2*

Previous nomenclature and gene symbolization:

Male sterile 2 = c_2(1).

Male sterile 2 = *ms2* (4).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 2HL (1, 11); *msg2.cb* is about 2.4 cM proximal from the *eog1* (elongated outer glume 1) locus (7); *msg2.cb* is less than 1 cM from the T2-7a translocation breakpoint and about 3 cM from the *eog1* locus (8); *msg2.cb* is associated with SNP markers 2_0674 to 2-0585 (positions 85.71 to 103.71 cM) in 2H bins 07 to 08 of a heterozygous plant from Bowman backcross-derived line BW554 (2).

Description:

Selfing - none (4).

Outcrossing - complete female fertility (4).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (10).

Pollen - non-staining, shrunken, and no normal grains (10).

Origin of mutant:

A spontaneous mutant in the F_2 progeny of Manchuria (CIho 2330) X CIho 4363 (4).

Mutational events:

msg2.cb (MSS046) in F_2 of Manchuria/CIho 4363 (4, 6); *msg2.ax* (MSS045) in Compana (PI 539111) (5, 6); *msg2.ed* (MSS379) in Ingrid (CIho 10083, NGB 2671) (3, 9).

Mutant used for description and seed stocks:

msg2.cb in Herta*10 (GSHO 2371, NGB 2664); *msg2.cb* in Manchuria*19 (MSS047); *msg2.cb* in Ogalitsu*14 (MSS048); *msg2.cb* in Trebi*19 (MSS050) (5); *msg2.cb* from Herta*10 in Bowman (PI 483237)*7 (GSHO 1890, BW554, NGB 23423).

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E.A. Hockett. 1971. Barley Genet. Newsl. 1:175-176.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:306.
J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:428.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:128-129.

BGS 359, Male sterile genetic 3, *msg3*

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

Previous nomenclature and gene symbolization:

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

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

Inheritance:

Monofactorial recessive (5).

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

Description:

Selfing - none (3, 5).

Outcrossing - complete female fertility (3, 5).

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

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

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
4. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
5. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. Can. J. Genet. Cytol. 2:397-415.
6. Lundqvist, U. (Unpublished).
7. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
8. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of

linkage studies in cultivated barley, *Hordeum* species: Supplement III. 1954-1963. Crop Sci. 5:33-43.

Prepared:

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

Revised:

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

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:130-131.

BGS 360, Male sterile genetic 4, *msg4*

Stock number:	BGS 360
Locus name:	Male sterile genetic 4
Locus symbol:	*msg4*

Previous nomenclature and gene symbolization:
Male sterile 4 = *ms4* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 1H (3); *msg4.cd* is near the centromere (3); *msg4.cd* is associated with SNP markers 2_0617 to 1_0552 (positions 50.96 to 88.33 cM) in 1H bins 05 to 08 of a heterozygous plant from the Bowman backcross-derived stock BW576 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (5).
Pollen - non-staining, shrunken, and no normal grains (5).
Origin of mutant:
A spontaneous mutant in Freja (CIho 7130, NGB 1485) (5).
Mutational events:
msg4.cd (MSS052, GSHO 2392) in Freja (CIho 7130, NGB 1485) (2, 4).
Mutant used for description and seed stocks:
msg4.cd (GSHO 2392) in Freja; *msg4.cd* in Bowman (PI 483237)*7 (GSHO 2043, BW576, NGB 23438.
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. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
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.
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5. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:177-178.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:308.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:100.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:132.

BGS 361, Male sterile genetic 5, *msg5*

Stock number:	BGS 361
Locus name:	Male sterile genetic 5
Locus symbol:	*msg5*

Previous nomenclature and gene symbolization:

Male sterile 5 = *ms5* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 3HS (7); *msg5.ce* is about 13.1 cM proximal from the *uzu1* (uzu 1) locus (2); *msg5.ce* is about 6.8 cM proximal from the *alm1* (albino lemma 1) locus (2); *msg5.ce* is associated with SNP marker 1_1191 (position 98.41 cM) in 3H bin 6 in a heterozygous plant from Bowman backcross-derived line BW587 (1); *msg5.ie* is associated with SNP markers 1_0926 to 2_0326 (positions 85.26 to 119.10 cM) in 3H bins 05 to 07 in a heterozygous plant from Bowman backcross-derived line BW971 (1).

Description:

Selfing - none (6).

Outcrossing - complete female fertility (6).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (9).

Pollen - non-staining, some normal-appearing grains (9).

Origin of mutant:

A spontaneous mutant in Carlsberg II (CIho 10114, NGB 5085) (6).

Mutational events:

msg5.ce (MSS053, GSHO 2403) in Carlsberg II (CIho 10114, NGB 5085) (6, 8); *msg5.s* (MSS087) in Schweigers Erika (CIho 11501) (4, 8); *msg5.fr* (MSS419) in Midas (PI 343078) (5); *msg5.ie* (MSS 484) in Universe (PI 410864) (3, 5).

Mutant used for description and seed stocks:

msg5.ce (GSHO 2403) in Carlsberg II; *msg5.ce* in Bowman (PI 483237)*7 (GSHO 1954, BW587, NGB 23447); *msg5.ie* in Bowman*6 (BW971. NGB 23466).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F., and W.L. McProud. 1974. Positioning of the male sterile 5 (*msg5*) on chromosome 3. Barley Genet. Newsl. 4:16-23.
3. Franckowiak, J.D. (Unpublished).
4. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. Barley Genet. Newsl. 2:139-144.
5. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. 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.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:178.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:309.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:133-134.

BGS 362, Male sterile genetic 6, *msg6*

Stock number:	BGS 362
Locus name:	Male sterile genetic 6
Locus symbol:	*msg6*

Previous nomenclature and gene symbolization:

Male sterile 6 = *ms6* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 6HS (5); *msg.cf* is near the centromere (4, 8); *msg6.cf* is about 1.0 cM distal from the *rob1* (orange lemma 1) locus (4); *msg6.cf* is associated with SNP markers 1_0061 to 1_0040 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 in a heterozygous plant from Bowman backcross-derived line BW589 (3), likely in 6H bin 06..

Description:

Selfing - none, but occasionally a few selfed seeds occur (4).

Outcrossing - complete female fertility (4).

Stamens - equal in size to normal anthers (4); stomium present, filament elongation (9).

Pollen - nearly normal stained in both field and greenhouse plants, most grains appear normal (9). The *msg6.cf* pollen grains are non-functional because aperture development is abnormal (1, 2). This mutant can be classified as a pollen sterile (3).

Cytology - normal development and differentiation of anthers (9, 10).

Origin of mutant:

A spontaneous mutant in Heines Hanna (PI 539131) (6, 7).

Mutational events:

msg6.cf (MSS054, GSHO 2405) in Heines Hanna (PI 539131) (6, 7).

Mutant used for description and seed stocks:

msg6.cf (GSHO 2405) in Heines Hanna; *msg6.cf* in Bowman (PI 483237)*7 (GSHO 2078, BW589, NGB 23449).

References:

1. Ahokas, H. 1975. Male sterile mutants of barley. I. Inaperturate pollen of the *msg6cf* mutant. Ann. Bot. Fenn. 12:17-21.
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3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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5. Falk, D.E. 1994. Creation of a marked telo 6S trisomic for chromosome 6. Barley Genet. Newsl. 23:32.
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9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
10. Roath, W.W., and E.A. Hockett. 1971. Pollen development in genetic male-sterile barley. p. 308-315. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet.

Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:178-179.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:310.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:135-136.

BGS 363, Male sterile genetic 7, *msg7*

Stock number: BGS 363
Locus name: Male sterile genetic 7
Locus symbol: *msg7*

Previous nomenclature and gene symbolization:

Male sterile 7 = *ms7* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5HL (2); *msg7.cg* is about 5.5 cM from the *raw1* (smooth awn 1) locus (2); the plant of the Bowman backcross-derived line for *msg7.cg* stock, BW590, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (2).

Description:

Selfing - none (6).

Outcrossing - complete female fertility (6).

Stamens - anthers much smaller than fertile sibs, no stomium or filament elongation (8).

Pollen - microspores degenerate before the free microspore stage, non-staining, no free grains (8, 9).

Cytology - normal development and differentiation of anthers until completion of meiosis, but degeneration of tapetal tissue at the tetrad stage (9).

Origin of mutant:

A spontaneous mutant in Dekap (CIho 3351) (5).

Mutational events:

msg7.cg (MSS055, GSHO 2406) in Dekap (CIho 3351) (3, 5); *msg7.ah* (MSS099) in HB 421/78 (CIho 13641) (3, 7); *msg7.fx* (MSS425) in Proctor (PI 269153) (4, 5).

Mutant used for description and seed stocks:

msg7.cg (GSHO 2406) in Dekap; *msg7.cg* in Bowman (PI 483237)*7 (GSHO 2109, BW590. NGB 24811).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
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4. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl.14:70-75.
5. Hockett, E.A. 1991. The identification of eight new loci and allelism of 14 additional mutants. Barley Genet. Newsl. 20:37-40.
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7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
9. Roath, W.W., and E.A. Hockett. 1971. Pollen development in genetic male-sterile barley. p. 308-315. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:179-180.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:311.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:137-138.

BGS 364, Male sterile genetic 8, *msg8*

Stock number:	BGS 364
Locus name:	Male sterile genetic 8
Locus symbol:	*msg8*

Previous nomenclature and gene symbolization:

Male sterile 8 = *ms8* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5HL (3, 6); *msg8.ch* is about 8.3 cM from the *raw1* (smooth awn 1) locus (3); *msg8.ch* is associated with adjacent SNP markers 2_0127 and 1_1507 (positions 111.21 and 111.56 cM) in 5H bin 10 in a homozygous male sterile plant from Bowman backcross-derived line BW591 (2).

Description:

Selfing - none (5).

Outcrossing - complete female fertility (5).

Stamens - anthers smaller than fertile sibs (5), stomium present, and filament elongation (1, 8).

Pollen - reduced staining (6.9% stains with 2,3,5-triphenyltetrazolium, 20.7% stains with acetocarmine), some grains appear normal (8, 9).

Cytology - normal development and differentiation of microspores up to the free microspore stage (9). Pollen grains are undeveloped, have a stainable ring at the apertural annulus without any actual pore; the exine staining with Fast Blue B is darker than in normal grains (1).

Origin of mutant:

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

Mutational events:

msg8.ch (MSS056, GSHO 2407) in Betzes (PI 129430) (5, 7); *msg8.au* (MSS313) in OAC 21 (CIho 1470) (4, 7).

Mutant used for description and seed stocks:

msg8.ch (GSHO 2407) in Betzes; *msg8.ch* in Bowman (PI 483237)*6 (GSHO 2110, BW591, NGB 23450).

References:

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2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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5. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
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7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

9. Roath, W.W., and E.A. Hockett. 1971. Pollen development in genetic male-sterile barley. p. 308-315. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:180.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:312.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:139-140.

BGS 365, Male sterile genetic 9, *msg9*

Stock number:	BGS 365
Locus name:	Male sterile genetic 9
Locus symbol:	*msg9*

Previous nomenclature and gene symbolization:

Male sterile 9 = *ms9* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HS (2, 4); *msg9.ci* is about 6 cM from the T2-7a translocation point (4); *msg9.ci* is over 18.7 cM distal from the *eog1* (elongated outer glume 1) locus (2); *msg9.ci* is associated with adjacent SNP markers 1_0786 to 2_1242 (position 133.59 cM) in 2H bin 09 in a plant from Bowman backcross-derived line BW592 (1). The position of the *msg9* locus based on SNP data does not correspond to the linkage based map distances.

Description:

Selfing - 10% at Bozeman, Montana and 24% at Tucson, Arizona, USA (4).

Outcrossing - complete female fertility (4).

Stamens - anthers smaller than fertile sib (4), stomium present and filament elongation occurs (5).

Pollen - stained in plants grown in the field and in the greenhouse, in some samples the grains appear normal (5).

Origin of mutant:

A spontaneous mutant in Vantage (CIho 7324) (4).

Mutational events:

msg9.ci (MSS057, GSHO 2408) in Vantage (CIho 7324) (4).

Mutant used for description and seed stocks:

msg9.ci (GSHO 2408) in Vantage; *msg9.ci* in Bowman (PI 483237)*7 (GSHO 1883, BW592, NGB 24138).

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:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:181.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:313.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:141.

BGS 366, Male sterile genetic 10, *msg10*

Stock number:	BGS 366
Locus name:	Male sterile genetic 10
Locus symbol:	*msg10*

Previous nomenclature and gene symbolization:

Male sterile 3 = *ms3* (6).

Male sterile 10 = *ms10* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HS (2, 5); *msg10.ay* is about 7.2 cM distal from the *nud1* (naked caryopsis 1) locus (3, 8); *msg10.ay* is about 14.1 cM from the *lks2* (short awn 2) locus (3); *msg10.ay* is about 2.0 cM from the *msg14* (male sterile genetic 14) locus (3); *msg10.ay* is associated with SNP markers 1_0056 to 2_0485 (positions 51.93 to 84.97 cM) in 7H bins 4 to 7 in a homozygous male sterile plant from Bowman backcross-derived line BW546 (1).

Description:

Selfing - none (4).

Outcrossing - complete female fertility (4).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (9).

Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (9).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (6).

Mutational events:

msg10.ay (MSS058, GSHO 1811) in Compana (PI 539111) (6, 7); *msg10.cy* (MSS059) in Manchuria (CIho 2330)*9 (4, 7).

Mutant used for description and seed stocks:

msg10.ay (GSHO 1811) in Compana; *msg10.ay* in Bowman (PI 483237)*7 (GSHO 1835, BW546, NGB 23471).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
3. Eslick, R.F., and E.A. Hockett. 1972. Recombination values of four genes on chromosome 1. Barley Genet. Newsl. 2:123-126.
4. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
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7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Jarvi, A.J., and R.F. Eslick. 1975. Shrunken endosperm mutants in barley. Crop Sci.

15:363-366.
9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:181-182.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:314.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:142-143.

BGS 367, Male sterile genetic 11, *msg11*

Stock number:	BGS 367
Locus name:	Male sterile genetic 11
Locus symbol:	*msg11*

Previous nomenclature and gene symbolization:

Male sterile 10 = *ms10* (2, 3, 4, 5, 7, 8).
Male sterile 11 = *ms11* (2, 9).
Male sterile 12 = *msg12* (2).

Inheritance:

Monofactorial recessive (2, 9).

Located in chromosome 5HS (1); *msg11.az* is associated with adjacent SNP markers 2_0206 to 2_0010 (positions 9.61 to 28.11 cM) in 5H bin 01 in a heterozygous plant from Bowman backcross-derived line BW547 (1).

Description:

Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (6).
Pollen - no staining in *msg11.ck* plants, but very low staining in *msg11.a*z plants, no normal-appearing grains (6).

Origin of mutant:

A spontaneous mutant in Gateway (CIho 10072) (5).

Mutational events:

msg11.ck (MSS060, GSHO 1812) in Gateway (CIho 10072) (4, 5); *msg11.az* (MSS061) in Svalöf 50-109 (CIho 10524) (2, 4).

Mutant used for description and seed stocks:

msg11.az (GSHO 1812) in Svalöf 50-109; *msg11.az* in Bowman (PI 483237)*7 (GSHO 2299, BW547, NGB 23419).

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. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. 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.
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5. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. Can. J. Genet. Cytol. 2:397-415.
6. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
7. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III. 1954-1963. Crop Sci. 5:33-43.
8. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.
9. Walker, G.W.R., K. Kasha, and R.A. Miller. 1958. Recombination studies in barley. Proc. Genet. Soc. Can. 3:41-43.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:182-183.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:315.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:144-145.

BGS 368, Male sterile genetic 13, *msg13*

Stock number:	BGS 368
Locus name:	Male sterile genetic 13
Locus symbol:	*msg13*

Previous nomenclature and gene symbolization:

Male sterile 13 = *ms13* (2).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 3HL (1); *msg13.cl* is associated with adjacent SNP markers 2_0063 to 2_1277 (positions 133.92 to 173.82 cM) in 3H bins 08 to 11 in a homozygous male sterile plant from Bowman backcross-derived line BW548 (1).

Description:

Selfing - none (2).

Outcrossing - complete female fertility (2).

Stamens - anthers smaller than those of fertile sibs, no stomium or filament elongation (4).

Pollen - no staining, shrunken, no normal-appearing grains (4).

Origin of mutant:

A spontaneous mutant in Haisa II (CIho 10420) (2).

Mutational events:

msg13.cl (MSS062, GSHO 1813) in Haisa II (CIho 10420) (2, 3).

Mutant used for description and seed stocks:

msg13.cl (GSHO 1813) in Haisa II; *msg13.cl* in Bowman (PI 483237)*7 (GSHO 2300, BW548, NGB 23420).

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. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
4. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:183.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:316.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:146.

1

BGS 369, Male sterile genetic 14, *msg14*

Stock number:	BGS 369
Locus name:	Male sterile genetic 14
Locus symbol:	*msg14*

Previous nomenclature and gene symbolization:

Male sterile 14 = *ms14* (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 7HS (2, 7); *msg14.cm* is about 2.0 cM from the *msg10* (male sterile genetic 10) locus (3); *msg14.cm* is associated with SNP markers 1_0983 to 2_0880 (positions 74.81 to 82.16 cM) in 7H bin 07 in a homozygous male sterile plant from Bowman backcross-derived line BW549 (1).

Description:

Selfing - none (6).

Outcrossing - complete female fertility (6).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (9).

Pollen - less than 1% staining with 2,3,5-triphenyltetrazolium, about 9% with acetocarmine, some normal-appearing grains (9).

Origin of mutant:

A spontaneous mutant in Unitan (CIho 10421) (6).

