# Barley Genetics Newsletter

# Volume 47 - 2017

Barley spikes infected with Fusarium head blight

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# <<Information about the Barley Genetics Newsletter>>

The Barley Genetics Newsletter is published electronically at
https://wheat.pw.usda.gov/ggpages/bgn

The Barley Genetics Newsletter (BGN) was first published in 1971, and in the years since then has served to disseminate to the barley community announcements, memoria, informal research reports, and detailed descriptions of barley genetic stocks.

In recent years, new forms of rapid communication of ideas and data, principally on-line, have reduced the demand for many aspects of BGN. At the 12th International Barley Genetics Symposium, held in Minneapolis, Minnesota, USA June 26-30, 2016, discussion of the fate of BGN resulted in the consensus that a forum for informal communication, memoria, documentation of resources, and any other topic of interest to the community was beneficial.

Thanks to resources provided by GrainGenes, past issues of BGN will be preserved and available in electronic format. GrainGenes will serve also as a mechanism for publishing new submissions from the barley community.

Contributions to the Barley Genetics Newsletter can be sent to Phil Bregitzer, phil.bregitzer@ars.usda.gov. Dr. Bregitzer can be reached also at 208-397-4162 ext. 116.

## Acknowledgements

BGN has been made possible by the contributors of research reports, the diligence of the many coordinators, and by the special efforts of leaders in the barley genetics community. Of special note, the compilation of the detailed and extensive new and updated barley genetic stock descriptions published in the last several issues of BGN has been made possible by the time and expertise of Jerry Franckowiak and Udda Lundqvist. Special thanks to the USDA-ARS GrainGenes team.

*Barley Genetics Newsletter (2017) 47;1-4.*

# Descriptions of Barley Genetic Stocks for 2017

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In this volume of the Barley Genetics Newsletter seventy revised and new Barley Genetic Stock (BGS) descriptions are published (Table 1). The current lists of new and revised BGS descriptions, including those in Table 1, are presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in another section of this issue. Information on the description location, recommended locus name, chromosomal location, previous gene symbols, and the primary genetic stock (GSHO number and/or NGB number) are included in these lists. The GSHO stocks are held in the USDA-ARS Barley Genetic Stocks collection at the National Small Grains Collection (U.S. Department of Agriculture – Agricultural Research Service, National Small Grains Germplasm Research Facility, 1691 S 2700 W) Aberdeen, ID 83210, USA. The NGB stocks are held in the Nordic Genetic Resource Center (NordGen), Smedjevägen 3, SE-230 53 Alnarp, Sweden. This information is available through the Internet at the following addresses:

**(1) www.ars.usda.gov.PacWest/Aberdeen**

**(2) www.ars-grin.gov:7000/npgs/descriptors/barley-genetics (GRIN)**

**(3) http://wheat.pw.usda.gov/ggpages/bgn/**

**(4) http:/www.nordgen.org/sesto**

**(5) http://www.nordgen.org/bgs**

**Table 1.** A listing of new and revised Barley Genetic Stock (BGS) descriptions published in volume 47 of the Barley Genetics Newsletter, giving recommended locus symbols and names, chromosomal locations, and stock source information.

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 1 | brh1 | br, ari-i | 7HS | Brachytic 1 | 47:50 | 25 |
| 51 | rtt1 | rt | 2HS | Rattail spike 1 | 47:53 | 216 |
| 65 | Eam1 | Ea, Ppd-H1 | 2HS | Early maturity 1 | 47:54 | 1316 |
| 67 | Vrs1.t | $V^t$ | 2HL | Six-rowed spike 1 (Deficiens 1) | 47:57 | 684 |
| 69 | Gth1 | G | 2HL | Toothed lemma1 | 47:59 | 309 |
| 79 | wst7 | rb | 2HL | White streak 7 | 47:61 | 247 |
| 82 | Zeo1 | Ert-r, Knd | 2HL | Zeocriton 1 | 47:63 | 1613 |
| 89 | ari-g | lk10 | 2H | Breviaristatum-g | 47:66 | 1655 |
| 97 | acr1 | acr, ril | 2HL | Accordion rachis 1 | 47:68 | 1617 |
| 102 | uzu1 | uz, ert-ii, HvBRI1 | 3HL | Uzu 1 or Semibrachytic 1 | 47:70 | 1300 |
| 118 | lnt1 | rnt, int-l | 3HL | Lower number of tillers 1 | 47:74 | 833 |
| 124 | vrs4 | v4, mul, int-e, HvRA2 | 3HL | Six-rowed spike 4 | 47:76 | 775 |
| 131 | gra-a | gran-a | 7H | Granum-a | 47:79 | 1757 |
| 155 | glf1 | gl1, cer-zh | 4HL | Glossy leaf 1 | 47:81 | 98 |
| 157 | brh2 | br2, ari-l | 4HL | Brachytic 2 | 47:84 | 573 |
| 165 | glf3 | gl3, cer-j | 4HL | Glossy leaf 3 | 47:86 | 577 |
| 172 | lks5 | lk5, ari-c | 4HL | Short awn 5 | 47:89 | 1297 |
| 178 | int-c | i, v5, HvTB1 | 4HS | Intermedium spike-c | 47:91 | 776 |
| 184 | Zeo3 | Mo1, Zeo2, cly1.c | 2HL | Zeocriton 3 | 47:95 | 1611 |
| 188 | Alp1 | Alp, Pht | 4HL | Aluminum tolerance 1 | 47:98 | 1297 |
| 189 | Acr2 | acr, lax | 4HL | Accordion rachis 2 | 47:101 | 1071 |
| 229 | cud2 | cud2 | 1HL | Curly dwarf 2 | 47:103 | 1712 |
| 238 | ari-t | ari-25 | 1H | Breviaristatum-t | 47:104 | 1611 |
| 241 | Acr3 | acr | 1HL | Accordion rachis 3 | 47:105 | 1071 |
| 258 | dsp9 | l9, ert-e | 6HL | Dense spike 9 | 47:107 | 1774 |
| 266 | ert-e | l9, dsp9 | 6HL | Erectoides-e | 47:109 | 477 |
| 275 | lfl1 | lfl | 6HL | Leafless 1 | 47:111 | 609 |
| 314 | vrs2 | v2, int-b | 5HL | Six-rowed spike 2 | 47:113 | 773 |
| 315 | vrs3 | v3, int-a | 1HL | Six-rowed spike 3 | 47:115 | 774 |
| 320 | int-b | vrs2 | 5HL | Intermedium spike-b | 47:118 | 1764 |
| 328 | ari-e | lk9, GPert | 5HL | Breviaristatum-e | 47:120 | 1653 |
| 332 | Ert-r | Zeo1 | 2HL | Erectoides-r | 47:123 | 492 |
| 352 | gsh2 | gs2, cer-b | 3HL | Glossy sheath 2 | 47:125 | 736 |
| 355 | gsh5 | gs5, cer-s | 2HL | Glossy sheath 5 | 47:128 | 739 |
| 402 | cer-g | cer-g | 2HL | Eceriferum-g | 47:131 | 428 |

Table 1. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| 439 | cer-zv | cer-zv | 4HL | Eceriferum-zv | 47:133 | 1529 |
| 473 | com1 | lax-270, bir1 | 5HL | Compositum 1 | 47:135 | 1702 |
| 475 | lax-c | lax-21 | 6HL | Laxatum-c | 47:137 | 1777 |
| 476 | lax-d | lax-83 | | Laxatum-d | 47:139 | |
| 477 | lax-f | lax-61 | | Laxatum-f | 47:140 | |
| 478 | lax-g | lax-25 | | Laxatum-g | 47:141 | |
| 479 | lax-h | lax-26 | 3H | Laxatum-h | 47:142 | |
| 480 | lax-i | lax-50 | | Laxatum-i | 47:144 | |
| 481 | lax-j | lax-49 | 2H | Laxatum-j | 47:145 | |
| 482 | lax-k | lax-84 | 2H/3H | Laxatum-k | 47:147 | |
| 483 | lax-l | lax-60 | 1H | Laxatum-l | 47:148 | |
| 484 | lax-m | lax-80 | | Laxatum-m | 47:149 | |
| 485 | lax-n | lax-67 | 2H/4HL /5H | Laxatum-n | 47:150 | |
| 486 | lax-o | lax-79 | | Laxatum-o | 47:152 | |
| 487 | lax-df | lax-204 | | Laxatum-df | 47:153 | |
| 488 | lax-ef | lax-225 | 2H | Laxatum-ef | 47:154 | |
| 489 | lax-ff | lax-216 | | Laxatum-ff | 47:156 | |
| 490 | lax-gf | lax-217 | | Laxatum-gf | 47:157 | |
| 491 | lax-hf | lax-244 | 2H/3HL /5H | Laxatum-hf | 47:158 | |
| 492 | lax-if | lax-246 | | Laxatum-if | 47:160 | |
| 493 | Lax-jf | lax-253 | 4HS | Laxatum-jf | 47:161 | 1571 |
| 494 | lax-kf | lax-295 | | Laxatum-kf | 47:163 | |
| 495 | lax-lf | lax-274 | | Laxatum-lf | 47:164 | |
| 496 | lax-mf | lax-302 | | Laxatum-mf | 47:165 | |
| 497 | lax-nf | lax-322 | 2HL/4H | Laxatum-nf | 47:166 | |
| 518 | sdw1 | denso, Hv20ox$_2$ | 3HL | Semidwarf 1 | 47:168 | 2513 |
| 525 | cer-yl | cer-yl | 4HL | Eceriferum-yl | 47:171 | 1545 |
| 526 | cer-ym | cer-ym | 4HL | Eceriferum-ym | 47:173 | 1546 |
| 554 | ari-m | brh1 | 7HS | Breviaristatum-m | 47:175 | 1661 |
| 614 | Zeo2 | Zeo, cly1.b, HvAP2 | 2HL | Zeocriton 2 | 47:177 | 637 |
| 679 | acr4 | acr-3 | 2H/6HL | Accordion rachis 4 | 47:181 | |
| 740 | Pbg1 | Pbg | 7H | Pubescence on glume 1 | 47:182 | |
| 741 | stb1 | stb | | Stubble 1 | 47:183 | |
| 743 | twk1 | tw | 7H | Tweaky spike 1 | 47:185 | |
| 744 | acr5 | acr-2 | 7H | Accordion rachis 5 | 47:187 | 2153 |

* Recommended locus symbols are based on utilization of a three letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

† Chromosome numbers and arm designations are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

‡ The seed stock associated with each BGS number is held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Grains Germplasm Research Facility, Aberdeen, Idaho, USA.

