

BGS 1, Brachytic 1, *brh1*

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

Previous nomenclature and gene symbolization:

Brachytic = *br* (10, 12).
Breviaristatum-i = *ari-i* (5, 8).
Dwarf x = *dx1* (6).

Inheritance:

Monofactorial recessive (10, 12).
Located in chromosome 7HS [1S] (3), about 9.3 cM distal from the *fch12* (chlorina seedling 12) locus (12), 0.8 cM distal from RFLP marker BCD129 (9), about 5.0 cM from AFLP marker E4134-8 in subgroup 1 of the Proctor/Nudinka map (11), and about 13.6 cM proximal from SSR marker HVM04 in bin 1H-02 (2).

Description:

Plants have short leaves, culms, spikes, awns, and kernels. The seedling leaf is about 2/3 normal length. A similar reduction in the size of other organs is observed, but the awns are less than 1/2 normal length (6). The mutant phenotype is easy to classify at all stages of growth. The approximately 20% reduction in kernels size is caused primarily by a reduction in kernel length. The yields of the *brh1* mutants are about 2/3 normal and lodging is greatly reduced in the Bowman *brh1* lines (2). Börner (1) reported that *ari-i.38* seedlings are sensitive to gibberellic acid. Powers (10) states that the assigned gene symbol for this mutant is *br* and that L.J. Stadler selected this symbol.

Origin of mutant:

A spontaneous mutant in Himalaya (Clho 1312) (10, 12).

Mutational events:

brh1.a in Himalaya (12); *brh1.c* (GSHO 229) in Moravian (PI 539135) (13); *ari-i.38* (NGB 115888, GSHO 1657) in Bonus (PI 189763) (8, 14); *brh1.e* (GSHO 1690) in Aramir (PI 467786) (14); *brh1.f* (*dx1*, GSHO 1422) in Domen (Clho 9562) (6); *brh1.t* (OUM136, GSHO 1691) in Akashinriki (PI 467400, OUM659); *brh1.x* (7125, DWS1224, GSHO 1692) in Volla (PI 280423); *brh1.z* (Hja80001) in Apo; *brh1.aa* (Hja80051) in a Hja80001 cross (4, 7); and *brh1.ae* (FN53) in Steptoe (Clho 15229) (4).

Mutant used for description and seed stocks:

brh1.a in Himalaya (GSHO 25); *brh1.a* in Bowman (PI 483237)*7 (GSHO 1820); *ari-i.38* in Bowman*6 (GSHO 1821); *brh1.e* in Bowman*7 (GSHO 1822); *brh1.t* in Bowman*7 (GSHO 1823); *brh1.x* in Bowman*7 (GSHO 1824); *brh1.z* in Bowman*7 (GSHO 2179).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *BGN* 1:104.

Revised:

T. Tsuchiya. 1980. *BGN* 10:100.

J.D. Franckowiak. 1997. *BGN* 26:44.

J.D. Franckowiak and L. S. Dahleen. 2007. *BGN* 37:188-189.

BGS 2, Chlorina seedling 12, *fch12*

Stock number: BGS 2
Locus name: Chlorina seedling 12
Locus symbol: *fch12*

Previous nomenclature and gene symbolization:

Chlorina seedling-c = *f_c* (3).
Chlorina seedling-fc = *clo-fc* (7).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 7HS [1S] (1, 4), about 3.6 cM distal from the *gsh3* (glossy sheath 3) locus (6), and about 9.3 cM proximal from the *brh1* (brachytic 1) locus (8), in bin 7H-02 about 2.3 cM from RFLP marker KFP027 and co-segregating with markers BCD130 and ABC327 (5).

Description:

Seedling leaves are yellow with green tips and new leaves show a yellow base and a green tip. As the plant develops, leaf color changes to pale green (3).
Plants are vigorous, but anthesis is delayed and seed yield may be low.

Origin of mutant:

A spontaneous mutant in Colseess (Clho 2792) (3).

Mutational events:

fch12.b (*f_c*) in Colseess (Colseess V) (3); *fch12.l* (Trebi chlorina 453, GSHO 155), *fch12.m* (Trebi V, GSHO 158), *fch12.n* (Trebi IX, GSHO 18), *fch12.o* (Trebi XI, GSHO 163) in Trebi (PI 537442) (2); *clo-fc.110* in Bonus (PI 189763) (7); *fch12.b* may be present in the brachytic chlorina stocks (GSHO 124 and GSHO 174) (9).

Mutant used for description and seed stocks:

fch12.b in Colseess (GSHO 36); *fch12.b* in Bowman (PI 483237)*7 (GSHO 1826).

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Prepared:

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T. Tsuchiya and T. E. Haus. 1971. BGN 1:105.

Revised:

T. Tsuchiya. 1980. BGN 10:101.

J.D. Franckowiak and A. Hang. 1997. BGN 26:45.

J.D. Franckowiak. 2007. BGN 37:190-191.

BGS 6, Six-rowed spike 1, *vrs1*

Stock number: BGS 6
Locus name: Six-rowed spike 1
Locus symbol: *vrs1*

Previous nomenclature and gene symbolization:

Two-row vs six-row = *Zz* (21).
Six-row vs two-row = *Aa* (6).
Two-rowed = *D* (17).
Six-row vs two-row = *Vv* (3).
Six-row vs two-row (*distichon*) vs two-row (*deficiens*) = *A*, *a^s*, *a^f* (8).
Reduced lateral spikelet appendage on the lemma = *lr* (9).
Allelic series *v*, *V^d*, *V*, and *V^t* (22).
Hexastichon mutants = *hex-v* (5, 6).
Intermedium spike-d = *Int-d* (4).
Reduced lateral spikelet appendage on the lemma = *v^r* (19).
The *vrs1* DNA sequence identified as *HvHox1* (10).

Inheritance:

A multiple allelic series, incomplete dominant allele interactions based on the size and shape of lateral spikelets (1, 19, 22).
Located in chromosome 2HL (3, 6, 12, 14), about 30.5 cM distal from the *eog1* (elongated outer glume 1) locus (18), in bin 2H-09 and in a 0.90-cM interval between markers cMWG699 and MWG865 (11).

Description:

Alleles at this complex locus modify development of the lateral spikelets and the associated lemma awn. The *vrs1.a* allele (*v* gene) is present in most six-rowed cultivars and produces well-developed lateral spikelets (6). Based on phylogenetic analysis of the six-rowed cultivars, the six-rowed gene originated independently at least three times (*vrs1.a1*, *vrs1.a2*, and *vrs1.a3*) from different wild type (*Vrs1.b*) alleles (10). The lemma awn of lateral spikelets will vary from 3/4 to nearly as long as those of central spikelets, depending upon alleles present at other loci. The *Vrs1.b* allele (*V* gene, *distichon*) is present in many two-rowed cultivars and reduces lateral spikelets to sterile bracts with a rounded tip. The *Vrs1.t* allele (*V^t* gene, *deficiens*) causes an extreme reduction in the size of lateral spikelets. The *lr* or *v^r* (*vrs1.c*) gene in Nudihaxtoni and Bozu types will not recombine with the *vrs1.a* allele (12, 19) and produces phenotypes similar to the *Vrs1.d* allele (*V^d* gene) of Svanhals (22). The series of induced mutants in two-rowed barley called *hex-v* and *Int-d* mutants differ in the size of lateral spikelets, but they interact with the *vrs1.a* allele as incomplete dominants (5). Many heterozygous combinations with *vrs1.a* have a pointed tip on the lemma of sterile lateral spikelets. Alleles at the *int-c* (intermedium spike-c) locus modify lateral size in the presence of *vrs1.a*, *Vrs1.b*, and *Vrs1.d*, but not when *Vrs1.t* is present (22). Multiple origins of *vrs1* alleles in six-rowed barley have been confirmed by molecular analysis (20). Komatsuda et al. (10) found that expression of the *Vrs1* gene was strictly localized in the lateral-spikelet primordia of immature spikes and suggested that the VRS1 protein suppresses development of lateral spikelets.

Origin of mutant:

Natural occurrence in six-rowed barley and induced frequently by mutagenic agents (10, 14).

Mutational events:

vrs1.a1 in most six-rowed cultivars (1, 10, 22); *vrs1.a2* in Dissa and Valenci (10), *vrs1.a3* in Natsudaikon Mugi (OUK735) (10), *Vrs1.b* in wild barley (10), *Vrs1.b2* in Pamella Blue (OUH630) (10), *Vrs1.b3* in Bonus (PI 189763) (10), *Vrs1.t* in a few two-rowed cultivars (10, 22); *vrs1.c* or *lr* in Nudihaxtoni (PI 32368) (12, 19); *Vrs1.d* in Svanhals (PI 5474) (22); 23 induced mutants from programs in Belgium, Germany, and Hungary (2); *hex-v.3* (NGB 115545), *-v.4* (NGB 115546), *-v.6* (NGB 115547), *-v.7* (NGB 115548), *-v.8* (NGB 115549), *-v.9* (NGB 115550), *-v.10* (NGB 115551), *-v.11* (NGB 115552), *-v.12* (NGB 115553), *-v.18* (NGB 115559), *-v.44* (NGB 115581), *-v.45* (NGB 115582), *-v.46* (NGB 115583), *-v.47* (NGB 115584), *-v.48* (NGB 115585), in Bonus, *-v.13* (NGB 115554), *-v.14* (NGB 115555), *-v.15* (NGB 115556), *-v.16* (NGB 115557), *-v.17* (NGB 115558), *-v.19* (NGB 115560), *-v.21* (NGB 115562), *-v.22* (NGB 115563), *-v.23* (NGB 115564), *-v.24* (NGB 115565), *-v.25* (NGB 115566), *-v.26* (NGB 115567), *-v.27* (NGB 115568), *-v.28* (NGB 115569), *-v.29* (NGB 115570), *-v.30* (NGB 115571), *-v.31* (NGB 115572), *-v.35* (NGB 115574) in Foma (CIho 11333), *-v.20* (NGB 115561) in Ingrid (CIho 10083), *-v.33* (NGB 115573), *-v.36* (NGB 115575), *-v.38* (NGB 115576), *-v.39* (NGB 115577), *-v.41* (NGB 115578), *-v.42* (NGB 115579), *-v.43* (NGB 115580) in Kristina (NGB 1500) (5, 14); *hex-v.49* (NGB 115586) in Bonus, *-v.50* (NGB 115587), *-v.51* (NGB 115588) in Sv 79353, *-v.52* (NGB 119353) in Golf (PI 488529) (13); *Int-d.11* (NGB 115429), *-d.12* (NGB 115430), *-d.22* (NGB 115440), *-d.24* (NGB 115442), *-d.28* (NGB 115446), *-d.36* (NGB 115454) in Foma, *-d.40* (NGB 115458), *-d.41* (NGB 115459), *-d.50* (NGB 115468), *-d.57* (NGB 115475), *-d.67* (NGB 115485), *-d.68* (NGB 115486), *-d.69* (NGB 115487) in Kristina (5, 15); *Int-d.73* (NGB 115491), *-d.80* (NGB 115498), *-d.82* (NGB 115500) in Bonus, *-d.93* (NGB 115511), *-d.94* (NGB 115512), *-d.96* (NGB 115514), *-d.97* (NGB 115515), *-d.100* (NGB 115518) in Hege (NGB 13692) (13); *vrs1.o* (*v1b*) in New Golden (16).

Mutant used for description and seed stock:

vrs1.a in Trebi (PI 537442, GSHO 196); *vrs1.a* in Bonneville (CIho 7248) (7); *vrs1.a* from Glenn (CIho 15769) in Bowman (PI 483237)*8 (GSHO 1907); *Int-d.12* in Bowman*7 (GSHO 1910).

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Prepared:

T.E. Haus. 1975. BGN 5:106.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:49-50.

U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:192-194.

BGS 7, Naked caryopsis 1, *nud1*

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

Previous nomenclature and gene symbolization:

Naked caryopsis = *k* (14).
Naked caryopsis = *s* (21).
Naked caryopsis = *n* (6, 9).
Hulless = *h* (10).

Inheritance:

Monofactorial recessive (6, 14, 19).
Located in chromosome 7HL [1L] (3, 11, 12, 14, 20), near the centromere (3, 11), about 9.6 cM proximal from the *lks2* (short awn 2) locus (15), about 10.5 cM proximal from the *dsp1* (dense spike 1) locus (15, 16), in bin 7H-07 about 13.1 cM distal from RFLP marker MWG808 (2), co-segregating with AFLP markers KT3 and KT7 and SCAR marker sKT7 (7), about 0.06 cM distal from SCAR marker sTK3 and the same distance proximal from sTK9 (17).

Description:

The lemma and palea do not adhere to the caryopsis and the grain will thresh free of the hull at maturity. The naked caryopsis trait is expressed in all environments (16). The naked lines fail to produce a cementing substance present in covered lines (4). The *nud1.a* mutant depressed the expression by 10 to 20% of other traits such as plant height, seed weight (1, 8) and altered malt quality parameters (8). The *nud1.a* gene is often associated with the *dsp1.a* (dense spike 1) gene in Japanese cultivars (16). Allele *IV* of the marker sKT7 near the *nud1* locus was the only one found in naked barley cultivars (18); however, the geographic distribution for haplotypes of allele *IV* suggest migration of naked types toward eastern Asia (18).

Origin of mutant:

In an unknown cultivar, but its origin was monophyletic probably in southwestern Iran (18), widespread in cultivated barley in Asia.

Mutational events:

nud1.a in Himalaya (CIho 1312) (21); *nud1.b* in Haisa (Mut 4129), *nud1.c* (Mut 3041/62) in Ackermann's Donaria (PI 161974) (13).

Mutant used for description and seed stocks:

nud1.a in Himalaya (GSHO 115), *nud1.a* from Sermo (CIho 7776) in Betzes (PI 129430)*7 (CIho 16559, GP 37), *nud1.a* from Sermo in Compana (CIho 5438)*7 (CIho 16185, GP 41), *nud1.a* from Sermo in Decap (CIho 3351)*7 (CIho 16563, GP 45) (5); *nud1.a* from Stamm (PI 194555) in Betzes*7 (CIho 16566, GP 48), *nud1.a* from Stamm in Compana*7 (CIho 16183, GP 50), *nud1.a* from Stamm*7 in Freja (CIho 7130)*7 (CIho 16568, GP 52) (5); *nud1.a* from R.I. Wolfe's Multiple Recessive Marker Stock in Bowman (PI 483237)*8 (GSHO 1847).

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- Prepared:
T. Tsuchiya and T.E. Haus. 1971. *BGN* 1:110.
- Revised:
J.D. Franckowiak and T. Konishi. 1997. *BGN* 26:51-52.
J.D. Franckowiak. 2007. *BGN* 37:195-196.

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* (15, 16).
Short awn = *lk* (14).
Short awn 2 = *lk₁* (7).
Short awn 2 = *lk2* (11).
Short awn 4 = *lk4* (2, 5).

Inheritance:

Monofactorial recessive (6, 7, 12).
Located in chromosome 7HL [1L] (6, 13), estimates range from 7.9 to 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (3, 12, 13), about 2.8 cM distal from molecular marker WG541 in bin 7H-05 (8), about 8.6 cM proximal from RFLP marker WG380B in bin 7H-08 (1).

Description:

Awns of both central and lateral spikelets are reduced to about 3/5 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 (13, 14). The awn length of heterozygotes in some crosses is shorter than that of the normal parent. Other plant characteristics are apparently unaltered by the *lks2.b* gene.

Origin of mutant:

Spontaneous occurrence in some cultivars distributed in China, Japan, Korea, and Nepal (5, 10, 12, 14).

Mutational events:

lks2.b in many cultivars of Oriental origin, often associated with the *dsp1.a* (dense spike 1) gene (6, 12, 14); a possible mutant in Morex (CIho 15773) (9, 10).

Mutant used for description and seed stocks:

lks2.b in Honen 6 (OUJ469, PI 307495, GSHO 566) (14); *lks2.b* from Sermo (CIho 7776) in Betzes (PI 129430)*7 (CIho 16558, GP 36), *lks2.b* from Sermo in Compana (CIho 5438)*7 (CIho 16188, GP 40), *lks2.b* from Sermo in Decap (CIho 3351)*7 (CIho 16562, GP 44) (4); *lks2.b* from R.I. Wolfe's Multiple Recessive Stock in Bowman (PI 483237)*9 (GSHO 1850).

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3. Eslick, R.F., and E.A. Hockett. 1972. Recombination values of four genes on chromosome 1. *BGN* 2:123-126.
4. Hockett, E.A. 1981. Registration of hullless and hullless short-awned spring barley germplasm (Reg. nos. GP 35 to 52). *Crop Sci.* 21:146-147.
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Prepared:

R. Takahashi. 1972. BGN 2:176.

Revised:

R. Takahashi and T. Tsuchiya. 1973. BGN 3:119.
J.D. Franckowiak and T. Konishi. 1997. BGN 26:54-55.
J.D. Franckowiak 2007. BGN 37:197-198.

BGS 22, Reaction to *Schizaphis graminum* 1, *Rsg1*

Stock number: BGS 22
Locus name: Reaction to *Schizaphis graminum* 1 (greenbug)
Locus symbol: *Rsg1*

Previous nomenclature and gene symbolization:

Greenbug resistance = *Grb* (8).

Resistance to *Schizaphis graminum* Rondani (greenbug) = *Rsg_{1,a}* (3).

Inheritance:

Monofactorial dominant (2, 3, 9).