Mutational events:

msg14.cm (MSS063, GSHO 1814) in Unitan (CIho 10421) (6, 8); *msg14.da* (MSS349) in Betzes (PI 129430) (4, 8); *msg14.dl* (MSS360) in Hector (CIho 15514) (5, 8).

Mutant used for description and seed stocks:

msg14.cm (GSHO 1814) in Unitan; *msg14.cm* in Bowman (PI 483237)*7 (GSHO 1836, BW549, NGB 23472).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
3. Eslick, R.F., and E.A. Hockett. 1972. Recombination values of four genes on chromosome 1. Barley Genet. Newsl. 2:123-126.
4. Hockett, E.A. 1975. The genetic male sterile collection. Barley Genet. Newsl. 5:84-86.
5. Hockett, E.A. 1979. The genetic male sterile collection. Barley Genet. Newsl. 9:124-128.
6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. 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.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:184.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:317.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:147-148.

BGS 370, Male sterile genetic 15, *msg15*

Stock number: BGS 370
Locus name: Male sterile genetic 15
Locus symbol: *msg15*

Previous nomenclature and gene symbolization:
Male sterile 15 = *ms15* (2).
Inheritance:
Monofactorial recessive (2).
Location is unknown.
Description:
Selfing - early tillers have 7.7% and late tillers have 46.2% at Bozeman, Montana, USA (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sibs (2).
The phenotype of *msg15.cn* plants differ from other male sterile genetic mutants because late tillers are fertile (2). Anthesis is delayed in relationship to spike emergence from the flag leaf (1). Only fully fertile plants were recovered from the attempt to develop a Bowman backcross-derived line for *msg15.cn* (1).
Origin of mutant:
A spontaneous mutant in a selection from the cross Atlas/2*Kindred (CIho 13446) (2).
Mutational events:
msg15.cn (MSS064, GSHO 1815) in Atlas/2*Kindred (CIho 13446) (2, 3).
Mutant used for description and seed stocks:
msg15.cn (GSHO 1815) in Atlas/2*Kindred.
References:
1. Franckowiak, J.D. (Unpublished).
2. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
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. 1971. Barley Genet. Newsl. 1:184-185.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:318.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:149.

BGS 371, Male sterile genetic 16, *msg16*

Stock number: BGS 371
Locus name: Male sterile genetic 16
Locus symbol: *msg16*

Previous nomenclature and gene symbolization:
Male sterile 16 = *ms16* (7).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 5HS (3, 7); *msg16.co* is 8.0 to 15.0 cM distal from the breakpoint in translocation stock T2-7a (10, 11); the plant of the Bowman backcross-derived line for *msg16.co* stock, BW550, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (2).
Description:
Selfing - none (4, 6).
Outcrossing - complete female fertility (6).
Stamens - anthers are almost equal in size to fertile sibs, stomium present, and filament elongation (6, 12).
Pollen - partial staining (15 to 35%) from plants grown under both field and greenhouse conditions, normal-appearing grains occur in some samples (12). Pollen appears immature based on staining with Fast Blue B, grains lack a pore or aperture, the exine is thinner, not distinctly two-layered, and bears fewer spicules than normal pollen (1).
Tapetal tissue degeneration was observed at the free microspore stage (9).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (6).
Mutational events:
msg16.co (MSS065, GSHO 1816) in Betzes (PI 129430) (6, 8); *msg16.bi* (MSS323) in Betzes (4, 5, 8).
Mutant used for description and seed stocks:
msg16.co (GSHO 1816) in Betzes; *msg16.co* in Bowman (PI 483237)*7 (GSHO 2116, BW550, NGB 24129.
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. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Hayes, J.D., and M.S. Rana. 1966. Investigations on genetic resistance to chemicals in spring barley. p. 47-48. Welsh Plant Breed. Station, Aberystwyth, Report for 1965.
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6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. 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.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Mian, H.R., J. Kuspira, G.W.R. Walker, and N. Muntjewerff. 1981. Macromolecular

changes and submicroscopic structure in the differentiation of *msg16* male-sterile barley anthers. p. 804-813. *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.

10. Ramage, R.T., and R.F. Eslick. 1975. Translocation linkage tests – T2-7a x male sterile genes. Barley Genet. Newsl. 5:46-48.

11. Ramage, R.T., M. Paluska, and G.A. Wiebe. 1973. Genetics and cytology of the translocation T2-7a. Barley Genet. Newsl. 3:47-49.

12. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:185.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:319.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:150-151.

BGS 372, Male sterile genetic 17, *msg17*

Stock number:	BGS 372
Locus name:	Male sterile genetic 17
Locus symbol:	*msg17*

Previous nomenclature and gene symbolization:

Male sterile 17 = *ms17* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL (1); *msg17.cp* is associated with SNP markers 2_0134 to 2_0388 (positions 163.29 to 230.08 cM) in 5H bins 10 to 12 in a heterozygous plant from Bowman backcross-derived line BW551 (1).

Description:

Selfing - 1% at Bozeman, Montana and 3% at Tucson, Arizona, USA (2).

Outcrossing - complete female fertility (2).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (4).

Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (4).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (2).

Mutational events:

msg17.cp (MSS066, GSHO 1817) in Compana (PI 539111) (2, 3).

Mutant used for description and seed stocks:

msg17.cp (GSHO 1817) in Compana; *msg17.cp* in Bowman (PI 483237)*7 (GSHO 2301, BW551, NGB 23421).

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. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
4. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:186.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:320.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:152.

BGS 373, Male sterile genetic 18, *msg18*

Stock number:	BGS 373
Locus name:	Male sterile genetic 18
Locus symbol:	*msg18*

Previous nomenclature and gene symbolization:

Male sterile 18 = *ms18* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5HL (2); *msg18.cq* is over 37.0 cM distal from the T2-7a translocation breakpoint (7); the plant of the Bowman backcross-derived line for *msg18.cq* stock, BW552, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (1).

Description:

Selfing - none (5).

Outcrossing - complete female fertility (5).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (8).

Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (8).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (5).

Mutational events:

msg18.cq (MSS067, GSHO 1818) in Compana (PI 539111) (5, 6); *msg18.z* (MSS093) in Betzes (PI 129430) (4, 6); *msg18.am* (MSS304) in Betzes (3, 6).

Mutant used for description and seed stocks:

msg18.cq (GSHO 1818) in Compana; *msg18.cq* in Bowman (PI 483237)*7 (GSHO 2117, BW552. NGB24130).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
3. Hockett, E.A. 1976. The genetic male sterile collection. Barley Genet. Newsl. 6:108.
4. Hockett, E.A. 1977. The genetic male sterile collection. Barley Genet. Newsl. 7:97-100.
5. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
7. Ramage, R.T., and R.F. Eslick. 1975. Translocation linkage tests – T2-7a x male sterile genes. Barley Genet. Newsl. 5:46-48.
8. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:186-187.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:321.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:153-154.

BGS 374, Male sterile genetic 19, *msg19*

Stock number:	BGS 374
Locus name:	Male sterile genetic 19
Locus symbol:	*msg19*

Previous nomenclature and gene symbolization:

Male sterile 19 = *ms19* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 5HS (2, 4); *msg19.cr* is between the centromere and the breakpoint in translocation stock T2-7a (6); *msg19.cr* is associated with SNP markers 1_0983 to 2_0880 (positions 74.81 to 82.16 cM) in 5H bins 04 to 06 in a heterozygous plant from Bowman backcross-derived line BW553 (1).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3).

Stamens - anthers smaller than fertile sib, no stomium or filament elongation (7).

Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (7).

Origin of mutant:

A spontaneous mutant in an introduction from Russia (CIho 14393) (3).

Mutational events:

msg19.cr (MSS068, GSHO 1819) in an introduction from Russia (CIho 14393) (3, 5).

Mutant used for description and seed stocks:

msg19.cr (GSHO 1819) in an introduction from Russia; *msg19.cr* in Bowman (PI 483237)*6 (GSHO 2118, BW553, NGB 23422).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
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4. 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.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
6. Ramage, R.T., M. Paluska, and G.A. Wiebe. 1973. Genetics and cytology of the translocation T2-7a. Barley Genet. Newsl. 3:47-49.
7. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:187.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:322.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:155.

BGS 375, Male sterile genetic 20, *msg20*

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

Previous nomenclature and gene symbolization:

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

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

Inheritance:

Monofactorial recessive (3).

Located in chromosome 4H (1); *msg20.ad* is associated with SNP markers 1_0942 to 1_1224 (positions 69.62 to 91.93 cM) in 4H bins 05 to 06 in a homozygous partially fertile plant from Bowman backcross-derived line BW555 (1). The *msg20.ad* mutant was previously associated with chromosome 1H (3).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3).

Stamens - anthers smaller than fertile sib (3). Selfed seed set in the Bowman backcross-derived line is 50 to 75% or more, but both the original stock and the Bowman backcross-derived line for *msg20.ad*, BW555, have short awns (3/4 normal length) (2).

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

msg20.ad (GSHO 2372) in Hannchen; *msg20.ad* in Bowman (PI 483237)*5 (GSHO 2059, BW555, NGB 23424). (The BW555 seed stock is maintained as homozygous for the *msg20.ad* allele.)

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
4. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
6. Robertson, D.W. 1971. Recent information of linkage and chromosome mapping. p. 220-242. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press.

Prepared:

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

Revised:

T. Tsuchiya. 1982. Barley Genet. Newsl. 12:107.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:323.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:139.
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J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:156.

BGS 376, Male sterile genetic 21, *msg21*

Stock number: BGS 376
Locus name: Male sterile genetic 21
Locus symbol: *msg21*

Previous nomenclature and gene symbolization:
Male sterile q = *msg,,q* (3, 4, 6).
Male sterile 21 = *ms 21* (3).

Inheritance:
Monofactorial recessive (3).
Located in chromosome 1HL (1*); msg21.q* is associated with SNP markers 2_0290 to 2_0780 (positions 102.33 to 154.89 cM) in 1HL bins 11 to 12 of the Bowman backcross-derived line BW556 (1).

Description:
Selfing - 3.8% at Bozeman, Montana and 2.9% at Tucson, Arizona, USA (3, 4).
Outcrossing - complete female fertility (3).
Stamens - anthers almost equal in size to fertile sibs (3). The Bowman backcross-derived line for *msg21.q*, BW556, had 70 to 85% or more selfed seed set and partially male fertile segregates were difficult to identify during backcrossing (2).

Origin of mutant:
A spontaneous mutant in a Midwest Bulk (CIho 13640) (4).

Mutational events:
msg21.q (MSS085, GSHO 2373) in CIho 13640 (CIho 13640) (3, 5).

Mutant used for description and seed stocks:
msg21.q (GSHO 2373) in CIho 13640; *msg21.q* in Bowman (PI 483237)*7 (GSHO 2302, BW556, NGB 23425). (The BW556 seed stock is maintained as homozygous for the *msg21.q* allele.)

References:
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Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:188-189.

Revised:
T. Tsuchiya. 1982. Barley Genet. Newsl. 12:108.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:324.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:101.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:157.

BGS 377, Shrunken endosperm genetic 1, *seg1*

Stock number:	BGS 377
Locus name:	Shrunken endosperm genetic 1
Locus symbol:	*seg1*

Previous nomenclature and gene symbolization:

Shrunken endosperm = *se1* (6).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 5H (1); *seg1.a* is linked to the *msg23* (male sterile genetic 23) locus (7); *seg1.a* is associated with SNP markers 1_0116 to 2_1275 (positions 75.85 to 104.73 cM) in 5H bins 04 to 06 in Bowman backcross-derived line BW834 (1). The *seg1.a* mutant was previously placed in chromosome 7HL (5), based on an incorrect position for the *msg23.b* mutant.

Description:

Kernels are long and thin and the 100-kernel weight is about 33% of normal. Good stands can be established in the field if optimum environmental conditions prevail during germination and emergence (5, 7). This mutant is associated with an increase in percentage lysine in the protein (7). Tannins are not deposited in *seg1* chalazal cell central vacuoles, but rather appeared to cause cytoplasmic disorganization and cell death (2). Light microscopy revealed that *seg1* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (2, 3). Compared to Bowman, plants of the Bowman backcross-derived line for *seg1.a*, BW834, appeared normal. However, kernels were thinner and had lower average weights, 3.7 vs. 5.7 mg. Test weight of BW834 grain was lower and yields were 1/2 to 2/3 those of Bowman (4).

Origin of mutant:

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

Mutational events:

seg1.a (GSHO 750) in Betzes (PI 129430) (5, 6).

Mutant used for description and seed stocks:

seg1.a (GSHO 750) in Betzes; *seg1.a* in Bowman (PI 483237)*7 (GSHO 1852, BW834, NGB 22274).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1984. Development of tannin vacuoles in chalazal and seed coat of barley in relation to early chalazal necrosis in the seg1 mutant. Planta 161:540-549.
3. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
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7. Jarvi, A.J., and R.F. Eslick. 1975. Shrunken endosperm mutants in barley. Crop Sci. 15:363-366.

Prepared:

A.J. Jarvi and R.F. Eslick. 1971. Barley Genet. Newsl.1:190.

Revised:

R.F. Eslick. 1976. Barley Genet. Newsl. 6:135.
T. Tsuchiya. 1980. Barley Genet. Newsl. 10:124.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:325.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:264.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:158-159.

BGS 379, Shrunken endosperm genetic 3, *seg3*

Stock number:	BGS 379
Locus name:	Shrunken endosperm genetic 3
Locus symbol:	*seg3*

Previous nomenclature and gene symbolization:

Shrunken endosperm = *se3* (6).

Proanthocyanidin-free 17 = *ant17* (4).

Inheritance:

Monofactorial recessive (7).

Located in chromosome 3HS (1, 7); *seg3.c* is over 30.8 cM from the centromere (7); *seg1.a* is associated with SNP marker 1_0601 (position 71.29 cM) in 3H bin 05 in Bowman backcross-derived line BW836 (2); *ant17.148* is associated with SNP markers 2_0607 to 1_0601 (positions 52.41 to 71.29 cM) in 3H bins 04 to 05 in Bowman backcross-derived line BW016 (2), in 3H bin 05.

Description:

The size of *seg3.c* kernels is reduced to about 33% of normal when grown under field conditions. Kernels are long and thin, but they are viable and good stand establishment is possible (7). Light microscopy revealed that the *seg3.c* mutant exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (3). The mutant *ant17.148* is an allele at the *seg3* locus (4); thus, all mutants at the proanthocyanidin-free 17 (*ant17*) locus might be alleles at the *seg3* locus. Alleles at the *seg3* locus in the Bowman backcross-derived lines BW016 (*ant17.148*) and BW836 (*seg3.c*) showed variable reductions in kernel weight: Kernels of BW016 and BW836 were thin, 3.2 vs. 3.8 mm, and weighed 1/3 to 1/2 of normal while those of *ant17.567*, another allele at the *ant17* locus, (8) were about 3/4 of normal (4). Plants of BW016 and BW836 were slightly shorter than Bowman plants and headed about two days later. Grain yields of BW016 and BW836 were 10 to 20% of those for Bowman (4). The strong effects of *seg3* mutants on grain development were not observed in all *ant17* mutants. Although the *seg3* locus was named before the *ant17* locus, but many more mutants were identified at the *ant17* locus. See BGS 599 for a complete listing of *ant1*7 mutants.

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (5).

Mutational events:

seg3.c (GSHO 752) in Compana (PI 539111) (5, 6), *ant17.148* (Galant, NGB 13698) in Triumph (PI 268180, NGB 13678) (4).

Mutant used for description and seed stocks:

seg3.c (GSHO 752) in Compana; *seg3.c* in Bowman (PI 483237)*7 (GSHO 1957, BW836, NGB 22273); *ant17.148* from Triumph in Bowman*4 (GSHO 1973, BW016, NGB 20424).

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Prepared:

A.J. Jarvi and R.F. Eslick. 1971. Barley Genet. Newsl. 1:191.
B. Jende-Strid. 1999. Barley Genet. Newsl. 29:88-89, as BGS 599, proanthocyanidin-free 17, *ant17*.

Revised:

R.F. Eslick. 1976. Barley Genet. Newsl. 6:137.
T. Tsuchiya. 1980. Barley Genet. Newsl. 10:126.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:327.
J.D. Franckowiak and U. Lundqvist. 2007 Barley Genet. Newsl. 37:265-266.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:160-161.

BGS 383, Male sterile genetic 22*, msg22*

Stock number: BGS 383
Locus name: Male sterile genetic 22
Locus symbol: *msg22*

Previous nomenclature and gene symbolization:
Male sterile e = *msg,,e* (5, 6).
Male sterile 22 = *ms22* (2, 5).
Inheritance:
Monofactorial recessive (5).
Located in chromosome 7H (5); *msg22.e* is associated with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73 cM) in 5H bins 04 to 06 in a homozygous male sterile plant from Bowman backcross-derived line BW557 (1).
Description:
Selfing - none (5).
Outcrossing - complete female fertility (5).
Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (3).
Origin of mutant:
A spontaneous mutant in a selection from Glacier/Compana (CIho 10861) (6).
Mutational events:
msg22.e (MSS073, GSHO 741, GSHO 2374) in a selection from Glacier/Compana (CIho 10861) (6, 7); *msg22.fc* (MSS404) in Proctor (PI 280420), *msg22.fo* (MSS416) in Zephyr (PI 339815) (3, 4).
Mutant used for description and seed stocks:
msg22.e (GSHO 741, GSHO 2374) in a selection from Glacier/Compana; *msg22.e* in Bowman (PI 483237)*7 (GSHO 1857, BW557, NGB 24131).
References:
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Prepared:
E.A. Hockett. 1972. Barley Genet. Newsl. 2:178 as BGS 377, Male sterile 22, *ms22*.
E.A. Hockett. 1973. Barley Genet. Newsl. 3:121.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:331.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:162.