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# Descriptions of Barley Genetic Stocks
# Tables 2 and 3 (2017)

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In this section of the Barley Genetics Newsletter volume 47, you will find two updated tables with new and revised barley locus descriptions. The descriptions are listed by BGS numbers (Table 2) and by alphabetic order using the existing and recommended locus symbols (Table 3). As research in barley is proceeding rapidly, it is necessary to update the latest research and findings about specific barley genes.

Table 2. A listing of Barley Genetic Stock (BGS) descriptions in volume 47 and recent issues of the Barley Genetics Newsletter with recommended locus symbols, recommended locus names, chromosome location information, description citation, and stock location information.

Table 3. An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on recommended locus names, recommended locus symbols, chromosomal locations, description citation, and original cultivars.

**Table 2.** A listing of Barley Genetic Stock (BGS) descriptions in recent issues of the Barley Genetics Newsletter with recommended locus symbols, recommended locus names, chromosome location information, description citation, and stock location information.

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 1 | brh1 | br, ari-i | 7HS | Brachytic 1 | 47: 50 | 25 |
| 2 | fch12 | $f_c$, clo-fc | 7HS | Chlorina seedling 12 | 41: 60 | 36 |
| 3 | yvs2 | $y_c$ | 7HS | Virescent seedling 2 | 26: 46 | 41 |
| 4 | abo8 | $a_{c2}$, alb-m | 7HS | Albino seedling 8 | 26: 47 | 61 |
| 5 | fch8 | f8 | 7HS | Chlorina seedling 8 | 41: 62 | 40 |
| 6 | vrs1 | v, Int-d | 2HL | Six-rowed spike 1 | 37:192 | 196 |
| 7 | nud1 | n, h | 7HL | Naked caryopsis 1 | 44: 51 | 115 |
| 9 | dsp1 | l | 7HS | Dense spike 1 | 43: 50 | 1232 |
| 10 | lks2 | lk2, lk4 | 7HL | Short awn 2 | 45: 80 | 566 |
| 11 | ubs4 | lks2, ari-d | 7HL | Unbranched style 4 | 45: 84 | 567 |
| 12 | des1 | lc | 7H | Desynapsis 1 | 42: 58 | 592 |
| 13 | des4 | des4 | 7H | Desynapsis 4 | 44: 54 | 595 |
| 14 | des5 | des5 | 7HL | Desynapsis 5 | 44: 56 | 596 |
| 15 | blx1 | bl | 4HL | Non-blue aleurone xenia 1 | 26: 60 | 185 |
| 16 | wax1 | wx, glx | 7HS | Waxy endosperm 1 | 42: 65 | 908 |
| 17 | fch4 | f4, yv | 7HL | Chlorina seedling 4 | 43: 54 | 1214 |
| 18 | fch5 | f5, yv2 | 7HS | Chlorina seedling 5 | 43: 56 | 1215 |
| 19 | blx2 | bl2 | 7HS | Non-blue aleurone xenia 2 | 26: 65 | 209 |
| 20 | Rym2 | Ym2 | 7HL | Reaction to BaYMV 2 | 26: 66 | 984 |
| 21 | Run1 | Un | 7HS | Reaction to *Ustilago nuda* 1 | 26: 67 | 1324 |
| 22 | Rsg1 | Grb | 7H | Reaction to *Schizaphis graminum* 1 | 37:199 | 1317 |
| 23 | wnd1 | wnd | 4HL | Winding dwarf 1 | 42: 74 | 2499 |
| 24 | fst3 | fs3 | 7HS | Fragile stem 3 | 41: 74 | 1746 |
| 25 | Xnt1 | $X_a$ | 7HL | Xantha seedling 1 | 26: 71 | 1606 |
| 26 | snb1 | sb | 7HS | Subnodal bract 1 | 26: 72 | 1217 |
| 27 | lbi3 | lb3 | 7HL | Long basal rachis internode 3 | 42: 79 | 536 |
| 28 | ert-a | ert-a | 7HS | Erectoides-a | 41: 76 | 468 |
| 29 | ert-d | ert-d | 7HS | Erectoides-d | 42: 82 | 475 |
| 30 | ert-m | ert-m | 7HS | Erectoides-m | 46: 47 | 487 |
| 31 | sex6 | ssIIa | 7HS | Shrunken endosperm xenia 6 | 45: 86 | 2476 |
| 32 | Rph9 | Pa9, Pa12 | 5HL | Reaction to *Puccinia hordei* 9 | 37:201 | 1601 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 33 | ant1 | rs, rub-a | 7HS | Anthocyanin-less 1 | 46: 49 | 1620 |
| 34 | msg50 | msg,,hm | 7HL | Male sterile genetic 50 | 45: 88 | 2404 |
| 35 | rsm1 | sm | 7HS | Reaction to BSMV 1 | 26: 84 | 2492 |
| 36 | xnt4 | $x_{c2}$ | 7HL | Xantha seedling 4 | 26: 85 | 42 |
| 37 | xnt9 | xan,,i | 7HL | Xantha seedling 9 | 26: 86 | 584 |
| 38 | smn1 | smn | 3H/5H | Seminudoides 1 | 43: 58 | 1602 |
| 39 | mss2 | mss2 | 7HS | Midseason stripe 2 | 44: 59 | 2409 |
| 40 | prm1 | prm | 7HS | Premature ripe 1 | 44: 60 | 2429 |
| 41 | brh7 | brh.w | 7H | Brachytic 7 | 42: 98 | 1687 |
| 42 | Pyr1 | Pyr.g, Pyr.i | 3HL | Pyramidatum 1 | 41: 78 | 1581 |
| 43 | mov1 | mo5 | 7HL | Multiovary 1 | 43: 59 | 3641 |
| 44 | brh16 | brh.v, ari-o | 7HL | Brachytic 16 | 45: 89 | 1686 |
| 45 | sdw4 | | 7HL | Semidwarf 4 | 46: 51 | |
| 48 | Rpt4 | QRpt7 | 7HL | Reaction to *Pyrenophora teres* 4 | 43: 61 | |
| 49 | sld8 | sld.i | 7HS/ 4HL | Slender dwarf 8 | 43: 63 | 2484 |
| 51 | rtt1 | rt | 2HS | Rattail spike 1 | 47: 53 | 216 |
| 52 | fch15 | or | 2HS | Chlorina seedling 15 | 40: 48 | 49 |
| 53 | abo2 | a2 | 2HS | Albino seedling 2 | 26: 89 | 70 |
| 55 | fch1 | f, lg | 2HS | Chlorina seedling 1 | 40: 49 | 112 |
| 56 | wst4 | wst4 | 2HL | White streak 4 | 44: 61 | 568 |
| 57 | eog1 | e, lep-e | 2HL | Elongated outer glume 1 | 43: 64 | 29 |
| 58 | vrs1 | lr, $v^{lr}$ | 2HL | Six-rowed spike 1 | 26: 94 | 153 |
| 59 | gpa1 | gp, gp2 | 2HL | Grandpa 1 | 45: 91 | 1379 |
| 60 | lig1 | li, aur-a | 2HL | Liguleless 1 | 45: 93 | 6 |
| 61 | trp1 | tr | 4HL | Triple awned lemma 1 | 41: 82 | 210 |
| 62 | sbk1 | sk, cal-a | 2HS | Subjacent hood 1 | 40: 51 | 267 |
| 63 | yvs1 | $y_x$, alb-c.7 | 2HS | Virescent seedling 1 | 26: 99 | 68 |
| 64 | des7 | des7 | 3H | Desynapsis 7 | 43: 67 | 598 |
| 65 | Eam1 | Ea, Ppd-H1 | 2HS | Early maturity 1 | 47: 54 | 1316 |
| 66 | vrs1 | $V^d$ | 2HL | Two-rowed spike 1 | 26:103 | 346 |
| 67 | vrs1.t | $V^t$ | 2HL | Deficiens 1 | 47: 57 | 684 |

Table 2. (continued)