Located in chromosome 7H [1] (4).

Description:

Resistant seedlings infested with greenbugs (aphids) are not killed, while susceptible seedlings are killed, eight weeks after infestation by the buildup of the greenbug population (2, 3, 4). The resistance provided by Post 90 (PI 549081), having the *Rsg1.a* gene, to most *S. graminum* biotypes was commonly 2 to 3 readings on a 1 to 9 scale (7). Accessions with the *Rsg1.a* gene conferred resistance to most, but not all greenbug populations (5).

Origin of mutant:

Natural occurrence in Bozu Omugi (OUJ028, PI 87181), Derbent (PI 76504), and Kearney (PI 539126, Clho 7580) (1, 3).

Mutational events:

Rsg1.a in Bozu Omugi, Derbent, Kearney, Dobaku (PI 87817), and Clho 5087 (PI 82683) (3, 7).

Mutant used for description and seed stocks:

Rsg1.a in Bozu Omugi (GSHO 1317); *Rsg1.a* in Post 90 (PI 549081) from Will () (5).

References:

1. Atkins, I.M., and R.G. Dahms. 1945. Reaction of small-grain varieties to greenbug attack. USDA Tech. Bull. 901.
2. Gardenshire, J.H. 1965. Inheritance and linkage studies on greenbug resistance in barley (*Hordeum vulgare* L.). Crop Sci. 5:28-29.
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Prepared:

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J.G. Moseman. 1976. BGN 6:119.

Revised:

J.D. Franckowiak. 1997. BGN 26:68.

J.D. Franckowiak. 2007. BGN 37:199-200.

BGS 32, Reaction to *Puccinia hordei* 9, *Rph9*

Stock number: BGS 32
Locus name: Reaction to *Puccinia hordei* 9 (barley leaf rust)
Locus symbol: *Rph9*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 9 = *Pa₉* (3, 7, 8).
Resistance to *Puccinia hordei* Otth 9 = *Pa9* (2).
Resistance to *Puccinia hordei* 12 = *Rph12* (1, 2, 9).

Inheritance:

Monofactorial dominant (1, 5, 6).
Located in chromosome 5HL [7L] (5), about 26.1 cM distal from the *raw1* (smooth awn 1) locus (5), in bin 5H-11 about 9.3 cM proximal from esterase 9 (*Est9*) and about 22.5 cM proximal from STS marker ABC155 (1), about 29.2 cM distal from the *var1* (variegated 1) locus (1).

Description:

Seedling reaction types range from 0; or necrotic fleck to 23- or reduced pustule size (4, 6), but 0; reactions are more common with the *Rph9.z* allele, formerly *Rph12.z* (1, 2, 5). The resistant reaction of the *Rph9.i* allele is temperature sensitive and is inactivated above 20°C (3). Heterozygotes show an intermediate reaction to pathogenic isolates of *Puccinia hordei* (5). The original cultivar 'Trumpf' was also marketed in the United Kingdom as 'Triumph'.

Origin of mutant:

Natural occurrence in Abyssinian (Hor 2596, Clho 1234) (3, 7); natural occurrence in *Hordeum vulgare* subsp. *spontaneum*, but transferred to the cultivar Trumpf (Triumph, PI 548762, GSHO 1590) (2, 9).

Mutational events:

Rph9.i in Abyssinian (3, 7); *Rph9.z* in Trumpf (2, 9).

Mutant used for description and seed stocks:

Rph9.i in Abyssinian (GSHO 1601); *Rph9.i* in Bowman (PI 483237)*8 (GSHO 1866); *Rph12.z* in Trumpf (GSHO 1590); *Rph12.z* in Bowman (PI 483237)*9 (GSHO 2145).

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Prepared:

J.D. Franckowiak and Y. Jin. 1997. BGN 26:81.

J.D. Franckowiak and Y. Jin. 1997. BGN 26:281 as BGS 333, Reaction to *Puccinia hordei* 12, *Rph12*.

Revised:

J.D. Franckowiak. 2007. BGN 37:201-202.

BGS 41, Brachytic 7, *brh7*

Stock number: BGS 41
Locus name: Brachytic 7
Locus symbol: *brh7*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS [7S] (1), approximately 4.6 cM proximal from SSR marker Bmac0113 in bin 5H-04 (1).

Description:

Plants are about 5/6 of normal height and awns are about 3/4 of normal length. The rachis internodes are slightly shorter than normal for Bowman. The seedling leaf of *brh7* plants is short and wide and leaf blades are wider than those of normal sibs. The Bowman line with *brh7* showed less lodging than Bowman. Although the kernels of *brh7* plants seem plumper and more globose shaped than those from normal sibs, the primary difference is a 10 to 15% reduction in kernel length. Kernel weights and grain yields of the *brh7* line are slightly lower than those of normal Bowman (1, 2).

Origin of mutant:

An induced mutant in Volla (PI 280423) (4).

Mutational events:

brh7.w in Volla (7101, DWS1211) (4, 5).

Mutant used for description and seed stocks:

brh7.w in Volla (GSHO 1687); *brh7.w* in Bowman (PI 483237)*7 (GSHO 1943).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
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5. Gaul, H. 1986. (Personal communications).

Prepared:

J.D. Franckowiak. 2002. BGN 32:81.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:203.

BGS 44, Brachytic 16, *brh16*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 7HL [1L] (1), approximately 7.4 cM proximal from SSR marker Bmag0135 in bin 7H-13 (1).

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 fasciated appearance because spikelets are very close together. The seed yield of the Bowman line with *brh16* was less than 1/3 of Bowman's yield. Since kernels per spikes and kernel size were not reduced, much of the yield loss was probably associated with reduced tillering (1). The original introduction (HE 2816) contained two dwarf mutants, but only *brh16.v* gene was isolated in the Bowman backcross-derived line.

Origin of mutant:

Probably an ethyl methanesulphonate induced mutant in Korál (PI 467778) (4).

Mutational events:

brh16.v in HE 2816 (DWS1176) from a cross between two semidwarf mutants (3, 4).

Mutant used for description and seed stocks:

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

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.
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3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
4. Váša, M. 1986. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:204.

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); about 25.1 cM distal from the *mtt4* (mottled leaf 4) locus (2); and near AFLP marker E3633-1 in subgroup 21 of the Proctor/Nudinka map (7).

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. Bowman backcross-derived lines with *lig1* gene are similar in agronomic traits and maturity to Bowman (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar, Muyoji (liguleless) (8).

Mutational events:

lig1.my as Muyoji (OUL007) (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 (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 (CIho 11333) (5); *aur-a.11* (NGB 114369), *aur-a.12* (NGB 114370, NGB 114371) in Kristina, *aur-a.13* (NGB 114372), *aur-a.14* (NGB 114373) in Bonus, *aur-a.15* (NGB 119377) in Golf (PI 488529) (6); *lig1.2* in Bonus, found in *eli-2* (*eligulum-2*) (NGB 115389) stock as the second mutant (2).

Mutant used for description and seed stocks:

lig1.my as Muyoji (GSHO 6); *lig1.my* in Bowman (PI 483237)*8 (GSHO 1930); *lig1.2* in Bowman*5 (2).

References:

1. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
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3. Hayashi, J., T. Konishi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VI. Ten mutant genes located on chromosomes 1 to 7, except 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:227-250.
4. Konishi, T. 1975. Reverse mutation at the ligule-less locus (*li*) of barley. *BGN* 5:21-23.
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 10. Woodward, R.W. 1957. Linkages in barley. *Agron. J.* 49:28-32.
- Prepared:
T. Tsuchiya and T.E. Haus. 1971. BGN 1:120.
- Revised:
J.D. Franckowiak, U. Lundqvist, T. Konishi. 1997. BGN26:96.
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:205-206.

BGS 79, White streak 7, *wst7*

Stock number: BGS 79
Locus name: White streak 7
Locus symbol: *wst7*

Previous nomenclature and gene symbolization:

Ribbon grass = *rb* (6).
White streak-k = *wst,,k* (10).
White streak-B = *wst,,B* (8).

Inheritance:

Monofactorial recessive (2, 11).
Located in chromosome 2HL (5, 7, 8,9), about 22.0 cM distal from the *gpa1* (grandpa 1) locus (2, 9), over 29.4 cM distal from the *lig1* (liguleless 1) locus (8), in bin 2H-15 about 6.1 cM from RFLP marker MWG949A (1).

Description:

Vertical white streaks of variable width and number develop in the leaf blades of young secondary tillers. Fewer white streaks and fewer tillers with white streaks occur as environmental conditions become warm. White streaks can be found until near maturity, but they are difficult to observe after heading under field conditions. Often the lower or first leaves on early tillers have more and wider streaks. The mutant has no apparent affect on agronomic traits in the Bowman backcross-derived line (4).

Origin of mutant:

A spontaneous mutant isolated by Robertson (6, 11).

Mutational events:

wst7.k in an unknown cultivar (2, 11).

Mutant used for description and seed stocks:

wst7.k in an unknown cultivar (GSHO 247); *wst7.k* from R.I. Wolfe's Multiple Recessive Marker Stock in Bowman (PI 483237)*7 (GSHO 1935).

References:

1. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopsisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. *Theor. Appl. Genet.* 103:415-424.
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4. Franckowiak, J.D. (Unpublished).
5. Kasha, K.J. 1982. Coordinator's report: Chromosome 6. *Barley Genet. Newsl.* 12:90-92.
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7. Schondelmaier, J., G. Fischbeck, and A. Jahoor. 1993. Linkage studies between morphological and RFLP markers in the barley genome. *Barley Genet. Newsl.* 22:57-62.
8. Shin, J.S., S. Chao, L. Corpuz, and T.K. Blake. 1990. A partial map of the barley genome incorporating restriction fragment length polymorphism,

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polymerase chain reaction, isozyme, and morphological marker loci. *Genome* 23:803-810.

9. Walker, G.W.R. 1974. Linkage data for *rb* and *mt3*. *Barley Genet. Newsl.* 4:90-91.

10. Wolfe, R.I., and J.D. Franckowiak. 1991. Multiple dominant and recessive genetic marker stocks in spring barley. *Barley Genet. Newsl.* 20:117-121.

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

Prepared:

J.D. Franckowiak and R.I. Wolfe. 1997. *BGN* 26:117.

Revised:

J.D. Franckowiak. 2007. *BGN* 37:207-208.

BGS 82, Zeocriton 1, *Zeo1*

Stock number: BGS 82
Locus name: Zeocriton 1
Locus symbol: *Zeo1*

Previous nomenclature and gene symbolization:

"Kurz und dicht" = *Knd* (6).

Inheritance:

Monofactorial incomplete dominant (5).

Located in chromosome 2HL, about 9.2 cM distal from the *lig1* (liguleless 1) locus (4), in bin 2H-13 about 7.3 cM distal from RFLP marker *cnx1* (1).

Description:

Plants heterozygous for *Zeo1* have short culms, compact spikes, and wide kernels. Homozygotes have shorter culms (short peduncle), very compact spikes, large outer glumes with long awns, and reduced fertility. Generally, the spike emerges from the side of the sheath in homozygotes. Although the name *zeocriton* is used for this gene, this gene is not from Spratt, the dense ear type described by Engledow (2).

Origin of mutant:

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

Mutational events:

Zeo1.a in Donaria (Mut 2657) (5); *Zeo1.b*, received as "Kurz und dicht" and placed in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614), was probably derived from Mut 2657 (3, 6).

Mutant used for description and seed stocks:

Zeo1.a in Donaria (GSHO 1613); *Zeo1.a* in Bowman (PI 483237)*5 (GSHO 1931); *Zeo1.b* in Bowman*9 (GSHO 1932).

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Prepared:

J.D. Franckowiak and R.I. Wolfe. 1997. BGN 26:120.
J.D. Franckowiak. 2007. BGN 37:209.

BGS 85, Yellow streak 4, *yst4*

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

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (2).
Located in chromosome 2HL, near the *vrs1* (six-rowed spike 1) locus (2), in bin 2H-07 near RFLP marker CDO537 (3).

Description:
Plants have a yellow-green color with numerous, vertical yellow streaks in the leaves. The yellow-green color is retained until maturity, but the yellow streaks may be difficult to observe after heading. Plant vigor and height are reduced, heading is delayed, and seed yields are low.

Origin of mutant:
A sodium azide induced mutant in Glenn (Clho 15769) (1).

Mutational events:
yst4.d in Glenn (DWS1059) (2).

Mutant used for description and seed stocks:
yst4.d in Glenn (GSHO 2502); *yst4.d* in Bowman (PI 483237)*7 (GSHO 1922).

References:
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3. Kleinhofs, A. 2002. Integrating molecular and morphological/physiological marker maps. Coordinator's Report. *Barley Genet. Newsl.* 32:152-159.

Prepared:
J.D. Franckowiak. 1997. BGN 26:123.

Revised:
J.D. Franckowiak. 2007. BGN 37:210.

BGS 87, Chlorina seedling 14, *fch14*

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

Previous nomenclature and gene symbolization:

Chlorina seedling 14 = *f14* (2).

Inheritance:

Monofactorial recessive (2, 4).

Located in chromosome 2HL (2), probably between the *vrs1* (six-rowed spike 1) and the *ant2* (anthocyanin-less 2) loci (2), likely in bin 2H-11 (3, 4).

Description:

Seedlings have a pale yellow-green color. The leaves gradually become greener starting at the tip of the leaf blade, and mutant plants are indistinguishable in color from normal sibs at heading (2). When grown in the field, plants produce slightly thinner kernels with about a 10% reduction in kernel weight (1).

Origin of mutant:

A spontaneous mutant in Shyri (Lignee 640//Kober/Teran 78) from Ecuador (2).

Mutational events:

fch14.w in Shyri (2, 5).

Mutant used for description and seed stocks:

fch14.w in Shyri (GSHO 1739); *fch14.w* in Bowman (PI 483237)*6 (GSHO 1911).

References:

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2. 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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Prepared:

J.D. Franckowiak. 1997. BGN 26:125.

Revised:

J.D. Franckowiak. 2007. BGN 37:211.

BGS 88, Reaction to *Puccinia hordei* 2, *Rph2*

Stock number: BGS 88
Locus name: Reaction to *Puccinia hordei* 2 (barley leaf rust)
Locus symbol: *Rph2*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia anomala* Rostr = *Pa* (2).
Resistance to *Puccinia hordei* Otth 2 = *Pa*₂ (9, 15).
Resistance to *Puccinia hordei* A = A (8, 9).

Inheritance:

Monofactorial incomplete dominant (2, 14).
Located in chromosome 5HS [7S] (1), not in the long arm (10), distal from the secondary constriction (1), in bin 5H-04 about 3.5 cM proximal from RFLP marker CDO749 (1).

Description:

The seedling reaction type is 0ⁿ - 1^c with race 4 culture 57-19 (2); heterozygotes have reaction types ranging from 1 to 3, depending on parents. Responses will vary for homozygotes and heterozygotes when different rust cultures are tested (8).

Origin of mutant:

Natural occurrence in Peruvian (Clho 935) and several other cultivars (2, 4, 6, 12, 15, 16).

Mutational events:

Rph2.b in Peruvian (4, 12); *Rph2.j* in Batna (Clho 3391) (7, 12); *Rph2.k* in Weider (No 22, PI 39398) (2, 11, 15); *Rph2.l* in Juliaca (PI 39151) (3, 12); *Rph2.m* in Kwan (PI 39367, GSHO 1392) (2, 4, 12); *Rph2.n* in Chilean D (PI 48136) (4, 14); an allele at the *Rph2* locus is present in Purple Nepal (Clho 1373), Modia (Clho 2483), Morocco (Clho 4975), Barley 305 (Clho 6015), Marco (PI 94877) (2); Austral (Clho 6358) (4, 6, 7, 12); Marocaine 079 (Clho 8334) (6); Q21861 (PI 584766), TR306 (1, 13); accessions with a second *Rph* gene besides the *Rph2* allele include Carre 180 (Clho 3390), Clho 14077 (12); Ricardo (PI 45492) (2, 14, 16); Ariana (Clho 14081) (11, 12, 16); Quinn (PI 39401) (8, 9); Bolivia (PI 36360) (2, 8, 9); Reka 1 (Clho 5051) (4, 6, 7, 12); tentative *Rph2* allele symbols are *Rph2.q* in Quinn, *Rph2.r* in Bolivia (GSHO 1598), *Rph2.s* in Ricardo, *Rph2.t* in Reka 1 (GSHO 1594), and *Rph2.u* in Ariana based on differential reactions and different cultivar origins (5, 8, 9, 12); *Rph2.y* from HJ198*3/HS2310 (PI 531841, GSHO 1595) (3).

Mutant used for description and seed stocks:

Rph2.b in Peruvian (GSHO 1593); *Rph2.b* in Bowman (PI 483237)*3 (GSHO 2320); *Rph2.t* from Rika 1 in Bowman*8 (GSHO 2321).

References

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Prepared:

Y. Jin and J.D. Franckowiak. 1997. BGN 26:126-127.

Revised:

J.D. Franckowiak. 2007. BGN 37:212-213.

BGS 96, Reaction to *Puccinia hordei* 15, *Rph15*

Stock number: BGS 96
Locus name: Reaction to *Puccinia hordei* 15 (barley leaf rust)
Locus symbol: *Rph15*

Previous nomenclature and gene symbolization:

Rph16 = Reaction to *Puccinia hordei* 16 (6, 9).

Inheritance:

Monofactorial dominant (1, 2).