BGS 384, Male sterile genetic 23, *msg23*

Stock number:	BGS 384
Locus name:	Male sterile genetic 23
Locus symbol:	*msg23*

Previous nomenclature and gene symbolization:

Male sterile b = *msg,,b* (4, 5).

Male sterile 23 = *ms23* (2, 4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5H (1); *msg23.b* is associated with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73 cM) in 5H bins 04 to 06 in a heterozygous plant from Bowman backcross-derived line BW558 (1). The *msg23.b* gene was previously associated with chromosome 7HL (4).

Description:

Selfing - none in *msg23.b* and *msg23.bg* (4), but 1.9 to 13.6% in *msg23.y* (3).

Outcrossing - complete female fertility (4).

Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (4).

Origin of mutant:

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

Mutational events:

msg23.b (MSS071, GSHO 2375) in Betzes (PI 129430) (5, 6); *msg23.y* (MSS092) in Betzes (3, 4, 6); *msg23.bg* (MSS321) in Betzes (2, 3, 6).

Mutant used for description and seed stocks:

msg23.b (GSHO 2375) in Betzes; *msg23.b* in Bowman (PI 483237)*8 (GSHO 1867, BW558, NGB 23426).

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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6. 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. 1972. Barley Genet. Newsl. 2:179 as BGS 378, Male sterile 23, *ms23*.

E.A. Hockett. 1973. Barley Genet. Newsl. 3:122.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:332.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:163.

BGS 385, Male sterile genetic 24, *msg24*

Stock number: BGS 385
Locus name: Male sterile genetic 24
Locus symbol: *msg24*

Previous nomenclature and gene symbolization:
  Male sterile v = *msg,,v* (6, 7).
  Male sterile 24 = *ms24* (3, 6).

Inheritance:
  Monofactorial recessive (6).
  Located in chromosome 4HL (6); *msg24.v* is over 11.0 cM proximal from the *Blx1* (Non-blue aleurone xenia 1) locus (9); the plant of the Bowman backcross-derived line for *msg24.v* stock, BW559, evaluated for SNP markers did not have any deviant markers in 4H from those of Bowman (2).

Description:
  Selfing - none (3, 6).
  Outcrossing - complete female fertility (6).
  Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (4).

Origin of mutant:
  A spontaneous mutant in Betzes (PI 129430) (7).

Mutational events:
  msg24.j (MSS078) in Betzes/Domen (CIho 13639) (7); *msg24.v* (MSS089, GSHO 2376) in Betzes (PI 129430 (7, 8); *msg24.ak* (MSS302) in Betzes (3, 7); *msg24.an* (MSS305) in Betzes (3, 8); *msg24.at* (MSS312) in OAC21 (CIho 1470), *msg24.bc* (MSS317) in Betzes (4, 8); *msg24.hg* (MSS460) in an unknown cultivar (1, 5).

Mutant used for description and seed stocks:
  msg24.v (GSHO 2376) in Betzes; *msg24.v* in Bowman (PI 483237)*7 (GSHO 2018, BW559, NGB 23427).

References:

1. Dawi, D.A., and C.A. Foster. 1983. Allelism studies of new genetic male sterile barley stocks in the WPBS collection. Barley Genet. Newsl. 13:9-11.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Kushnak, G.D. 1972. Linkage of *Bl* and *ms-v* on chromosome 4. Barley Genet. Newsl. 2:45-46.

Prepared:
  E.A. Hockett. 1973. Barley Genet. Newsl. 3:123.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:333.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:164-165.

BGS 395, Male sterile genetic 26, *msg26*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (5, 6).

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

Description:

Selfing - none (6).

Outcrossing - complete female fertility (6).

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

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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5. Hockett, E.A. 1974. The genetic male sterile collection. Barley Genet. Newsl. 4:121-123.
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8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.

Prepared:

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

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

Revised:

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

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:137.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:166-167.

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

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

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 3HL (2); *cer-r.19* is about 4.3 cM distal from the *uzu1* (uzu 1) locus (11, 12, 13, 14); *cer-r.19* is associated with SNP markers 1_0601 to 1_0047 (positions 71.29 to 119.1 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW121 (1); likely in 3H bin 06.

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
U. Lundqvist. 1975. Barley Genet. Newsl. 5:129.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:361.
U. Lundqvist and J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:145-146.
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:168-169.

BGS 455, Shrunken endosperm genetic 8, *seg8*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7H (6); *seg8.k* in a 4.6 cM interval flanked by markers GBM1516 and Bmag341 (8); *seg8.k* is associated with SNP markers 1_0772 to 1_0169 (positions 71.81 to 142.56 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW840 (1), likely in 7H bin 07.

Description:

Seed size is reduced and maturity is delayed. Seed weights of 24, 23, and 27% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (6). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg8.k* plants can be used to establish stands under field conditions (6). Endosperms of *seg8.k* plants developed as two-filled lateral lobes with no central endosperm lobe, resulting in a distinct dorsal crease (2). This is evidence that the endosperm is divided into three lobes as explained by the phytomeric triad model (4). Kernels of the Bowman backcross-derived line for *seg8.k*, BW840, were very thin 3.0 vs. 3.8 mm in width and weighed much less, 1.7 vs. 5.6 mg, compared to those of Bowman. BW840 plants were similar to Bowman morphologically, but their grain yield was about 1/20 that of Bowman (3).

Origin of mutant:

A spontaneous mutant in 60Ab1810-53 (CIho 15686) (7).

Mutational events:

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

Mutant used for description and seed stocks:

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

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endosperm genes *seg8* and *sex1* in barley (*Hordeum vulgare* L.) Genome 49:1209-1214.

Prepared:

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

Revised:

R.T. Ramage. 1983. Barley Genet. Newsl. 13:116 as BGS 453.
T. Tsuchiya. 1983. Barley Genet. Newsl. 13:117. BGS number changed to BGS 455.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:405.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:272.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:150-151.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:170-171.

BGS 460, Curly 4, *cur4*

Stock number:	BGS 460
Locus name:	Curly 4
Locus symbol:	*cur4*

Previous nomenclature and gene symbolization:

Curly 4 = *cu4* (13).
Spiral neck = *spn* (5, 11, 12).
Globosum-d = *glo-d* (6).

Inheritance:

Monofactorial recessive (6, 8, 12, 13).

Located in chromosome 2HL (5, 6, 9, 14); *glo-d.1006* is close to the *Gth1* (Toothed lemma 1) locus based on linkage drag (3); *cur4.f* is associated with SNP markers 1_0297 to 2_1258 (positions 85.71 to 114.96 cM) in 2H bins 07 to 08 of Bowman backcross-derived line BW223 (1); *glo-d.1006i* is associated with SNP markers 2_0674 to 2_0528 (positions 85.28 to 118.78 cM) in 2H bins 07 to 08 of Bowman backcross-derived line BW395 (1); *cur4.i* is associated with SNP markers 1_0216 to 2_0833 (positions 47.48 to 115.90 cM) in 2H bins 04 to 08 of Bowman backcross-derived line BW224 (1), in 2H bin 08.

Description:

Diagnostic characteristics for *cur4* mutants can be observed from the seedling stage to maturity. Roots are curved compared to straight roots in normal plants (12). Leaf blades tend to coil or bend and have wrinkles at the margins. Culms are bent slightly at the nodes and about 3/4 normal length, peduncles are spiral or kinky, and awns are frequently slightly coiled (6, 12). Compared to Bowman, plants of the Bowman backcross-derived line for *cur4.f*, BW223, headed 2 to 4 days later and had 2 to 5 more kernels per spike. BW223 plants were 5 to 10% shorter and have slightly shorter peduncles, awns, and rachis internodes. Kernels of BW223 were shorter, 7.4 vs. 9.4 mm, and weighed less, 4.7 vs.5.4 mg. Grain yields of BW223 were 10 to 30% lower than Bowman yields (4). Compared to Bowman, the morphological effects of the g*lo-d.1006* mutant in the Bowman backcross-derived line BW395 were slightly less than observed with BW223. BW224 plants with *cur4.i* was morphologically similar to BW223 plants (4). The delayed heading and more kernels per spike of the BW lines for *cur4* mutants could be attributed to retention of the late maturity allele at the *Eam6* or *mat-c* (early maturity 6 or praematurum-c) locus in 2HS (4).

Origin of mutant:

An X-ray induced mutant in Asahi 5 (OUJ509) (5, 13).

Mutational events:

cur4.f (Kmut 118, GSHO 1708) in Asahi 5 (OUJ509) (5, 13); *glo-d.1006* (1114/66, GSHO 1754) in Donaria (PI 161974) (2, 6); *glo-d.13* (*glo-d.1009*) (NGB 115631), *glo-d.14* (NGB 115632) in Bonus (PI 189763, NGB 14657) (7, 8); *cur4.i* (OUM163, GSHO 1709) in Akashinriki (OUJ659, PI 467400) (4, 10).

Mutant used for description and seed stocks:

cur4.f (GSHO 1708) in Asahi 5; *cur4.f* in Bowman (PI 483237)*7 (GSHO 1915, BW223, NGB 22050); *glo-d.1006* from Donaria in Bowman*7 (GSHO 1917. BW395, NGB 20633); *cur4.i* from Akashinriki in Bowman*7 (GSHO 1916, BW224, NGB 22051).

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Prepared:
T. Tsuchiya. 1984. Barley Genet. Newsl. 14:97.

Revised:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:406.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:172-173.

BGS 464, Male sterile genetic 27, *msg27*

Stock number:	BGS 464
Locus name:	Male sterile genetic 27
Locus symbol:	*msg27*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 8).

Located in chromosome 2HS (1, 2, 3); *msg27.ae* did not recombine with the *vrs1* (six-rowed spike 1) locus (2); *msg27.ae* is about 20.5 cM distal from the *vrs1* locus (3); *msg27.ae* is associated with SNP markers 2_1366 to 2_1153 (positions 50.56 to 89.09 cM) in 2H bins 05 to 06 in a heterozygous plant from Bowman backcross-derived line BW562 (1); likely in 2H bin 05.

Description:

Selfing - none (5, 7, 8).

Outcrossing - complete female fertility (8).

Stamens - anthers rudimentary, no stomium or filament elongation (5, 8).

Origin of mutant:

A spontaneous mutant in Firlbecks III (PI 223985) (8).

Mutational events:

msg27.ae (MSS097, GSHO 2379) in Firlbecks III (PI 223985) (4, 7, 8); *msg27.jr* (MSS523) in Mona (NGB 1499, PI 466726) (5, 6).

Mutant used for description and seed stocks:

msg27.ae (GSHO 2379) in Firlbecks III; *msg27.ae* in Bowman (PI 483237)*7 (GSHO 1921, BW562, NGB 24805).

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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:

E.A. Hockett. 1986. Barley Genet. Newsl. 16:47.

Revised:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:94.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:411.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:174.

BGS 465, Male sterile genetic 28, *msg28*

Stock number:	BGS 465
Locus name:	Male sterile genetic 28
Locus symbol:	*msg28*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 6).

Located in chromosome 2HS (1); *msg28.as* is associated with SNP markers 2_1015 to 2_0864 (positions 48.68 to 55.52 cM) in 2HS bin 05 of a plant presumed to be a heterozygous plant from the Bowman backcross-derived line BW563 (1). The *msg28.as* mutant was previously mapped in chromosome 6H near the *rob1* (orange lemma 1) locus (2).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3, 6).

Stamens - anthers rudimentary, with no stomium or filament elongation (6).

Pollen - non-staining, shrunken, and no normal-appearing grains (6).

Cytology - normal meiosis (6).

Origin of mutant:

A spontaneous mutant in York (CIho 10075) (6).

Mutational events:

msg28.as (MSS311, GSHO 2380) in York (CIho 10075) (4, 5, 6).

Mutant used for description and seed stocks:

msg28.as (GSHO 2380) in York; *msg28.as* in Bowman (PI 483237)*7 (GSHO 2079, BW563, NGB 24132).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:

E.A. Hockett. 1986. Barley Genet. Newsl. 16:48.

Revised:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:95.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:412.
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:173.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:175.

BGS 466, Male sterile genetic 29, *msg29*

Stock number:	BGS 466
Locus name:	Male sterile genetic 29
Locus symbol:	*msg29*

Previous nomenclature and gene symbolization:

Male sterile a = *msg,,a* (4).

Male sterile = 63msx1 and 63msx2 (*ms-aa*) (5).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL (2); *msg29.a* is about 22.7 cM from the *raw1* (smooth awn 1) locus (2); the plant of the Bowman backcross-derived line for *msg29.a* stock, BW564, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (1).

Description:

Selfing - none (4).

Outcrossing - complete female fertility (4).

Stamens - anthers smaller than fertile sibs, with no stomium or filament elongation (4).

Origin of mutant:

A spontaneous mutant in Ackermans MGZ (CIho 11491) (5).

Mutational events:

msg29.a (MSS069, GSHO 2381) in Ackermans MGZ (CIho 11491) (3, 6); *msg29.aa* in Ackermans MGZ (MSS070) (4, 6).

Mutant used for description and seed stocks:

msg29.a (GSHO 2381) in Ackermans MGZ; *msg29.a* in Bowman (PI 483237)*7 (GSHO 2140, BW564, NGB 24133).

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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6. 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. 1986. Barley Genet. Newsl. 16:47.

Revised:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:94.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:413.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:176.

BGS 467, Male sterile genetic 30, *msg30*

Stock number:	BGS 467
Locus name:	Male sterile genetic 30
Locus symbol:	*msg30*

Previous nomenclature and gene symbolization:

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

Male sterile = msx2 (*msa*) (6).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7HL (2); *msg30.c* is about 11.4 cM from the *lks2* (short awn 2) locus (2); *msg30.c* is associated with SNP markers 2_0282 to 2_0485 (positions 107.40 to 128.28 cM) in 7H bin 07 in a heterozygous plant from Bowman backcross-derived line BW566 (1), in 7H bin 07.

Description:

Selfing - 0.7% at Bozeman, Montana, USA (5).

Outcrossing - complete female fertility (5), open pollinated seed set of 15% at Bozeman, MT and 2% at Elimäki, Finland (4).

Stamens - anthers smaller than fertile sibs, stomium present and the filament elongates (4).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (6).

Mutational events:

msg30.c (MSS072, GSHO 2382) in Compana (PI 539111) (3, 6, 7).

Mutant used for description and seed stocks:

msg30.c (GSHO 2382) in Compana; *msg30.c* in Bowman (PI 483237)*7 (GSHO 1859, BW566, NGB 23431).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
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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. 1986. Barley Genet. Newsl. 16:50.

Revised:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:97.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:414.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:177.

BGS 468, Male sterile genetic 31, *msg31*

Stock number:BGS 468
Locus name: Male sterile genetic 31
Locus symbol: *msg31*

Previous nomenclature and gene symbolization:
Male sterile d = *msg,,d* (4).
Male sterile dwarf = *msdwf* (4).

Inheritance:
Monofactorial recessive (3).
Located in chromosome 1HL (1); *msg31.d* is distal from the *sls1* (small lateral spikelet 1) locus (3); *msg31.d* is associated with SNP markers 1_0434 to 2_0267 (positions 127.71 to 149.80 cM) in 1HL bin 11 and with SNP markers 1_1098 to 2_1274 (positions 161.08 to 218.47 cM) in 2HL bins 11 to 13 of a heterozygous plant from the Bowman backcross-derived line BW567 (1).

Description:
Selfing - none (6).
Outcrossing - complete female fertility (6).
Stamens - anthers rudimentary, no stomium or filament elongation (5).
In addition to male sterility, mutant plants are weak and short (about 1/2 normal height), show delayed development, and appear to lack surface wax on the spike (wax code - ++ ++) (2, 4).

Origin of mutant:
A spontaneous mutant in the six-rowed line 51Ab4934 (CIho 15245) (6).

Mutational events:
msg31.d (MSS306, GSHO 2383) in 51Ab4934 (CIho 15245) (4, 6).

Mutant used for description and seed stocks:
msg31.d (GSHO 2383) in 51Ab4934; *msg31.d* in Bowman (PI 483237)*6 (GSHO 2031, BW567, NGB 23432).

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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. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
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5. Hockett, E.A. 1979. The genetic male-sterile barley collection. Barley Genet. Newsl. 9:124-128.
6. 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. 1986. Barley Genet. Newsl. 16:51.

Revised:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:98.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:415.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:117.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:178.

BGS 469, Male sterile genetic 32, *msg32*

Stock number:	BGS 469
Locus name:	Male sterile genetic 32
Locus symbol:	*msg32*

Previous nomenclature and gene symbolization:

Male sterile w = *msg,,w* (4).

Male sterile = 63msx7 (5).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7H (2, 4); *msg32.w* is linked to the *nud1* (naked caryopsis 1) locus (2); *msg32.w* is associated with SNP markers 1_0327 to 2_0911 (positions 55.54 to 107.44 cM) in 7H bins 05 to 07 in a homozygous male sterile plant from Bowman backcross-derived line BW568 (1).

Description:

Selfing - none (4).

Outcrossing - complete female fertility (4).

Stamens - anthers smaller than fertile sibs, no stomium or filament elongation 4).

Origin of mutant:

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

Mutational events:

msg32.w (MSS090, GSHO 2384) in Betzes (PI 129430) (3, 4, 6).

Mutant used for description and seed stocks:

msg32.w (GSHO 2384) in Betzes; *msg32.w* in Bowman (PI 483237)*7 (GSHO 1860, BW568, NGB 23433).

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. 1988. Mapping four male sterile genes on chromosome 1. Barley Newsl. 31:111.
3. Hockett, E.A. 1979. The genetic male sterile barley collection. Barley Genet. Newsl. 9:124-128.
4. 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.
5. 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.
6. 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. 1986. Barley Genet. Newsl. 16:52.

Revised:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:99.