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 68 | Pvc 16 | $P_c$ | 2HL | Purple veined lemma 1 | 44: 67 | 132 |
| 69 | Gth 1 | G | 2HL | Toothed lemma 1 | 47: 59 | 309 |
| 70 | Rph1 | Pa | 2H | Reaction to *Puccinia hordei* 1 | 26:107 | 1313 |
| 71 | com2 | bir2 | 2HS | Compositum 2 | 45: 95 | 1700 |
| 74 | flo-c | flo-a | 6HL | Extra floret-c | 45: 97 | 1743 |
| 75 | Lks1 | Lk | 2HL | Awnless 1 | 41: 84 | 44 |
| 76 | Pre2 | Re2, P | 2HL | Red lemma and pericarp 2 | 46: 53 | 234 |
| 77 | hcm1 | h | 2HL | Short culm 1 | 26:113 | 2492 |
| 78 | mtt4 | mtt,,e, mt | 2HL | Mottled leaf 4 | 41: 86 | 1231 |
| 79 | wst7 | rb | 2HL | White streak 7 | 47: 61 | 247 |
| 80 | ant2 | pr, rub | 2HL | Anthocyanin-less 2 | 46: 55 | 1632 |
| 81 | gsh7 | gs7 | 1H/2H /5H | Glossy sheath 7 | 40: 55 | 1759 |
| 82 | Zeo1 | Knd, Ert-r | 2HL | Zeocriton 1 | 47. 63 | 1613 |
| 83 | sld2 | sld2 | 2HS | Slender dwarf 2 | 44: 74 | 2491 |
| 84 | mss1 | mss | 5H | Midseason stripe 1 | 44: 75 | 1404 |
| 85 | yst4 | yst4 | 2HL | Yellow streak 4 | 44: 76 | 2502 |
| 86 | fch13 | f13 | 5HL | Chlorina seedling 13 | 44: 77 | 16 |
| 87 | fch14 | f14 | 2HL | Chlorina seedling 14 | 44: 78 | 1739 |
| 88 | Rph2 | Pa2, A | 5HS | Reaction to *Puccinia hordei* 2 | 37:212 | 1593 |
| 89 | ari-g | lk10 | 2H | Breviaristatum-g | 47: 66 | 1655 |
| 90 | ert-j | ert-j | 2H | Erectoides-j | 43: 70 | 484 |
| 91 | ert-q | ert-q | 6H | Erectoides-q | 43: 71 | 1562 |
| 92 | ert-u | br5, ari-o | 7HL | Erectoides-u | 45:100 | 496 |
| 93 | ert-zd | br7, ari-o | 7HL | Erectoides-zd | 45:102 | 504 |
| 94 | abo4 | a4 | 2H | Albino seedling 4 | 26:133 | 167 |
| 95 | abo13 | alb,,p | 2HL | Albino seedling 13 | 26:134 | 585 |
| 96 | Rph15 | Rph16 | 2HS | Reaction to *Puccinia hordei* 15 | 37:214 | 1586 |
| 97 | acr1 | acr, ril | 2HL | Accordion rachis 1 | 47: 68 | 1617 |
| 98 | Eam6 | Ea6, Ea, HvCEN | 2HS | Early maturity 6 | 46: 57 | |
| 99 | lin1 | s, rin | 2HL | Lesser internode number 1 | 41: 92 | 2492 |
| 100 | sld4 | sld.d | 2HS | Slender dwarf 4 | 43: 72 | 2479 |
| 101 | als1 | als | 3HL | Absent lower laterals 1 | 43: 74 | 1065 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 102 | uzu1 | uz, ert-ii, HvBRI1 | 3HL | Uzu 1 or semi brachytic 1 | 47: 70 | 1300 |
| 104 | yst1 | yst, ys | 3HS | Yellow streak 1 | 42:178 | 1140 |
| 105 | xnt3 | $x_c$, vir-l | 3HS | Xantha seedling 3 | 26:139 | 66 |
| 106 | abo6 | $a_c$ | 3HS | Albino seedling 6 | 46: 60 | 30 |
| 107 | wst1 | wst, wst3 | 3HL | White streak 1 | 41: 97 | 159 |
| 108 | alm1 | al, ebu-a | 3HS | Albino lemma 1 | 46: 61 | 270 |
| 109 | yst2 | yst2 | 3HS | Yellow streak 2 | 44: 81 | 570 |
| 111 | dsp10 | $l_c$ | 3HL | Dense spike 10 | 41: 99 | 71 |
| 112 | abo9 | $a_n$ | 3HS | Albino seedling 9 | 26:146 | 348 |
| 113 | xnt6 | $x_s$ | 3HS | Xantha seedling 6 | 26:147 | 117 |
| 114 | cur2 | cu2 | 3HL | Curly 2 | 44: 82 | 274 |
| 115 | btr1 | bt1 | 3HS | Non-brittle rachis 1 | 43: 78 | 1233 |
| 116 | btr2 | bt2 | 3HS | Non-brittle rachis 2 | 43: 80 | 842 |
| 117 | fch2 | f2, lg5 | 3HL | Chlorina seedling 2 | 46: 63 | 107 |
| 118 | lnt1 | rnt, int-l | 3HL | Low number of tillers 1 | 47: 74 | 833 |
| 119 | des2 | ds | 3H | Desynapsis 2 | 43: 84 | 593 |
| 120 | zeb1 | zb | 3HL | Zebra stripe 1 | 43: 86 | 1279 |
| 121 | Rph3 | Pa3 | 7HL | Reaction to *Puccinia hordei* 3 | 26:156 | 1316 |
| 122 | Rph5 | Pa5, Pa6 | 3HS | Reaction to *Puccinia hordei* 5 | 37:224 | 1597 |
| 123 | Ryd2 | Yd2 | 3HL | Reaction to BYDV 2 | 26:158 | 1315 |
| 124 | vrs4 | v4, int-e, HvRA2 | 3HL | Six-rowed spike 4 | 47: 76 | 775 |
| 125 | lzd1 | dw4 | 3H | Lazy dwarf 1 | 43: 87 | 1787 |
| 126 | sld1 | dw1 | 3HL | Slender dwarf 1 | 41:103 | 2488 |
| 127 | Pub1 | Pub | 3HL | Pubescent leaf blade 1 | 44: 84 | 1576 |
| 128 | sca1 | sca | 3HS | Short crooked awn 1 | 44: 85 | 2439 |
| 129 | wst6 | wst,,j | 3HL | White streak 6 | 41:105 | 2500 |
| 130 | eam10 | $ea_{sp}$ | 3HL | Early maturity 10 | 44: 86 | 2504 |
| 131 | gra-a | gran-a | 7H | Granum-a | 47: 79 | 1757 |
| 132 | ari-a | ari-a, lk7 | 3HS | Breviaristatum-a | 41:106 | 1648 |
| 133 | sdw2 | sdw-b | 3HL | Semidwarf 2 | 45:108 | 2466 |
| 134 | ert-c | ert-c | 3HL | Erectoides-c | 41:108 | 471 |
| 135 | ert-ii | uzu1 | 3HL | Erectoides-ii | 45:104 | 483 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 136 | Rph7 | Pa7, Pa5 | 3HS | Reaction to *Puccinia hordei* 7 | 37:228 | 1318 |
| 137 | Rph10 | Rph10 | 3HL | Reaction to *Puccinia hordei* 10 | 26:174 | 1588 |
| 138 | nec4 | nec4 | 3H | Necrotic leaf spot 4 | 43: 88 | |
| 139 | nec5 | nec5 | 3H | Necrotic leaf spot 5 | 43: 89 | |
| 140 | xnt8 | xan,,h | 3HS | Xantha seedling 8 | 26:177 | 582 |
| 141 | rym5 | Ym | 3HL | Reaction to barley yellow mosaic virus 5 | 32: 90 | |
| 142 | brh8 | brh.ad | 3HL | Brachytic 8 | 42:232 | 1671 |
| 143 | sex8 | sex.j | 3HS | Shrunken endosperm xenia 8 | 43: 90 | 2471 |
| 144 | sld5 | sld5 | 3HS | Slender dwarf 5 | 44: 90 | 2483 |
| 146 | cal-d | cal-d | 3H | Calcaroides-d | 40: 58 | 1698 |
| 147 | mov2 | mo | 3HS | Multiovary 2 | 43: 91 | 3642 |
| 148 | brh14 | brh.q,<br>ari-o | 7HL | Brachytic 14 | 45:111 | 1682 |
| 149 | Rpc1 | | 3H | Reaction to *Puccinia coronata* var. *hordei* 1 | 37:232 | 1601 |
| 150 | scl-b | scl-5 | 3H/6H | Scirpoides leaf-b | 40: 60 | |
| 151 | fch9 | f9 | 4HS | Chlorina seedling 9 | 44: 92 | 571 |
| 152 | Kap1 | K | 4HS | Hooded lemma 1 | 26:179 | 985 |
| 155 | glf1 | gl, cer-zh | 4HL | Glossy leaf 1 | 47: 81 | 98 |
| 156 | lbi2 | lb2, ert-i | 4HS | Long basal rachis internode 2 | 44: 93 | 572 |
| 157 | brh2 | br2, ari-l | 4HL | Brachytic 2 | 47: 84 | 573 |
| 158 | yhd1 | yh | 4HL | Yellow head 1 | 42:250 | 574 |
| 160 | min2 | en-min | | Enhancer of minute 1 | 26:186 | 266 |
| 161 | min1 | min | 4HL | Semi-minute dwarf 1 | 44: 97 | 987 |
| 163 | sgh1 | sh1 | 4HL | Spring growth habit 1 | 26:188 | 575 |
| 164 | Hln1 | Hn | 4HL | Hairs on lemma nerves 1 | 44: 99 | 576 |
| 165 | glf3 | gl3, cer-j | 4HL | Glossy leaf 3 | 47: 86 | 577 |
| 166 | msg25 | msg,,r | 4HL | Male sterile genetic 25 | 45:113 | 744 |
| 167 | rym1 | Ym | 4HL | Reaction to barley yellow mosaic virus 1 | 32: 96 | |
| 168 | glo-a | glo-a | 4H | Globosum-a | 45:115 | 1328 |
| 169 | lgn2 | lg2 | 4HS | Light green 2 | 42:264 | 171 |
| 170 | lgn3 | lg3, lg7 | 1HL | Light green 3 | 44:103 | 171 |
| 171 | lgn4 | lg4, lg1 | 4HL | Light green 4 | 44:105 | 681 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 172 | lks5 | lk5, ari-c | 4HL | Short awn 5 | 47: 89 | 1297 |
| 173 | blx3 | bl3 | 4HL | Non-blue aleurone xenia 3 | 26:198 | 2506 |
| 174 | blx4 | bl4 | 4HL | Non-blue (pink) aleurone xenia 4 | 26:199 | 2507 |
| 176 | ovl1 | ovl | 4H | Ovaryless 1 | 35:191 | |
| 177 | fch10 | | 4H | Chlorina seedling 10 | 43: 95 | 1737 |
| 178 | int-c | i, vrs5 HvTB1 | 4HS | Intermedium spike-c | 47: 91 | 776 |
| 179 | Hsh1 | Hs | 4HL | Hairy leaf sheath 1 | 44:107 | 986 |
| 180 | sid1 | nls | 4HL | Single internode dwarf 1 | 43: 97 | 2477 |
| 181 | eam9 | ea,,c | 4HL | Early maturity 9 | 26:204 | 1732 |
| 182 | flo-a | flo-a | 6HL | Extra floret-a | 45:116 | 1741 |
| 183 | Ynd1 | Yn | 4HS | Yellow node 1 | 44:109 | 1607 |
| 184 | Zeo3 | Zeo2, cly1.c | 4HL | Zeocriton 3 | 47: 95 | 1611 |
| 185 | brh5 | brh.m | 4HS | Brachytic 5 | 44:110 | 1678 |
| 186 | sld3 | ant17.567 | 4HS | Slender dwarf 3 | 40: 63 | 2480 |
| 187 | brh9 | brh.k | 4HL | Brachytic 9 | 43: 99 | 1676 |
| 188 | Alp1 | Alp, Pht | 4HL | Aluminum tolerance 1 | 47: 98 | |
| 189 | Acr2 | acr, lax | 4HL | Accordion rachis 2 | 47:101 | 1071 |
| 190 | tfm1 | | 1HL | Thick filament 1 | 40: 67 | |
| 191 | fch17 | vy | 1H/3H | Chlorina seedling 17 | 40: 68 | 1079 |
| 193 | viv-b | viv-6 | 4HS | Viviparoides-b | 43:100 | |
| 194 | sld7 | sld.f | 4HL | Slender dwarf 7 | 43:101 | 2481 |
| 195 | sex9 | sex.l | 4HL | Shrunken endosperm xenia 9 | 43:102 | 2473 |
| 196 | sdw7 | sdw.u | 4HL | Semidwarf 7 | 43:103 | 2462 |
| 197 | nec34 | nec.k | 4HS | Necroticans 34 | 43:104 | |
| 198 | Rpt8 | QRpts4 | 4HS | Reaction to *Pyrenophora teres* 8 | 43:105 | |
| 201 | fch7 | f7, clo-f7 | 1HL | Chlorina seedling 7 | 41:113 | 4 |
| 202 | trd1 | t, bra-c | 1HL | Third outer glume 1 | 46: 65 | 227 |
| 203 | Blp1 | B | 1HL | Black lemma and pericarp 1 | 46: 67 | 988 |
| 207 | abo1 | $a_t$ | 1HL | Albino seedling 1 | 26:210 | 51 |
| 208 | fst2 | fs2 | 1HL | Fragile stem 2 | 41:114 | 578 |
| 213 | Sgh3 | Sh3 | 1HL | Spring growth habit 3 | 26:212 | 764 |
| 214 | eam8 | $ea_k$, mat-a | 1HL | Early maturity 8 | 46: 69 | 765 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 215 | des6 | des6 | 1HL/5HL | Desynapsis 6 | 43:106 | 597 |
| 218 | Rph4 | Pa4 | 1HS | Reaction to *Puccinia hordei* 4 | 42:302 | 1314 |
| 220 | fch3 | f3 | 1HS | Chlorina seedling 3 | 40: 71 | 851 |
| 221 | wst5 | wst5 | 1HL | White streak 5 | 46: 73 | 591 |
| 222 | nec1 | sp,,b | 1HL | Necrotic leaf spot 1 | 43:108 | 989 |
| 223 | zeb3 | zb3, $zb_c$ | 1HL | Zebra stripe 3 | 40: 72 | 1451 |
| 224 | ert-b | ert-b | 1HL | Erectoides-b | 40: 74 | 470 |
| 225 | clh1 | clh | 7H/5H | Curled leaf dwarf 1 | 40: 76 | 1212 |
| 226 | rvl1 | rvl | 1HL | Revoluted leaf 1 | 40: 77 | 608 |
| 227 | sls1 | sls | 1HL | Small lateral spikelet 1 | 40: 78 | 2492 |
| 228 | Sil1 | Sil | 1H | Subcrown internode length 1 | 40: 79 | 1604 |
| 229 | cud2 | cud2 | 1HL | Curly dwarf 2 | 47:103 | 1712 |
| 230 | glo-e | glo-e | 3HL | Globosum-e | 45:117 | 1755 |
| 231 | cur5 | cu5 | 2HS | Curly 5 | 41:120 | 1710 |
| 232 | Lys4 | sex5 | 1HS | High lysine 4 | 40: 80 | 2475 |
| 233 | xnt7 | xan,,g | 1HL | Xantha seedling 7 | 26:231 | 581 |
| 234 | mov3 | mo-a | 1H | Multiovary 3 | 32:102 | |
| 235 | lel1 | lel | 2H | Leafy lemma 1 | 46:74 | 1780 |
| 237 | Rpt2 | Rpt2c | 1HS | Reaction to *Pyrenophora teres* 2 | 43:110 | |
| 238 | ari-t | ari-25 | 1H | Breviaristatum-t | 47:104 | |
| 239 | sci-b | sci-4 | 1H/6H | Scirpoides-b | 46: 76 | |
| 240 | sdw6 | sdw.f | 1H/7H | Semidwarf 6 | 46:77 | 2449 |
| 241 | Acr3 | acr | 1HL | Accordionrachis 3 | 47:105 | 1071 |
| 242 | sld6 | sld.g | 1H | Slender dwarf 6 | 40: 87 | 2482 |
| 244 | dsp11 | dsp.am, dsp.ao | 1HL | Dense spike 11 | 41:121 | 1722<br>1723 |
| 251 | mul2 | mul2 | 6HL | Multiflorus 2 | 26:232 | 1394 |
| 252 | eam7 | HvCO7 | 6HS | Early maturity 7 | 45:118 | 579 |
| 253 | cul2 | uc2 | 6HL | Uniculm 2 | 43:112 | 531 |
| 254 | rob1 | o, rob-o | 6HS | Orange lemma 1 | 46: 78 | 707 |
| 255 | xnt5 | $x_n$ | 6HL | Xantha seedling 5 | 26:237 | 43 |
| 257 | raw5 | r,,e | 6HL | Smooth awn 5 | 44:112 | 785 |
| 258 | dsp9 | l9, ert-e | 6HL | Dense spike 9 | 47:107 | 1774 |