Located in chromosome 2HS (1, 6); over 32.3 cM proximal from the *vrs1* (six-rowed spike 1) locus (1); in bin 2H-6 near molecular markers MWG874 (6) and MWG2133 (9); cosegregation with AFLP marker P13M40 (9); about 25.2cM distal from the centromere (9); about 14 cM proximal from the *Eam1* (Early maturity 1) locus (3).

Description:

The seedling reaction to most isolates of *Puccinia hordei* is a relatively large necrotic fleck, hypersensitive reaction (1). The seedling infection type of heterozygotes is indistinguishable from that of homozygous resistant seedlings. Alleles at this locus were found in six of the first seven *Rph* genes from *Hordeum vulgare* subsp *spontaneum* evaluated in Bowman backcross-derived lines (1, 2). The *Rph15* locus is likely allelic to *Rph16* based on the failure to recover susceptible recombinants (9). Only one of the 350 leaf rust isolates (90-3 from Israel) was found to be virulent on *Rph15* lines (4, 9). Resistance to isolate 90-3 was observed in progeny from a cross between a line with *Rph15* to another source of leaf rust resistance (8). *Rph15* represents one of the most effective leaf rust resistance genes reported in *Hordeum vulgare* (9).

Origin of mutant:

Natural occurrence in accession PI 355447 of *Hordeum vulgare* subsp *spontaneum*, but isolated in a selection that contained one *Rph* gene from the original accession crossed to Bowman (PI 483237) (1, 7).

Mutational events:

Rph15.ad in PI 355447 (1, 2, 5), PI 354937, PI 391024, PI 391069, PI 391089, and PI 466245 (1, 2); *Rph15.ae* from HS084 (6, 9); PI 466245 has at least two genes for leaf rust resistance (7).

Mutant used for description and seed stocks:

Rph15.ad in selection from a cross to Bowman (GSHO 1586); *Rph15.ad* in Bowman*8 (GSHO 2330).

References:

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amplified fragment length polymorphism marker into a co-dominant marker in the
mapping of the *Rph15* gene conferring resistance to barley leaf rust, *Puccinia*
hordei Otth. Theor. Appl. Genet. 108:712-719.

Prepared:

J.D. Franckowiak and O. Chicaiza. 1998. BGN 28:29.

Revised:

J.D. Franckowiak. 2005. BGN 35:186.

J.D. Franckowiak. 2007. BGN 37:214-215.

BGS 98, Early maturity 6, *Eam6*

Stock number: BGS 98
Locus name: Early maturity 6
Locus symbol: *Eam6*

Previous nomenclature and gene symbolization:

Early heading = *Ea* (9).
Early maturity 6 = *Ea6* (7).

Inheritance:

Monofactorial dominant (9).
Located in chromosome 2HS, about 13.5 cM proximal from the *vrs1* (six-rowed spike 1) locus (9), near the *gsh5* (glossy sheath 5) locus based on linkage drag (1, 2), near molecular marker ABC167b in bin 2H-08 (5, 8).

Description:

Alleles at the *Eam6* locus alter the timing of floral initiation when barley is grown under long-day conditions. In temperate climates, the *Eam6.h* gene induces spring barley to head two to five days earlier than plants with the recessive allele (1, 5). A much stronger response to long photoperiods is associated with the *Eam1* gene. Tohno-oka et al. (8) reported that *Eam6* gene from Morex (CIho 15773) is effective when the photoperiod is 13 hours or longer and that the *Eam1* gene from Steptoe (CIho 15229) induces early heading when the photoperiod is 14 hours or longer. In North Dakota, plants with both the *Eam1* and *Eam6* genes head one to two days earlier than those with only the *Eam1* gene (1). The factors, *Eam1* and *Eam6*, for early heading were studied possibly by Yasuda (10) and named "A" and "B", respectively. A QTL for long-day photoperiod response in North American two-rowed and six-rowed barleys in the *Eam6* region of 2H was reported by Moralejo et al. (6) and Horsley et al. (3), respectively. *Eam6* may interact with other maturity genes because a QTL for early heading was detected in 2HS under both short- and long-day environments in the Harrington/Morex mapping population (4).

Origin of mutant:

Natural occurrence in many spring, six-rowed barley, represented by the cultivar Morex (CIho 15773) (8).

Mutational events:

Eam6.h in an unknown cultivar (8), possibly Trebi (CIho 936) (1); *Eam6.h* in Morex (4, 5, 8).

Mutant used for description and seed stocks:

Eam6.h in Morex (CIho 15773, GSHO 2492); *Eam6.h* from Nordic (CIho 15216) in Bowman (PI 483237) (1).

References:

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Prepared:

J.D. Franckowiak and T. Konishi. 2002. *BGN* 32:86-87.

Revised:

J.D. Franckowiak. 2007. *BGN* 37:216-217.

Barley Genetics Newsletter (2007) 37: 188-301

BGS 100, Slender dwarf 4, *sld4*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (5, 6).

Located in chromosome 7HS [5S] (4), near AFLP marker E 4134-2 in subgroup 6 of the Proctor/Nudinka map (4).

Description:

Plants with the *sld4.d* gene have reduced vigor and are light green in color during early stages of growth (6). The *sld4.d* mutant is apparently very environmentally sensitive in the Bowman derived line. Plants can vary from less than 1/2 to 3/4 of normal height and heading can be delayed over 10 days in certain environments. The number of fertile spikelets per spike varies from 2/3 normal to near normal. Depending on the delay in heading, kernels vary from very thin to near normal. Grain yield of the Bowman backcross-derived line can vary from very low to nearly normal (1).

Origin of mutant:

A neutron induced mutant in Two-row Glacier (5). (Glacier is available as Clho 6976.)

Mutational events:

sld4.d in Two-row Glacier (80-T-5899-2-13, DWS1368) (2, 3, 5).

Mutant used for description and seed stocks:

sld4.d in Two-row Glacier (GSHO 2479); *sld4.d* in Bowman (PI 483237)*7 (GSHO 1880).

References:

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Prepared:

J.D. Franckowiak. 2002. BGN 32:89.

Revised:

J.D. Franckowiak. 2007. BGN 37:218.

BGS 101, Absent lower laterals 1, *als1*

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

Previous nomenclature and gene symbolization:

Absent lower laterals = *als* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HL (2, 3, 5, 6), about 31.2 cM distal from the *uzu1* (*uzu* 1) locus (2), about 39.7 cM proximal from the *cur2* (*curly* 2) locus (3), and near AFLP marker E4234-11 in subgroup 28 of the Proctor/Nudinka map (4).

Description:

Lateral spikelets at the base of the spike fail to develop or are partially developed. Tillers are large, coarse, and stiff, and only 1 or 2 tillers are produced in the six-rowed stock. The plants resemble those of the (*cul2*) unicum 2 mutant (2). Plants of the Bowman backcross-derived line commonly produce 3 to 5 tillers with short spikes; and seed yields are very low (1).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (Clho 7149) (2).

Mutational events:

als1.a in Montcalm (Alb Acc 281) (2).

Mutant used for description and seed stocks:

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

References:

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *BGN* 1:123.

Revised:

J.D. Franckowiak. 1997. *BGN* 26:135.

J.D. Franckowiak. 2007. *BGN* 37:219.

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* (12).
Uzu = *u* (4).
Uzu (semi-brachytic) = *uz* (11).
Uzu 2 = *uz2* (3, 13, 15).
Uzu 3 = *uz3* (3, 13, 15).
Hordeum vulgare BR-insensitive 1 = *HvBRI1* (1).

Inheritance:

Monofactorial recessive (4, 7, 9, 11).
Located in chromosome 3HL (5, 6, 11), about 17.6 cM proximal from the *alm1* (albino lemma 1) locus (10), in bin 3H-06 near cDNA marker, C1271 (1).

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (8, 9, 11). 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 (9, 13, 14). The temperature sensitive reduction in culm length of *uzu1.a* plants ranges from less than 15% in cool environments to over 75% in warm ones. Chono et al. (1) reported that the *uzu1.a* or *HvBRI1* gene is caused by a mutation that changed a highly conserved residue of the kinase domain of *BRI1* (*Arabidopsis* BR-insensitive 1) (brassinosteroids) receptor protein from His-857 to Arg-857.

Origin of mutant:

Natural occurrence in many cultivars of Japanese origin (8, 9).

Mutational events:

uzu1.a in many Japanese cultivars (9, 13, 15); *uzu1.b* (092AR) in Aramir (PI 467781) (2).

Mutant used for description and seed stocks:

uzu1.a in Baitori 11 (OUJ371, PI 182624, GSHO 1300); *uzu1.a* in Bowman (PI 483237)*7 (GSHO 1963).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. BGN 1:124.

Revised:

T. Tsuchiya. 1984. BGN 14:92.

J.D. Franckowiak and T. Konishi. 1997. BGN 26:136-137.

J.D. Franckowiak. 2007. BGN 37:220-221.

BGS 108, Albino lemma 1, *alm1*

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

Previous nomenclature and gene symbolization:

Albino lemma = *al* (9).
Eburatum = *ebu-a* (3).

Inheritance:

Monofactorial recessive (9).
Located in chromosome 3HS (9), about 16.5 cM distal from the *uzu1* (*uzu 1*) locus (2, 5, 6, 7, 8, 9), in bin 3H-04 about 4.8 cM proximal from RFLP marker MWG844B (1).

Description:

The lemma and palea are white in color and mostly devoid of chlorophyll, but they terminate into green tips with green awns. The basal part of lower leaf sheaths and stem nodes are devoid of chlorophyll. Ligules and joints between the leaf sheath and blade are white in color (9, 10). Plant vigor is reduced slightly and maturity is delayed in the Bowman backcross-derived line.

Origin of mutant:

Spontaneous occurrence in an unknown cultivar (Russia 82) (OUU086, NSL 43389) (9).

Mutational events:

alm1.a in Russia 82 (9); *alm1.b* in Liberty (Clho 9549) (2); *alm1.c* (Mut 966/61) in Proctor (PI 280420) (4); *ebu-a.1* (NGB 115236), *-a.2* (NGB 115237), *-a.3* (NGB 115238) in Foma (Clho 11333) (3, 10); *ebu-a.4* (NGB 115239), *-a.5* (NGB 115240) in Foma (6).

Mutant used for description and seed stocks:

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

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. BGN 1:130.

Revised:

T. Tsuchiya. 1980. BGN 10:111.

J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:143.

J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:222-223.

BGS 122, Reaction to *Puccinia hordei* 5, *Rph5*

Stock number: BGS 122
Locus name: Reaction to *Puccinia hordei* 5 (barley leaf rust)
Locus symbol: *Rph5*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 5 = *Pa*₅ (6, 7).
Resistance to *Puccinia hordei* B = *B* (5).
Resistance to *Puccinia hordei* Otth = *X* (5, 6).
Resistance to *Puccinia hordei* Otth = *Pa*_x (6).
Resistance to *Puccinia hordei* 6 = *Rph6.f* (11).

Inheritance:

Monofactorial incomplete dominant (3, 5, 6).
Located in chromosome 3HS (4, 11); about 7.0 cM distal from *Rph7* (11), about 0.5 cM proximal from RFLP marker CDO549 (11), about 2.5 cM distal from RFLP marker MWG2021 (4).

Description:

Rph5.e in Magnif 102 showed a seedling infection type of 0 - 0;^c with race 4 culture 57-19, and *Rph6.f* from Bolivia had a 0;ⁿ - 1^c seedling infection type with race 4 culture 57-19. (3). Heterozygotes frequently show an intermediate response (type 2 or 3 reaction) to inoculation with pathogenic races, and incomplete dominance is observed in segregating progenies (3, 5, 6). Zhong et al. (11) demonstrated that *Rph5.e* is allelic to the *Rph6.f* gene extracted from Bolivia (PI 36360). *Rph6.f* was identified as a monofactorial dominant, but an allele at the *Rph2* (reaction to *Puccinia hordei* 2) locus is present in the original cultivar Bolivia (PI 36360) (5, 6, 8).

Origin of mutant:

Natural occurrence in Quinn (PI 39401) (6, 10); natural occurrence in Bolivia (PI 36360) (2, 5).

Mutational events:

Rph5.e in Magnif 102 (PI 337140) (10), *Rph5.f* (formerly *Rph6.f*) in Bolivia (11), *Rph5.ai* in Quinn along with *Rph2.q* (5, 6).

Mutant used for description and seed stocks:

Rph5.e in Malteria Heda*4/Quinn (Magnif 102, GSHO 1597) (10); *Rph5.e* in Bowman (PI 483237)*8 (GSHO 1865); *Rph5.f* in Bowman*8 (GSHO 2323); *Rph6.f* in Bolivia (GSHO 1598); *Rph6.f* (without an *Rph2* allele) in Bowman (PI 483237)*4 (GSHO 2323) (1).

References:

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Prepared:

C.W. Roane. 1976. BGN 6:122.

J.D. Franckowiak and Y. Jin. 1997. BGN 26:501, as BGS 575, Reaction to *Puccinia hordei* 6, *Rph6*.

Revised:

J.D. Franckowiak and Y. Jin. 1997. BGN 26:157.

J.D. Franckowiak and B.J. Steffenson. 2005. BGN 35:188.

J.D. Franckowiak. 2007. BGN 37:224-225.

BGS 130, Early maturity 10, *eam10*

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

Previous nomenclature and gene symbolization:

Early maturity sp = *ea_{sp}* (8).

Inheritance:

Monofactorial recessive (8).

Located in chromosome 3HL (8); about 2.0 ± 5.8 cM from the *Est1-Est4* (esterase 1, esterase 4) locus (8); about 5.8 cM distal from RFLP marker Xmwg546 (1).

Description:

In winter nurseries at Ciudad Obregón, Sonora, Mexico and Davis, California, USA, plants of Super Precoz 2H head about 11 days earlier than lines with the genes *eam7.g* or *eam8.k* for photoperiod insensitivity from Atsel and Sv Mari, respectively (8). The *eam10.m* gene appears to suppress expression of the *eam7.g* and *eam8.k* genes (8). Plants expressing *eam10.m* become chlorotic (yellow green) under photothermal stress. Zeaxanthin increases at the expense of chlorophyll and other pigments (7). The chlorotic appearance is similar to that observed in plants homozygous for other recessive genes for early maturity (*eam7*, *eam8*, and *eam9*) (2, 5, 7). Plants in the Bowman *eam10.m* line head two days earlier than Bowman under long days and are slightly shorter (5).

Origin of mutant:

Present in Super Precoz 2H (PI 527381) from Russia (7), but originating probably as an induced mutant in MC20 (3, 4, 7).

Mutational events:

eam10.m in Super Precoz 2H plus a dominant maturity enhancer (4, 5, 7);

eam10.m in Amber Nude without the enhancer (4).

Mutant used for description and seed stocks:

eam10.m in Super Precoz 2H (GSHO 2504); *eam10.m* in Amber Nude (GSHO 2505); *eam10.m* from Super Precoz in Bowman (PI 483237)*5.

References:

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31:256-261.

Prepared:

L.W. Gallagher and J.D. Franckowiak. 1997. BGN 26:166.

Revised:

J.D. Franckowiak. 2007. BGN 37:226-227.

BGS 136, Reaction to *Puccinia hordei* 7, *Rph7*

Stock number: BGS 136
Locus name: Reaction to *Puccinia hordei* 7 (barley leaf rust)
Locus symbol: *Rph7*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth y = *Pay* (7).
Resistance to *Puccinia hordei* Otth 5 = *Pa₅* (10).
Resistance to *Puccinia hordei* Otth 7 = *Pa7* (8).

Inheritance:

Monofactorial dominant (7, 10).
Located in chromosome 3HS (14, 15), linkage to markers in the centromeric region was reported (11), about 24.0 cM from the *ant17* (proanthocyanidin-free 17) locus (5), in bin 3H-01 about 1.3 cM distal from RFLP marker cMWG691 (6), about 3.2 cM from receptor-like kinase gene *Hv3Lrk* (2), about 7.0 cM proximal from *Rph5* locus (16).

Description:

The seedling reaction type is 0;ⁿ - 1^c (4, 11). Temperature studies show that resistance conferred by the *Rph7.g* gene is not expressed well above 20°C (4, 15). Cebada Capa is indistinguishable from the cultivar Forrajera Klein (possibly identical to PI 331904) (1). The *Rph7* regions from Morex (*rph7*) and Cebada Capa (*Rph7*) were sequenced and compared to similar regions from 39 other cultivars. The data suggest that a large amount of haplotype variability exists in the cultivated barley gene pool and indicate rapid and recent divergence at this locus (12).

Origin of mutant:

Natural occurrence in Cebada Capa (PI 53911) (7, 8, 10).

Mutational events:

Rph7.g in Cebada Capa (7, 8, 10); *Rph7.g* in France 7 and France 21 (7);
Rph7.g in Dabat, Gondar (PI 199964), and La Estanzuela (9, 13, 16); *Rph7.ac* in Tu17a, a Bowman backcross-derived line from Tunisia 17 (3).

Mutant used for description and seed stocks:

Rph7.g in Cebada Capa (GSHO 1318); *Rph7.g* in Bowman (PI 483237)*8 (GSHO 1994).

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- Prepared:
J.D. Franckowiak and Y. Jin. 1997. BGN 26:173.
- Revised:
J.D. Franckowiak. 2007. BGN 37:228-229.

BGS 142, Brachytic 8, *brh8*

Stock number: BGS 142
Locus name: Brachytic 8
Locus symbol: *brh8*

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5, 6).