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:416.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:179.

BGS 470, Male sterile genetic 33, *msg33*

Stock number: BGS 470
Locus name: Male sterile genetic 33
Locus symbol: *msg33*

Previous nomenclature and gene symbolization:
Male sterile x = *msg,,x* (6).
Male sterile = 63msx8 (7).

Inheritance:
Monofactorial recessive (6).
Located in chromosome 2HS (2); *msg33.x* is about 5.2 cM distal from the centromere and 25.6 cM proximal from the *vrs1* (six-rowed spike 1) locus (3); *msg33.x* is associated with SNP markers 2_0458 to 1_1250 (positions 96.47 to 161.08 cM) in 2H bins 07 to 11 in a heterozygous plant from Bowman backcross-derived line BW569 (1).

Description:
Selfing - 20% at Bozeman, Montana, 17% at Tucson, Arizona, USA, and 0% at Elimäki, Finland (5).
Outcrossing - complete female fertility (6).
Stamens - anthers smaller than fertile sibs, stomium present, and filament elongation (6).

Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (7).

Mutational events:
msg33.x (MSS091, GSHO 2385) in Betzes (PI 129430) (4, 6, 7, 8).

Mutant used for description and seed stocks:
msg33.x (GSHO 2385) in Betzes; *msg33.x* in Bowman (PI 483237)*7 (GSHO 1884, BW569, NGB 24807).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Franckowiak, J.D. (Unpublished).
4. Hockett, E.A. 1979. The genetic male sterile barley collection. Barley Genet. Newsl. 9:124-128.
5. Hockett, E.A., and H. Ahokas. 1979. Male and female fertility levels of genetic male sterile barley grown at two different latitudes. Hereditas 91:65-71.
6. Hockett, E.A., and R.F. Eslick. 1971. Genetic male sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA. Washington State Univ. Press, Pullman.
7. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.

Prepared:
E.A. Hockett. 1986. Barley Genet. Newsl. 16:53.

Revised:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:100.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:417.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:180.

BGS 471, Male sterile genetic 34, *msg34*

Stock number: BGS 471
Locus name: Male sterile genetic 34
Locus symbol: *msg34*

Previous nomenclature and gene symbolization:

Male sterile av = *msg,,av* (4).
Male sterile = 63msy1 (4).

Inheritance:

Monofactorial recessive (4, 7, 8).

Located in chromosome 6HS or 7HS (2, 3); *msg34.av* is associated with SNP markers 1_0775 to 1_0744 (positions 26.42 to 39.34 cM) in 1H bins 03 to 05 in a homozygous plant from Bowman backcross-derived line BW570 (1). Previously recombination between *msg34.av* and the *rob1* (orange lemma 1) locus was not observed (2).

Description:

Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers rudimentary, with no stomium or filament elongation (4).
Heterozygotes show reduced fertility (75 to 85% seed set), and male sterile plants always have a Long glume awn 1 (*Lga1.a* in 7HS) gene from Paragon. Thus, the *msg34.av* mutant may involve a translocation between chromosomes 6HS and 7HS (3).

Origin of mutant:

A spontaneous mutant in Paragon (CIho 13649) (8).

Mutational events:

msg34.av (MSS314, GSHO 2386) in Paragon (CIho 13649) (5, 6).

Mutant used for description and seed stocks:

msg34.av (GSHO 2386) in Paragon; *msg34.av* in Bowman (PI 483237)*7 (GSHO 2070, BW570, NGB 24134).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Franckowiak, J.D. (Unpublished).
4. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. Barley Genet. Newsl. 2:139-144.
5. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
7. Ramage, R.T., and R.F. Eslick. 1975. Translocation linkage tests – T2-7a x male sterile genes. Barley Genet. Newsl. 5:46-48.
8. Sharma, R.K. 1970. Studies of sterility mutants in spring barley (*Hordeum vulgare* L.). Ph.D. Thesis. Univ. of Guelph, Ontario.

Prepared:

E.A. Hockett. 1986. Barley Genet. Newsl. 16:54.

Revised:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:101.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:418.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:181-182.

BGS 498, Male sterile genetic 35, *msg35*

Stock number:	BGS 498
Locus name:	Male sterile genetic 35
Locus symbol:	*msg35*

Previous nomenclature and gene symbolization:

Male sterile genetic,,dr = *msg,,dr* (3).
Male sterile = 76Y17 (3).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 2HL (2); *msg35.dr* is about 23.0 cM from the *wst7* (white streak 7) locus (2); *msg35.dr* is associated with SNP markers 1_1118 to 2_0715 (positions 180.85 to 213.08 cM) in 2H bins 11 to 13 in a homozygous male sterile plant from Bowman backcross-derived line BW571 (1).

Description:

Selfing - none (3).
Outcrossing - complete female fertility (3).
Stamens - anthers smaller than fertile sib, with no stomium of filament elongation (3).

Origin of mutant:

A spontaneous mutant in Karl (CIho 15487) (3).

Mutational events:

msg35.dr (MSS366, GSHO 2387) in Karl (CIho 15487) (3, 4, 5).

Mutant used for description and seed stocks:

msg35.dr (GSHO 2387) in Karl; *msg35.dr* in Bowman (PI 483237)*7 (GSHO 1933, BW571, NGB 23435).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Hockett, E.A. 1979. The genetic male sterile barley collection. Barley Genet. Newsl. 9:124-128.
4. Hockett, E.A. 1986. Male sterile genes. Barley Genet. Newsl. 16:36-37.
5. Hockett, E.A., and C.F. McGuire. 1983. Male sterile facilitated recurrent selection for malting barley. Barley Newsl. 27:67.

Prepared:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:102.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:424.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:183.

BGS 499, Male sterile genetic 36, *msg36*

Stock number:	BGS 499
Locus name:	Male sterile genetic 36
Locus symbol:	*msg36*

Previous nomenclature and gene symbolization:

Male sterile bk = *msg,,bk* (6).

Male sterile = 867N-89 (6).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 6HS (2*); msg36.bk* is about 10.8 cM distal from the *rob1* (orange lemma 1) locus (2, 3, 9); *msg36.bk* is associated with two groups of SNP markers separated by a gap, 1_0244 to 1_0013 (positions 71.39 to 74.97) in 6H bin 06 and markers 1_1261 to 1_1246 (positions 107.28 to 134.55 cM) in 6H bins 07 to 08 in a heterozygous plant from Bowman backcross-derived line BW572 (1), likely in 6H bin 06.

Description:

Selfing - about 1.1% (6).

Outcrossing - complete female fertility (6).

Stamens - anthers nearly normal sized with stomium and filament elongation (6).

Origin of mutant:

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

Mutational events:

msg36.bk (MSS325, GSHO 2388) in Betzes (PI 129430) (5, 6, 8); *msg36.eg* (MSS382) in Pavo P57 (4, 7).

Mutant used for description and seed stocks:

msg36.bk (GSHO 2388) in Betzes; *msg36.bk* in Bowman (PI 483237)*7 (GSHO 2067, BW 572, NGB 23436).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F., R.T. Ramage, and D.R. Clark. 1974. Two genetic male steriles, *msg6* and *msg,,bk*, assigned to chromosome 6. Barley Genet. Newsl. 4:11-15.
3. Falk, D.E., M.J. Swartz, and K.J. Kasha. 1980. Linkage data with genes near the centromere of barley chromosome 6. Barley Genet. Newsl. 10:13-16.
4. Franckowiak, J.D. (Unpublished).
5. Franckowiak, J.D., and E.A. Hockett. 1987. Allelism tests for the genetic male sterile *msg,,bk*. Barley Genet. Newsl. 17:77-78.
6. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. Barley Genet. Newsl. 2:139-144.
7. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Ramage, R.T., and M. Paluska. 1975. Mapping chromosome 6. Barley Genet. Newsl. 5:49-51.

Prepared:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:103.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:425.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:184-185.

BGS 500, Male sterile genetic 37, *msg37*

Stock number:	BGS 500
Locus name:	Male sterile genetic 37
Locus symbol:	*msg37*

Previous nomenclature and gene symbolization:

Male sterile hl = *msg,,hl* (4).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 3HL most likely (1), *msg37.jx* is associated with SNP markers 3_1220 (position 182.97 cM) in 3H bin 12 in the homozygous partially sterile Bowman backcross-derived line BW573; *msg37.hl* is associated with SNP markers 2_0797 to 1_1516 (positions 5.45 to 249.75 cM) in 3H bins 01 to 16, plus SNP markers in all other chromosomes, in a heterozygous plant from Bowman backcross-derived line BW970 (1).

Description:

Selfing - none to 6% or more (4), the degree of selfing seems sensitive to environmental conditions, favored by cool conditions (3).

Outcrossing - complete female fertility (4).

Stamens - anthers shrunken, no stomium or filament elongation (5) to nearly normal (4).

The level of self-fertility in *msg37.hl* and *msg37.jx* plants gradually increased as more backcrosses to Bowman were made. The level of self-fertility approached 80% in BW573, a selection with the *msg37.jx* allele from the sixth backcross to Bowman (3).

Origin of mutant:

A spontaneous mutant in Clermont (PI 343724) (4).

Mutational events:

msg37.hl (MSS465, GSHO 2389) in Clermont (PI 343724) (2, 4); *msg37.jx* (MSS529, GSHO 2389) in a dwarf mutant 17:17:2 (*sdw.ax*, DWS1009, GSHO 2437) selected from Birgitta (NSGC 1870, NGB 1494) (2, 4).

Mutant used for description and seed stocks:

msg37.hl (GSHO 2389) in Clermont; *msg37.hl* in Bowman (PI 483237)*5 (BW970, NGB 24149; *msg37.jx* (GSHO 2437) from Birgitta; *msg37.jx* in Bowman (PI 483237)*7 (GSHO 2303, BW573), (The BW573 seed stock is maintained as homozygous for the *msg37.jx* allele).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D., and E.A. Hockett. 1988. Identification of three new loci which control male sterility of barley. Barley Genet. Newsl. 18:11-13.
3. Franckowiak, J.D. (Unpublished).
4. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
5. Hockett, E.A. 1988. New mutants in the genetic male sterile barley collection. Barley Genet. Newsl. 18:70-73.

Prepared:

E.A. Hockett. 1991. Barley Genet. Newsl. 20:104.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:426.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:186.

BGS 501, Male sterile genetic 38, *msg38*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3H (1); *msg38.jl* is associated with SNP markers 2_1533 to 1_0728 (positions 87.01 to 96.85 cM) in 3H bins 05 to 06 in a heterozygous plant from Bowman backcross-derived line BW574 (1).

Description:

Selfing - none (3).

Outcrossing - complete female fertility (3).

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

Origin of mutant:

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

Mutational events:

msg38.jl (MSS51, GSHO 2390) in Ingrid (CIho 10083, NGB 2671) (2, 3).

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. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D., and E.A. Hockett. 1988. Identification of three new loci which control male sterility of barley. Barley Genet. Newsl. 18:11-13.
3. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.

Prepared:

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

Revised:

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

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:187.

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 bin 12 of a heterozygous plant from the Bowman backcross-derived stock BW575 (2), in 3H bin 12. The *msg36.dm* and *msg39.ff* mutants were 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). Pollen shower is normal (1).

The pollen grains of the *msg39.dm* and *msg39.dn* mutants are non-functional because aperture development is abnormal. These mutants can be classified as pollen steriles (1).

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. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:188-189.

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* (5, 7).
    Male sterile = ms-C (7).

Inheritance:
    Monofactorial recessive (5).
    Located in chromosome 6HL (1, 2); *msg40.ac* is over 27.8 cM from the *rob1* (orange lemma 1) locus (2); *msg40.ac* is associated with SNP markers 2_1025 to 2_0036 (positions 147.51 to 169.88 cM) in 6H bins 09 to 11 in a heterozygous plant from Bowman backcross-derived line BW577 (1).

Description:
    Selfing - none (5).
    Outcrossing - less than 30% in crosses and in the Bowman backcross-derived line (3, 5).
    Stamens - anthers are smaller than those of fertile sibs, no stomium or filament elongation (5).

Origin of mutant:
    A spontaneous mutant in Conquest (CIho 11683) (6).

Mutational events:
    msg40.ac (MSS095, GSHO 2393) in Conquest (CIho 11683) (4, 5, 7).

Mutant used for description and seed stocks:
    msg40.ac (GSHO 2393) in Conquest; *msg40.ac* in Bowman (PI 483237)*6 (GSHO 2081, BW577, NGB 24808).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Franckowiak, J.D. (Unpublished).
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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. 20:107.

Revised:
    J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:429.
    J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:190.

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* (6).

Male sterile = 65msx166 (7).

Inheritance:

Monofactorial recessive (6).

Located in chromo some 6HS (1); *msg41.aj* is associated with SNP markers 1_0061 to 1_1250 (positions 70.15 to 82.43 cM) in 6H bins 05 to 06 in a heterozygous plant from Bowman backcross-derived line BW976 (1); the plant of the Bowman backcross-derived line for the *msg41.dk* stock, BW578, evaluated for SNP markers did not have any deviant markers from those of Bowman (1).

Description:

Selfing - none (4, 6).

Outcrossing - complete female fertility (6).

Stamens - anthers rudimentary, no stomium or filament elongation (4, 6).

Origin of mutant:

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

Mutational events:

msg41.aj (MSS101, GSHO 2394) in Betzes (PI 129430) (5, 7, 8); *msg41.dk* (MSS359) in Betzes (2, 5, 8); *msg41.do* (MSS363) in Maris Baldric (PI 294512) (3, 5, 8); *msg41.ef* (MSS381) in Hector (CIho 15514), *msg41.el* (MSS387) in Sabarlis (CIho 15484), *msg41.eq* (MSS392) in Sel 12387Co; *msg41.fa* (MSS402) in Midas (PI 343078), *msg41.gl* (MSS439) in Maris Mink (PI 467824), *msg41.ij* (MSS489) in Mazurka (PI 410868) (4, 5).

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* (MSS359) in Betzes; *msg41.dk* in Bowman*6 (GSHO 2305, BW578, NGB 23440).

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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.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:191-192.

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* (3).
Male sterile = B68-N-109 (3).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 3H (2); *msg42.db* is over 18.9 cM from the *alm1* (albino lemma 1) locus (2); *msg42.db* is associated with SNP markers 1_0672 to 1_1191 (positions 58.56 to 98.41 cM) in 3H bins 04 to 06 in a heterozygous plant from Bowman backcross-derived line BW579 (1).

Description:

Selfing - none (3, 4).
Outcrossing - complete female fertility (3, 4).
Stamens - anthers rudimentary, no stomium or filament elongation (3, 4).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (3).

Mutational events:

msg42.db (MSS350, GSHO 2395) in Betzes (PI 129430) (2, 5, 6); *msg42.gt* (MSS447) in Berac (PI 355136), *msg42.hw* (MSS476) in Sel 15025Co, *msg42.iy* (MSS504) in Sv73608 (5, 6).

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).

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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5. 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.
6. 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.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:193.

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* (2).
  Male sterile = B65msx38 (2).
Inheritance:
  Monofactorial recessive (2).
  Located in chromosome 2HL (1); *msg43.br* is associated with SNP markers 2_0064 to 2_1274 (positions 179.99 to 218.47 cM) in 2H bins 11 to 13 in a heterozygous plant from Bowman backcross-derived line BW580 (1).
Description:
  Selfing - none (2).
  Outcrossing - complete female fertility (2).
  Stamens - anthers rudimentary, no stomium or filament elongation (2).
Origin of mutant:
  A spontaneous mutant in Betzes (PI 129430) (2).
Mutational events:
  msg43.br (MSS332, GSHO 2396) in Betzes (PI 129430) (2, 3, 4).
Mutant used for description and seed stocks:
  msg43.br (GSHO 2396) in Betzes; *msg43.br* in Bowman (PI 483237)*7 (GSHO 2306, BW580, NGB 24809).
References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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4. 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.
  J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:194.

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* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 5HL (1); *msg44.cx* is associated with SNP markers 1_1249 to 1_1290 (positions 109.27 to 145.57 cM) in 5H bins 06 to 09 in a heterozygous plant from Bowman backcross-derived line BW581 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers rudimentary, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in selection HA6-33-02 (CIho 15835) (2).
Mutational events:
msg44.cx (MSS346, GSHO 2397) in HA6-33-02 (CIho 15835) (2, 3, 4).
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. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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4. 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.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:195.

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* (2).

Male sterile = 76Y2 (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 5HL or 7HS (1); *msg45.dp* is associated with SNP markers 2_1150 to 2_1168 (positions 145.57 to 168.17 cM) in 5H bins 09 to 10 and with SNP markers 1_0949 to 2_0993 (positions 0.00 to 44.83 cM) in 7H bins 01 to 03 in a heterozygous plant from Bowman backcross-derived line BW582 (1).

Description:

Selfing - none (2).

Outcrossing - complete female fertility (2).

Stamens - anthers rudimentary, no stomium or filament elongation (2).

Origin of mutant:

A spontaneous mutant in selection RPB439-71 (CIho 15838) (2).

Mutational events:

msg45.dp (MSS364, GSHO 2398) in RPB439-71 (CIho 15838) (2, 3, 4).

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).

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Prepared:

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

Revised:

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

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:196.

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* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 2H or 6H (1); *msg46.ec* is associated with SNP markers 1_0602 to 2_0182 (positions 95.53 to 185.53 cM) in 2H bins 07 to 12 and with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 06 to 07 in a heterozygous plant from Bowman backcross-derived line BW583 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than those of fertile sibs, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in Hector (CIho 15514) (2).
Mutational events:
msg46.ec (MSS378, GSHO 2399) in Hector (CIho 15514) (2, 3, 4).
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:
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Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:113.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:435.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:197.