Table 2. (continued)

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 260 | fch11 | f11 | 6HL | Chlorina seedling 11 | 45:120 | 1738 |
| 261 | nec2 | nec2 | 6HS | Necrotic leaf spot 2 | 26:241 | 1224 |
| 262 | cur1 | cu1 | 3HL | Curly 1 | 46: 81 | 1705 |
| 263 | cur3 | cu3 | 6HL | Curly 3 | 41:125 | 1707 |
| 264 | mtt5 | mt,,f | 6HL | Mottled leaf 5 | 41:126 | 2410 |
| 265 | nec3 | nec3 | 6HS | Necrotic leaf spot 3 | 43:116 | 1330 |
| 266 | ert-e | l9, dsp9 | 6HL | Erectoides-e | 47:109 | 477 |
| 267 | Rph11 | Rph11 | 6HL | Reaction to *Puccinia hordei* 11 | 26:247 | 1589 |
| 268 | lax-b | lax-b | 6HL | Laxatum-b | 44:113 | 1776 |
| 269 | lys6 | lys6 | 6H | High lysine 6 | 44:114 | 1786 |
| 270 | abo14 | alb,,q | 6HL | Albino seedling 14 | 26:250 | 586 |
| 271 | abo15 | alb,,t | 6HS | Albino seedling 15 | 26:251 | |
| 272 | Rpt5 | Pt$_a$ | 6HL | Reaction to *Pyrenophora teres* 5 | 43:120 | |
| 274 | ari-x | ari-22 | 6H | Breviaristatum-x | 43:124 | |
| 275 | lfl1 | lfl, lfs | 6HL | Leafless 1 | 47:111 | 609 |
| 301 | fst1 | fs | 5HL | Fragile stem 1 | 26:252 | 629 |
| 302 | mtt2 | mt2 | 5HL | Mottled leaf 2 | 41:127 | 1398 |
| 303 | var3 | va3 | 5HL | Variegated 3 | 44:115 | 1277 |
| 304 | wst2 | wst2 | 5HL | White streak 2 | 46: 83 | 766 |
| 305 | crm1 | cm | 5HL | Cream seedling 1 | 26:256 | 20 |
| 306 | var1 | va | 5HL | Variegated 1 | 37:259 | 1278 |
| 308 | lbi1 | lb, rac-a | 5HL | Long basal rachis internode 1 | 43:125 | 580 |
| 309 | Sgh2 | Sh2 | 5HL | Spring growth habit 2 | 26:259 | 770 |
| 311 | dex1 | sex2 | 5HS | Defective endosperm xenia 1 | 26:260 | |
| 312 | raw1 | r | 5HL | Smooth awn 1 | 46: 84 | 27 |
| 313 | fch6 | f6, yv | 5HL | Chlorina seedling 6 | 44:116 | 1390 |
| 314 | vrs2 | v2, int-b | 5HL | Six-rowed spike 2 | 47:113 | 773 |
| 315 | vrs3 | v3, int-a | 1HL | Six-rowed spike 3 | 47:115 | 774 |
| 317 | ddt1 | ddt | 5HS | Reaction to DDT 1 | 26:266 | 331 |
| 319 | rpg4 | rpg4 | 5HL | Reaction to *Puccinia graminis* 4 | 26:267 | 2438 |
| 320 | int-b | vrs2 | 5HL | Intermedium spike-b | 47:118 | 1764 |
| 321 | srh1 | s, l | 5HL | Short rachilla hair 1 | 46: 86 | 27 |
| 322 | dsk1 | dsk | 5HL | Dusky 1 | 41:128 | 1714 |
| 323 | nld1 | nld | 5HL | Narrow leafed dwarf 1 | 46: 88 | 769 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 324 | cud1 | cud | 5HL | Curly dwarf 1 | 26:272 | |
| 325 | crl1 | crl, cl | 6H | Curly lateral 1 | 41:129 | |
| 326 | blf1 | bb | 5HL | Broad leaf 1 | 46: 90 | |
| 327 | flo-b | flo-a | 6HL | Extra floret-b | 45:121 | |
| 328 | ari-e | lk9, GPert | 5HL | Breviaristatum-e | 47:121 | |
| 329 | ari-h | 1k11 | 5HL | Breviaristatum-h | 26:277 | |
| 330 | ert-g | ert-g, br3 | 1HL | Erectoides-g | 41:133 | |
| 331 | ert-n | ert-n | 5HL | Erectoides-n | 44:120 | 488 |
| 332 | Ert-r | Zeo1 | 2HL | Erectoides-r | 47:123 | 492 |
| 333 | Rph12 | Pa12, Pa9 | 5HL | Reaction to *Puccinia hordei* 12 | 26:281 | 1590 |
| 334 | raw6 | r6 | 5HL | Smooth awn 6 | 26:282 | 2437 |
| 335 | msg49 | msg,,jw | 5HL | Male sterile genetic 49 | 45:122 | 2402 |
| 337 | blf2 | bb2, nlh | 5HL | Broad leaf 2 | 41:137 | 1667 |
| 338 | lys1 | lys | 5HL | High lysine 1 | 26:286 | 1784 |
| 339 | lys3 | sex3 | 5HL | High lysine 3 | 43:127 | 1785 |
| 340 | raw2 | r2 | 5HL | Smooth awn 2 | 46: 92 | 27 |
| 341 | abo12 | alb,,o | 5HS | Albino seedling 12 | 26:290 | 583 |
| 342 | glo-f | glo-e | 5HL | Globosum-f | 26:291 | |
| 343 | Lfb1 | Lfb | 5HL | Leafy bract 1 | 41:140 | 1577 |
| 344 | var2 | va2 | 5HL | Variegated 2 | 32:104 | 2496 |
| 345 | rym3 | ym3 | 5HS | Reaction to barley yellow mosaic virus 3 | 32:105 | |
| 346 | yst5 | yst5 | 7HS | Yellow streak 5 | 43:130 | 2501 |
| 347 | mnd4 | m4 | 5HL | Many noded dwarf 4 | 44:122 | 1798 |
| 348 | Eam5 | HvPhyC-e | 5HL | Early maturity 5 | 45:123 | |
| 349 | brh4 | brh.j | 2HL | Brachytic 4 | 42:407 | 1675 |
| 350 | brh6 | brh.s | 5HS | Brachytic 6 | 42:408 | 1683 |
| 351 | gsh1 | gs1, cer-q | 2HS | Glossy sheath 1 | 46: 94 | 735 |
| 352 | gsh2 | gs2, cer-b | 3HL | Glossy sheath 2 | 47:125 | 736 |
| 353 | gsh3 | gs3, cer-a | 7HS | Glossy sheath 3 | 41:143 | 737 |
| 354 | gsh4 | gs4, cer-x | 6HL | Glossy sheath 4 | 41:146 | 738 |
| 355 | gsh5 | gs5, cer-s | 2HL | Glossy sheath 5 | 47:128 | 739 |
| 356 | gsh6 | gs6, cer-c | 2HS | Glossy sheath 6 | 46:101 | 740 |
| 357 | msg1 | ms1 | 1HL | Male sterile genetic 1 | 45c:126 | 1810 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 358 | msg2 | ms2 | 2HL | Male sterile genetic 2 | 45:128 | 2371 |
| 359 | msg3 | ms3 | 2HS | Male sterile genetic 3 | 45:130 | 1130 |
| 360 | msg4 | ms4 | 1H | Male sterile genetic 4 | 45:132 | 2392 |
| 361 | msg5 | ms5 | 3HS | Male sterile genetic 5 | 45:133 | 2403 |
| 362 | msg6 | ms6 | 6HS | Male sterile genetic 6 | 45:135 | 2405 |
| 363 | msg7 | ms7 | 5HL | Male sterile genetic 7 | 45:137 | 2406 |
| 364 | msg8 | ms8 | 5HL | Male sterile genetic 8 | 45:139 | 2407 |
| 365 | msg9 | ms9 | 2HS | Male sterile genetic 9 | 45:141 | 2408 |
| 366 | msg10 | ms10 | 7HS | Male sterile genetic 10 | 45:142 | 1811 |
| 367 | msg11 | ms11 | 5HS | Male sterile genetic 11 | 45:144 | 1812 |
| 368 | msg13 | ms13 | 3HL | Male sterile genetic 13 | 45:146 | 1813 |
| 369 | msg14 | ms14 | 7HS | Male sterile genetic 14 | 45:147 | 1814 |
| 370 | msg15 | ms15 | | Male sterile genetic 15 | 45:149 | 1815 |
| 371 | msg16 | ms16 | 5HS | Male sterile genetic 16 | 45:150 | 1816 |
| 372 | msg17 | ms17 | 5HL | Male sterile genetic 17 | 45:152 | 1817 |
| 373 | msg18 | ms18 | 5HL | Male sterile genetic 18 | 45:153 | 1818 |
| 374 | msg19 | ms19 | 5HS | Male sterile genetic 19 | 45:155 | 1819 |
| 375 | msg20 | Msg,,ad | 4H | Male sterile genetic 20 | 45:156 | 2372 |
| 376 | msg21 | ms21 | 1HL | Male sterile genetic 21 | 45:157 | 2373 |
| 377 | seg1 | se1 | 7HL | Shrunken endosperm genetic 1 | 45:158 | 750 |
| 378 | seg2 | se2 | 7HS | Shrunken endosperm genetic 2 | 26:326 | 751 |
| 379 | seg3 | se3, ant17 | 3H | Shrunken endosperm genetic 3 | 45:160 | 752 |
| 380 | seg4 | se4 | 7HL | Shrunken endosperm genetic 4 | 37:267 | 753 |
| 381 | seg5 | se5 | 7HS | Shrunken endosperm genetic 5 | 26:329 | 754 |
| 382 | sex1 | lys5 | 6HL | Shrunken endosperm xenia 1 | 26:330 | 755 |
| 383 | msg22 | ms22 | 7H | Male sterile genetic 22 | 45:162 | 741,<br>2374 |
| 384 | msg23 | ms23 | 7HL | Male sterile genetic 23 | 45:163 | 2375 |
| 385 | msg24 | ms24 | 4HL | Male sterile genetic 24 | 45:164 | 2376 |
| 386 | des3 | des3 | 2H/ 5HL | Desynapsis 3 | 43:140 | 594 |
| 387 | des8 | des8 | 3H | Desynapsis 8 | 41:151 | 599 |
| 388 | des9 | des9 | 7HL | Desynapsis 9 | 44:131 | 600 |
| 389 | des10 | des,,p | 5HL | Desynapsis 10 | 41:152 | 601 |