Located in chromosome 3HS (4), near the *btr1* (non-brittle rachis 1) locus based on linkage drag (4), about 26.3 cM proximal from SSR marker HVM60 in bin 3H-08 (1).

Description:

In the Bowman backcross-derived line, *brh8* plants are 3/4 to 5/6 of normal height and awns are 2/3 to 3/4 of normal length. The peduncle is 3/4 normal length. The seedling leaf of *brh8* plants is shorter and wider than those of normal sibs and the leaf blades are slightly wider. Kernels of *brh8* plants are shorter than that of normal sibs and their weights are nearly 15% lower. Heading dates are 2 or 3 days later, spikes have 3 to 4 more kernels, and rachis internodes are about 20% shorter. Grain yield is nearly normal (1, 2).

Origin of mutant:

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

Mutational events:

brh8.ad in Birgitta (17:16:1, DWS1008) (5, 6).

Mutant used for description and seed stocks:

brh8.ad in Birgitta (GSHO 1671); *brh8.ad* in Bowman (PI 483237)*8 (GSHO 1944).

References:

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Prepared:

J.D. Franckowiak. 2002. BGN 32:92.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:230.

BGS 148, Brachytic 14, *brh14*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 3HL (2), approximately 24.9 cM proximal from SSR marker Bmac0029 in bin 3H-15 (2).

Description:

Plants are about 2/3 normal height and awns, peduncles are about 2/3 normal length, and rachis internodes are about 7/8 normal length (2, 6, 7). Seedling leaves of *brh14.q* plants are relatively short, but they do respond to gibberellic acid treatment (1). Leaf blades are about 3/4 normal length. The kernels of *brh14* plants are slightly shorter and smaller than those of normal sibs, but there are slightly more kernels per spike. However, the grain yields of the *brh14* line to average 1/3 to 1/4 of those for Bowman reduced because tillering was reduced. Plants show an erect growth habit (2, 3). Failure of the internode below the peduncle to elongate was observed in double dwarfs involving *brh14.q* in the Akashinriki genetic background (7).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (6, 7).

Mutational events:

brh14.q in Akashinriki (OUM131, dw-d, DWS1035, GSHO 1682) (4, 5, 6, 7).

Mutant used for description and seed stocks:

brh14.q in Akashinriki (GSHO 1682); *brh14.q* in Bowman (PI 483237)*6 (GSHO 2175).

References:

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Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:231.

BGS 149, Reaction to *Puccinia coronata* var. *hordei* 1, *Rpc1*

Stock number: BGS 149
Locus name: Reaction to *Puccinia coronata* var. *hordei* 1
Locus symbol: *Rpc1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (3).

Located in chromosome 3H centromeric region (1), approximately 2.5 cM from RAPD marker OPO08-700 (1).

Description:

Crown rust of barley was identified as a new disease of barley in North America (2). In seedling tests, resistant cultivars exhibited necrotic or chlorotic flecks (0; to ; infection types) at infection sites and no sporulation (3). Adult plant reactions of Hor2596 were resistant to moderately resistant (3). Hor 2596 is one of the differential lines for barley leaf rust (caused by *Puccinia hordei*), see BGS 032, *Rph9.i* (reaction to *Puccinia hordei* 9). The F1 plants from the Bowman/Hor2596 cross exhibited slightly higher infection types (1,2 reaction) than the resistant parent (3).

Origin of mutant:

Natural occurrence in Abyssinian (Hor 2596, Clho 1234) (3).

Mutational events:

Rpc1.a in Hor 2596 (3).

Mutant used for description and seed stocks:

Rpc1.a in Hor 2596 (GSHO 1601) (3).

References:

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Prepared:

Y. Jin and J.D. Franckowiak. 2007. BGS 37:232.

BGS 155, Glossy leaf 1, *glf1*

Stock number: BGS 155
Locus name: Glossy leaf 1
Locus symbol: *glf1*

Previous nomenclature and gene symbolization:

Waxless bloom on leaves = *w1* (11).

Glossy = *gl* (9).

Glossy leaves = *gl* (16).

Glossy leaf = *gl* (15).

Glossy seedling 2 = *gl2* (3, 9).

Eceriferum-zh = *cer-zh* (4).

Inheritance:

Monofactorial recessive (9).

Located in chromosome 4HL (3, 9, 12, 14), about 7.5 cM distal from the *lbi2* (long basal rachis internode 2) locus (1), and about 4.8 cM distal from the *Mlg* (*Reg2*, reaction to *Erysiphe graminis* 2) locus (1).

Description:

Surface wax coating on the leaf blade appears absent from the seedling stage to near maturity, and leaves have a shiny appearance (wax code ++ ++ -) (4).

Plants are semidwarf, relatively weak, and late in heading. The stock in the Bonus is highly sterile (4), but the Bowman backcross-derived line has nearly complete fertility. The lack of surface waxes reduces the ability of growing germ tube of certain fungi to find the stomata openings (10).

Origin of mutant:

A radiation induced mutant in Himalaya (Clho 1312) (9, 13), an X-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

glf1.a, *glf1.b* (*gl2*, GSHO 22) in Himalaya (13); *glf1.f* in 34-119-1, *glf1.g* in II-34-199-7-2 (GSHO 89) (2); *cer-zh.54* (NGB 110938) in Bonus (4, 5); *cer-zh.266* (NGB 111153), *-zh.308* (NGB 111195), *-zh.357* (NGB 111244, NGB 117254), *-zh.366* (NGB 111253), *-zh.432* (NGB 111320), *-zh.433* (NGB 111321, NGB 117256) in Foma (Clho 11333) (5, 8); *cer-zh.325* (NGB 111212) in Foma (5); *cer-zh.373* (NGB 111260) in Foma (6); *cer-zh.865* (NGB 111753) in Bonus (7).

Mutant used for description and seed stocks:

glf1.a in Himalaya (GSHO 98); *cer-zh.54* in Bonus (GSHO 455) is used for allelism tests; *glf1.a* in Bowman (PI 483237)*8 (GSHO 2015).

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Prepared:

- T.E. Haus and T. Tsuchiya. 1971. BGN 1:141 as BGS 155, Glossy seedling, *gl*; and BGN 1:145 as BGS 159, Glossy seedling 2, *gl2*.
U. Lundqvist. 1975. BGN 5:144 as BGS 426, Eceriferum-zh, *cer-zh*.

Revised:

- T. Tsuchiya. 1980. BGN 10:114 as BGS 155, Glossy seedling, *gl*; and BGN 10:116 as BGS 159, Glossy seedling 2, *gl2*.
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:181-182.
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:233-234.

BGS 157, Brachytic 2, *brh2*

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

Previous nomenclature and gene symbolization:

Brachytic 2 = *br2* (9).
Breviaristatum-1 = *ari-1* (4, 5).

Inheritance:

Monofactorial recessive (8).
Located in chromosome 4HL (8), about 1.5 cM proximal from the *glf3* (glossy leaf 3) locus (3, 8), over 22.8 cM proximal from the *Kap1* (hooded lemma 1) locus (8), near AFLP marker E4140-7 in subgroup 38-40 of the Proctor/Nudinka map (7), and about 15.9 cM distal from SSR marker Bmag0353 near the boundary between bins 4H-06 and 4H-07 (2).

Description:

Plant height and vigor are reduced to about 2/3 normal; the awn is less than 1/4 normal length; the spike is semi-compact; and the leaf, kernel, glume and glume awn, rachilla, and coleoptile are shorter than in the original cultivar. Auricles are well developed and larger than those of the original cultivar (9). In the Bowman backcross-derived lines, the peduncle is about 1/2 normal length, kernel weights are slightly over 2/3 normal, yield is about 1/2 normal; however, rachis internode lengths are normal (2). The *ari-1.3* allele at the *brh2* locus is sensitive to gibberellic acid treatment (1).

Origin of mutant:

An X-ray induced mutant in Svanhals (PI 5474) (9).

Mutational events:

brh2.b in Svanhals (Kmut 28, OUM283) (8); *ari-1.3* (NGB 115848) in Bonus (PI 189763) (5); *ari-1.132* (NGB 115942) in Foma (CIho 11333) (6); *ari-1.135* (NGB 115945), *-1.145* (NGB 115956), *-1.214* (NGB 116023), *-1.237* (NGB 116047) in Foma, *-1.257* (NGB 116066) in Kristina (NGB 1500) (5).

Mutant used for description and seed stocks:

brh2.b in Svanhals (GSHO 573); *ari-1.3* in Bonus (GSHO 1660); *brh2.b* in Bowman (PI 483237)*7 (GSHO 2016); *ari-1.3* in Bowman*7 (GSHO 2017).

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2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
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Barley Genet. Newsl. 1:51-58.

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. BGN 1:143.

Revised:

T. Tsuchiya. 1980. BGN 10:115.

J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:184.

J.D. Franckowiak and L. S. Dahleen. 2007. BGN 37:235-236.

BGS 178, Intermedium spike-c, *int-c*

Stock number: BGS 178
Locus name: Intermedium spike-c
Locus symbol: *int-c*

Previous nomenclature and gene symbolization:

Intensifer for $Z = W$ (22).
Infertile intermedium = *i* (12, 20, 21).
Allelic series I^h, I, i (12, 23).
Intermedium spike-c = *int-c* (6, 7, 17, 18).
Six-rowed spike 5 = $v5$ (24).

Inheritance:

Monofactorial recessive (4, 5, 21, 24).
Located in chromosome 4HS (3, 5, 18, 21, 24), about 13.1 cM proximal from the *fch9* (chlorina seedling 9) locus, about 14.5 cM distal from the *Kap1* (hooded lemma 1) locus (2, 3, 4, 5, 11), and about 3.5 cM from AFLP marker E4143-5 in subgroup 8 of the Proctor/Nudinka map (19).

Description:

Alleles at the *int-c* ($v5$) locus alter the size of lateral spikelets. The lemma apex of lateral kernels is rounded or weakly pointed, awnless or short-awned (1, 9, 16). Lower lateral spikelets may develop poorly in some *int-c* mutants (4), while seed development may occur in all lateral spikelets of others (6, 15). Variability in lateral spikelet development exists among the *int-c* mutants and environmental conditions can alter expressivity. The *Int-c.a* (formerly *I*) allele in six-rowed barley increases the size of lateral spikelets, while the *int-c.b* (formerly *i*) allele in two-rowed barley prevents anther development in lateral spikelets (9, 22). The *int-c.5* mutant in Bonus produces fertile stamens in lateral spikelets (9). In the presence of the *Int-c.h* (formerly I^h) allele of Mortoni, lateral spikelets are male fertile and may occasionally set seed (8, 12). Spikes of *vrs5.n* ($v5$) plants appear similar to those of six-rowed barley, but lateral spikelets are smaller (less than half the size of the central spikelets) and broader (3, 4).

Origin of mutant:

Natural occurrence in many two-rowed barley cultivars; an X-ray induced mutant in Gamma 4 (3, 5).

Mutational events:

int-c.b (*i*) in two-rowed barley (23); *Int-c.h* (I^h) in Mortoni (CIho 2210, GSHO 72) (8, 12); *vrs5.n* ($v5$) in Gamma 4 (38X-197, OUM338) (3, 5, 14); *int-c.5* (NGB 115423) in Bonus (PI 189763) (15, 18); *int-c.7* (NGB 115425), -c.62 (NGB 116835), -c.63 (NGB 115481) in Bonus, -c.13 (NGB 115431), -c.15 (NGB 115433), -c.16 (NGB 115434), -c.18 (NGB 115436), -c.25 (NGB 115443), -c.29 (NGB 115447) in Foma (CIho 11333), -c.33 (NGB 115451), -c.38 (NGB 115456), -c.45 (NGB 115463), -c.48 (NGB 115466), -c.49 (NGB 115467), -c.53 (NGB 115471), -c.56 (NGB 115474), -c.60 (NGB 115478) in Kristina (NGB 1500) (15); *int-c.70* (NGB 115488), -c.76 (NGB 115494), -c.78 (NGB 115496), -c.84 (NGB 115502) in Bonus, -c.95 (NGB 115513) in Hege (NGB 13692) (13).

Mutant used for description and seed stocks:

vrs5.n in Gamma 4 (GSHO 776); *int-c.b* in *Hordeum distichon* var. *nigrinudum* (GSHO 988); *int-c.5* in Bonus (GSHO 1765); *int-c.b* from Compana (CIho 5438) in Bonneville (CIho 7248)*6 (CIho 16176) (10); *vrs5.n* in Bowman (PI 483237)*6 (GSHO 2002); *int-c.5* in Bowman*6 (GSHO 2003).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:200-201.

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Revised:

U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:237-239.

BGS 179, Hairy leaf sheath 1, *Hsh1*

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

Previous nomenclature and gene symbolization:

Hairy leaf sheath = *Hs* (7).

Inheritance:

Monofactorial dominant (4, 5, 6).

Located in chromosome 4HL (6), over 8.7 cM proximal from the *yhd1* (yellow head 1) locus, and over 22.5 cM distal from the *mlo* (reaction to *Erysiphe graminis hordei-o*) locus (3, 5), in bin 4H-12 about 1.1 cM proximal from RFLP marker HVM067 (2).

Description:

Short hairs (1 to 3 mm) are scattered or in rows on leaf sheaths of the basal part of the plant. The density of hairs varies considerably among cultivars and with changes in growing conditions. With few exceptions, no hairs are observed on the sheath of upper leaves (4, 5). Heterozygotes and smooth awned cultivars seem to have fewer hairs.

Origin of mutant:

Natural occurrence in a few cultivars and in some accessions of *Hordeum vulgare* subsp *spontaneum* (1, 5, 6).

Mutational events:

Hsh1.a introduced into cultivated barley from its wild progenitor (5).

Mutant used for description and seed stocks:

Hsh1.a in Kimugi (OUL012, GSHO 986) (5, 6); *Hsh1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)*10 (GSHO 2026).

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Prepared:

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R. Takahashi. 1972. BGN 2:184 as BGS 158.

Revised:

J.D. Franckowiak and T. Konishi. 1997. BGN 26:202.

J.D. Franckowiak. 2007. BGN 37:240-241.

BGS 185, Brachytic 5, *brh5*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 4HS (4), near the *int-c* (intermedium spike-c) locus (4), about 13.0 cM proximal from SSR marker Bmac0310 near the boundary between bins 4H-06 and 4H-07 (1).

Description:

Plants are about 3/4 normal height and awns are about 3/4 of normal length. Peduncles are less than 2/3 normal length. Seedling leaves of *brh5* plants are relatively short. The kernels of *brh5* plants are shorter than those of normal sibs and weigh about 30% less. Plants lodge easily and the grain yield is about 1/2 normal (1, 2).

Origin of mutant:

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

Mutational events:

brh5.m in Birgitta (17:18:2, DWS1010) (5, 6).

Mutant used for description and seed stocks:

brh5.m in Birgitta (GSHO 1678); *brh5.m* in Bowman (PI 483237)*7 (GSHO 2001).

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Prepared:

J.D. Franckowiak. 2002. BGN 32:100.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:242.

BGS 186, Slender dwarf 3, *sld3*

Stock number: BGS 186
Locus name: Slender dwarf 3
Locus symbol: *sld3*

Previous nomenclature and gene symbolization:

Anthocyanin-free = *ant-567* (5).
Proanthocyanidin-free 17.567 = *ant17.567* (4).
Slender dwarf e = *sld.e* (3).

Inheritance:

Monofactorial recessive (1).
Located in chromosome 4HS, based on linkage drag with the *int-c* (intermedium spike-c) locus (2).

Description:

Plants show reduced vigor and are about 3/4 normal height. The number of spikelets per spike is about 3/4 that of normal sibs and kernels are slightly smaller. Rachis internodes can be slightly longer and grain yields are about 3/4 normal (1). The mutant gene *sld3.e* was isolated as a second mutant in the stock *ant17.567* (proanthocyanidin-free 17) (1). The Bowman backcross-derived line for *sld3.e* does not show a reduction in anthocyanin pigmentation or the large reduction in kernel size (1).

Origin of mutant:

A sodium azide induced mutant isolated with *ant-567* in Manker (CIho 15549) (5).

Mutational events:

sld3.e in *ant17.567* (DWS1050) (1).

Mutant used for description and seed stocks:

sld3.e in Bowman/*ant17.567* (GSHO 2480); *sld3.e* in Bowman (PI 483237)*7 (GSHO 1998).

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Prepared:

J.D. Franckowiak. 2002. BGN 32:101.

Revised:

J.D. Franckowiak. 2007. BGN 37:243.

BGS 187, Brachytic 9, *brh9*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 4HS (1), about 11.7 cM distal from SRR marker

Bmac0310 in bin 4H-06 (1).

Description:

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

Origin of mutant:

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

Mutational events:

brh9.k in Birgitta (17:14:4, DWS1006) (4, 5).

Mutant used for description and seed stocks:

brh9.k in Birgitta (GSHO 1676); *brh9.k* in Bowman (PI 483237)*6 (GSHO 2170).

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Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:244.

BGS 203, Black lemma and pericarp 1, *Blp1*

Stock number: BGS 203
Locus name: Black lemma and pericarp 1
Locus symbol: *Blp1*

Previous nomenclature and gene symbolization:

Black lemma and caryopsis = *B* (6).
Black pericarp = *Bk* (1).
Black lemma and pericarp = *B* (7).