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* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HS or 7HS (1); *msg47.ep* is associated with SNP markers 2_0159 to 2_0742 (positions 6.31 to 29.05 cM) in 3H bins 01 to 02 and with SNP markers 2_1270 to 1_0299 (positions 93.97 to 101.23 cM) in 7H bins 01 to 02 in a homozygous male sterile plant from Bowman backcross-derived line BW584 (1).

Description:

Selfing - none (2).

Outcrossing - complete female fertility (2).

Stamens - anthers rudimentary, no stomium or filament elongation (2).

Origin of mutant:

A spontaneous mutant in Sel 12384Co (2).

Mutational events:

msg47.ep (MSS391, GSHO 2400) in Sel 12384Co (2, 3).

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 24810).

References:

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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. 20:114.

Revised:

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

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:198.

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 Bowman backcross-derived line BW585, plus small heterozygous regions in chromosomes 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:

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Prepared:

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

Revised:

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

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:199.

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* (11).
Erectoides-56 = *ert-56* (7); *ert-u.56* (see BGS 092).
Brachytic 5 = *br5* (14).
Erectoides-159 = *ert-159* (12); *ert-zd.159* (see BGS 093).
Brachytic 7 = *br7* (14).
Brachytic-q = *brh.q* (4); *brh14.q* (see BGS 148) (2).
Brachytic-af = *brh.af* (2, 5); *brh14.af* (see BGS 148) (2).
Brachytic-v = *brh.v* (4); *brh16.v* (see BGS 044) (2).

Inheritance:

Monofactorial recessive (11).

Located in chromosome 7HL (3); *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 (3); *ari-o.40* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (2) in the barley genome map (13).

Description:

Plants of the *ari-o.40* mutant have reduced awn length (11), but they are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (4). 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 (11). 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 (5). As with other mutants at the *ari-o* locus*, ari-o.40* shows a brassinosteroid-deficient phenotype that includes a short culm, about 70% of normal, caused largely by an extreme shortening of the second culm internode (2). Other common traits include shorter rachis internodes, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (2). The six Bowman backcross-derived lines with a mutation at the *ari-o* or *HvDIM* locus, *ari-o.40*, *brh14.af*, *brh14.q*, *brh16.v*, *ert-u.56*, and *ert-zd.159*, have retained a small, common genetic donor parent interval (2). The sequence of *HvDIM*, encoding the barley Δ^5-sterol-Δ^{24}-reductase DIMINUTO, corresponds directly to single-nucleotide polymorphism (SNP) marker 1_0547 located in the telomere on the long arm of chromosome 7H (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763, NGB 14657) (11).

Mutational events:

ari-o.40 (NGB 115890, GSHO 1663)*, -o.43* (NGB 115894) in Bonus (PI 189763, NGB 14657) (11); *ari-o.143* (NGB 115953) in Foma (CIho 11333, NGB 14659) (12); *ert-u.56* (NGB 112655, GSHO 496) in Bonus (PI 189763, NGB 14657) (2, 7); *ert-zd.159* (NGB 112758, GSHO 504) in Bonus (2, 12); *brh14.q* (OUM131, *dw-d,* DWS1035, GSHO 1682) in Akashinriki (OUJ659, PI 467400) (2, 5, 7, 9, 10); *brh14.af* (FN46, GSHO 3706) in Steptoe (CIho 15229) (2, 3, 8); *brh16.v* in HE 2816 (DWS1176, GSHO 1686) from a cross between two semidwarf mutants (6, 15). Previously *ari-o.297* (*uzu1.297*, NGB 116118), *ari-o.301* (*uzu1.301*, NGB 116124), *ari-o.306* (*uzu1.306*, NGB 116133) in Kristina (NGB 1500, NGB 14661) were recorded as alleles at the *ari-o* locus (12), but retesting demonstrated allelism at the uzu 1 (*uzu1*) locus and the mutants were renamed (2). The *ari-o.304* (*ari-u.304*, NGB 116129) mutant in Kristina was shown to be an allele at *ert-t* (*HvBRD*) locus and renamed *ari-u.304* (2).

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); *ert-u.56* in Bonus (NGB 112655, GSHO 496); *ert-u.56* in Bowman (PI 483237)*8 (GSHO 1904, BW325, NGB 22120); *ert-zd.159* in Bonus (GSHO 504, NGB 112758); *ert-zd.159* in Bowman (PI 483237)*7 (GSHO 1901, BW333, NGB 22128); *brh14.q* (GSHO 1682) in Akashinriki; *brh14.q* in Bowman (PI 483237)*6 (GSHO 2175, BW085, NGB 20492); *brh14.af* (GSHO 3706) from Steptoe in Bowman*7 (BW072, NGB 20479); *brh16.v* in HE 2816/Bowman (GSHO 1686); *brh16.v* in Bowman (PI 483237)*7 (GSHO 2177, BW087, NGB 20494).

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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.

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:200-202.

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* (10).
Brachytic 4 = *br4* (15).
Brachytic-g = *brh.g* (2, 5).
Brachytic-h = *brh.h* (2, 5).
Brachytic-i = *brh.i* (2, 5).
Brachytic-y = *brh.y* (2, 5).
Brachytic 3 = *brh3* (2, 6).
Breviaristatum-245 = *ari.245* (3, 11).
Breviaristatum-o.304 = *ari-o.304* (3, 13).
Hordeum vulgare brassinosteroid-6-oxidase = *HvBRD* (3).

Inheritance:

Monofactorial recessive (4, 10, 14).

Located in chromosome 2HS (2, 3, 4); *ert-t.55* is 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 (4); *brh3.g* is associated with markers 2_0609 to 1_1059 (positions unmapped to 17.96) in 2H bin 02 of the Bowman backcross-derived line BW091 (4); *brh3.y* is associated with 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 (4); the *brh3* mutants are in the *HvBRD* locus, which encodes for a brassinosteroid-6-oxidase, and is located in the telomeric region of 2HS (3); *ari-u.245* is associated with SNP markers 2_0609 to 2_1377 (positions about 13.0 to 20.11 cM) in 2H bin 02 of the Bowman backcrossed-derived line BW031 (4); except for *ert-t.55*, mutants at the *ert-t* locus were reported to be structural changes in the *HvBRD* locus (3); in 2H bin 02.

Description:

Spikes of the *ert-t.55* mutant are semi-compact, rachis internode length is about 2.7 mm, and culm length is about 2/3 of normal. These phenotypic traits plus short awns are inherited together (14). Based on general appearance of the plants, the *ert-t.55* mutant can be placed in the brachytic class of semidwarf mutants (5, 15). Awns are about 2/3 normal length and curled or coiled near their tips. The *ert-t.55* mutant has short seedling leaf blades and is sensitive to gibberellic acid treatment (1). When the Bowman backcross-derived lines for *brh3.g* (BW091), *brh3.i* (BW093), *brh3.y* (BW094), and *ert-t.55* (BW324) were compared to Bowman, peduncles and plants were about 2/3 of normal length, rachis internodes were slightly shorter, and lodging was reduced. Kernels are shorter and slightly lighter and grain yields were about 1/2 normal (2). Mutants at the *ert-t* or *HvBRD* locus exhibited the brassinosteroid-deficient phenotype: shorter rachis internode length, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (3).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763, NGB14657) (7).

Mutational events:

ert-t.55 (NGB 112654, GSHO 494) in Bonus (PI 189763, NGB14657) (10); *ert-t.437* NGB 112953) in Foma (CIho 11333, NGB 14659) (3, 13); *brh3.g* (17:10:1, GSHO 1672), *brh3.h* (17:11:3, GSHO 1673), *brh3.i* (17:12:1, GSHO 1674) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (2, 5, 6, 12); *brh3.y* (10001, GSHO 1688) in Bido (PI 399485) (2, 5, 9); *ari-u.245* (NGB 116054) in Foma (CIho 11333, NGB 14659) (3, 11, 13); *ari-u.304* (previously named *ari-o.304*) (NGB 116129) in Kristina (NGB 1500, NGB 14661) (3. 13).

Mutant used for description and seed stocks:

ert-t.55 (NGB 112654, GSHO 494) in Bonus; *ert-t.55* in Bowman (PI 483237)*5 (GSHO 2257); *ert-t.55* in Bowman*7 (BW324, NGB 22119); *brh3.g* in Bowman*7 (GSHO 2167, BW 091, NGB 20497); *brh3.h* in Bowman*2 (GSHO 2168, BW092, NGB 20498); *brh3.i* in Bowman*6 (GSHO 2169); *brh3.i* in Bowman *7 (BW093, NGB 20499); *brh3.y* from Bido in Bowman*5 (GSHO 2178); *brh3.y* from Bido in Bowman*6 (BW094, NGB 20500); *ari-u.245* from Foma via ND14701 in Bowman (PI 483237)*5 (BW031, NGB 20439).

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Prepared:

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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.

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:203-204.

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* (3).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7HL (1); *ert-zb.132* is associated with SNP markers 2_0824 to 2_1363 (positions 146.97 to 198.70 cM) in 7H bins 9 to 12 of the Bowman backcross-derived line BW331 (1).

Description:

Plants are 3/4 normal height and spikes tend to emerge prematurely (3). Compared to Bowman, plants of the backcross-derived line for *ert-zb.132*, BW331, headed 2 to 4 days later and were 15 to 20% shorter. Peduncles were 2/3 normal length and rachis internodes were about 10% shorter. Kernel weights for BW331 averaged 15% less than those of Bowman, 5.1 vs.5.8 mg, and grain yields were about 25% lower (2).

Origin of mutant:

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

Mutational events:

ert-zb.132 (NGB 112731, GSHO 502) in Bonus (PI 189763, NGB 14657) (3).

Mutant used for description and seed stocks:

ert-zb.132 (NGB 112731, GSHO 502) in Bonus; *ert-zb.13 2* in Bowman (PI 483237)*5 (GSHO 2262, BW331, NGB 22126).

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. 26:498.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:205.

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* (3).

Inheritance:

Monofactorial recessive (3).

Located probably in chromosome 7HS (1); *ert-zc.149* is associated with SNP markers 2_0722 to 1_0056 (positions 23.45 to 51.93 cM) in 7H bins 2 to 4 and with SNP markers 1_1497 to 2_0545 (positions 237.41 to 244.39 cM) in 5H bin 12 of the Bowman backcross-derived line BW332 (1).

Description:

Spikes are semicompact and plants are semidwarf (3/4 normal height). The basal rachis internode is slightly elongated (3). Compared to Bowman, plants of the backcross-derived line for *ert-zc.149*, BW332, were about 10 cm shorter, peduncles were 4 to 8 cm shorter, and rachis internodes were 10 to 20% shorter. BW332 plants headed 2 to 3 days later than Bowman plants. Kernels of BW332 weighed 5 to 10% less than those of Bowman, but both lines had similar grain yields (2).

Origin of mutant:

An ethylene oxide induced mutant in Bonus (PI 189763, NGB 14657) (3).

Mutational events:

ert-zc.149 (NGB 112748, GSHO 503) in Bonus (PI 189763, NGB 14657) (3).

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

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:206.

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* (3).

Inheritance:
Monofactorial recessive (3).
Located probably in chromosome 5HS (1); *ert-ze.105* is associated with SNP markers 1_0974 to 2_1244 (positions 41.99 to 91.0 cM) in 5H bins 2 to 5 and with SNP markers 2_1374 to 2_1122 (positions 192.0 to 198.33 cM) in 4H bin 5 of the Bowman backcross-derived line BW334 (1).

Description:
Spikes are semicompact, but other phenotypic traits appear normal (3). Compared to Bowman, plants of the backcross-derived line for *ert-ze.105*, BW334, headed 2 days later and were up to 20 cm shorter. The Bowman stocks for *ert-ze.105* and *ert-za.102* might have been mixed during the backcrossing process (2).

Origin of mutant:
A spontaneous mutant in Bonus (PI 189763, NGB 14657) (3).

Mutational events:
ert-ze.105 (NGB 112704, GSHO 505) in Bonus (PI 189763, NGB 14657) (3).

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. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:500.
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:207.

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* (5).
Early maturity-d = *ea-d* (10).

Inheritance:

Monofactorial incomplete dominant (5).

Located in chromosome 4HL or 6HL (2); the narrow leaf blade trait from *mat-d.14* is associated with SNP markers 2_1130 to 1_1019 (positions 175.48 to 183.54 cM) in 4H bins 12 to 13 and with SNP markers 1_0734 to 2_0379 (positions 159.32 to 163.56 cM) in 6H bins 12 to 13 of the Bowman backcrossed-derived line BW509 (2).

Description:

Early heading mutants at the *mat-d* locus (6) have a moderate increase in earliness (heading 3 days earlier than the parents) under field cultivation in Sweden (7, 8). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (4). 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, 5). Retention of the *mat-d.14* mutant in the Bowman backcross-derived line, BW509, needs to be confirmed because only plants with narrower leaf blades were recovered in progenies from crosses to Bowman. An error could have been made during backcrossing because BW509 retained SNP molecular markers in chromosome 4HL that are identical to those retain in BW513, the Bowman backcross-derived line for *mat-h.36* (see BGS 584) (2). Phenotypically BW509 and BW513 were very similar (3). BW509 and Bowman plants were phenotypically similar except for reduce leaf blade width and slightly lower grain yield (3).

Origin of mutant:

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

Mutational events:

mat-d.14 (NGB 110014, GSHO 1790) in Bonus (PI 189763, NGB 14657) (3); *mat-d.124* (NGB 110124) in Foma (CIho 11333, NGB 14659) (7, 8, 9).

Mutant used for description and seed stocks:

mat-d.14 (NGB 110014, GSHO 1790) in Bonus; *mat-d.14* in Bowman (PI 483237)*6 (BW509, NGB 20737).

References:

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Prepared:

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Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:208-209.

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); *mat-f.23* is associated with SNP markers 1_0764 to 1_1326 (positions 61.55 to 82.35 cM in 1H) in 1H bins 06 to 08 and with markers 1_0310 to 2_0152 (positions 285.74 to 298.99) in 5HL bin 15 of the Bowman backcross-derived line BW511 (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 for *mat-f.23*, BW511, was similar in maturity to Bowman and for other agronomic traits when grown in Scotland. In New Zealand, plants were 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, NGB 14657) (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 117439), *-f.932* (NGB 117463) in Bonus (PI 189763, NGB 14657); *-f.983* (NGB 117514) in Sv 79353.(5, 6, 7).

Mutant used for description and seed stocks:

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

References:

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Prepared:

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Revised:

J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:137.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:210-211.

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* (3).

Inheritance:

Monofactorial recessive (3).

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 (3, 5). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (3). The Bowman backcross-derived line, BW513, line with the *mat-h.36* mutant is similar to BW509 line with the *mat-d.14* mutant in terms of both chromosomal SNP markers retained and phenotype attributes (1, 2). Plants with narrow leaves were found in progeny from the cross of the *mat-h.36* stock to Bowman. An error may have been made during backcrossing because the SNP molecular markers retained in chromosome 4HL of BW513 are identical to those retain in BW509 (see BGS 580) (1). BW513 and Bowman plants were phenotypically similar except for reduce leaf blade width and slightly lower grain yields (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763, NGB 14657) (7).

Mutational events

mat-h.36 (NGB 110036, GSHO 1794)*, -h.935* (NGB 117466) in Bonus (PI 189763, NGB 14657) (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. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155*:*617-627.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:511.

Revised:

U. Lundqvist and J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:662.
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:212-213.

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* (7).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 7HL (1); *mat-i.37* is associated with SNP markers 1_0885 to 3_0593 (positions 192.14 to 198.70 cM) in 7H bins 11 to 12 of the Bowman backcross-derived line BW514 (1).

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 (6, 7). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (5). Spikes of mutants are relatively short (7). The expression of earliness was relatively strong in BW514, the Bowman backcross-derived line for *mat-i.37*, was about 4 days earlier heading under long days and up to 15 days earlier under short days (2). Depend on heading dates, BW514 plants were 10 to 40% shorter than Bowman plants and grain yields were up to 50% lower (2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (PI 189763, NGB 14657) (7).

Mutational events:

mat-i.37 (NGB 110037, GSHO 1795), *-i.76* (NGB 110076) in Bonus (PI 189763, NGB 14657), *-i.303* (NGB 110303) in Foma (CIho 11333, NGB 14659), *-i.742* (NGB 110742) in Kristina (NGB 1500, NGB 14661), *-i.901* (NGB 116856), *-i.914* (NGB 117445) in Bonus (5, 6, 7).

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).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:512.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:214.

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* (2).

Inheritance:

Monofactorial recessive (2).

Location is unknown; compared to Bowman no polymorphisms were observed in the Bowman backcross-derived line for *yhd2.b*, BW921 (1).

Description:

The *yhd2.b* 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 (3). Plants of the Bowman backcross-derived line for *yhd2.b*, BW921, headed 3 to 5 days later than Bowman and were 5 to 10% shorter. Other morphological traits of BW921 including yield were not different from the range of values recorded for Bowman (3).

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (2).

Mutational events:

yhd2.b (Golden Compana, GSHO 757) in Compana (PI 539111) (2, 3).

Mutant used for description and seed stocks:

yhd2.b (GSHO 757 compared to Bowman no polymorphisms were observed in the Bowman backcross-derived line for *yhd2.b*, BW921 (1).) in Compana; *yhd2.b* in Bowman (PI 483237)*6 (GSHO 2037): *yhd2.b* in Bowman*8 (BW921, NGB 22350).

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Prepared:

J.D. Franckowiak. 1998. Barley Genet. Newsl. 28:33.

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:215.

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 with 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 *ant4* mutant plants. The amount of anthocyanin pigmentation was clearly decreased compared to the mother cultivars (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). Earlier heading of BW024 was observed under glasshouse and short-day conditions, but not under long-day conditions (2). 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 of BW024 were 10 to15% lighter and grain yields were slightly lower than those of Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333, NGB 14659) (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 (CIho 11333, NGB 14659) (7); *ant4.32* (NGB 114587) in Foma (5); *ant4.37* (NGB 114592) in Foma (7); *ant4.40* (NGB 114595) in Bonus (PI 189763, NGB 14657) (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).