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| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 390 | des11 | des11 | 3HL | Desynapsis 11 | 44:132 | 602 |
| 391 | des12 | des12 | 3H | Desynapsis 12 | 44:133 | 603 |
| 392 | des13 | des13 | 3H | Desynapsis 13 | 44:134 | 604 |
| 393 | des14 | des14 | 7H | Desynapsis 14 | 44:135 | 605 |
| 394 | des15 | des15 | 3HL | Desynapsis 15 | 44:136 | 606 |
| 395 | msg26 | msg,,u | 7HS | Male sterile genetic 26 | 45:166 | 745 |
| 396 | seg6 | se6 | 3HL | Shrunken endosperm genetic 6 | 44:138 | 2467 |
| 397 | seg7 | se7 | | Shrunken endosperm genetic 7 | 37:269 | 2468 |
| 399 | cer-d | cer-d | 5HL | Eceriferum-d | 41:153 | 425 |
| 400 | cer-e | cer-e | 1HL | Eceriferum-e | 40:102 | 1518 |
| 401 | cer-f | cer-f | 1H | Eceriferum-f | 40:104 | 427 |
| 402 | cer-g | cer-g | 2HL | Eceriferum-g | 47:131 | 428 |
| 403 | cer-h | cer-h | 4HS | Eceriferum-h | 41:157 | 429 |
| 404 | cer-i | cer-i | 5HL | Eceriferum-i | 41:158 | 430 |
| 405 | cer-k | cer-k | 4HL | Eceriferum-k | 41:160 | 432 |
| 406 | cer-l | cer-l | 3HL | Eceriferum-l | 44:142 | 433 |
| 407 | cer-m | cer-m | 1HL/ 3HL | Eceriferum-m | 41:161 | 434 |
| 408 | cer-n | gs9 | 2HL | Eceriferum-n | 44:143 | 435 |
| 409 | cer-o | cer-o | 1HL | Eceriferum-o | 40:106 | 436 |
| 410 | cer-p | cer-p | 7HL | Eceriferum-p | 41:162 | 437 |
| 411 | cer-r | cer-r | 3HL | Eceriferum-r | 45:168 | 439 |
| 413 | gsh8 | cer-u, gs8 | 2HS | Glossy sheath 8 | 46:105 | 442 |
| 414 | cer-v | cer-v | 2HS | Eceriferum-v | 44:147 | 443 |
| 415 | cer-w | cer-w | 5HL | Eceriferum-w | 41:166 | 1519 |
| 417 | cer-y | cer-y | 1HS | Eceriferum-y | 44:149 | 446 |
| 418 | cer-z | cer-z | 7HS | Eceriferum-z | 44:150 | 447 |
| 419 | cer-za | cer-za | 5HL | Eceriferum-za | 43:144 | 1521 |
| 420 | cer-zb | cer-zb | 5HS | Eceriferum-zb | 42:508 | 1522 |
| 421 | cer-zc | cer-zc | 4HL/ 2HS | Eceriferum-zc | 42:510 | 450 |
| 422 | cer-zd | cer-zd | 3HL | Eceriferum-zd | 40:110 | 451 |
| 423 | cer-ze | gl5 | 7HS | Eceriferum-ze | 44:152 | 452 |
| | | | | | | |

Table 2. (continued)

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 424 | cer-zf | cer-zf | 3H/7HS | Eceriferum-zf | 42:516 | 453 |
| 425 | cer-zg | cer-zg | 4HL | Eceriferum-zg | 26:377 | 454 |
| 427 | cer-zi | cer-zi | 1HL | Eceriferum-zi | 41:168 | 456 |
| 428 | cer-zj | cer-zj | 5HL | Eceriferum-zj | 42:520 | 457 |
| 429 | cer-zk | cer-zk | 2H | Eceriferum-zk | 43:146 | 458 |
| 430 | cer-zl | cer-zl | | Eceriferum-zl | 26:382 | 459 |
| 431 | cer-zn | cer-zn | 1H | Eceriferum-zn | 40:112 | 1523 |
| 432 | cer-zo | cer-zo | 3HS | Eceriferum-zo | 44:154 | 462 |
| 433 | cer-zp | cer-zp | 5HL | Eceriferum-zp | 26:385 | 463 |
| 434 | cer-zq | cer-zq | | Eceriferum-zq | 26:386 | 1524 |
| 435 | cer-zr | cer-zr | 5HL | Eceriferum-zr | 44:155 | 1525 |
| 436 | cer-zs | cer-zs | | Eceriferum-zs | 44:156 | 1526 |
| 437 | cer-zt | cer-zt | 2HS | Eceriferum-zt | 44:157 | 1527 |
| 438 | cer-zu | cer-zu | 1HS | Eceriferum-zu | 41:170 | 1528 |
| 439 | cer-zv | cer-zv | 4HL | Eceriferum-zv | 47:133 | 1529 |
| 440 | cer-zw | cer-zw | | Eceriferum-zw | 26:392 | 1530 |
| 441 | cer-zx | cer-zx | 3H | Eceriferum-zx | 46:109 | 1531 |
| 442 | cer-zy | cer-zy | 1HS | Eceriferum-zy | 40:116 | 1532 |
| 443 | cer-zz | cer-zz | 3HL | Eceriferum-zz | 44:159 | 1533 |
| 444 | cer-ya | cer-ya | 3HS | Eceriferum-ya | 26:396 | 1534 |
| 445 | cer-yb | cer-yb | 2HL | Eceriferum-yb | 41:171 | 1535 |
| 446 | cer-yc | cer-yc | 6H/7HS | Eceriferum-yc | 41:172 | 1536 |
| 447 | cer-yd | cer-yd | 3HS | Eceriferum-yd | 26:399 | 1537 |
| 448 | cer-ye | cer-ye | 4H | Eceriferum-ye | 43:149 | 1538 |
| 449 | cer-yf | cer-yf | 7H | Eceriferum-yf | 44:160 | 1539 |
| 450 | cer-yg | cer-yg | 7HS | Eceriferum-yg | 44:161 | 1540 |
| 451 | cer-yh | cer-yh | 3HS | Eceriferum-yh | 26:403 | 1541 |
| 453 | fer1 | | | Few roots 1 | 46:112 | 2538 |
| 454 | blx5 | bl5 | 7HL | Non-blue aleurone xenia 5 | 26:404 | 2509 |
| 455 | seg8 | seg8 | 7H | Shrunken endosperm genetic 8 | 45:170 | 2469 |
| 460 | cur4 | cu4, glo-d | 2HL | Curly 4 | 45:172 | 1708 |
| 461 | zeb2 | zb2, fch10 | 4HS | Zebra stripe 2 | 43:152 | 93 |
| 462 | yst3 | yst,,c | 3HS | Yellow streak 3 | 44:163 | 48 |