Inheritance:

Monofactorial dominant (1, 4, 6).
Located in chromosome 1HL [5L] (3, 5), about 16.0 cM proximal from the *trd1* (third outer glume 1) locus (3), in bin 1H-13 about 8.8 cM proximal from RFLP marker ABC261 (2).

Description:

Black pigmentation of the lemma and pericarp develops slightly before maturation of the spike. Pigmented organs may include all parts of the spike, awns, the upper portion of the stem, and upper leaves. The intensity of pigmentation associated with each of the dominant alleles at the *Blp1* locus is characteristic of that allele, and is relatively stable over environments (7). Black seed is produced by melanin-like pigment in the pericarp (1). Woodward (7) reports that the dominance ranking of alleles at the *Blp1* locus is related to the intensity of black pigmentation they confer, with the *Blp1.b* (*B*) allele conferring extreme black pigmentation. The *Blp1.mb* (*B^{mb}*) allele is associated with medium black and a reduced distribution pattern; and the *Blp1.g* (*B^g*) allele is associated with light black or gray coloration (7, 8).

Origin of mutant:

Natural occurrence in several cultivars (6, 7).

Mutational events:

Blp1.b (*B*) in *Hordeum distichon* var *nigrinudum* No 1 (7); *Blp1.mb* (*B^{mb}*) in Clho 2970 (GSHO 226) (7); *Blp1.g* (*B^g*) in Blackhull (Clho 878, GSHO 199) and Black Smyrna (Clho 191, GSHO 222) (7).

Mutant used for description and seed stocks:

Blp1.b in *Hordeum distichon* var *nigrinudum* No 1 (GSHO 988); *Blp1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1580) in Bowman (PI 483237)*8 (GSHO 2054).

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. BGN 1:148.

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:209.

J.D. Franckowiak. 2007: BGN 37:245-246.

BGS 214, Early maturity 8, *eam8*

Stock number: BGS 214
Locus name: Early maturity 8
Locus symbol: *eam8*

Previous nomenclature and gene symbolization:

Early heading k = *ea_k* (26).
Early maturity-a = *ea-a* (8, 21).
Praematurum-a = *mat-a* (3, 8, 13, 14, 26).
Erectoides-o = *ert-o* (8, 18).

Inheritance:

Monofactorial recessive (3, 7).
Located in chromosome 1HL [5L] (21), about 11.4 cM distal from the *trd1* (third outer glume 1) locus and 20.9 cM distal from the *Blp1* (black lemma and pericarp 1) locus (21, 24).

Description:

Early heading is associated with decreased culm length, spike length, kernels per spike, and grain yield (16, 24, 26). When grown in the fall at Kurashiki, Japan, plants head about 20 days earlier than the standard mid-season cultivar, Akashinriki, because they are day-length neutral or photoperiod insensitive (26). Day-length neutrality is observed in early heading mutants isolated from spring barley in Sweden (2, 9). Under controlled environmental conditions, number of days to heading does not change as photoperiod is altered (2, 10). All *mat-a* induced mutants are characterized by yellowish-green seedlings at an early stage of development under controlled environmental conditions (1). Other *eam8* mutants show a similar response by becoming yellow green under specific growing conditions, 8 to 12 hours of illumination at low temperatures (below 10°C) plus high temperature (20°C or higher) during the dark period (5, 21, 24). The color change is caused by photothermal stress, which increases the zeaxanthin content at the expense of chlorophyll and other pigments (5, 19, 24). The mutant stock *mat-a.8* was released as the cultivar Mari (9, 11). When grown under 12 h days, the levels of phytochrome B (*phyB*) decreases in light-grown BMDR-1 plants, containing an allele at the *eam8* locus, compared to normal plants (12). The instability of *phyB* content was reported to be responsible for photoperiod insensitivity of *eam8* mutants (12). Under continuous light and with far-red light treatment for seven days, most differences in heading date between BMDR-1 and BMDR-8 (Shabet) are eliminated (19).

Origin of mutant:

An X-ray induced mutant in Maja (PI 184884, NGB 8815) (6, 7, 10); natural occurrence in Kinai 5 (OUJ493) and Kagoshima Gold (OUJ219) (21, 25).

Mutational events:

ert-o.16 (NGB 112618) in Maja (6); *eam8.k* in Kagoshima Gold, Kinai 5 (CIho 11560), and Kindoku (OUU332) (21, 22, 25); *mat-a.8* (NGB 1491, NGB 4694, NGB 14656, NGB 110008), *-a.11* (NGB 110011), *-a.12* (NGB 110012) in Bonus (PI 189763) (7, 14); *mat-a.27* (NGB 110027), *-a.45* (NGB 110045), *-a.46* (NGB 110046), *-a.48* (NGB 110048), *-a.62* (NGB 110062) in Bonus, *-a.110* (NGB 110110), *-a.130* (NGB 110130), *-a.153* (NGB 110153), *-a.221* (NGB 110221), *-a.238* (NGB 110238), *-a.255* (NGB 110255), *-a.272* (NGB 110272), *-a.274* (NGB 110274), *-a.287* (NGB 110287), *-a.289* (NGB 110289), *-a.294* (NGB 110294), *-a.325* (NGB 110325), *-a.338* (NGB 110338), *-a.370* (NGB 110370), *-a.384* (NGB

110384), -a.390 (NGB 110390), -a.404 (NGB 110404), -a.406 (NGB 110406), -a.407 (NGB 110407) in Foma (CIho 11333), -a.509 (NGB 110509), -a.641 (NGB 110641), -a.703 (NGB 110703), -a.733 (NGB 110733), in Kristina (NGB 1500), -a.753 (NGB 110753), -a.796 (NGB 110796), -a.797 (NGB 110797), -a.813 (NGB 110813), -a.832 (NGB 110832), -a.903 (NGB 116858), -a.909 (NGB 117440), -a.921 (NGB 117452) in Bonus, -a.961 (NGB 117492), -a.970 (NGB 117501), -a.976 (NGB 117507), -a.984 (NGB 117515), -a.1011 (NGB 117542), in Sv 79353, -a.1032 (NGB 117563), -a.1033 (NGB 117564), -a.1034 (NGB 117565), -a.1035 (NGB 117566), -a.1036 (NGB 117567), -a.1037 (NGB 117568), -a.1039 (NGB 117570), -a.1040 (NGB 117571), -a.1041 (NGB 117572), -a.1042 (NGB 117573), -a.1043 (NGB 117574), -a.1044 (NGB 117575), -a.1045 (NGB 117576), -a.1046 (NGB 117577), -a.1047 (NGB 117578), -a.1048 (NGB 117579), -a.1049 (NGB 117580) in Sv Vg74233 (13); *mat-a.1050* (NGB 117581), -a.1051 (NGB 117582), -a.1052 (NGB 117583), -a.1053 (NGB 117584), -a.1054 (NGB 117585), -a.1055 (NGB 117586), -a.1056 (NGB 117587), -a.1057 (NGB 117588), -a.1058 (NGB 117589), -a.1059 (NGB 117590), -a.1060 (NGB 117591), -a.1061 (NGB 117592), -a.1062 (NGB 117593), -a.1063 (NGB 117594), -a.1064 (NGB 117595), -a.1065 (NGB 117596), -a.1067 (NGB 117598), -a.1069 (NGB 117600), -a.1070 (NGB 117601), -a.1071 (NGB 117602), -a.1072 (NGB 117603), -a.1073 (NGB 117604), -a.1074 (NGB 117605) in Sv Vg74233 (15); *eam8.q* (Ea8), *eam8.r* (Ea9), *eam8.s* (Ea10), *eam8.t* (Ea16) in Chikurin Ibaraki 1 (OUJ069, CIho 7370, GSHO 783) (23); *eam8.u* (Mut 2571) in Donaria (PI 161974) (5, 17); *eam8.v* in Munsing (CIho 6009, GSHO 636) (4, 19, 20); *eam8.w* in Early Russian (CIho 13839) (4), BMDR-1 (*eam8.y*) from the original mutant in a dwarf line backcrossed to Shabet (CIho 13827) (19).

Mutant used for description and seed stocks:

eam8.k in Kinai 5 (OUJ439, GSHO 765); *ert-o.16* in Maja (GSHO 489); *eam8.k* in Bonus*5 (25); *mat-a.8* in Tochigi Golden*5 (25); *eam8.u* in Munsing/7*Titan (CIho 16526) (20); *eam8.k* in Bowman (PI 483237)*7 (GSHO 2063); *ert-o.16* in Bowman*7 (GSHO 2064).

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- Prepared:
S. Yasuda. 1972. *BGN* 2:198.
- Revised:
J.D. Franckowiak, U. Lundqvist, T. Konishi, and L.W. Gallagher. 1997. *BGN* 26:213-215.

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J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:247-250.

BGS 222, Necrotic leaf spot 1, *nec1*

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

Previous nomenclature and gene symbolization:

Mutant no. 10 (2).
Parkland spot = *sp,,b* (1).

Inheritance:

Monofactorial recessive (2, 4).
Located in chromosome 1HL [5L] (1, 2, 4), near the centromere (1), about 34.5 cM proximal from the *wst5* (white streak 5) locus (3, 5), about 10.0 cM distal from the *msg1* (male sterile genetic 1) locus (4, 6), in bin 5H-09 near EST marker BF630384 (7).

Description:

Small black-brown spots develop on all light-exposed parts of the plant starting near the leaf tip at the three-leaf stage (1, 2). The spots are oval (the longest dimension is parallel to the leaf veins) and generally less than 1 to 2 mm in size. The spots are concentrated in awn and the most distal parts of the leaf blade, but may occur on all plant parts (2, 4). The *nec1* locus is an orthologue of *Arabidopsis* necrotic mutant *HLM1* that encodes the cyclic nucleotide-gated ion channel 4 (7).

Origin of mutant:

A mutant induced by combined treatment with gamma-rays and diethyl sulfate of Carlsberg II (CIho 10114, NGB 5085) (2).

Mutational events:

nec1.a in Carlsberg II (Mutant no 10) (2, 3); *sp,,b* (GSHO 1284) in Parkland (CIho 10001) (1, 4); a mutant in Morex (CIho 15773) (6); FN085 and FN370 in Steptoe (CIho 15229) (7); FN338 in Morex (CIho 15773) (7).

Mutant used for description and seed stocks:

nec1.a in Carlsberg II (GSHO 989); *nec1.a* from R.I. Wolfe's Chromosome 5 Marker Stock in Bowman (PI 483237)*7 (GSHO 2052).

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nucleotide-gated ion channel 4 homologous to the *Arabidopsis Hlm1*. Mol. Gen. Genomics 275:159-168.

Prepared:

J. Jensen. 1981. BGN 11:101.

Revised:

J.D. Franckowiak. 1997. BGN 26:220.

J.D. Franckowiak. 2007. BGN 37:251-252.

BGS 253, Uniculm 2, *cul2*

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

Previous nomenclature and gene symbolization:
Uniculm 2 = *uc2* (8).

Inheritance:

Monofactorial recessive (8).

Located in chromosome 6HL (4, 6), about 1.3 cM distal from the *gsh4* (glossy sheath 4) locus (3, 5), about 11.4 cM from the *msg36* (male sterile genetic 36) locus (3, 5), about 2.2 cM proximal from the *rob1* (orange lemma 1) locus (3, 4, 5), about 8.8 cM from RFLP markers cMWG679 and ABG458 (1), and about 6.2 cM from AFLP marker E4343-10 in subgroup 54 of the Proctor/Nudinka map (7).

Description:

The *cul2* plants have a single elongated culm (stem), the stem is much greater in diameter than normal, and plants are usually earlier than normal (8). The *cul2* plants initiate vegetative axillary meristems, but tillers fail to develop (1). Irregular placement of some spikelets and male fertility in lateral spikelets occur in the original stock (5) and in the Bowman backcross-derived line (1). Yield of uniculm plants is not restored when grown under high plant populations (2). Double mutant combinations with most other mutants that affect tiller number resulted in a uniculm vegetative phenotype (1).

Origin of mutant:

A thermal neutron induced mutant in Kindred (CIho 6969) (8).

Mutational events:

cul2.b in Kindred (GBC379) (5), *cul2.k* (*unc^k*) in an unknown cultivar from the Max-Planck-Institut für Züchtungsforschung (7).

Mutant used for description and seed stocks:

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

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Prepared:

C.R. Burnham. 1971. BGN 1:156.

Revised:

J.D. Franckowiak. 1997. BGN 26:234.

J.D. Franckowiak. 2007. BGN 37:253-254.

BGS 254, Orange lemma 1, *rob1*

Stock number: BGS 254
Locus name: Orange lemma 1
Locus symbol: *rob1*

Previous nomenclature and gene symbolization:

Orange lemma = *pl* (14).
Orange lemma = *br* (1, 2).
Orange lemma = *o* (15).
Robiginosum-o = *rob-o* (6).

Inheritance:

Monofactorial recessive (1, 2, 14, 15).
Located in chromosome 6HS (4, 5, 17, 18), about 10.8 cM proximal from the *msg36* (male sterile genetic 36) locus (5, 9), and about 2.2 cM distal from the *cul2* (unculm 2) locus (5, 7, 9), in bin 6H-06 near RFLP marker HVM031 (3).

Description:

The lemma, palea, and rachis have an orange pigmentation that is present in immature spikes, can be observed at heading, and is retained in mature grain and spikes (2, 15). The orange pigmentation is visible at the base of sheath of seedlings and in exposed nodes after jointing. Internodes have a layer of orange tissue and stems have an orange color as the straw dries. The mutant stock for *rob1.f* (OUM189) has a lighter orange lemma color than that in other mutants at the *rob1* locus (10). The Bowman backcross-derived line with the *rob1* gene had slightly lower acid-detergent lignin (ADL) content than Bowman (13), but it was also more susceptible to common root rot, caused by *Bipolaris sorokiniana* (11).

Origin of mutant:

A spontaneous mutant in Clho 5649 (15).

Mutational events:

rob1.a in Clho 5649 (GBC340, GSHO 707) (8, 15); *rob1.b* (OUM185), *rob1.c* (OUM186), *rob1.d* (OUM187), *rob1.e* (OUM188), *rob1.f* (OUM189) in Akashinriki (OUJ659, PI 467400) (10); *rob1.1* (NGB 115071, NGB 119367), *rob1.2* (NGB 115072, NGB 119368) in Bonus (PI 189763), *rob1.3* (NGB 115073, NGB 119369), *rob1.4* (NGB 115074, NGB 119370), *rob1.5* (NGB 115075, NGB 119371), *rob1.6* (NGB 115076, 119372) in Foma (Clho 11333), *rob1.7* (NGB 115077, NGB 119373) in Kristina (NGB 1500) (12); *rob1.g* (200A12/8/2) from Emir (Clho 11790) isolated following a cross to *Hordeum bulbosum* (16).

Mutant used for description and seed stocks:

rob1.a in Clho 5649 (GSHO 707); *rob1.a* in Bowman (PI 483237)*8 (GSHO 2069).

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13. Meyer, D.W., J.D. Franckowiak, and R.D. Nudell. 2006. Forage quality of barley hay. *Agronomy Abstracts* 2006.

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Prepared:

C.R. Burnham. 1971. *BGN* 1:157.

Revised:

J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997. *BGN* 26:235-236.

J.D. Franckowiak and U. Lundqvist. 2007. *BGN* 37:255-256.

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

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

Previous nomenclature and gene symbolization:

Erectoides-17 = *ert-17* (2).
Dense spike = *la* (4).
Dense spike 9 = *l9* (4).

Inheritance:

Monofactorial recessive (2, 4, 8).
Located in chromosome 6HL (3, 7, 8), about 27.2 cM distal from the *xnt5* (xantha seedling 5) locus (5), over 26.9 cM distal from the *Aat2* (aspartate aminotransferase 2) locus (11).

Description:

Spikes are very compact with rachis internode length values from 1.2 to 1.5 mm. Plants are about 2/3 normal height. Partial fertility and reduced vigor are noted among *ert-e* mutants. The peduncle is very short and spikes often emerge from the side of the flag sheath (7, 9). A large deficiency of mutant plants is frequently noted in segregating populations (7). Spike density decreases greatly when plants are treated with GA₃ as the flag leaf emerges (10). The mutant *ert-e.17* is allelic to mutant *dsp9.i* (dense spike 9, see BGS 258) (1).

Origin of mutant:

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

Mutational events:

ert-e.17 (NGB 112619), *-e.65* (NGB 112664) in Bonus (2); *ert-e.94* (NGB 112693), *-e.143* (NGB 112742) in Bonus, *-e.331* (NGB 112846), *-e.396* (NGB 114150) in Foma (CIho 11333) (9); *dsp9.i* (OUM113) in Akashinriki (4); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118) in Akashinriki (6).

Mutant used for description and seed stocks:

ert-e.17 in Bonus (GSHO 477); *ert-e.17* in Bowman (PI 483237)*6 (GSHO 2091); *dsp9.i* in Akashinriki (GSHO 1774); *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090).

References:

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:246.

Revised as BGS 258:

T. Konishi and J.D. Franckowiak. 1997. BGS 258, Dense spike 9, *dsp9*. BGN 26:239.

Revised:

J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:257-258.

BGS 306, Variegated 1, *var1*

Stock number: BGS 306
Locus name: Variegated 1
Locus symbol: *var1*

Previous nomenclature and gene symbolization:

Variegated = *va* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL [7L] (4), about 4.6 cM proximal from the *raw1* (smooth awn 1) locus (3, 4), in bin 5H-09 about 29.2 cM proximal from the *Rph9* (reaction to *Puccinia hordei* 9) locus (1).