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Prepared:

B. Jende-Strid. 1999. Barley Genet. Newsl. 29:83.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:189-190.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:216-217.

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 (5, 6).

Located in chromosome 3HS (1); *ant17.148* is associated with SNP markers 2_0607 to 1_0601 (positions 52.41 to 71.29 cM) in 3H bins 04 to 05 in Bowman backcross-derived line BW016 (2); the *ant17.148* mutant has been shown to be an allele at the *seg3* (shrunken endosperm genetic 3, see BGS 379) locus (3). The seed stock for the Bowman backcross derived line for *ant17.567*, BW017, is incorrect because the same SNP markers were retained in both BW016 and BW017 (2, 3). The correct seed lot for BW017 has been increased as NGB 20425

Description:

Under normal growing conditions no anthocyanin pigmentation is observed in the *ant17* mutant plants. The testa layers of the grain of the *ant17* mutants lack proanthocyanidins and catechins, but accumulate homoeriodictyol and chrysoeriol (8, 11). 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* (13). 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 (8, 13). The mutant line *ant17.148* was released as cultivar Galant (12). Alleles at the *seg3* locus in the Bowman backcross-derived lines BW016 (*ant17.148*) and BW836 (*seg3.c*) showed variable reductions in kernel weight: Kernels of BW016 and BW836 were 1/3 to 1/2 normal weight while those of BW017, the backcross-derived line for *ant17.567*, were about 3/4 normal (3). Grain yields of BW017 were about 3/4 those of Bowman (3).

Origin of mutant:

A sodium azide induced mutant in Nordal (NGB 13680) (4).

Mutational events:

ant17.103, *17.104*, *17.105*, *17.139* (NGB 13697), *17.140*, *17.142*, *17.143*, *17.145* in Nordal (NGB 13680) (5); *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) (5); *ant17.352* in Triumph (6); *ant17.160* in Gula Abed (NGB 13681) (5); *ant17.165*, *17.167*, *17.169*, *17.171*, *17.174*, *17.182* in Ark Royal (PI 447006) (5); *ant17.192*, *17.193* in Georgie (PI 447012, NGB 13683) (5); *ant17.199* in Secobra 4681 (4); *ant17.200* in Secobra 4681 (6); *ant17.208* in Hege 876 (4); *ant17.210*, *17.211*, *17.217* in Hege 802 (5); *ant 17.216* in Hege 802 (6); *ant17.220*, *17.221*, *17.224*, in Secobra 4743 (NGB 13679) (5); *ant17.227* in Ca 59995 (6); *ant17.231* in Tron (5); *ant17.237*, *17.239*, *17.241*, *17.242*, *17.247*, *17.249* in Gunhild (PI 464655, NGB 13690) (5); *ant17.243*, *17.246* in Gunhild (6); *ant17.250*, *17.251*, *17.252*, *17.253*, *17.255* in Tokak (PI 264251) (5); *ant17.267*, *17.268*, *17.269* in Secobra 18193 (NGB 13684) (5); *ant17.270* in Secobra 18193 (6); *ant17.280* in Hege 550/75 (NGB 13692) (10); *ant17.288*, *17.289*, *17.290* in Hege 550/75 (5); *ant17.293*, *17.294, 17.295*, *17.296* in Bonus (NGB 14597, PI 189763) (5); *ant17.297*, *17.298*, 17.300, *17.301*, *17.307* in Ca 41507 (5); *ant17.306*, *17.340* in Ca 41507 (6); *ant17.316* in Ca 33787 (NGB 13693) (6); *ant17.318*, *17.321*, *17.326* in Harry (PI 491575) (6); *ant17.331* in Hege A2/A4 (6);

ant17.335, *17.336*, *17.338* in Ackermann 724/5/7 (6); *ant17.359* in Hege15/74-1A (6); *ant17.370* in Ackermann 72/440 (6); *ant17.372*, *17.413*, *17.414*, *17.417*, *17.418*, *17.419*, *17.444* in Kaya (6); *ant17.375* in Fanette (7); *ant17.379*, 17.382, *17.383*, 17.386, *17.387*, *17.388*, *17.389*, *17.390*, *17.391*, *17.464*, 17.465 in Irene (6); *ant17.405* in Odin (7); *ant17.408* in KMJ 326 (6); *ant17.410*, *17.447* in Catrin (6); *ant17.421* in VBS 18707 (6); *ant17.422*, *17.423*, *17.424*, *17.426* in NZ 3789 (6); *ant17.432* in NZ 1836-3 (6); *ant17.438*, *17.439* in NZ 732.01 (6); *ant17.440* in Nordal (NGB 13680) (6); *ant17.450* in Ca 601427 (6); *ant17.453*, *17.455*, *17.457*, *17.458* in Ackermann 1734/5 (6); *ant17.462* in Pamela (6); *ant17.469* (NGB 23018), *17.470* (NGB 23019) in Grit (PI 548764, NGB 13685) (6); *ant17.475* in Zenit (PI 564447, NGB 13686) (6); *ant17.476* in Zenit (7); *ant17.480* in Secobra 9709 (6); ant17.501 in Advance (CIho 15804) (5); *ant17.504* in Karla (CIho 15860) (5); *ant17.506*, *17.507*, *17.508*, *17.509* in OR 9114 (5); *ant17.515*, *17.516*, *17.518* in WA9037-75 (5); *ant17.520* in WA9044-75 (5); *ant17.530* in Morex (CIho15773) (5); *ant17.537*, *17.595*, *17.619*, *17.620* in Advance (6); *ant17.560*, *17.561*, *17.563*, *17.565*, *17.567* in Manker (CIho 15549) (6); *ant17.597* in Morex (7); *ant17.598* in Morex (6); *ant17.600* in S 80351 (6); *ant17.601* in Moravian 111 (CIho 15812) (6); *ant17.604* in Harrington (7); *ant17.612* in Andre, (PI 469107) (6); *ant17.624* in Klages (CIho 15478) (6); *ant17.625* in Robust (M36, PI 476976) (6); *ant17.630* in Azure (CIho 15865) (14); *ant17.636*, *17.658* in Cougbar (PI 496400) (14); *ant17.637* in 8892-78 (14); *ant17.661* in Crest (PI 561409) (14); *ant17.1502*, *17.1505*, *17.1519* in Amagi-Nijo (5); *ant17.1510*, *17.1511* in Haruna- Nijo (5); *ant17.1515* in Nirakei 61 (5); *ant17.1537* in Nirakei 62 (6); *ant17.1544* in Nirakei 63 (6); *ant17.1534* in Nirasaki-Nijo 14 (6); *ant17.2022*, *17.2067* in Natasha (PI 592171) (7); *ant17.2084* in Hege 694/82 (10); *ant17.2106* in Ca 708912 (9); *ant17.5019* in Sonja (PI 302047) (10); *ant17.5024* in Ackermann 72/27/4 (7); *ant17.5028* in Trigger (PI 473541) (10); *ant17.5034* in Kaskade (10); *ant17.5035*, *17.5036*, *17.5037* in Video (7); *ant17.5038*, *17.5039*, *17.5040*, *17.5042* in Sonja (7); *ant17.5044* in Ackermann 27/220/8 (7).

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* (GSHO 1629) in Manker; *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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Revised:
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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 (5, 6).

Located in chromosome 3H (2); *ant18.102* is associated with SNP markers 2_0666 to 2_0063 (positions 67.01 to 133.92 cM) in 3H bins 05 to 08 in Bowman backcross-derived line BW018 (2). An *ant18* mutant was previously associated with chromosome 7HL (1).

Description:

No anthocyanin pigmentation is observed in the *ant18* mutant plants. The ripe grains of the *ant18* mutants have a shrunken appearance (6). The testa layers of the grains of the *ant18* mutants lack proanthocyanidins and catechins but accumulate small amounts of dihydroquercetin (10, 11). 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 (12). The *ant18* gene is the structural gene coding for the dihydroflavonol reductase enzyme, which catalyzes the conversion of dihydroflavonols into leucoanthocyanidins (10, 12, 15). 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 (13). Plants of the Bowman backcross-derived line for *ant18.102*, BW018, were similar to Bowman, but kernels were thinner and lighter, 4.6 vs.5.7 mg. Grain yields of BW018 were 1/2 to 3/4 those of Bowman (3).

Origin of mutant:

A sodium azide induced mutant in Nordal (NGB 13680) (4).

Mutational events:

ant18.102 (GSHO 1630), *18.141*, *18.144* in Nordal (NGB 13680) (5); *ant18.106*, *18.111* in Alf (NGB 13682) (5); *ant18.146*, *18.186* in Triumph (PI 268180, NGB 13678) (5); *ant18.159* (NGB 13699),*18.161* (NGB 13700), *18.162* (NGB 13701), *18.164* (NGB 13702), *18.183* in Gula Abed (NGB 13681) (5); *ant18.166*, *18.170*, *18.175*, *18.176*, *18.177*, *18.178*, *18.179* in Ark Royal (PI 447006) (5); *ant18.168* in Triumph (6); *ant18.195*, *18.196*, *18.197* in Georgie (PI 447012, NGB 13683) (5); *ant18.198*, *18.204* in Secobra 4681 (5); *ant18.206* in Hege 876 (5); *ant18.209* in Hege 802 (5); *ant18.215*, *18.226* in Hege 802 (6); *ant18.234*, *18.235* in Tron (5); *ant18.236*, *18.240*, *18.244*, *18.248* in Gunhild (PI 464655, NGB 13690) (5); *ant18.254* in Tokak (PI 264251) (6); *ant18.256*, *18.257*, *18.258*, *18.259*, *18.260*, *18.261*, *18.262*, *18.263* in Tokak (5); *ant18.275*, *18.276*, *18.279* in VP116 (NGB 13691) (5); *ant18.281*, *18.286*, *18.291* in Hege 550/75 (NGB 13692) (5); *ant18.292* in Bonus (NGB 14657, PI 189763) (5); *ant18.299*, *18.302*, *18.303*, *18.304*, *18.309*, *18.339*, *18.341* in Ca 41507 (5); *ant18.319*, *18.323*, *18.324*, *18.325* in Harry (PI 491575) (6); *ant18.332* in Ca 603801 (6); *ant18.337* in Ackermann 724/5/7 (6); *ant18.342* in Secobra 18193 (*NGB* 13684) (5); *ant18.344* in NZ 716.01 (6); *ant18.356*, *18.357* in Hege 841/80 (6); ant18.365, *18.366* in Ca 36167 (6); *ant18.367* in Gimpel (PI 564720) (6); *ant18.374*, *18.376*, *18.377* in Fanette (6); *ant18.378* in Ca 33787 (NGB 13693) (6); *ant18.380*, *18.392*, *18.463* in Irene (6); *ant18.402* in Odin (6); *ant18.415* in Kaya (6); *ant18.425* in NZ 3789 (6); *ant18.427* in NZ 3789 (7); *ant18.428*, *18.429*, *18.431*, *18.433*, *18.435*, *18.436* in NZ 1836-3 (6); *ant18.442* in Ca 710516 (6); *ant18.448* in Catrin (6); *ant18.451* in Ca 601427 (6); *ant18.454*, *18.456*, 18.459 in Ackermann 1734/5 (6); *ant18.460* in Pamela (6); *ant18.467* (NGB 23020), *18.468* (NGB 23021), *18.471* (NGB 23022) in Grit (PI 548764, NGB 13685) (6); *ant18.473*, *18.474* in Almudena (7); *ant18.478* in Zenit (PI 574447, NGB 13686) (6); *ant18.481* in Secobra 9709 (6); *ant18.505* in WA 8953-75 (5); *ant18.512* in 72AB3484 (5); *ant18.519* in WA9044-75 (5); *ant18.532*, *18.533*, *18.591*, 18.592, *18.617*, *18.618*, *18.621* in Advance (CIho 15804) (6); *ant18.610*, *18.611*, *18.613* in Andre, (PI 469107) (6); *ant18.623* in Klages (CIho 15478) (6); *ant18.638* in 8892-78 (14); *ant18.659*, *18.660* in Cougbar (PI 496400) (14); *ant18.1503*, *18.1506*, *18.1517*, *18.1518* in Amagi-Nijo (5); *ant18.1509* in Haruna-Nijo (5); *18.1531*, *18.1532* in Nirasaki-Nijo 14 (6); *ant18.1536* in Nirakei 62 (6); *ant18.1539* in Nirakei 63 (6); *ant18.5001*, *18.5002*, *18.5003*, *18.5004*, *18.5005*, *18.5008*, *18.5009*, *18.5010* in Igri (PI 428488) (8); *ant18.5018*, *18.5022*, *18.5023*, *18.5030*, *18.5041* in Sonja (PI 392047) (9); *ant18.5027* in Video (9); *ant18.5043* in Ackermann 27/4/98 (9); *ant18.5046*, 1*8.5048* in Lucia (9); *ant18.5049* in Marinka (9).

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* from Nordal in Bowman (PI 483237)*3 (GSHO 1856); *ant18.102* in Bowman*7 (BW018, NGB 20426).

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Prepared:

B. Jende-Strid. 1999. Barley Genet. Newsl. 29:90-91.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:221-223.

BGS 613, Branched 1, *brc1*

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

Revised locus symbol:

The *brc1.5* mutant is one of the alleles at the *com2* (compositum 2) locus (3). See BGS 071 for more information on the alleles at the *com2* locus.

Previous nomenclature and gene symbolization:

Branched-5 = *brc-5* (1, 2, 3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 2HS (2); *brc1.5* is about 2.5 cM from AFLP marker E3636-2 and proximal from molecular marker CDO665A (2, 4); the BLASTn association of *brh1.5* is with rice gene *FUZZY PANICLE* (*FZP*) (3, 4), in bin 2H bin 05.

Description:

A second-order ramification of the barley spike is observed in the *brc1.5* mutant. Basal parts of the spike elongate to form rachis-like branches, and thus generating a ramified spike phenotype (1, 2). The *brc1.5* (*com2*) mutant disrupts production of COM2 containing an AP2/ERF (an ethylene-responsive element DNA binding factor) domain that represses inflorescence branch formation (3).

Origin of mutant:

Natural occurrence in line BGRC 13145 from the Braunschweig seed collection (*Hordeum vulgare* L. convar. *distichon* (L.) Alef. var. *inerme* Körn.) (5).

Mutational events:

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

Mutant used for description and seed stocks:

brc1.5 (G22) in BGRC 13145; *brc1.5* in Bowman (PI 483237)*2 (BW071, NGB 20408).

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Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:224-225.

BGS 624, Opposite spikelets 1, *ops1*

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

Previous nomenclature and gene symbolization:

Opposite spikelets-3 = *op-3* (4, 5).

Inheritance:

Monofactorial recessive (4).

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

Description:

Plants with the *ops1.3* gene have a reduced number of tillers and very few late tillers (5). Variable lengths of the rachis internodes caused an irregular arrangement of spikelets in the spike. Compared to normal sibs, *ops1.3* plants were slightly shorter and lower yielding (3, 5). Plants of the Bowman backcross-derived line for *ops1.3*, BW641, yielded 1/4 to 1/2 as much grain as Bowman plants. Kernels of BW641 were slightly larger than those of Bowman in low stress environments and slightly smaller in higher stress environments (3). In field environments, a variable number of kernels of BW641 exhibited a slightly split palea (3) caused by failure of the two glumes that form the palea to fuse completely (2).

Origin of mutant:

A sodium azide induced mutant in Bonus (PI 189763, NGB 14657) (5).

Mutational events:

ops1.3 (NGB 115379, GSHO 2427) in Bonus (PI 189763, NGB 14657) (5).

Mutant used for description and seed stocks:

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

References:

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

Prepared:

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

Revised:

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

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:226.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 2H (2); *viv-a.5* is associated with SNP markers 2_0177 to 2_0528 (positions 63.96 to 116.78 cM) in 2H bins 05 to 08 of the Bowman backcross-derived line BW896 (2).

Description:

Tillers of *viv-a* plants may remain vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as the culm elongates. Occasionally a short, malformed spike is formed in a lateral position (1, 5). For the Bowman backcross-derived line for *viv-a.5*, BW896, only a few tiller exhibited the typical viviparoides phenotype in most environments. BW896 plants were 5 to 20 cM shorter than Bowman and they lodged easily. Peduncle and awn lengths were slightly reduced and heading was delayed about six days. Kernels of BW896 were thinner, 3.5 vs. 4.0 mm, and weighed less, 4.2 vs. 5.6 mg. Grain production varied almost none to nearly 50% of that for Bowman (3).

Origin of mutant:

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

Mutational events:

viv-a.5 (NGB 115364, GSHO 2498) in Foma (CIho 11333, NGB 14659) (5).

Mutant used for description and seed stocks:

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

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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4. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
5. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. Barley Genet. Newsl. 32:128.

Revised:

U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:227.

BGS 629, Mottled leaf 6, *mtt6*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HS (1); *mtt6.g* is associated with SNP markers 1_0851 to 2_1437 (positions 17.32 to 20.56 cM) in 7H bin 02 of the Bowman backcross-derived line BW604 (1).

Description:

When grown in the greenhouses, the *mtt6.g* seedlings are slightly pale green in color and develop a white necrotic region partially across the blade of the first leaf. Occasionally white necrotic blotches or region develop in subsequent leaf blades. Plants are taller than normal sibs and remain a slightly pale shade of green until maturity. Plant vigor appears normal (2). Plants of the Bowman backcross-derived line for *mtt6.g*, BW604, headed 1 to 4 days later than Bowman plants. BW604 plants varied from slightly taller to shorter, had slightly longer peduncles and larger leaf blades, and had 2 to 4 more kernels per spike. Compared to Bowman, kernels of BW604 were 5 to 10% lighter and grain yields varied from 30 to 95% of those for Bowman (2).