Table 2. (continued)

| BGS no. | Locus symbol[*] |  | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
|  | Rec. | Prev. |  |  |  |  |
|  |  |  |  |  |  |  |
| 463 | gig1 | gig, sf | 2HL | Gigas 1 | 44:164 | 1650 |
| 464 | msg27 | msg,,ae | 2HS | Male sterile genetic 27 | 45:174 | 2379 |
| 465 | msg28 | msg,,as | 2HS | Male sterile genetic 28 | 45:175 | 2380 |
| 466 | msg29 | msg,,a | 5HL | Male sterile genetic 29 | 45:176 | 2381 |
| 467 | msg30 | msg,,c | 7HL | Male sterile genetic 30 | 45:177 | 2382 |
| 468 | msg31 | msg,,d | 1HL | Male sterile genetic 31 | 45:178 | 2383 |
| 469 | msg32 | msg,,w | 7H | Male sterile genetic 32 | 45:179 | 2384 |
| 470 | msg33 | msg,,x | 2HS | Male sterile genetic 33 | 45:180 | 2385 |
| 471 | msg34 | msg,,av | 6HS/ 7HS | Male sterile genetic 34 | 45:181 | 2386 |
| 472 | abr1 | abr | 2HL | Accordion basal rachis internode 1 | 26:419 | 1563 |
| 473 | com1 | lax-270, bir1 | 5HL | Compositum 1 | 47:135 |  |
| 474 | lax-a | lax-a | 5HL | Laxatum-a | 46:113 |  |
| 475 | lax-c | lax-21 | 6HL | Laxatum-c | 47:137 |  |
| 476 | lax-d | lax-83 |  | Laxatum-d | 47:139 |  |
| 477 | lax-f | lax-61 |  | Laxatum-f | 47:140 |  |
| 478 | lax-g | lax-25 |  | Laxatum-g | 47:141 |  |
| 479 | lax-h | lax-26 | 3H | Laxatum-h | 47:142 |  |
| 480 | lax-i | lax-50 |  | Laxatum-i | 47:144 |  |
| 481 | lax-j | lax-49 | 2H | Laxatum-j | 47:145 |  |
| 482 | lax-k | lax-84 | 2H/3H | Laxatum-k | 47:147 |  |
| 483 | lax-l | lax-60 | 1H | Laxatum-l | 47:148 |  |
| 484 | lax-m | lax-80 |  | Laxatum-m | 47:149 |  |
| 485 | lax-n | lax-67 | 2H/4HL /5H | Laxatum-n | 47:150 |  |
| 486 | lax-o | lax-79 |  | Laxatum-o | 47:152 |  |
| 487 | lax-df | lax-204 |  | Laxatum-df | 47:153 |  |
| 488 | lax-ef | lax-225 | 2H | Laxatum-ef | 47:154 |  |
| 489 | lax-ff | lax-216 |  | Laxatum-ff | 47:156 |  |
| 490 | lax-gf | lax-217 |  | Laxatum-gf | 47:157 |  |
| 491 | lax-hf | lax-244 | 2H/3HL /5H | Laxatum-hf | 47:158 |  |
| 492 | lax-if | lax-246 |  | Laxatum-if | 47:160 |  |
| 493 | Lax-jf | lax-253 | 4HS | Laxatum-jf | 47:161 |  |

Table 2. (continued)

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 494 | lax-kf | lax-295 | | Laxatum-kf | 47:163 | |
| 495 | lax-lf | lax-274 | | Laxatum-lf | 47:164 | |
| 496 | lax-mf | lax-302 | | Laxatum-mf | 47:165 | |
| 497 | lax-nf | lax-322 | 2HL/4H | Laxatum-nf | 47:166 | |
| 498 | msg35 | msg,,dr | 2HL | Male sterile genetic 35 | 45:183 | 2387 |
| 499 | msg36 | msg,,bk | 6HS | Male sterile genetic 36 | 45:184 | 2388 |
| 500 | msg37 | msg,,hl | 3HL | Male sterile genetic 37 | 45:186 | 2389 |
| 501 | msg38 | msg,,jl | 3H | Male sterile genetic 38 | 45:187 | 2390 |
| 502 | msg39 | msg,,dm | 3H | Male sterile genetic 39 | 45:188 | 2391 |
| 503 | msg40 | msg,,ac | 6HL | Male sterile genetic 40 | 45:190 | 2393 |
| 504 | msg41 | msg,,aj | 6HS | Male sterile genetic 41 | 45:191 | |
| 505 | msg42 | msg,,db | 3H | Male sterile genetic 42 | 45:193 | |
| 506 | msg43 | msg,,br | 2HL | Male sterile genetic 43 | 45:194 | |
| 507 | msg44 | msg,,cx | 5HL | Male sterile genetic 44 | 45:195 | |
| 508 | msg45 | msg,,dp | 5HL/7HS | Male sterile genetic 45 | 45:196 | |
| 509 | msg46 | msg,,ec | 2H/6H | Male sterile genetic 46 | 45:197 | |
| 510 | msg47 | msg,,ep | 3HS/7HS | Male sterile genetic 47 | 45:198 | |
| 511 | Rpg1 | T | 7HS | Reaction to *Puccinia graminis* 1 | 26:437 | |
| 512 | Rpg2 | T2 | | Reaction to *Puccinia graminis* 2 | 26:439 | |
| 513 | xnt2 | $x_b$ | | Xantha seedling 2 | 26:440 | |
| 515 | Rsp1 | Sep | | Reaction to *Septoria passerinii* 1 | 26:441 | 2510 |
| 516 | Rsp2 | Sep2 | | Reaction to *Septoria passerinii* 2 | 37:275 | 2511 |
| 517 | Rsp3 | Sep3 | | Reaction to *Septoria passerinii* 3 | 37:276 | 2512 |
| 518 | sdw1 | denso, Hv20ox$_2$ | 3HL | Semidwarf 1 | 47:168 | 2513 |
| 519 | mnd1 | m | 2H | Many-noded dwarf 1 | 43:154 | 253 |
| 520 | msg48 | msg,,jt | 1H | Male sterile genetic 48 | 45:199 | 2401 |
| 521 | mtt1 | mt. mt3 | 1HL | Mottled leaf 1 | 41:179 | 622 |
| 522 | cer-yi | cer-yi | 2H | Eceriferum-yi | 41:180 | 1542 |
| 523 | cer-yj | cer-yj | 1HS | Eceriferum-yj | 40:124 | 1543 |
| 524 | cer-yk | cer-yk | 7HL | Eceriferum-yk | 44:167 | 1544 |
| 525 | cer-yl | cer-yl | 4HL | Eceriferum-yl | 47:171 | 1545 |
| 526 | cer-ym | cer-ym | 4HL | Eceriferum-ym | 47:173 | 1546 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 527 | cer-yn | cer-yn | 1H | Eceriferum-yn | 40:125 | 1547 |
| 528 | cer-yo | cer-yo | 4HS | Eceriferum-yo | 44:168 | 1548 |
| 529 | cer-yp | cer-yp | 5HS | Eceriferum-yp | 44:169 | 1549 |
| 530 | cer-yq | cer-yq | 5H | Eceriferum-yq | 44:170 | 1550 |
| 531 | cer-yr | cer-yr | 5HL | Eceriferum-yr | 44:171 | 1551 |
| 532 | cer-ys | cer-ys | 2HL | Eceriferum-ys | 44:172 | 1552 |
| 533 | cer-yt | cer-yt | 1H/5H | Eceriferum-yt | 40:126 | 1553 |
| 534 | cer-yu | cer-yu | 1H | Eceriferum-yu | 40:127 | 1554 |
| 535 | cer-yx | cer-yx | 1H/3H /5H | Eceriferum-yx | 40:128 | 1555 |
| 536 | Cer-yy | Gle1 | 1HS | Eceriferum-yy | 40:129 | 1556 |
| 537 | cer-yz | cer-yz | 1H/5H | Eceriferum-yz | 44:173 | 1557 |
| 538 | cer-xa | cer-xa | 2HL/4H /5HL | Eceriferum-xa | 44:174 | 1558 |
| 539 | cer-xb | cer-xb | 4H | Eceriferum-xb | 44:175 | 1559 |
| 540 | cer-xc | cer-xc | 1H | Eceriferum-xc | 44:176 | 1560 |
| 541 | cer-xd | cer-xd | 4H/5HL | Eceriferum-xd | 44:177 | 1561 |
| 542 | Dwf2 | Dwf2 | | Dominant dwarf 2 | 24:170 | |
| 544 | int-h | int-h | 5H | Intermedium spike-h | 44:179 | 1768 |
| 545 | int-i | int-i | 2HS | Intermedium spike-i | 41:181 | 1769 |
| 546 | int-k | int-k | 7H | Intermedium spike-k | 44:180 | 1770 |
| 547 | int-m | int-m | 5HL | Intermedium spike-m | 44:181 | 1772 |
| 548 | Fol-b | Ang | 1HS | Angustifolium-b | 40:131 | 17 |
| 549 | Lga1 | Log | 7HS | Long glume awn 1 | 44:183 | 835 |
| 550 | ari-b | ari-b | | Breviaristatum-b | 44:185 | 1649 |
| 551 | ari-f | ari-21 | 7H | Breviaristatum-f | 41:182 | 1654 |
| 552 | ari-j | ari-32 | | Breviaristatum-j | 44:186 | 1658 |
| 553 | ari-k | ari-504 | 3H | Breviaristatum-k | 44:187 | 1659 |
| 554 | ari-m | brh1 | 7HS | Breviaristatum-m | 47:175 | 1661 |
| 555 | ari-n | ari-45 | 7H | Breviaristatum-n | 41:185 | 1662 |
| 556 | ari-o | ert-u,<br>ert-zd | 7HL | Breviaristatum-o | 45:200 | 1663 |
| 557 | ari-p | ari-27 | | Breviaristatum-p | 46:120 | 1664 |
| 558 | ari-q | ari-271 | 4H | Breviaristatum-q | 44:188 | 1665 |