Description:

Narrow white stripes develop on young leaves, but they are not as well defined than those of white streak 7 (*wst7*). White stripes are visible on the foliage and stems of older plants (3). When sown in plots, selections homozygous for the *var1.a* gene have a whitish cast until heading (2). The Bowman backcross-derived line for *var1* shows slightly delayed heading and may be slightly shorter (2).

Origin of mutant:

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

Mutational events:

var1.a in Montcalm (Alb Acc 311) (4).

Mutant used for description and seed stocks:

var1.a in Montcalm (GSHO 1278); *var1.a* in Bowman (PI 483237)*7 (GSHO 2121).

References:

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. BGN 1:165.

Revised:

J.D. Franckowiak. 1997. BGN 26:257.

J.D. Franckowiak. 2007. BGN 37:259.

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* (5, 8).
Early maturity 3 = *Ea3* (2, 3).
Early maturity 5 = *Ea5* (4).
Early maturity 8 = *Ea8* (6).

Inheritance:

Monofactorial dominant (9).
Located in chromosome 5HL [7L] (2), very close to the *raw1* (smooth awn 1) locus (1, 8, 9).

Description:

Plants with the *Eam5* gene head 3 to 10 days earlier than normal sibs under short-day conditions (1, 5). Early heading is commonly associated a shorter stature compared to normal sibs. The slight reduction in height is also observed under long-day conditions. Peduncles and rachis internodes are slightly shortened (1). The *Eam5* 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 (1, 9). Takahashi and Yasuda (7) classified plants that were about 10 days earlier than normal spring barley as having the *Sgh2.//* (spring growth of habit 2, grade 2) gene, but an earliness factor closely linked to the rough awn gene was earlier identified in spring barley (8).

Origin of mutant:

Natural occurrence in Indian cultivars (2, 3) and isolated from ICARDA/CIMMYT selection CMB85-533-H-1Y-1B-0Y-5B (Higuerilla*2/Gobernadora) (1).

Mutational events:

Eam5.x in CMB85-533 (1), *Eam5.x* in a number of Chinese cultivars planted in the fall (9).

Mutant used for description and seed stocks:

Eam5.x in CMB85-533; *Eam5.x* in Bowman (PI 483237)*6 (GSHO 3424).

References:

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9. Yu, G. 2006. Development of early maturing two-rowed malting barley with *Fusarium* head blight resistance. Ph.D. Thesis. North Dakota State University, Fargo.

Prepared:

J.D. Franckowiak. 2002. BGN 32:109.

Revised:

J.D. Franckowiak and G. Yu. 2007. BGN 37:260-261.

BGS 349, Brachytic 4, *brh4*

Stock number: BGS 349
Locus name: Brachytic 4
Locus symbol: *brh4*

Previous nomenclature and gene symbolization:

Brachytic-j = *brh.j* 4, 5).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 2HL (3), about 14.1 cM distal from SSR marker EBmac0850 in bin 2H-08 (1).

Description:

Seedling leaves of *brh4* plants are short and wide compared to those of Bowman. Plants are 3/4 to 5/6 normal height and awns are about 3/4 of normal length. Plants have a rather erect growth habit. Peduncle length is about 3/4 normal and rachis internodes are slightly shortened. Heading is delayed by about 2 days and the fertile spikelet number is increased by over 3, but these effects could be caused by pleiotropism or linkage drag with the *Eam6* (early maturity 6) locus. The kernels of *brh4* plants are slightly shorter (8.3 vs. 9.4 mm), more globose shaped, and slightly smaller (46 vs. 56 mg) than those of Bowman. The yield reduction was non-significant in comparisons between the *brh4.j* Bowman line and Bowman (1, 2).

Origin of mutant:

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

Mutational events:

brh4.j in Birgitta (17:13:6, DWS1005) (5, 6).

Mutant used for description and seed stocks:

brh4.j in Birgitta (GSHO 1675); *brh4.j* in Bowman (PI 483237)*7 (GSHO 2130).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
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5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
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Prepared:

J.D. Franckowiak. 2002. BGN 32:110.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:262.

BGS 350, Brachytic 6, *brh6*

Stock number: BGS 350
Locus name: Brachytic 6
Locus symbol: *brh6*

Previous nomenclature and gene symbolization:

Brachytic-r = *brh.r* (3).
Brachytic-s = *brh.s* (3).

Inheritance:

Monofactorial recessive (4, 5).
Located in chromosome 5HS [7S] (4), about 12.0 cM distal from SSR marker Bmag0394 in bin 5H-03 (1).

Description:

Plants of the Bowman backcross-derived line are 2/3 to 3/4 normal height and awns are 1/2 to 2/3 normal length. The seedling leaf of *brh6* plants is shorter than that of normal sibs (1, 2). Peduncles and leaf blades are 2/3 normal length and the grain is nearly normal (1). However, kernels are nearly 20% lighter than those of Bowman with both decreased length and width (1, 2). Although grain yield of the near-isogenic line for *brh6* was lower than those of tall Akashinriki, the *brh6* line was considered a high yielding dwarf (7).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (6, 7).

Mutational events:

brh6.r in Akashinriki (OUM133, dw-h, DWS1036, GSHO 1683), *brh6.s* in Akashinriki (OUM135, DWS1037, GSHO 1684) (3, 5, 6).

Mutant used for description and seed stocks:

brh6.r in Akashinriki (GSHO 1683); *brh6.r* in Bowman (PI 483237)*7 (GSHO 2132).

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.
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Prepared:

J.D. Franckowiak and T. Konishi. 2002. BGN 32:111.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:263.

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* (4).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 7HL [1L] (3), linked to the *msg23* (male sterile genetic 23) locus (5).

Description:

Seed is 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 (3, 5). This mutant is associated with an increase in percentage lysine in the protein (5). Tannins are not deposited in *seg1* chalazal cell central vacuoles, but rather appeared to cause cytoplasmic disorganization and cell death (1). 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).

Origin of mutant:

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

Mutational events:

seg1.a in Betzes (3, 4).

Mutant used for description and seed stocks:

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

References:

1. 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.
2. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. *Amer. J. Bot.* 72:248-256.
3. Jarvi, A.J. 1970. Shrunken endosperm mutants in barley, *Hordeum vulgare*. Ph.D. Thesis. Montana State Univ., Bozeman.
4. Jarvi, A.J., and R.F. Eslick. 1971. BGS 377, Normal vs. shrunken endosperm, *se1*. *Barley Genet. Newsl.* 1:190.
5. 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. BGN 1:190.

Revised:

R.F. Eslick. 1976. BGN 6:135.

T. Tsuchiya. 1980. BGN 10:124.

J.D. Franckowiak. 1997. BGN 26:325.

J.D. Franckowiak. 2007. BGN 37:264.

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* (5).
Proanthocyanidin-free 17 = *ant17* (3).

Inheritance:

Monofactorial recessive (3).
Located in chromosome 3HS (1, 6), over 30.8 cM from the centromere (6).

Description:

Seed size is reduced to about 33% of normal when grown under field conditions. Seeds are long and thin similar to those from *seg1* plants; seeds are viable and good stand establishment is possible (6). Light microscopy revealed that *seg3* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (2). The mutant *ant17.148* is an allele at the *seg3* locus (3); thus, all mutants at the proanthocyanidin-free 17 (*ant17*) locus might be alleles at the shrunken endosperm genetic 3 locus. Alleles at the *seg3* locus that have been examined in the Bowman genetic background showed a variable reduction in kernel weight: *ant17.148* and *seg3.c* about 1/3 normal and *ant17.567* about 3/4 normal (3). The *seg3* locus was named before the *ant17* locus, but many more mutants were identified at the *ant17* locus. Therefore, see BGS 599 for a complete listing of *ant17* mutants.

Origin of mutant:

A spontaneous mutant in Compana (PI 539111) (4).

Mutational events:

seg3.c in Compana (4, 5), *ant17.148* (Galant, NGB 13698) in Triumph (PI 268180, NGB 13678) (3).

Mutant used for description and seed stocks:

seg3.c in Compana (GSHO 752); *seg3.c* in Bowman (PI 483237)*7 (GSHO 1957), *ant17.148* in Bowman*4 (GSHO 1973).

References:

1. Boyd, P.W., and D. E. Falk. 1990. (Personal communications).
2. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
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5. Jarvi, A.J., and R.F. Eslick. 1971. BGS 379, Normal vs. shrunken endosperm, *se3*. Barley Genet. Newsl. 1:191.
6. 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. BGN 1:191.
B. Jende-Strid. 1999. BGN 29:88-89, as BGS 599, proanthocyanidin-free 17, *ant17*.

Revised:

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R.F. Eslick. 1976. BGN 6:137.

T. Tsuchiya. 1980. BGN 10:126.

J.D. Franckowiak. 1997. BGN 26:327.

J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:265-266.

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BGS 380, Shrunken endosperm genetic 4, *seg4*

Stock number: BGS 380
Locus name: Shrunken endosperm genetic 4
Locus symbol: *seg4*

Previous nomenclature and gene symbolization:

Shrunken endosperm = *se4* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 7HL [1L] (2), over 34.0 cM from the centromere (4).

Description:

Under field conditions in the original mutant, seed size is reduced to about 38% of normal and seed set is about 50% of normal. Stand establishment is poor under field conditions (2, 4). Endosperms of *seg4* were characterized by progressively distorted, disorganized growth, but the quantity of endosperm tissue at maturity varied from severely reduced to near normal (1). The stock described in the 1997 revision was incorrect and was in fact a mixture with GSHO 755 (BGS 382, shrunken endosperm xenia 1, *sex1*), which was identified by Dr. Marion Röder, IPK, Gatersleben.

Origin of mutant:

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

Mutational events:

seg4.d in Compana (2, 3).

Mutant used for description and seed stocks:

seg4.d in Compana (GSHO 753).

References:

1. 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.
2. Jarvi, A.J. 1970. Shrunken endosperm mutants in barley, *Hordeum vulgare*. Ph.D. Thesis. Montana State Univ., Bozeman.
3. Jarvi, A.J., and R.F. Eslick. 1971. BGS 380, Normal vs. shrunken endosperm, *se4*. *Barley Genet. Newsl.* 1:192.
4. 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. BGN 1:192.

Revised:

R.F. Eslick. 1976. BGN 6:138.

T. Tsuchiya. 1980. BGN 10:127.

J.D. Franckowiak. 1997. BGN 26:328.

J.D. Franckowiak. 2007. BGN 37:267.

Barley Genetics Newsletter (2007) 37: 188-301

BGS 396, Shrunken endosperm genetic 6, *seg6*

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

Previous nomenclature and gene symbolization:

Shrunken endosperm = *se6* (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HL (4).

Description:

Seed size is reduced, but the degree reduction is affected by environment. Seed weights of 25, 50, and 75% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (4). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg6.g* plants can be used to establish stands under field conditions (4). Light microscopy revealed that *seg6* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (1).

Origin of mutant:

A spontaneous mutant in Ingrid (CIho 10083) (3).

Mutational events:

seg6.f in an unknown hybrid, *seg6.g* in Ingrid (3).

Mutant used for description and seed stocks:

seg6.g in Ingrid (GSHO 2467); *seg6.g* in Bowman (PI 483237)*4 (GSHO 1975).

References:

1. 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.
2. Ramage, R.T. 1983. Chromosome location of shrunken endosperm mutants *seg6g* and *seg8k*. *Barley Genet. Newsl.* 13:64-65.
3. Ramage, R.T., and R.F. Eslick. 1975. BGS 396, Shrunken endosperm, *xenia*, *se6*. *Barley Genet. Newsl.* 5:114.
4. Ramage, R.T., and J.F. Scheuring. 1976. Shrunken endosperm mutants *seg6* and *seg7*. *Barley Genet. Newsl.* 6:59-60.

Prepared:

R.T. Ramage and R.F. Eslick. 1975. BGN 5:114.

Revised:

- R.T. Ramage and R.F. Eslick. 1976. BGN 6:141.
T. Tsuchiya. 1980. BGN 10:130.
R.T. Ramage. 1983. BGN 13:115.
J.D. Franckowiak. 1997. BGN 26:344.
J.D. Franckowiak. 2007. BGN 37:268.

BGS 397, Shrunken endosperm genetic 7, *seg7*

Stock number: BGS 397
Locus name: Shrunken endosperm genetic 7
Locus symbol: *seg7*

Previous nomenclature and gene symbolization:

Shrunken endosperm = *se7* (4).

Inheritance:

Monofactorial recessive (3).

Location is unknown.

Description:

Seed size is reduced less than other *seg* mutants, but the degree reduction is affected by environment. Seed weights of 40, 75, and 90% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (4). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg7.h* plants can be used to establish stands under field conditions (4). The shrunken endosperm trait was very difficult to detect in the crosses to Bowman (2). Light microscopy revealed that *seg7* 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 (1).

Origin of mutant:

A spontaneous mutant in Ingrid (CIho 10083) (3).

Mutational events:

seg7.h in Ingrid (4).

Mutant used for description and seed stocks:

seg7.h in Ingrid (GSHO 2468); *seg7.h* in Bowman (PI 483237)*3 (GSHO 2352).

References:

1. 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.
2. Franckowiak, J.D. (Unpublished).
3. Ramage, R.T., and R.F. Eslick. 1975. BGS 397, Shrunken endosperm, *xenia, se7*. *Barley Genet. Newsl.* 5:115.
4. Ramage, R.T., and J.F. Scheuring. 1976. Shrunken endosperm mutants *seg6* and *seg7*. *Barley Genet. Newsl.* 6:59-60.

Prepared:

R.T. Ramage and R.F. Eslick. 1975. BGN 5:115.

Revised:

R.T. Ramage and R.F. Eslick. 1976. BGN 6:142.

T. Tsuchiya. 1980. BGN 10:131.

J.D. Franckowiak. 1997. BGN 26:345.

J.D. Franckowiak. 2007. BGN 37:269.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Location in chromosome 2HS (1), in bin 2H-01 about 16.8 distal from SSR marker Bmac0134 (1).

Description:

Surface wax coating on the spike appears slightly reduced (wax code + ++ ++)
(3). The reduction in the surface wax seemed greater in plants selected from the backcrosses to Bowman (wax code +/- ++ ++).

Origin of mutant:

An ethyl methanesulfonate and neutron induced mutant in Foma (CIho 11333)
(2).

Mutational events:

cer-zt.389 (NGB 111276), *-zt.479* (NGB 111367) in Foma (2).

Mutant used for description and seed stocks:

cer-zt.389 in Foma (GSHO 1527); *cer-zt.389* in Bowman (PI 483237)*2 (GSHO 2205).

References:

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

Prepared:

U. Lundqvist. 1975. *BGN* 5:155.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. *BGN* 26:389.

U. Lundqvist and J.D. Franckowiak. 2007. *BGN* 37:270.

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

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

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Location is unknown.

Description:
Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (3). In the Bowman backcross-derived line, mutant plants have pale green leaves, heading is delayed by several days, and plants are slightly shorter (1).

Origin of mutant:
A neutron induced mutant in Bonus (PI 189763) (2).

Mutational events:
cer-yf.652 (NGB 111540), *-yf.804* (NGB 111692) in Bonus (3).

Mutant used for description and seed stocks:
cer-yf.652 in Bonus (GSHO 1539); *cer-yf.652* in Bowman (PI 483237)*3 (GSHO 2212).

References:
1. Franckowiak, J.D. (Unpublished).
2. Lundqvist, U. (Unpublished).
3. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the *eceriferum* mutants II. *Barley Genet. Newsl.* 3:110-112.

Prepared:
U. Lundqvist. 1975. *BGN* 5:167.

Revised:
U. Lundqvist and J.D. Franckowiak. 1997. *BGN* 26:401.

Revised:
U. Lundqvist. 2007. *BGN* 37:271.

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 (2).
Located in chromosome 7H [1] (4).

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 (4). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg8.k* plants can be used to establish stands under field conditions (4). Endosperms of *seg8* developed as two-filled lateral lobes with no central endosperm lobe, resulting in a distinct dorsal crease (1).

Origin of mutant:
A spontaneous mutant in 60Ab1810-53 (Clho 15686) (3).

Mutational events:
seg8.k in 60Ab1810-53 (3, 4).

Mutant used for description and seed stocks:
seg8.k in 60Ab1810-53 (GSHO 2469); *seg8.k* in Bowman (PI 483237)*5 (GSHO 1854).

References:
1. 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.
2. Ramage, R.T. 1983. Chromosome location of shrunken endosperm mutants *seg6g* and *seg8k*. *Barley Genet. Newsl.* 13:64-65.
3. Ramage, R.T., and C.L. Crandall. 1981. BGS 453, Shrunken endosperm, *seg8*. *Barley Genet. Newsl.* 11:103.
4. Ramage, R.T., and C.L. Crandall. 1981. Shrunken endosperm mutant *seg8*. *Barley Genet. Newsl.* 11:34.

Prepared:
R.T. Ramage and C.L. Crandall. 1981. BGN 11:103 as BGS 453.

Revised:
R.T. Ramage. 1983. BGN 13:116 as BGS 453.
T. Tsuchiya. 1983. BGN 13:117. BGS number changed to BGS 455.
J.D. Franckowiak. 1997. BGN 26:405.
J.D. Franckowiak. 2007. BGN 37:272.

BGS 474, Laxatum-a, *lax-a*

Stock number: BGS 474
Locus name: Laxatum-a
Locus symbol: *lax-a*

Previous nomenclature and gene symbolization:

Laxatum-01 = *lax-01* (3, 6, 11).