Origin of mutant:

A spontaneous mutant in selection ND6809 from a ND2654-31/Karl cross (2).

Mutational events:

mtt6.g (GSHO 2411) in ND6809-1 (2).

Mutant used for description and seed stocks:

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

References:

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

Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:228.

BGS 631, Brachytic 3, *brh3*

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

Revised locus symbol:

The *brh3* mutants are alleles at the *ert-t* (Erectoides-t) or *BRASSINOSTEROID-6-OXIDASE* (*HvBRD*) locus, which encodes a barley brassinosteroid-6-oxidase (2). See BGS 566 for more information on the alleles at the *ert-t* or *HvBRD* locus.

Previous nomenclature and gene symbolization:

Brachytic-g = *brh.g* (4).
Brachytic-h = *brh.h* (1, 4).
Brachytic-i = *brh.i* (1, 4).
Brachytic-y = *brh.y* (1, 4).
Erectoides-t.55 = *ert-t.55* (1, 8, 10).
Brachytic 4 = *br4* (11).

Inheritance:

Monofactorial recessive (4, 6).

Located in chromosome 2HS (1, 3); *brh3.g* is approximately 11.4 cM distal from SSR marker Bmac0134 (1), near the boundary between 2H bins 01 and 02 (1); *brh3.g* is associated with 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 with 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 different from those of Bowman were retained in 2HS Bowman backcross-derived line for *brh3.i*, BW093 (3); the *brh3* mutants are in the *HvBRD* locus, which encodes for a brassinosteroid-6-oxidase, and is located in the telomeric region of 2HS (2); in 2H bin 02.

Description:

The seedling leaf of *brh3* plants is shorter than that of normal sibs. Plants are 2/3 to 3/4 of normal height and the number of tillers per plant is reduced. Awns are fine with slightly curly tips and are about 1/2 normal length. Spikes of *brh3* plants have a slightly elongated first rachis internode. Seed set may be reduced when plants are grown under greenhouse conditions (5). 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, included the dense spike and short awn, are inherited together (1, 5). Based on general appearance of the plants, the *ert-t.55* mutant can be placed in the brachytic class of semidwarf mutants (1, 11). The *brh3* mutants exhibited the brassinosteroid-deficient phenotype: shorter rachis internode length, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (2). The Bowman backcross-derived lines for *brh3.g* and *brh3.y*, BW091 and BW094, had kernels that were shorter, 8.7 vs 9.7 mm, and lighter, 4.6 vs 5.6 mg, than those of Bowman. Grain yields of BW091 and BW094 varied from 1/3 to 2/3 those of Bowman (5).

Origin of mutant:

Probably sodium azide induced mutants in Birgitta (NSGC 1870, NGB 1494 and 14667) (9).

Mutational events:

brh3.g (GSHO 1672, 17:10:1, DWS1002) in Birgitta (NSGC 1870, NGB 1494 and 14667) (1, 4, 6); *brh3.h* (GSHO 1673, 17:11:3, DWS1003) in Birgitta; *brh3.i* (GSHO 1674, 17:12:1, DWS1004) in Birgitta (4, 6, 9); *brh3.y* (GSHO 1688, 10001, DWS1230) in Bido

(PI 399485) (1, 4, 7). The *brh3.g* and *brh3.h* lines may be the same mutational event as a seed mixture was observed in the original seed lots (5) and both stocks have the same nonsense mutation in the *ert-t* (*HvBRD*) coding region (2).

Mutant used for description and seed stocks:

brh3.g (GSHO 1672) in Birgitta; *brh3.g* in Bowman (PI 483237)*7 (GSHO 2167, BW 091, NGB 20497); *brh3.h* in Bowman*2 (GSHO 2168, BW092, NGB 20498); *brh3.i* in Bowman*6 (GSHO 2169); *brh3.i* in Bowman *7 (BW093, NGB 20499); *brh3.y* from Bido in Bowman*5 (GSHO 2178); *brh3.y* in Bowman*6 (BW094, NGB 20500). See BGS 566 for information about additional mutants at this locus.

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.
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4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
5. Franckowiak, J.D. (Unpublished).
6. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
7. Gaul, H. 1986. (Personal communications).
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9. Lehmann, L. 1985. (Personal communications).
10. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
11. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and erectoides mutants. Barley Genet. Newsl. 6:79-81.

Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:229-230.

BGS 653, Brachytic 10, *brh10*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 2HS (1); *brh10.l* is approximately 12.9 cM distal from SSR marker Bmac0850 in 2H bin 08 (1); *brh101.l* is associated with SNP markers 1_1054 to 2_0960 (positions 83.83 to 120.83 cM) in 2H bins 06 to 09 of the Bowman backcross-derived line BW081 (2).

Description:

Plants of the *brh10.l* mutant are about 3/4 normal height and peduncles are over 3/4 normal length. Awns are about 3/4 of normal length. Rachis internodes are slightly shorter than those of normal sibs, but the number of fertile rachis nodes is increased by over 2. Seedling leaves of *brh10.l* plants are relatively short (1, 3). Kernels of the Bowman backcross-derived line for *brh10.l*, BW081, were shorter (7.9 vs. 9.6 mm) and 10 to 20% lighter than those of Bowman. BW081 plants showed an erect growth habit and grain yields averaged 20% less than those of Bowman (1, 3). Awns of BW081 were slightly shorter, 8 vs. 11 cm beyond terminal kernel, and rachis internodes were shorter, 3.7 vs.4.5 mm. BW081 plants headed 2 to 4 days later than Bowman and had 2 to 3 more kernels per spike (3).

Origin of mutant:

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

Mutational events:

brh10.l (17:15:2, DWS1007, GSHO 1677) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5, 6).

Mutant used for description and seed stocks:

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

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
6. Lehmann, L.C. 1985. (Personal communications).

Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:231.

BGS 654, Brachytic 11, *brh11*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 5HS (1); *brh11.n* is about 6.7 cM proximal from SSR marker Bmac0113 in 5H bin 04 (1); *brh11.n* is associated with SNP markers 1_0688 to 2_1121 (positions 52.12 to 105.90 cM) in 5H bins 03 to 06 and with SNP markers 2_0062 to 2_1151 (positions 51.44 to 78.94 cM) in 4H bins 06 to 08 of the Bowman backcross-derived line BW082 (2).

Description:

Plants of the *brh11.n* mutant are 2/3 to 3/4 normal height and peduncles are 3/4 to 5/6 normal length. The length of the rachis internodes is about 3/4 as long as those of normal sibs. Seedling leaves of *brh11.n* plants are relatively short (1, 3). Kernels of the Bowman backcross-derived line for *brh11.n*, BW082, were shorter (7.2 vs. 9.6 mm) and about 25% lighter (4.6 vs. 5.7 mg) than those of Bowman. BW082 plants had an erect growth habit and grain yields averaged less than 1/2 of those for Bowman (1, 3). Rachis internodes of BW082 were shorter, 3.4 vs. 4.5 mm. Also, peduncles were shorter. 22 vs. 30 cm, and awns were slightly shorter. BW082 plants headed 2 to 4 days later than Bowman (3).

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
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Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:232.

BGS 655, Brachytic 12, *brh12*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 5HS (1); *brh12.o* is approximately 13.5 cM distal from SSR marker Bmag0387 in 5H bin 03 (1); *brh12.o* is associated with SNP markers 1_1198 to 2_1244 (positions 73.70 to 91.0 cM) in 5H bins 04 to 05 of the Bowman backcross-derived line BW083 (2).

Description:

Plants of the *brh12.o* mutant are 2/3 to 3/4 of normal height. Awns and peduncles are about 3/4 normal length. The length of the rachis internodes is about 3/4 of normal sibs. Seedling leaves of *brh12.o* plants are relatively short (1, 3). Kernels of the Bowman backcross-derived line for *brh12.o*, BW083, were shorter (7.3 vs. 9.2 mm) and about 20% lighter than those of Bowman. Grain yields of BW083 averaged slightly more than 1/2 of those for Bowman (1, 3).

Origin of mutant:

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

Mutational events:

brh12.o (17:20:2, DWS1012, GSHO 1680) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5, 6).

Mutant used for description and seed stocks:

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

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, j. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
6. Lehmann, L.C. 1985. (Personal communications).

Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:233.

BGS 656, Brachytic 13, *brh13*

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

Previous nomenclature and gene symbolization:

Brachytic-p = *brh.p* (5).

Brachytic-ac = *brh.ac* (2, 5).

Hordeum vulgare Constitutive Photomorphic Dwarf = *HvCPD* (2).

Inheritance:

Monofactorial recessive (5, 7).

Located in chromosome 5HS (1, 2, 3); *brh13.p* is approximately 8.7 cM distal from SSR marker Bmag0387 in 5H bin 03 (1); *brh13.p* is associated with SNP markers 2_1324 to 2_1121 (positions 47.40 to 105.91 cM) in 5H bins 02 to 06 of the Bowman backcross-derived line BW084 (3); the Bowman backcross-derived line for *brh13.ac* (*brh18.ac*), BW089, was not evaluated by Druka et al. (3); the *brh13* (*HvCPD*) locus is positioned at 44.24 cM (2) on the barley genome map (9, 10).

Description:

Plants of the *brh13.p* mutant are about 2/3 normal height, and their awns are about 1/2 normal length. Peduncles and leaf blades are about 2/3 and 3/4 normal length, respectively (1, 6). The length of the rachis internodes is about 5/6 that of Bowman, 3.8 vs 4.3 mm. The spikelets at the tip of the spike are close together giving a fascinated appearance. Seedling leaves of *brh13.p* plants are relatively short. Plants lodge relatively easily (1, 6). Kernels of the Bowman backcross-derived line for *brh13.p*, BW084, were about the same size as those of Bowman, but kernel weights averaged about 20% less and test weight was lower. BW084 plants had erect growth habit and their grain yields averaged about 1/2 those of Bowman (6). The *brh13.p* mutant shows a brassinosteroid deficient phenotype including reduced culm length due to short upper internodes, irregular rachis internode length, short awns, acute leaf angles, and strongly undulating leaf margins (2). The *brh13.p* mutant is at the *brh13* (Brachytic 13) or *CONSTITUTIVE PHOTOMORPHOGENIC DWARF* (*HvCPD*) locus, which encodes the barley C-23α-hydroxylase cytochrome P450 90A1 (CYP90A1) (2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (8).

Mutational events:

brh13.p (18:02:4, DWS1013, GSHO 1681) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (6, 7); *brh13.ac* (*brh18.ac*) (402B, DWS1277, GSHO 1670) in Mo6/4*Triumph (CIho 11612, GSHO 2465) (2, 4, 5, 7); based on allelism tests conducted by Dockter et al. (2) *brh18.ac* (BGS659) is renamed *brh13.ac*.

Mutant used for description and seed stocks:

brh13.p (GSHO 1681) in Birgitta; *brh13.p* in Bowman (PI 483237)*6 (GSHO 2174, BW084, NGB 20491); *brh13.ac* (GSHO 1670) in Mo6/4*Triumph; *brh13.ac* in Bowman*6 (GSHO 2182, BW089, NGB 22474).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.

2. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson.

2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.
3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
4. Falk, D. 1985. (Personal communications).
5. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
6. Franckowiak, J.D. (Unpublished).
7. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
8. Lehmann, L.C. 1985. (Personal communications).
9. Mayer, K.F. , M. Martis, P.E. Hedley, H. Simková, H. Liu, J.A. Morris, B. Steuernagel, S. Taudien, S. Roessner, H. Gundlach, M. Kubalákoyá, P. Suchánková, F. Murat, M. Felder, T. Nussbaumer, A. Graner, J. Salse, T. Endo, H. Sakai, T. Tanaka, T. Itoh, K. Sato, M. Platzer, T. Matsumato, U. Schotz, J. Dolezel, R. Waugh, and N. Stein. 2011. Unlocking the barley genome by chromosomal and comparative genomics. Plant Cell 23:1249-1263.
10. The International Barley Genome Sequencing Consortium. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature 491:711-716.

Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:234-235.

BGS 658, Brachytic 17, *brh17*

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

Previous nomenclature and gene symbolization:

Semidwarf mutant = Mo4 (6).

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 5HS (1); *brh17.ab* is approximately 11.6 cM proximal from SSR marker Bmag0387 in 5H bin 03 (1); *brh17.ab* is associated with SNP markers 1_0688 to 2_1344 (positions 52.12 to 98.42 cM) in 5H bins 03 to 06 of the Bowman backcross-derived line BW088 (2).

Description:

Plants of the *brh17.ab* mutant are about 3/4 normal height and awns are 5/6 of normal length. Peduncles are slightly shortened. Rachis internodes are about 20% shorter than those of normal sibs. Seedling leaves of *brh17.ab* plants are relatively short (1, 3). Compared to Bowman, kernels of the Bowman backcross-derived line for *brh17.ab*, BW088, were shorter (7.7 vs. 9.7 mm) and nearly 20% lighter, 5.0 vs. 5.9 mg. Lodging was reduced in BW088 and grain yields averaged 2/3 those of Bowman (1, 3). BW088 plants headed 1 to 2 days later than Bowman plants, were 10 to 15 cm shorter and had slightly shorter awns and peduncles (3).

Origin of mutant:

A sodium azide induced mutant in Morex (CIho 15773) (7).

Mutational events:

brh17.ab (Wa14355-83, Mo4, DWS1260, GSHO 1669) in Morex (CIho 15773) (5, 6).

Mutant used for description and seed stocks:

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

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
6. Nedel, J.L., S.E. Ullrich, J.A. Clancy, and W.L. Pan. 1993. Barley semidwarf and standard isotype yield and malting quality response to nitrogen. Crop Sci. 33:258-263.
7. Ullrich, S.E., and Aydin, A. 1988. Mutation breeding for semi-dwarfism in barley. p. 135-144. *In* Semi-dwarf Cereal Mutants and Their Use in Cross-breeding III. IAEA-TECDOC-455. IAEA, Vienna.

Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:236.

BGS 659, Brachytic 18, *brh18*

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

Revised locus symbol:

The *brh18.ac* mutant is an allele at the *brh13* (Brachytic 13) or *CONSTITUTIVE PHOTOMORPHOGENIC DWARF* (*HvCPD*) locus, which encodes the barley C-23α-hydroxylase cytochrome P450 90A1 (CYP90A1) (2). See BGS 656 for more information on the alleles at the *brh13* or *HvCPD* locus.

Previous nomenclature and gene symbolization:

Brachytic-ac = *brh.ac* (5).
Brachytic 18.ac = *brh18.ac*.

Inheritance:

Monofactorial recessive (5, 7).

Located in chromosome 5HS (1); *brh13.ac* (*brh18.ac*) is approximately 9.2 cM distal from SSR marker Bmac0163 in 5H bin 01 (1); *brh13.ac* was not evaluated by Druka et al. (3); the *brh13.ac* mutant is in the *HvCPD* gene and is positioned at 44.24 cM (2) on the barley genome map (8, 9).

Description:

Plants of the *brh13.ac* mutant are about 2/3 normal height and awns are less than 2/3 of normal length. Seedling leaves of *brh13.ac* plants are relatively short (1, 4). Peduncles are slightly coiled and about 3/4 as long as those of normal sibs (1, 2, 5). Rachis internodes of the Bowman backcross-derived line for *brh13.ac* mutant, BW089, were about 20% shorter than those of Bowman. BW089 plants were about 2/3 the height of Bowman plants and the extension of awns beyond the tip of the spike was about half as far. Kernels of BW089 plants were slightly lighter than those of Bowman, but about 10% shorter. Lodging was reduced, but grain yields averaged about 1/2 that for Bowman (6). The *brh13.ac* mutant shows a brassinosteroid deficient phenotype including reduced culm length due to short upper internodes, irregular rachis internode length, short awns, acute leaf angles, and undulating leaf margins (2).

Origin of mutant:

An induced mutant backcrossed into Triumph (CIho 11612, GSHO 2465) (4).

Mutational events:

brh13.ac (402B, DWS1277, GSHO 1670) in Mo6/4*Triumph (CIho 11612, GSHO 2465) (4, 5, 7); *brh13.p* mutant (18:2:4, DWS 1013, GSHO 1681) in Birgitta (NSCG 1870, NGB 1494, NGB 14667) (2).

Mutant used for description and seed stocks:

brh13.ac (GSHO 1670) in Mo6/4*Triumph; *brh13.ac* in Bowman (PI 483237)*6 (GSHO 2182, BW089, NGB 22474).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.

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

4. Falk, D. 1985. (Personal communications).

5. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.

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

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

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9. The International Barley Genome Sequencing Consortium. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature 491:711-716.

Prepared:

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

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:237-238.

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

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

Revised locus symbol:

The *ari-u.245* mutant is an allele at the *ert-t* (Erectoides-t) or *BRASSINOSTEROID-6-OXIDASE* (*HvBRD*) locus, which encodes a barley brassinosteroid-6-oxidase (1). See BGS 566 for more information on the alleles at the *ert-t* or *HvBRD* locus.

Previous nomenclature and gene symbolization:

Breviaristatum-245 = *ari.245* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HS (1, 2); *ari-u.245* is associated with SNP markers 2_0609 to 2_1377 (positions about 13.0 to 20.11 cM) in 2H bin 02 of the Bowman backcrossed-derived line BW031 (2); the *ari-u.245* mutant is an allele at the *ert-t* or *HvBRD* locus, which encodes for a brassinosteroid-6-oxidase, and is located in the telomeric region of 2HS (1); in 2H bin 02.