Table 2. (continued)

| BGS no. | Locus symbol[*] |  | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
|  | Rec. | Prev. |  |  |  |  |
|  |  |  |  |  |  |  |
| 559 | ari-r | ari-14 | 5H | Breviaristatum-r | 41:187 | 1666 |
| 560 | ert-f | ert-f | 1H | Erectoides-f | 40:133 | 478 |
| 561 | ert-h | ert-h | 5HL | Erectoides-h | 44:189 | 481 |
| 562 | ert-k | ert-k | 6H | Erectoides-k | 46:121 | 485 |
| 563 | ert-l | ert-l |  | Erectoides-l | 26:489 | 486 |
| 564 | ert-p | ert-p |  | Erectoides-p | 26:490 | 490 |
| 565 | ert-s | ert-s |  | Erectoides-s | 26:491 | 493 |
| 566 | ert-t | brh3 | 2HS | Erectoides-t | 45:203 | 494 |
| 567 | ert-v | ert-v | 6H | Erectoides-v | 41:188 | 497 |
| 568 | ert-x | ert-x | 1H/7H | Erectoides-x | 40:136 | 498 |
| 569 | ert-y | ert-y |  | Erectoides-y | 26:495 | 499 |
| 570 | ert-z | ert-z |  | Erectoides-z | 26:496 | 500 |
| 571 | ert-za | ert-za | 5H | Erectoides-za | 44:190 | 501 |
| 572 | ert-zb | ert-zb | 7HL | Erectoides-zb | 45:205 | 502 |
| 573 | ert-zc | ert-zc | 7HS | Erectoides-zc | 45:206 | 503 |
| 574 | ert-ze | ert-ze | 5HS | Erectoides-ze | 45:207 | 505 |
| 575 | Rph6 | Pa6 |  | Reaction to *Puccinia hordei* 6 | 26:501 | 1598 |
| 576 | Rph8 | Pa8 |  | Reaction to *Puccinia hordei* 8 | 26:502 | 1600 |
| 577 | Rsg2 | Rsg2 |  | Reaction to *Schizaphis graminum* 2 | 37:283 | 2513 |
| 578 | mat-b | mat-b | 7HL | Praematurum-b | 46:123 | 1788 |
| 579 | mat-c | Eam6, HvCEN | 2H | Praematurum-c | 46:125 | 1789 |
| 580 | mat-d | mat-d | 4Hl/6HL | Praematurum-d | 45:208 | 1790 |
| 581 | mat-e | mat-e |  | Praematurum-e | 26:508 | 1791 |
| 582 | mat-f | mat-f | 1H | Praematurum-f | 45:210 | 1792 |
| 583 | mat-g | mat-g |  | Praematurum-g | 26:510 | 1793 |
| 584 | mat-h | mat-h | 4HL | Praematurum-h | 45:212 | 1794 |
| 585 | mat-i | mat-i | 7HL | Praematurum-i | 45:214 | 1795 |
| 586 | bra-d | bra-d | 1HL | Bracteatum-d | 40:139 | 1696 |
| 587 | abo3 | a2, alb-za |  | Albino seedling 3 | 26:514 | 165 |
| 588 | abo10 | $a_{t2}$ |  | Albino seedling 10 | 26:515 | 57 |
| 589 | abo11 | $a_{t3}$, $alb^{t}$ |  | Albino seedling 11 | 26:516 | 233 |
| 590 | Rph13 | Rph13 |  | Reaction to *Puccinia hordei* 13 | 28: 31 | 1591 |
| Table 2. (continued) |  |  |  |  |  |  |

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 591 | Rph14 | Rph14 | | Reaction to *Puccinia hordei* 14 | 28: 32 | 1592 |
| 592 | yhd2 | yh2 | | Yellow head 2 | 45:215 | 757 |
| 593 | adp1 | adp | 3HL | Awned palea 1 | 43:158 | 1618 |
| 594 | ant3 | rub | | Anthocyanin-deficient 3 | 29: 82 | 1641 |
| 595 | ant4 | ant4 | 4H | Anthocyanin-deficient 4 | 45:216 | 1642 |
| 596 | ant5 | rs2 | | Anthocyanin-deficient 5 | 29: 84 | 1643 |
| 597 | ant6 | ant6 | | Anthocyanin-deficient 6 | 29: 85 | 1644 |
| 598 | ant13 | ant13 | 6HL | Proanthocyanin-free 13 | 29: 86 | 1624 |
| 599 | ant17 | ant17 | 3HS | Proanthocyanin-free 17 | 46:128 | 1628 |
| 600 | ant18 | ant18 | | Proanthocyanin-free 18 | 45:221 | 1630 |
| 601 | ant19 | ant19 | | Proanthocyanin-free 19 | 29: 92 | 1631 |
| 602 | ant20 | ant20 | | Anthocyanin-rich 20 | 29: 93 | 1633 |
| 603 | ant21 | ant21 | 6H | Proanthocyanin-free 21 | 29: 94 | 1634 |
| 604 | ant22 | ant22 | 2HL | Proanthocyanin-free 22 | 41:191 | 1635 |
| 605 | ant25 | ant25 | | Proanthocyanin-free 25 | 29: 96 | 1638 |
| 606 | ant26 | ant26 | | Proanthocyanin-free 26 | 29: 97 | 1639 |
| 607 | ant27 | ant27 | | Proanthocyanin-free 27 | 29: 98 | 1640 |
| 608 | ant28 | ant28 | 3HL | Proanthocyanin-free 28 | 46:131 | |
| 609 | ant29 | ant29 | | Proanthocyanin-free 29 | 29:100 | |
| 610 | ant30 | ant30 | | Proanthocyanin-free 30 | 29:101 | |
| 611 | Nec6 | Sp | 7HS | Necrotic leaf spot 6 | 43:159 | 977 |
| 612 | gig2 | gig2 | 4HL | Gigas 2 | 44:191 | 1750 |
| 613 | brc1 | brc-5, com2 | 2HS | Branched 1 | 45:224 | |
| 614 | Zeo2 | cly1.b, HvAP2 | 2HL | Zeocriton 2 | 47:177 | 637 |
| 615 | wxs1 | wxs1 | 7H/ 2HL | Waxy spike 1 | 43:160 | 3649 |
| 616 | cul3 | cul3 | 3HL | Uniculme 3 | 43:161 | 2494 |
| 617 | cul4 | uc-5, uc-3 | 3HL | Uniculme 4 | 46:132 | 2495 |
| 618 | mnd3 | mn3, m3 | 4HS | Many noded dwarf 3 | 44:194 | 1797 |
| 619 | bra-a | bra-a | 7H | Bracteatum-a | 44:196 | 1693 |
| 620 | cal-b | cal-b | 5HL | Calcaroides-b | 44:197 | 1697 |
| 621 | Cal-c | Cal-c | 5HL | Calcaroides-c | 41:195 | 1567 |
| Table 2. (continued) | | | | | | |

| BGS no. | Locus symbol[*] | | Chr. loc.[†] | Locus name or phenotype | Descr. vol. p. | GSHO no.[‡] |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 622 | cal-e | cal-23 | 5HS | Calcaroides-e | 32:123 | |
| 623 | eli-a | lig-a | | Eligulum-a | 44:199 | 3647 |
| 624 | ops1 | op-3 | 7HS | Opposite spikelets 1 | 45:226 | 2427 |
| 625 | sci-a | sci-3 | 5H | Scirpoides 1 | 44:200 | |
| 626 | scl-a | scl-6 | 1HL | Scirpoides leaf-a | 44:201 | |
| 627 | viv-a | viv-5 | 2H | Viviparoides-a | 45:227 | 2498 |
| 628 | sex7 | sex.i | 5HL | Shrunken endosperm 7 | 32:129 | 2470 |
| 629 | mtt6 | mtt6 | 7HS | Mottled leaf 6 | 45:228 | 2411 |
| 630 | Ari-s | ari-265 | 5H/7H | Breviaristatum-s | 41:197 | |
| 631 | brh3 | brh.g, ert-t | 2HS | Brachytic 3 | 45:229 | 1672 |
| 632 | mnd5 | mnd5 | 7HL | Many noded dwarf 5 | 44:202 | |
| 633 | mnd6 | den-6 | 5HL | Many noded dwarf 6 | 44:203 | 1713 |
| 634 | pmr2 | nec-50 | | Premature ripe 2 | 32:135 | 2421 |
| 635 | nec7 | nec-45 | 1H/6H /7H | Necroticans 7 | 43:166 | 2420 |
| 636 | tst2 | | 4HL | Tip sterile 2 | 43:167 | 1781 |
| 637 | nar1 | nar1 | 6HS | NADH nitrate reductase-deficient 1 | 35:194 | 2431 |
| 638 | nar2 | nar2 | 5HL | NADH nitrate reductase-deficient 2 | 35:195 | 2415 |
| 639 | nar3 | nar3 | 7HS | NADH nitrate reductase-deficient 3 | 35:196 | 2416 |
| 640 | nar4 | nar4 | 2Hl | NADH nitrate reductase-deficient 4 | 35:197 | |
| 641 | nar5 | nar5 | 5HL | NADH nitrate reductase-deficient 5 | 35:198 | 2417 |
| 642 | nar6 | nar6 | 2HL | NADH nitrate reductase-deficient 6 | 35:199 | |
| 643 | nar7 | nar7 | 6HL | NADH nitrate reductase-deficient 7 | 35:200 | 2418 |
| 644 | nar8 | nar8 | 6HS | NADH nitrate reductase-deficient 8 | 35:201 | |
| 645 | bsp1 | | | Bushy spike 1 | 43:168 | 3652 |
| 646 | ovl2 | ovl2 | | Ovaryless 2 | 43:169 | 3655 |
| 647 | tst1 | tst1 | 6HL | Tip sterile 1 | 43:170 | 3644 |
| 648 | mov4 | mo8 | | Multiovary 4 | 43:171 | 3643 |
| 649 | asp1 | asp1 | | Aborted spike 1 | 43:172 | 3654 |
| 650 | sun1 | sun1 | | Sensitivity to *Ustilago nuda* 1 | 43:173 | 3650 |
| 651 | lam1 | lam1 | | Late maturity 1 | 43:174 | 3653 |
| 652 | ylf1 | ylf1 | 7HS | Yellow leaf 1 | 43:175 | |
| 653 | brh10 | brh.l | 2HS | Brachytic 10 | 45:231 | 1677 |
| 654 | brh11 | brh.n | 5HS | Brachytic 11 | 45:232 | 1679 |