Laxatum-a = *lax-a*⁰¹ (12).

Inheritance:

Monofactorial recessive (7, 11).

Located in chromosome 5HL [7L] (7, 10), about 2.4 cM proximal from the *ari-e* (breviaristatum-e) locus (5, 14), and about 3.1 cM from the *ert-g* (erectoides-g) locus (5, 12, 13).

Description:

Florets have five anthers with two developing from transformed lodicules (3, 15); however, the extra anthers are deficient in having two rather than four microsporangia (1). The grain is thin and angular and caryopses are exposed between the lemma and palea. The awn has a very wide base, without a distinct notch in the lemma attachment region. Rachis internodes are 13% longer than normal. Tillers arise at oblique angles giving isolated plants an appearance of a tufty growth habit (6). Treatment of leaves after tillering with GA₃ increases rachis internode length (15).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (2, 6, 9).

Mutational events:

lax-a.01 (NGB 116334), *-a.4* (NGB 116338), *-a.8* (NGB 116342), *-a.20* (NGB 116354), *-a.37* (NGB 116372), *-a.39* (NGB 116374), *-a.54* (NGB 116388) in Bonus (6, 9); *lax-a.92* (NGB 116425, NGB 116426) in Bonus (9); *lax-a.208* (NGB 116435, NGB 116436), *-a.218* (NGB 116446), *-a.222* (NGB 116450), *-a.229* (NGB 116457, NGB 116458), *-a.249*, *-a.256* (NGB 116483), *-a.278* (NGB 116503), *-a.286* (NGB 116510) in Foma (CIho 11333) (6, 8); *-a.353* (NGB 116559, NGB 116560), *-a.369* (NGB 116578, 116579), *-a.373* (NGB 116583), *-a.398* (NGB 116608), *-a.405* (NGB 116613), *-a.406* (NGB 116614) in Kristina (NGB 14661) (7); *-a.413* (NGB 116621, NGB 116622), *-a.434* (NGB 116647), *-a.437* (NGB 116650), *-a.444* (NGB 116658, NGB 116659), *-a.448* (NGB 116664), *-a.450* (NGB 116667, NGB 116668), *-a.455* (NGB 116674, NGB 116675), *-a.472* (NGB 116695) in Bonus (8); a *lax-a* mutant (Mut 2100/61) in Proctor (PI 280420) (4).

Mutant used for description and seed stocks:

lax-a.8 in Bonus (GSHO 1775); *lax-a.8* in Bowman (PI 483237)*7 (GSHO 2103).

References:

1. Bossinger, G., W. Rohde W, U. Lundqvist U, and F. Salamini F. 1992. Genetics of barley development: mutant phenotypes and molecular aspects. p. 231-264. In P.R. Shewry (ed.) Barley: Genetics, Biochemistry, Molecular Biology and Biotechnology. CAB International, Oxford.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:257-278.
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.

4. Häuser, H., and G. Fischbeck. 1972. Translocations and genetic analysis of other mutants. BGN 2:28-29.
5. Jensen, J. 1981. Construction of a barley chromosome 7 linkage map. p. 927-939. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.) Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp., Edinburgh. Edinburgh Univ. Press, Edinburgh.
6. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
7. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. Hereditas 103:269-279.
8. Lundqvist, U. (Unpublished).
9. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley II. Hereditas 63:1-28.
10. Persson, G., and A. Hagberg. 1965. Localization of nine induced mutations in the barley chromosomes. Barley Newsl. 8:52-54.
11. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
12. Søgaaard, B. 1974. Three-point tests on chromosome 1 and 7. BGN 4:70-73.
13. Søgaaard, B. 1977. The localization of eceriferum loci in barley. IV. Three point tests of genes on chromosome 7 in barley. Carlsberg Res. Commun. 42:35-43.
14. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.
15. Wettstein, D. von, Å. Gustafsson, and L. Ehrenberg. 1959. Mutationsforschung und Züchtung. p. 7-50. *In* Arbeitsgemeinschaft für Forschung des Landes Nordrhein-Westfalen, Heft 73. Westdeutscher Verlag Köln und Opladen.

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. BGN 16:57.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:421-422.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:273-274.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial incomplete dominant (2).

Location in chromosome 1HS [5S] (3), about 3.9 cM from the *Rsp3* (reaction to *Septoria passerinii* 3) locus (2), cosegregation with SCAR marker E-ACT/M-CAA-170a and close to the *Rsp3* locus (3), about 17.6 cM proximal from marker RFLP Act8 (3).

Description:

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

Origin of mutant:

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

Mutational events:

Rsp2.b in PI 70837.

Mutant used for description and seed stocks:

Rsp2.b in PI 70837 (GSHO 2511).

References:

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

Prepared:

D.C. Rasmusson. 1988. BGN 18:85 as BGS 466.

Revised:

J.D. Franckowiak. 1997. BGN 26:442.

J.D. Franckowiak. 2007. BGN 37:275.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial incomplete dominant (2).

Location in chromosome 1HS [5S] (3), about 3.9 cM from the *Rsp2* (reaction to *Septoria passerinii* 2) locus (2), cosegregation with SCAR marker E-ACT/M-CAA-170a and close to the *Rsp2* locus (3), about 17.6 cM proximal from marker RFLP Act8 (3).

Description:

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

Origin of mutant:

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

Mutational events:

Rsp3.c in Clho 10644.

Mutant used for description and seed stocks:

Rsp3.c in Clho 10644 (GSHO 2512).

References:

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

Prepared:

D.C. Rasmusson. 1988. BGN 18:86 as BGS 467.

Revised:

- J.D. Franckowiak. 1997. BGN 26:443.
J.D. Franckowiak. 2007. BGN 37:276.

BGS 518, Semidwarf 1, *sdw1*

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

Previous nomenclature and gene symbolization:

Denso dwarf = *denso* (5, 12).

Inheritance:

Monofactorial recessive (5, 13), although some F_1 's tend to be intermediate in height compared to their parents (1, 8).

Location in chromosome 3HL (2, 9), probably proximal from the *gsh2* (glossy sheath 2) locus, near RFLP marker PSR170 (9), in bin 3H-11 (7), near RFLP marker R1545 (16).

Description:

Plants homozygous for the *sdw1.a* gene range from 10 to 30 cm shorter than normal sibs, with expression partial dependent on environment (1, 12, 14). Spike length is variable, but fully as long as normal barley. The stock used for description of the *sdw1.a* gene, M21, has the short straw and long spike of the original 'Jotun Mutant' as well as a large culm diameter from its parent 'Vantage' (1, 14). The semidwarf mutants, 'Diamant' and 'Abed Denso', are alleles at the *sdw1* locus (5, 10). Alleles at the *sdw1* locus are associated with semiprostrate juvenile growth (5, 12), delayed maturity (4, 6, 12, 15), and reduced malt quality (4, 6, 12). The *sdw1* mutants are GA sensitive (3, 16), and they are very likely mutants in an orthologue of the rice *sd1* gene (16), which encodes a GA-oxidase that produces lower levels of GA and therefore causes the dwarf phenotype (11). The original cultivar 'Trumpf' was also marketed in the United Kingdom as 'Triumph'.

Origin of mutant:

An X-ray induced mutant in the Norwegian cultivar Jotun (PI 467357) isolated as Jotun 22 by Knut Mikaelson (1, 8).

Mutational events:

sdw1.a in Jotun (66/86, GSHO 1414) (14); *sdw1.c* (*denso*) in Abed Denso (PI 361639) (5); *sdw1.d* (Diamant) in Valticky (5); *sdw1.e* (Risø 9265) in Bomi (PI 43371) (5).

Mutant used for description and seed stocks:

sdw1.a in M21 (Clho 15481, GSHO 2513) from the cross Jotun Mutant/Kindred//Vantage (13); *sdw1.d* in Trumpf (Triumph, PI 548762, GSHO 2465); *sdw1.a* from a Jotun derivative in Bowman (PI 483237)*7 (GSHO 1978); *sdw1.d* from Trumpf in Bowman*4 (GSHO 1979).

References:

1. Ali, M.A.M., O. Okiror, and D.C. Rasmusson. 1978. Performance of semidwarf barley. *Crop Sci.* 18:418-422.
2. Barau, U.M., K.J. Chambers, W.T.B. Thomas, C.A. Hackett, V. Lea, P. Jack, B.P. Forster, R. Waugh, and W. Powell. 1993. Molecular mapping of genes determining height, time to heading, and growth habit in barley (*Hordeum vulgare*). *Genome* 36:1080-1087.
3. Boulger, M.C., R.G. Sears, and W.E. Kronstad. 1982. An investigation of the association between dwarfing sources and gibberellic acid response in barley. p. 550-553. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.)

Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp., Edinburgh. Edinburgh Univ. Press, Edinburgh.

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10. Mickelson, H.R., and D.C. Rasmusson. 1994. Genes for short stature in barley. *Crop Sci.* 34:1180-1183.
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Prepared:

D.C. Rasmusson. 1988. BGN 18:87 as BGS 468.

Revised:

J.D. Franckowiak. 1997. BGN 26:444-445.

J.D. Franckowiak. 2007. BGN 37:277-278.

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

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

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (3).
Located in chromosome 7H [1] (2) in the centromeric region closely linked to markers Bmag0217 and Bmac0162 in bins 6 to 7 (2).

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

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

Mutational events:
int-k.47 in Kristina (3).

Mutant used for description and seed stocks:
in-k.47 in Kristina (GSHO 1770, NGB 115465); *int-k.47* in Bowman (PI 483237)*6.

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

Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. *BGN* 26:472.

Revised:
U. Lundqvist and J.D. Franckowiak. 2007. *BGN* 37:279.

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

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

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Location is unknown.

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

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

Mutational events:
int-m.85 (NGB 115503) in Bonus (3); *int-m.la* (GSHO 1773) in Lamont (PI 512036) (2).

Mutant used for description and seed stocks:
int-m.85 in Bonus (GSHO 1772); *int-m.85* in Bowman (PI 483237)*7 (GSHO 2273); *int-m.la* in Bowman (PI 483237)*5 (GSHO 2274).

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

Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:473.

Revised:
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:280.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 5, 7, 9).
Located in chromosome 2HS (2), approximately 11.4 cM distal from SSR marker Bmac0134 (2), near the boundary between bins 2H-01 and 2H-02 (2).

Description:

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

Origin of mutant:

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

Mutational events:

ert-t.55 in Bonus (NGB 112654) (7); *brh3.g* (17:10:1, DWS1002), *brh3.h* (17:11:3, DWS1003), *brh3.i* (17:12:1, DWS1004) in Birgitta (NGB 1494, NGB 14667) (2, 3, 4, 8); *brh3.y* (10001, DWS1230, GSHO 1688) in Bido (PI 399485) (2, 3, 6).

Mutant used for description and seed stocks:

ert-t.55 in Bonus (GSHO 494); *ert-t.55* in Bowman (PI 483237)*7 (GSHO 2257); *brh3.g* in Birgitta (GSHO 1672); *brh3.g* in Bowman*7 (GSHO 2167); *brh3.y* in Bowman*6 (GSHO 2178).

References:

1. Börner, A. 1996. GA response in semidwarf barley. Barley Genet. Newsl. 25:24-26.
2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. BGN 24:56-59.
4. Franckowiak. 2002. BGS 631, Brachytic 3, *brh3*. BGN 32:132.
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. Gaul, H. 1986. (Personal communications).
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530.

8. Lehmann, L.C. 1985. (Personal communications).

9. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.

10. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and *erectoides* mutants. *Barley Genet. Newsl.* 6:79-81.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:492.

J.D. Franckowiak. 2002. BGS 631, Brachytic 3, *brh3*. BGN 32:132.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:281-282.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Location is unknown.

Description:

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

Origin of mutant:

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

Mutational events:

Rsg2.b in PI 426756 (1).

Mutant used for description and seed stocks:

Rsg2.b in PI 426756 (GSHO 2513).

References:

1. Merkle, O.G., J.A. Webster, and G.H. Mogen. 1987. Inheritance of a second source of greenbug resistance in barley. *Crop Sci.* 27:241-243.
2. Porter, D.R., J.D. Burd, and D.W. Mornhinweg. 2007. Differentiating greenbug resistance genes in barley. *Euphytica* 153:11-14.
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Prepared:

J.D. Franckowiak. 1997. BGN 26:503.

Revised:

J.D. Franckowiak. 2007. BGN 37:283.

BGS 586, Bracteatum-d, *bra-d*

Stock number: BGS 586
Locus name: Bracteatum-d
Locus symbol: *bra-d*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (1).

Located in chromosome 1HL [5L] (5), about 4.1 cM from AFLP marker E3634-7 (5), probably in bin 1H-14 based on the association with *trd1* (third outer glume 1) (2, 5).

Description:

The characteristic trait of this mutant is the presence of a bract (third outer glume) outside the two empty glumes of the central spikelet. The bract subtending the lowest spikelet is always the largest, embracing in some cases about one-half the spike. Bracts become progressively smaller toward the tip of the spike. Mutants have elongated basal rachis internodes (3, 4). Pozzi et al. (5) suggested that *bra-d.7* is allelic to *trd1* (third outer glume 1) or near the *trd1* locus. Allelism studies demonstrated that *bra-d.7* is not an allele at the *trd1* locus (3).

Origin of mutant:

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

Mutational events:

bra-d.7 (NGB 114310) in Foma (3).

Mutant used for description and seed stocks:

bra-d.7 in Foma (GSHO 1696); *bra-d.7* in Bowman (PI 483237)*3 (GSHO 2185).

References:

1. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
2. Kleinhofs, A. 2006. Integrating molecular and morphological/physiological marker maps. *Barley Genet. Newsl.* 36:66-82.
3. Lundqvist, U. (Unpublished).
4. Nybom, N. 1954. Mutation types in barley. *Acta Agric. Scand.* 4:430-456.
5. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *BGN* 26:513.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. *BGN* 37:284.

BGS 593, Awned palea 1, *adp1*

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

Previous nomenclature and gene symbolization:

Awned palea = *adp* (1).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 3HL (2), about 5.8 cM distal from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (2).

Description:

This mutant was isolated as a partially female sterile plant with abnormal spikes. The palea is elongated to form two awns (2), which are derived from two fused bracts that form the palea (3). Pistils are often transformed into leafy buds and result in low female fertility and greatly reduced seed set. Two of the anthers appear normal and the third is deformed to some extent (1). Pollen fertility is good (1).

Origin of mutant:

A spontaneous mutant in an inbred line (1).

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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

Prepared:

J.D. Franckowiak. 1998. BGN 28:34.

Revised:

J.D. Franckowiak. 2007. BGN 37:285.

BGS 599, Proanthocyanidin-free 17, *ant17*

Stock number: BGS 599
Locus name: Proanthocyanidin-free 17
Locus symbol: *ant17*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 3HS (1), it has been shown that *ant17.148* is an allele at the *seg3* (shrunken endosperm genetic 3, see BGS 379) locus (2).

Description:

Under normal growing conditions no anthocyanin pigmentation is observed in the mutant plants. The testa layers of the grain of the *ant17* mutants lack proanthocyanidins and catechins, but accumulate homoeriodictyol and chrysoeriol (7, 10). A full length cDNA clone from barley, coding for a protein consisting of 377 amino acids (42 kDa), has been isolated. It shows a homology of 71% to the flavanone-3-hydroxylase enzyme protein from *Antirrhinum majus* (12). It is likely that the *ant17* gene codes for one subunit and the *ant22* gene for the other subunit of the dimeric flavanone 3-hydroxylase enzyme, which catalyzes the conversion of flavanones into dihydroflavanols (7, 12). The mutant stock *ant17.148* was released as cultivar Galant (11). Alleles at the *ant17* locus that have been examined in the Bowman genetic background showed a variable reduction in kernel weight: *ant17.148* and *seg3.c* about 1/3 normal and *ant17.567* about 3/4 normal (2).

Origin of mutant:

A sodium azide induced mutant in Nordal (NGB 13680) (3).