Description:

Plants of the *ari-u.245* mutant have reduced awn length, about 2/3 of normal with an undulated awn tip and an erect or brachytic growth habit (4). In the Bowman backcross-derived line for *ari-u.245*, BW031, a brachytic-like growth habit was observed, but expression of morphological traits was variable among nurseries with plant growth more reduced in moisture stressed nurseries. BW031 plants were 10 to 40% shorter and peduncles were 20 to 40% shorter compared to Bowman plants. Awn lengths of BW031 plants were 2/3 to 3/4 those for Bowman and rachis internode length varied from 2.9 to 4.3 mm compared to about 4.5 mm for Bowman. Kernels of BW031 were slightly smaller and 20% lighter. Grain yields varied from less than 1/3 to 3/4 of the Bowman yields (3). The variability in trait expression over environments observed in BW031 could be described as phenotypic plasticity, see Lacaze et al. (5). The *ari-u.245* mutant in BW031 plants exhibited the brassinosteroid-deficient phenotype: shorter rachis internode length, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (1).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Foma (CIho 11333, NGB 14659) (4, 6).

Mutational events:

ari-u.245 (NGB 116055) in Foma (CIho 11333, NGB 14659) (4, 6); *ari-u.304* (previously named *ari-o.304*) (NGB 116129) in Kristina (NGB 1500, NGB 14661) (1. 6).

Mutant used for description and seed stocks:

ari-u.245 (NGB 116055) in Foma; *ari-u.245* via ND14701 in Bowman (PI 483237)*5 (BW031, NGB 20439).

References:

1. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.

3. Franckowiak, J.D. (Unpublished).
4. Kucera, J., U. Lundqvist, and Å. Gustafsson. 1975. Inheritance of breviaristatum mutants in barley. Hereditas 80:263-278.
5. Lacaze, X., P. M. Hayes, and A. Korol. 2009. Genetics of phenotypic plasticity: QTL analysis in barley, *Hordeum vulgare.* Heredity 102:163-173.
6. Lundqvist, U. (Unpublished).

Prepared:
J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:200.
Revised:
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:239-240.

BGS 716, Intense blue aleurone 1, *ibl1*

Stock number:	BGS 716
Locus name:	Intense blue aleurone 1
Locus symbol:	*ibl1*

Previous nomenclature and gene symbolization:

Intense blue aleurone = *ibl* (1, 2).

Inheritance:

Monofactorial recessive (1).

Location is unknown.

Description:

The *ibl1.a* variant was identified based on mature aleurone color. Two new colors, brick red and intense blue, were found in the Abyssinian lines, Ethiopian 637 and Ab 2231, respectively. Aleurone color expression is influenced by the environment in much the same way as that of normal blue, but they are reasonably distinct from normal blue and white aleurones in well grown material (1). The *ibl1.a* gene intensifies the red anthocyanin pigmentation of base of seedlings and on the culms of maturing plants (3).

Origin of mutant:

Natural occurrence in Ethiopian 637 (GSHO 2508) (1).

Mutational events:

ibl1.a in Ethiopian accessions Ethiopian 637 (GSHO 2508) and in Ab 2231 (1, 2).

Mutant used for description and seed stocks:

ibl1.a in Ethiopian 637; *ibl1.a* with *blx4.d* (blue aleurone 4) and *nud1.a* (naked caryopsis 1) in Bowman*4/ICARDA Green//Ethiopian 637 (BW417, NGB 20650) produces red aleurone color; *ibl1.a* with *Blx1.a* (Blue aleurone 1) and *nud1.a* (naked caryopsis 1) in Bowman*4/ICARDA Green//Ethiopian 637 (BW418, NGB 20651) produces deep blue aleurone color.

References:

1. Finch, R.A., and G.E. Porter. 1976. A single gene determining two new aleurone colours in barley. Barley Genet. Newsl. 6:26-27.
2. Finch, R. A., and E. Simpson. 1978. New colours and complementary colour genes in barley. Z. Pflanzenzücht. 81:40-53.
3. Franckowiak, J.D. (Unpublished).

Prepared:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:241.

BGS 730, Labile 1, *lab1*

Stock number: BGS 730
Locus name: Labile 1
Locus symbol: *lab1*

Previous nomenclature and gene symbolization:

Hordeum irregulare (2, 5).

Hordeum vulgare L. convar. *labile* (Schiem.) Mansf.) (6, 7).

Inheritance:

Located in chromosome 5HL (6); *lab1.a* is at approximately 80 cM of 5HL in an interval of 5.7 cM between closely linked markers BAR and ge00066s01 (6), likely in 5H bins 08 or 09.

Description:

The *lab1.a* variant causes variable spikelet development at rachis nodes and is characterized by missing kernels or a variable number of fertile spikelets at each rachis node in six-rowed spikes (2, 5). The genetic background for *labile* phenotype is based on a six-rowed genotype with the recessive allele *vrs1.a* at the six-rowed spike 1 locus and dominant *Int-c.a* allele present at the intermedium spike-c loci (7). Suppression of lateral spikelet development starts in late stamen primordium (6).

Origin of mutant:

Natural occurrence in barley accessions from Ethiopia (1, 2, 3, 4, 5).

Mutational events:

lab1.a in PI 95306 and PI 25672 from Ethiopia.

Mutant used for description and seed stocks:

lab1.a in HOR2573 and HOR5465 from Ethiopia (6).

References:

1. Abay, F., and A. Bjørnstad. 2009. Specific adaptation of barley varieties in different locations in Ethiopia. Euphytica 167:181-195.
2. Åberg, E., and G.A. Wiebe. 1945. Irregular barley, *Hordeum irregulare*, sp. nov. J. Wash. Acad. Sci. 35:161-164.
3. Bjørnstad, A., and F. Abay. 2010. Multivariate patterns of diversity in Ethiopian barleys. Crop Sci. 50:1579-1586.
4. Hadado, T.T., D. Rau, E. Bitocchi, and R. Papa. 2009. Genetic diversity of barley (*Hordeum vulgare* L.) landraces from the central highlands of Ethiopia: comparison between the Belg and Meher growing seasons using morphological traits. Genet. Resour. Crop Evol. 56:1131-1148.
5. Harlan, H.V. 1914. Some distinctions in cultivated barleys with reference to their use in plant breeding. Vol 137 Gov. Print. Off., U.S. Dept. Agr. Bull., illus. p. 38. Washington.
6. Youssef, H.M., R. Koppolu, T. Rutten, V. Korzun, P. Schweizer, and T. Schnurbusch. 2014. Genetic mapping of the labile (*lab*) gene: a recessive locus causing irregular spikelet fertility in labile-barley (*Hordeum vulgare* convar. *labile*). Theor. Appl. Genet. 127:1123-1131.
7. Youssef, H.M., R. Koppolu, and T. Schnurbusch. 2012. Re-sequencing of *vrs1* and *int-c* loci shows that *labile*-barleys (*Hordeum vulgare* convar. *labile*) have a six-rowed genetic background. Genet. Resour. Crop Evol. 59:1319-1328.

Prepared:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:242.

BGS 731, Required for *Puccinia graminis* resistance 2, *rpr2*

Stock number: BGS 731
Locus name: Required for *Puccinia graminis* resistance 2
Locus symbol: *rpr2*

Previous nomenclature and gene symbolization:

ɣ08-118; R43-22#1 (3).

Inheritance:

Monofactorial recessive (2, 3)

Location in chromosome 6H (2); mapped to a 0.6 cM interval in 6H between markers Locus_6H_331 and GMS006 (2).

Description:

The *rpr2.b* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, which has the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr2.b* mutant has been partially characterized (2) with infection type (IT) range of 2.1; to 3; with a mode 3.2 (rated by 1), or IT of 3-2 to 3 (rated by 2), or IT of 2-3- (rated by 5). The *rpr2.b* mutant is not allelic to *rpr1.a*, *rpr3.c*, *rpr4.d; rpr5.e*, or *rpr6.f* (2, 3). Barley often exhibits mesothetic reactions with two or more ITs on a single leaf; therefore, ITs observed are recorded in order of their prevalence (4). Overall the *rpr2.b* mutant stock is moderately susceptible as opposed to the parent line Morex, which is typically rated as moderately resistant. (3, 4). The RPG1 protein is present in the *rpr2.b* line and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3). [Infection type (IT) for wheat stem rust (*Puccinia graminis* f. sp. *tritici*) seedling reaction is based on a 0-4 scale, defined by Stackman et al. (4), where 0 is highly resistant and 4 is highly susceptible with the in between numbers representing intermediate reactions which are further modified by + or – and a fleck which indicates a small necrotic area. IT1 indicates minute uredinia; IT2 small uredinia with chlorosis; IT3 medium uredinia often with chlorosis; and IT4 indicates large uredinia with chlorosis (4).]

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:

rpr2.b (ɣ08-118; R43-22#1, GSHO 3693) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

rpr2.b (ɣ08-118; R43-22#1, GSHO 3693) in Morex; *rpr2.b* in F_2 seed lots GSHO 3694 and GSHO 3695 (3).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:243.

BGS 732, Required for *Puccinia graminis* resistance 3, *rpr3*

Stock number: BGS 732
Locus name: Required for *Puccinia graminis* resistance 3
Locus symbol: *rpr3*

Previous nomenclature and gene symbolization:
ɣ08-112; R12-31#3 (3).
Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.
Description:

The *rpr3.c* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr3.c* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): range of 3- to 3+ (rated by 2); or MR with an IT range of 1.2 to 2 (rated by 1); or an It of 2.3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpg3.c* mutant is not allelic to *rpr1.a, rpr2.b, rpr4.d, rpr5.e, or rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).

Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).
Mutational events:
rpr3.c (γ08-112; R12-31#3, GSHO 3696) in Morex (CIho 15773) (2, 3).
Mutant used for description and seed stocks:
rpr3.c (γ08-112; R12-31#3, GSHO 3696) in Morex.
References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:244.

BGS 733, Required for *Puccinia graminis* resistance 4, *rpr4*

Stock number:	BGS 733
Locus name:	Required for *Puccinia graminis* resistance 4
Locus symbol:	*rpr4*

Previous nomenclature and gene symbolization:

γ08-114; R36-37#1 (3).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

The *rpr4.d* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr4.d* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 2.1 to 3.2 with a mode 3.2 (rated by 1); IT range of 3- to 3+ (rated by 2), or IT range of 3.3+ to 3.3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr4.d* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr5.e*, or *rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:

rpr4.d (γ08-114; R36-37#1, GSHO 3697) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

rpr4.d (γ08-114; R36-37#1, GSHO 3697) in Morex.

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:245.

BGS 734, Required for *Puccinia graminis* resistance 5, *rpr5*

Stock number:	BGS 734
Locus name:	Required for *Puccinia graminis* resistance 5
Locus symbol:	*rpr5*

Previous nomenclature and gene symbolizartion:

γ08-117; R42-33#5 (same as γ08-116) (3).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

The *rpr5.e* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr5.e* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 2 to 3.2 with a mode 2.3,3.2 (rated by 1); IT range of 3- to 3 (rated by 2), or 3.3-.2 (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr5.e* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, or *rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:

rpr5.e (γ08-117; R42-33#5, GSHO 3699) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

rpr5.e (γ08-117; R42-33#5, GSHO 3699) in Morex; *rpr5.e* (γ08-116; R42-33#1, GSHO 3699) in Morex (3). (These are selections from the same original seed lots, but they were both submitted and assigned different GSHO numbers).

References:

1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:246.

BGS 735, Required for *Puccinia graminis* resistance 6, *rpr6*

Stock number: BGS 735
Locus name: Required for *Puccinia graminis* resistance 6
Locus symbol: *rpr6*

Previous nomenclature and gene symbolization:
γ08-119; R47-23#1 (1).

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

Description:

The *rpr6.f* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr6.f* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 2.3- to 3+ (rated by 1) or IT range of 2.3- to 3.3- (rated by 4) based on a 0-4 scale, defined by Stakman et al. (3). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr6.f* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, or *rpr5.e* (1, 2) The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (1, 2).

Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (2).

Mutational events:
rpr6.f (γ08-119; R47-23#1, GSHO 3700) in Morex (CIho 15773) (1, 2).

Mutant used for description and seed stocks:
rpr6.f (γ08-119; R47-23#1, GSHO 3700) in Morex.

References:

1. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
2. Kleinhofs, A. (Unpublished).
3. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
4. Steffenson, B.J. (Unpublished).

Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:247.

BGS 736, Required for *Puccinia graminis* resistance 7, *rpr7*

Stock number: BGS 736
Locus name: Required for *Puccinia graminis* resistance 7
Locus symbol: *rpr7*

Previous nomenclature and gene symbolization:
γ08-115; R3-18#3 (2).

Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.

Description:
The *rpr7.g* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr7.g* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 1,2 to 3 with a mode 2.3-3.2 (rated by 1); IT of 3 (rated by 2), or IT range of 2.3 to 3.3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr7.g* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, *rpr5.e*, or *rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).

Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:
rpr7.g (γ08-115; R3-18#3, GSHO 3701) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:
rpr7.g (γ08-115; R3-18#3, GSHO 3701) in Morex.

References:
1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:248.

BGS 737, Required for resistance to *Cochliobolus sativus* 1, *rcr1*

Stock number:	BGS 737
Locus name:	Required for resistance to *Cochliobolus sativus*
Locus symbol:	*rcr1*

Previous nomenclature and gene symbolization:

γ08-122; (R4-29) (2).

Inheritance:

Monofactorial recessive (2, 3).
Location is unknown.

Description:

Plants with the *rcr1.a* mutant at the *rcr1* locus exhibited a susceptible reaction following inoculation with *Cochliobolus sativus* (Ito & Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] isolate ND85F. When rated following inoculation at the seedling stage, 10 individual plants of the *rcr1.a* mutant stock ranged from 5.5 to 6.5 with a mean 6.1 compared to rating of 3.5 to 4.5 with a mean of 3.7 for its moderately resistant parent Morex (2, 3). The six-rowed spring barley cultivar Morex has been reported to have the *Rcs5.e* (Reaction to *Cochliobolus sativus* 5) gene and at least two other QTL that in combination confer resistance to *C. sativus* (1, 4, 5).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (2).

Mutational events:

rcr1.a (γ08-122; R4-29, GSHO 3702) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

rcr1.a (γ08-122; R4-29, GSHO 3702) in Morex.

References:

1. Bilgic, H., B.J. Steffenson, and P.M. Hayes. 2005. Comprehensive genetic analyses reveal differential expression of spot blotch resistance in four populations of barley. Theor. Appl. Genet. 111:1238-1250.
2. Kleinhofs, A. (Unpublished).
3. Steffenson, B.J. (Unpublished).
4. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.
5. Zhou, H., and B. Steffenson. 2013. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breeding 32:139-154.

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:249.

BGS 738, Required for resistance to *Cochliobolus sativus* 2, *rcr2*

Stock number:	BGS 738
Locus name:	Required for resistance to *Cochliobolus sativus* 2
Locus symbol:	*rcr2*

Previous nomenclature and gene symbolization:

γ08-123; (R14-40) (2).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

Plants with the *rcr2.b* mutant at the *rcr2* locus exhibit a susceptible reaction following inoculation with *Cochliobolus sativus* (Ito & Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] isolate ND85F. When rated following inoculation at the seedling stage, 10 individual plants of the *rcr2.b* mutant stock ranged from 3.5 to 4.5 with a mean 4.0 compared to rating of 3.5 to 4.5 with a mean of 3.7 for its moderately resistant parent Morex (2, 3). The six-rowed spring barley cultivar Morex has been reported to have the *Rcs5.e* (Reaction to *Cochliobolus sativus* 5) gene and at least two other QTL that in combination confer resistance to *C. sativus* (1, 4, 5).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (2).

Mutational events:

A gamma-ray induced mutant in Morex (CIho 15773) (2).

Mutant used for description and seed stocks:

rcr2.b (γ08-123; R14-40, GSHO 3703) in Morex.

References:

1. Bilgic, H., B.J. Steffenson, and P.M. Hayes. 2005. Comprehensive genetic analyses reveal differential expression of spot blotch resistance in four populations of barley. Theor. Appl. Genet. 111:1238-1250.
2. Kleinhofs, A. (Unpublished).
3. Steffenson, B.J. (Unpublished).
4. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.
5. Zhou, H., and B. Steffenson. 2013. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breeding 32:139-154.

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:250.

BGS 739, Required for resistance to *Cochliobolus sativus* 3, *rcr3*

Stock number:	BGS 739
Locus name:	Required for resistance to *Cochliobolus sativus* 3
Locus symbol:	*rcr3*

Previous nomenclature and gen symbolization:

γ08-124 (2).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

Plants with the *rcr3.c* mutant at the *rcr3* locus exhibit a susceptible reaction following inoculation with *Cochliobolus sativus* (Ito & Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] isolate ND85F. When rated following inoculation at the seedling stage, 10 individual plants of the *rcr3.c* mutant stock ranged from 4.0 to 4.3 with a mean 4.1 compared to rating of 3.5 to 4.5 with a mean of 3.7 for its moderately resistant parent Morex (2, 3). The six-rowed spring barley cultivar Morex has been reported to have the *Rcs5.e* (Reaction to *Cochliobolus sativus* 5) gene and at least two other QTL that in combination confer resistance to *C. sativus* (1, 4, 5).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (2).

Mutational events:

rcr3.c (γ08-124, GSHO 3704) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

rcr3.c (γ08-124, GSHO 3704) in Morex.

References:

1. Bilgic, H., B.J. Steffenson, and P.M. Hayes. 2005. Comprehensive genetic analyses reveal differential expression of spot blotch resistance in four populations of barley. Theor. Appl. Genet. 111:1238-1250.
2. Kleinhofs, A. (Unpublished).
3. Steffenson, B.J. (Unpublished).
4. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.
5. Zhou, H., and B. Steffenson. 2013. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breeding 32:139-154.

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:251.