Mutational events:

ant17.103, *17.104*, *17.105*, *17.139*, *17.140*, *17.142*, *17.143*, *17.145* in Nordal (4); *ant17.107* in Alf (NGB13682) (4); *ant17.147*, *17.148* (Galant) (NGB 13698), *17.150*, *17.151*, *17.153*, *17.154*, *17.180*, *17.185* in Triumph (PI 268180, NGB 13678) (4); *ant17.352* in Triumph (5); *ant17.160* in Gula Abed (NGB 13681) (4); *ant17.165*, *17.167*, *17.169*, *17.171*, *17.174*, *17.182* in Ark Royal (PI 447006) (4); *ant17.192*, *17.193* in Georgie (PI 447012, NGB 13683) (4); *ant17.199* in Secobra 4681 (4); *ant17.200* in Secobra 4681 (5); *ant17.208* in Hege 876 (4); *ant17.210*, *17.211*, *17.217* in Hege 802 (4); *ant 17.216* in Hege 802 (5); *ant17.220*, *17.221*, *17.224*, in Secobra 4743 (NGB 13679) (4); *ant17.227* in Ca 59995 (5); *ant17.231* in Tron (4); *ant17.237*, *17.239*, *17.241*, *17.242*, *17.247*, *17.249* in Gunhild (PI 464655, NGB 13690) (4); *ant17.243*, *17.246* in Gunhild (5); *ant17.250*, *17.251*, *17.252*, *17.253*, *17.255* in Tokak (PI 264251) (4); *ant17.267*, *17.268*, *17.269* in Secobra 18193 (NGB 13684) (4); *ant17.270* in Secobra 18193 (5); *ant17.280* in Hege 550/75 (NGB 13692) (9); *ant17.288*, *17.289*, *17.290* in Hege 550/75 (4); *ant17.293*, *17.294*, *17.295*, *17.296* in Bonus (PI 189763) (4); *ant17.297*, *17.298*, *17.300*, *17.301*, *17.307* in Ca 41507 (4); *ant17.306*, *17.340* in Ca 41507 (5); *ant17.316* in Ca 33787 (NGB 13693) (5); *ant17.318*, *17.321*, *17.326* in Harry (PI 491575) (5); *ant17.331* in Hege A2/A4 (5); *ant17.335*, *17.336*, *17.338* in Ackermann 724/5/7 (5); *ant17.359* in Hege15/74-1A (5); *ant17.370* in Ackermann 72/440 (5); *ant17.372*, *17.413*, *17.414*, *17.417*, *17.418*, *17.419*, *17.444* in Kaya (5); *ant17.375* in Fanette (6); *ant17.379*, *17.382*, *17.383*, *17.386*, *17.387*, *17.388*, *17.389*, *17.390*, *17.391*, *17.464*, *17.465* in Irene (5); *ant17.405* in Odin (6);

ant17.408 in KMJ 326 (5); ant17.410, 17.447 in Catrin (5); ant17.421 in VBS 18707 (5); ant17.422, 17.423, 17.424, 17.426 in NZ 3789 (5); ant17.432 in NZ 1836-3 (5); ant17.438, 17.439 in NZ 732.01 (5); ant17.440 in Nordal (5); ant17.450 in Ca 601427 (5); ant17.453, 17.455, 17.457, 17.458 in Ackermann 1734/5 (5); ant17.462 in Pamela (5); ant17.469, 17.470 in Grit (PI 548764, NGB 13685) (5); ant17.475 in Zenit (PI 564447, NGB 13686) (5); ant17.476 in Zenit (6); ant17.480 in Secobra 9709 (5); ant17.501 in Advance (Clho 15804) (4); ant17.504 in Karla (Clho 15860) (4); ant17.506, 17.507, 17.508, 17.509 in OR 9114 (4); ant17.515, 17.516, 17.518 in WA9037-75 (4); ant17.520 in WA9044-75 (4); ant17.530 in Morex (Clho15773) (4); ant17.537, 17.595, 17.619, 17.620 in Advance (5); ant17.560, 17.561, 17.563, 17.565, 17.567 in Manker (Clho 15549) (5); ant17.597 in Morex (6); ant17.598 in Morex (5); ant17.600 in S 80351 (5); ant17.601 in Moravian 111 (Clho 15812) (5); ant17.604 in Harrington (6); ant17.612 in Andre, (PI 469107) (5); ant17.624 in Klages (Clho 15478) (5); ant17.625 in Robust (M36, PI 476976) (5); ant17.630 in Azure (Clho 15865) (13); ant17.636, 17.658 in Cougarbar (PI 496400) (13); ant17.637 in 8892-78 (13); ant17.661 in Crest (PI 561409) (13); ant17.1502, 17.1505, 17.1519 in Amagi-Nijo (4); ant17.1510, 17.1511 in Haruna- Nijo (4); ant17.1515 in Nirakei 61 (4); ant17.1537 in Nirakei 62 (5); ant17.1544 in Nirakei 63 (5); ant17.1534 in Nirasaki-Nijo 14 (5); ant17.2022, 17.2067 in Natasha (PI 592171) (6); ant17.2084 in Hege 694/82 (9); ant17.2106 in Ca 708912 (8); ant17.5019 in Sonja (PI 302047) (9); ant17.5024 in Ackermann 72/27/4 (6); ant17.5028 in Trigger (PI 473541) (9); ant17.5034 in Kaskade (9); ant17.5035, 17.5036, 17.5037 in Video (6); ant17.5038, 17.5039, 17.5040, 17.5042 in Sonja (6); ant17.5044 in Ackermann 27/220/8 (6).

Mutant used for description and seed stock:

ant17.139 in Nordal (NGB 13697); ant17.148 (Galant) in Triumph (NGB 13698, GSHO 1628); ant17.148 in Bowman (PI 483237)*4 (GSHO 1973); ant17.567 in Manker (GSHO 1629); ant17.567 in Bowman*5 (GSHO 1974), seg3.c in Bowman (PI 483237)*7 (GSHO 1957).

References:

1. Boyd, P.W., and D. E. Falk. 1990. (Personal communications).
2. Franckowiak, J.D. (Personal communications).
3. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. *Barley Genet. Newsl.* 8:55-57.
4. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. *Barley Genet. Newsl.* 14:76-79.
5. Jende-Strid, B. 1988. Coordinator's report: Anthocyanin genes. Stock list of ant mutants kept at the Carlsberg Laboratory. *Barley Genet. Newsl.* 18:74-79.
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7. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. *Hereditas* 119:187-204.
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10. Jende-Strid, B., and K.N. Kristiansen. 1987. Genetics of flavonoid biosynthesis in barley. p. 445-453. *In: S. Yasuda and T. Konishi (eds.) Barley Genetics V. Proc. Fifth Int. Barley Genet. Symp., Okayama 1986. Sanyo Press Co., Okayama.*

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13. Ullrich, S., and J. Cochran. 1998. (Personal communications).

Prepared:

B. Jende-Strid. 1999. BGN 29:88-89.

Revised:

B. Jende-Strid and U. Lundqvist. 2007. BGN 37:286-288.

BGS 617, Uniculme 4, *cul4*

Stock number: BGS 617
Locus name: Uniculme 4
Locus symbol: *cul4*

Previous nomenclature and gene symbolization:

Uniculme-5 = *uc-5* (3).

Inheritance:

Monofactorial recessive (3).

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

Description:

Plants produce 1 to 4 tillers that are twisted and have slightly bowed culm internodes. All secondary tillers are shorter than the primary tiller and have a curly appearance. Often secondary tillers are trapped at the base of the primary tiller (2, 4). Compared to normal sibs, *cul4* plants have peduncles that are slightly to 50% longer. Rachis internodes are slightly elongated, and kernels are slightly longer. Plant height varies from 2/3 normal to slightly taller than Bowman. The mutant *cul4.15* exhibits the most variation in height over environments (2). Under greenhouse conditions, Bowman line for *cul4.5* developed only two axillary tillers, and it was unicum when combined with the *cul2.b* (unicum 2) gene (1).

Origin of mutant:

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

Mutational events:

cul4.3 in Bonus (GSHO 2495, NGB 115062), *cul4.5* in Bonus (NGB 115063), *cul4.15* (NGB 115064) in Foma (CIho 11333), *cul4.16* in Bonus (NGB 115065) (4).

Mutant used for description and seed stocks:

cul4.5 in Bonus (GSHO 2493, NGB 115063); *cul4.5* in Bowman (PI 483237)*7 (GSHO 2361).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unicum2 (*cul2*) mutant. *Theor. Appl. Genet.* 106:846–857.
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4. Lundqvist, U. (Unpublished).
5. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. BGN 32:118.

Revised:

J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:289.

BGS623, Eligulum-a, *eli-a*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2).
Location is unknown.

Description:

Plants do not have ligules in the junction between the sheath and leaf blade, auricles are rudimentary and asymmetrically displaced. Plants are about 2/3 of normal height and have very wide leaves (3, 4). The peduncle is short and spike emergence from the sheath of the flag leaf is poor. Spikes have a compact arrangement of spikelets and are extremely compacted near the tip (1, 3). The culm breaks very easily just below the nodes. The Bowman backcross-derived lines have glume awns that are nearly twice as long as those of Bowman, but the lemma awns are about 2/3 of normal (1).

Origin of mutant:

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

Mutational events:

eli-a.2 (NGB 115389), *eli-a.3* (NGB 115390), *-a.7* (NGB 115392), *-a.9* (NGB 115393), *-a.10* (NGB 115394) in Foma (3); *eli-a.11* (NGB 115395), *-a.14* (NGB 115397) in Kristina (NGB 1500); *eli-a.15* (NGB 115398), *-a.16* (NGB 151399) in Bonus (PI 189763 (4), *-a.216* (FN216) in Steptoe (Clho 15229) (1, 3).

Mutant used for description and seed stocks:

eli-a.3 in Foma (NGB 115390); *eli-a.3* in Bowman (PI 483237)*3.

References:

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

Prepared:

U. Lundqvist and J.D. Franckowiak. 2002. BGN 32:126.

Revised:

J.D. Franckowiak and A. Kleinhofs. 2005. BGN 35:192.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:290.

Barley Genetics Newsletter (2007) 37: 188-301

BGS 633, Many noded dwarf 6, *mnd6*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4).

Located in chromosome 5HL [7L] (5), near AFLP marker E3743-3 in subgroup 65 of the Proctor/Nudinka map (5).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

mnd6.6 in Bonus (GSHO 1713), *mnd6.6* in Bowman (PI 483237)*7 (GSHO 2235).

References:

1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
4. Lundqvist, U. (Unpublished).
5. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.

Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. BGN 32:134.

Revised:

U. Lundqvist and J. D. Franckowiak. 2007. BGN 37:291.

BGS 636, Tip sterile 2, *tst2*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).
Location is unknown.

Description:

Spikes of *tst2.b* plants are 1/4 to 1/2 of normal length because seed set fails in the upper portion of the spike. Slow or poor development of the spike reduces both the number of rachis internodes and number of fertile spikelets (1, 4). Most spikes of the Bowman backcross-derived line set less than 10 seeds. Plants are shorter than are normal sibs because peduncles fail to elongate normally. Both rachis internode length and awn length are reduced in *tst2* plants (1).

Origin of mutant:

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

Mutational events:

tst2.b in Donaria (Mut. 2249, DWS1337) (2, 3).

Mutant used for description and seed stocks:

tst2.b in Donaria (GSHO 1781); *tst2.b* in Bowman (PI 483237)*5 (GSHO 2280).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
3. Scholz, F. 1956. Mutationsversuche an Kulturpflanzen. V. Die Vererbung zweier sich variabel manifestierender Übergangsmerkmale von bespelzter zu nackter Gerste bei röntgeninduzierten Mutanten. Kulturpflanze 4:228-246.
4. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l.l. Kulturpflanze 6:123-166.

Prepared:

J.D. Franckowiak and U. Lundqvist. 2002. BGN 32:137.

Revised:

J.D. Franckowiak. 2005. BGN 35:193. (Locus symbol was changed from *lin2*.)
J.D. Franckowiak. 2007. BGN 37:292.

BGS 653, Brachytic 10, *brh10*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

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

Description:

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

Origin of mutant:

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

Mutational events:

brh10.1 in Birgitta (17:15:2, DWS1007) (4, 5).

Mutant used for description and seed stocks:

brh10.1 in Birgitta (GSHO 1677); *brh10.1* in Bowman (PI 483237)*7 (GSHO 2171).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:293.

BGS 654, Brachytic 11, *brh11*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS [7S] (1), about 6.7 cM proximal from SSR marker Bmac0113 in bin 5H-04 (1).

Description:

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

Origin of mutant:

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

Mutational events:

brh11.n in Birgitta (17:19:2, DWS1011) (4, 5).

Mutant used for description and seed stocks:

brh11.n in Birgitta (GSHO 1679); *brh11.n* in Bowman (PI 483237)*6 (GSHO 2172).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:294.

BGS 655, Brachytic 12, *brh12*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS [7S] (1), approximately 13.5 cM distal from SSR marker Bmag0387 in bin 5H-03 (1).

Description:

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

Origin of mutant:

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

Mutational events:

brh12.o in Birgitta (17:20:2, DWS1012) (4, 5).

Mutant used for description and seed stocks:

brh12.o in Birgitta (GSHO 1680); *brh12.o* in Bowman (PI 483237)*7 (GSHO 2173).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:295.

BGS 656, Brachytic 13, *brh13*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS [7S] (1), approximately 8.7 cM distal from SSR marker Bmag0387 in bin 5H-03 (1).

Description:

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

Origin of mutant:

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

Mutational events:

brh13.p in Birgitta (18:02:4, DWS1013) (4, 5).

Mutant used for description and seed stocks:

brh13.p in Birgitta (GSHO 1681); *brh13.p* in Bowman (PI 483237)*6 (GSHO 2174).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:296.

BGS 657, Brachytic 15, *brh15*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown (1).

Description:

Plants have numerous tillers with small leaves, spikes, and kernels. Prior to heading plants appear to be grassy culms similar to those produced by the *sld2* (slender dwarf 2) and *sld4* (slender dwarf 4) mutants, but heading is not drastically delayed. Culms and peduncles are about 1/2 normal length. Awns and rachis internodes are slightly shorter than those of normal sibs. Leaf blades are narrow and about 1/2 normal length. Mutant plants headed 2 to 3 days later than normal sibs. No lodging was observed. Spikes of *brh15* plants had nearly 4 fewer kernels than those of Bowman. Kernels of the Bowman *brh15* line are slightly shorter (8.6 vs. 9.6 mm), thinner (3.4 vs. 3.8 mm), and about 30% lighter than those of Bowman. The grain yield of the *brh15* line averaged about 2/3 of that recorded for Bowman (1, 2).

Origin of mutant:

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

Mutational events:

brh15.u in Julia (409 JK, DWS1156) (4, 6).

Mutant used for description and seed stocks:

brh15.u in 409 JK/Bowman (GSHO 1685); *brh15.u* in Bowman (PI 483237)*5 (GSHO 2176).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Micke, A. and M. Maluszynski, M. 1984. List of semi-dwarf cereal stocks. *In* Semi-dwarf Cereal Mutants and Their Use in Cross-breeding II. IAEA-TECDOC-307. IAEA, Vienna.
6. Szarejko I., M. Maluszynski, M. Nawrot, and B. Skawinska-Zydron, 1988. Semi-dwarf mutants and heterosis in barley. II. Interaction between several mutant genes responsible for dwarfism in barley. p. 241-246. *In* Semi-dwarf Cereal Mutants and their Use in Cross-breeding III. IAEA- TECDOC-455, IAEA, Vienna.

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:297.

BGS 658, Brachytic 17, *brh17*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).
Located in chromosome 5HS [7L] (1), approximately 11.6 cM proximal from SSR marker Bmag0387 in bin 5H-03 (1).

Description:

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

Origin of mutant:

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

Mutational events:

brh17.ab in Morex (Wa14355-83, Mo4, DWS1260) (4, 5).

Mutant used for description and seed stocks:

brh17.ab in Morex (GSHO 1669); *brh17.ab* in Bowman (PI 483237)*6 (GSHO 2181).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Nedel, J.L., S.E. Ullrich, J.A. Clancy, and W.L. Pan. 1993. Barley semidwarf and standard isotype yield and malting quality response to nitrogen. *Crop Sci.* 33:258-263.
6. Ullrich, S.E., and Aydin, A. 1988. Mutation breeding for semi-dwarfism in barley. p. 135-144. *In Semi-dwarf Cereal Mutants and Their Use in Cross-breeding III.* IAEA-TECDOC-455. IAEA, Vienna.

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:298.

BGS 659, Brachytic 18, *brh18*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 5HS [7L] (1), approximately 9.2 cM distal from SSR marker Bmac0163 in bin 5H-01(1).

Description:

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

Origin of mutant:

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

Mutational events:

brh18.ac in mo6/4*Triumph (402B, DWS1277) (4, 5).

Mutant used for description and seed stocks:

brh18.ac in Mo6/4*Triumph (GSHO 1670); *brh18.ac* in Bowman (PI 483237)*6 (GSHO 2182).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Falk, D. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:299.

BGS 660, Narrow leafed dwarf 2, *nld2*

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

Previous nomenclature and gene symbolization:
None.

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

Description:
Mutant plants have narrow, dark green leaves, which are erect with well-developed midribs. Auricles degenerate to tiny projections, but ligules are normal. Stem internodes are short, and the upper ones are curved. Spikelets are relatively narrow and small, and seed set may be low. Kernels of the Bowman *nld2* line are thinner (3.2 vs. 3.8 mm) and about 35% lighter than those of Bowman (1). Plants are 1/2 to 1/3 of normal height, the spike commonly emerges from the side of the sheath before anthesis. Awns of the *nld2.b* line are similar in length to those of Bowman. The *nld2.b* Bowman line is more vigorous than *nld1.a* in Christchurch, New Zealand and in North Dakota greenhouse nurseries, but *nld1.a* was more vigor in the Dundee, Scotland nursery. Seed yields are generally less than 20% of those of Bowman (1).

Origin of mutant:
A fast neutron induced mutant in Steptoe (Clho 15229) (2).

Mutational events:
nld2.b in Steptoe (2).

Mutant used for description and seed stocks:
nld2.b in Steptoe; *nld2.b* in Bowman (PI 483237)*6.

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

Prepared:
J.D. Franckowiak and A. Kleinhofs. 2007. BGN 37:300.

BGS 661, Double seed 1, *dub1*

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

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (2).
Located in chromosome 5HL [7L] (2), near AFLP marker E4038-4 in subgroups 66 to 67 of the Proctor/Nudinka map (2).

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

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

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

Mutant used for description and seed stocks:
dub1.1 (NGB 114331) in Bonus (2).

References:
1. Lundqvist, U. (Unpublished).
2. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.

Prepared:
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:301.