Table 2. (continued)

| BGS no. | Locus symbol* | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 655 | brh12 | brh.o | 5HS | Brachytic 12 | 45:233 | 1680 |
| 656 | brh13 | brh.p | 5HS | Brachytic 13 | 45:234 | 1681 |
| 657 | brh15 | brh.u | 2HL | Brachytic 15 | 44:205 | 1685 |
| 658 | brh17 | brh.ab | 5HS | Brachytic 17 | 45:236 | 1669 |
| 659 | brh18 | brh13 | 5HS | Brachytic 18 | 45:237 | 1670 |
| 660 | nld2 | | 5H/6H /7H | Narrow leafed dwarf 2 | 43:176 | 3645 |
| 661 | dub1 | | 5HL | Double seed 1 | 37:301 | |
| 663 | sdw3 | gai | 2HS | Semidwarf 3 | 46:134 | |
| 667 | Rpt1 | Pt | 3HL | Reaction to *Pyrenophora teres* 1 | 43:177 | |
| 671 | nec8 | nec.w | 5HL | Necrotic leaf spot 8 | 43:179 | 3600 |
| 672 | nec9 | | 3HL | Necrotic leaf spot 9 | 43:181 | 3599 |
| 673 | cst1 | cs | 5HL | Corn stalk | 41:199 | |
| 674 | mtt8 | Mut 1661 | | Mottled leaf 8 | 43:182 | 3597 |
| 675 | mtt9 | Mut 2721 | | Mottled leaf 9 | 44:207 | 3598 |
| 676 | fch16 | clo.117 | 2HS | Chlorina seedling 16 | 40:144 | |
| 677 | mtt7 | mtt.h | 2HS | Mottled leaf 7 | 42:753 | |
| 678 | ari-u | ari-245 | 2HS | Breviaristatum-u | 45:239 | |
| 679 | acr4 | acr-3 | 2H/6HL | Accordion rachis 4 | 47:181 | |
| 680 | ari-v | ari-137 | 5HS | Breviaristatum-v | 41:202 | |
| 681 | nec10 | necS 1-1 | 3H | Necroticans 10 | 43:184 | 3607 |
| 682 | nec11 | | 1H | Necroticans 11 | 43:185 | 3610 |
| 683 | nec12 | | | Necroticans 12 | 43:186 | 3613 |
| 684 | nec13 | | | Necroticans 13 | 43:187 | 3616 |
| 685 | nec14 | | | Necroticans 14 | 43:188 | 3619 |
| 686 | nec15 | | | Necroticans 15 | 43:189 | 3620 |
| 687 | nec16 | | | Necroticans 16 | 43:190 | 3621 |
| 688 | nec17 | | | Necroticans 17 | 43:191 | 3622 |
| 689 | nec18 | | | Necroticans 18 | 43:192 | 3623 |
| 690 | nec19 | | | Necroticans 19 | 43:193 | 3624 |
| 691 | nec20 | | | Necroticans 20 | 43:194 | 3625 |
| 692 | nec21 | | | Necroticans 21 | 43:195 | 3626 |
| 693 | Nec22 | | | Necroticans 22 | 43:196 | 3627 |
| 694 | nec23 | | | Necroticans 23 | 43:197 | 3628 |
| Table 2. (continued) | | | | | | |

| BGS no. | Locus symbol | | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| | Rec. | Prev. | | | | |
| | | | | | | |
| 695 | Nec24 | | | Necroticans 24 | 43:198 | 3629 |
| 696 | nec25 | | | Necroticans 25 | 43:199 | 3630 |
| 697 | Nec26 | | | Necroticans 26 | 43:200 | 3631 |
| 698 | nec27 | | | Necroticans 27 | 43:201 | 3633 |
| 699 | nec28 | | | Necroticans 28 | 43:202 | 3635 |
| 700 | nec29 | | | Necroticans 29 | 43:203 | 3636 |
| 701 | nec30 | | | Necroticans 30 | 43:204 | 3637 |
| 702 | nec31 | | | Necroticans 31 | 43:205 | 3638 |
| 703 | nec32 | | | Necroticans 32 | 43:206 | 3639 |
| 704 | nec33 | | | Necroticans 33 | 43:207 | 3640 |
| 707 | Rpr1 | | 4H | Required for *Puccinia graminis* resistance 1 | 42:757 | |
| 711 | Rpt3 | QRptts2 | 2HS | Reaction to *Pyrenophora teres* 3 | 43:208 | |
| 713 | Rpt6 | | 5HL | Reaction to *Pyrenophora teres* 6 | 43:210 | |
| 714 | Rpt7 | Qrpts4 | 4HL | Reaction to *Pyrenophora teres* 7 | 43:211 | |
| 716 | ibl1 | ibl1 | 5HL | Intense blue aleurone 1 | 46:136 | |
| 718 | ops2 | op-2 | 5HL | Opposite spikelets 2 | 43:213 | 2426 |
| 719 | ops3 | op-1 | 5HS | Opposite spikelets 3 | 43:214 | 2425 |
| 720 | viv-c | viv-1 | 5H | Viviparoides-c | 43:215 | 2497 |
| 721 | ari-w | ari-153 | 7H | Breviaristatum-w | 43:216 | |
| 722 | ari-y | ari-9 | 5H | Breviaristatum-y | 43:217 | |
| 723 | mov5 | mov.o | | Multiovary 5 | 43:218 | 3671 |
| 724 | lks6 | lks.q | 1H/5H /6H | Short awn 6 | 43:219 | 3674 |
| 725 | ovl3 | | | Ovaryless 3 | 43:220 | 3687 |
| 726 | mnd7 | | | Many noded dwarf 7 | 43:221 | 3686 |
| 727 | ubs5 | | | Unbranched style 5 | 43:222 | 3675 |
| 728 | fxp1 | | | Fenoxaprop-p-ethyl reaction 1 | 43:223 | 3684 |
| 729 | dsk2 | msg,,df | 7HL | Dusky 2 | 44:208 | |
| 730 | lab1 | | 5HL | Labile1 | 46:137 | |
| 731 | rpr2 | γ08-118; R43-22#1 | 6H | Required for *Puccinia graminis* resistance 2 | 46:139 | |
| 732 | rpr3 | γ08-112; R12-31#3 | | Required for *Puccinia graminis* resistance 3 | 46:141 | 3696 |

Table 2: continued

| BGS no. | Locus symbol Rec. | Prev | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | GSHO no.‡ |
|---|---|---|---|---|---|---|
| 733 | rpr4 | γ08-114;<br>R36-37#1 | | Required for *Puccinia graminis* resistance 4 | 46:142 | 3697 |
| 734 | rpr5 | γ08-117;<br>R42-33#5 | | Required for *Puccinia graminis* resistance 5 | 46:143 | 3699 |
| 735 | rpr6 | γ08-119;<br>R47-23#1 | | Required for *Puccinia graminis* resistance 6 | 46:144 | 3700 |
| 736 | rpr7 | γ08-115;<br>R3-18#3 | | Required for *Puccinia graminis* resistance 7 | 46:145 | 3701 |
| 737 | rcr1 | γ08-122;<br>(R4-29) | | Required for resistance to *Cochliobolus sativus* 1 | 45:249 | 3703 |
| 738 | rcr2 | γ08-123;<br>(R4-40) | | Required for resistance to *Cochliobolus sativus* 2 | 45:250 | 3704 |
| 739 | rcr3 | γ08-124 | | Required for resistance to *Cochliobolus sativus* 3 | 45:251 | 3705 |
| 740 | Pbg1 | Pbg | 7H | Pubescence on glume 1 | 47:182 | |
| 741 | stb1 | stb | | Stubble1 | 47:183 | |
| 743 | twk1 | tw | 7H | Tweaky spike 1 | 47:185 | |
| 744 | acr5 | acr-2 | 7H | Accordion rachis 5 | 47:187 | |

* Recommended locus symbols are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 5 1996.

† Chromosome numbers and arm designations are based on a resolution passed at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on August 05 1996. The Burnham and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

‡ The seed stock associated with each BGS number is held as a GSHO stock number in the Barley Genetics Stock Collection at the USDA-ARS National Small Grains Germplasm Research Facility, Aberdeen, ID 83210, USA.

**Table 3.** An alphabetic listing of recently published Barley Genetic Stock (BGS) descriptions for loci in barley (*Hordeum vulgare*), including information on recommended locus names, recommended locus symbols, chromosomal locations, description citation, and original cultivars.

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| abo1 | $a_t$ | 207 | 1HL | Albino seedling 1 | 26:210 | Trebi |
| abo2 | a2 | 53 | 2HS | Albino seedling 2 | 26: 89 | Nilsson-Ehle No 2 |
| abo3 | alb-za | 587 | | Albino seedling 3 | 26:514 | Unknown cultivar |
| abo4 | a4 | 94 | 2H | Albino seedling 4 | 26:133 | Unknown cultivar |
| abo6 | $a_c$ | 106 | 3HS | Albino seedling 6 | 46: 60 | Colsess |
| abo8 | $a_{c2}$ | 4 | 7HS | Albino seedling 8 | 26: 47 | Coast |
| abo9 | $a_n$ | 112 | 3HS | Albino seedling 9 | 26:146 | Nigrinudum |
| abo10 | $a_{t2}$ | 588 | | Albino seedling 10 | 26:515 | Canadian Thorpe |
| abo11 | $a_{t3}$ | 589 | | Albino seedling 11 | 26:516 | Trebi |
| abo12 | alb,,o | 341 | 5HS | Albino seedling 12 | 26:290 | Titan |
| abo13 | alb,,p | 95 | 2HL | Albino seedling 13 | 26:134 | Titan |
| abo14 | alb,,q | 270 | 6HL | Albino seedling 14 | 26:250 | Shabet |
| abo15 | alb,,t | 271 | 6HS | Albino seedling 15 | 26:251 | Betzes |
| abr1 | abr | 472 | 2HL | Accordion basal rachis internode 1 | 26:419 | Bonus |
| acr1 | acr, ril | 97 | 2HL | Accordion rachis 1 | 47: 68 | ACBV89B229 |
| Acr2 | acr, lax | 189 | 4HL | Accordion rachis 2 | 47:101 | CIho 6164 |
| Acr3 | acr | 241 | 1HL | Accordion rachis 3 | 47:105 | Burma Girl |
| acr4 | acr-3 | 679 | 2H/ 6HL | Accordion rachis 4 | 47:181 | Bonus |
| acr5 | acr-2 | 744 | 7H | Accordion rachis 5 | 47:187 | |
| adp1 | adp | 593 | 3HL | Awned palea 1 | 43:158 | Unknown line |
| alm1 | al | 108 | 3HS | Albino lemma 1 | 46: 61 | Russia 82 |
| Alp1 | Alp, Pht | 188 | 4HL | Aluminum tolerance 1 | 47: 98 | |
| als1 | als | 101 | 3HL | Absent lower laterals 1 | 43: 74 | Montcalm |
| ant1 | rs | 33 | 7HS | Anthocyanin-less 1 | 46: 49 | Bonus |
| ant2 | pr | 80 | 2HL | Anthocyanin-less 2 | 46: 55 | Foma |
| ant3 | | 594 | | Anthocyanin-deficient 3 | 29: 82 | Bonus |
| ant4 | | 595 | 4H | Anthocyanin-deficient 4 | 45:216 | Foma |
| ant5 | | 596 | | Anthocyanin-deficient 5 | 29: 84 | Bonus |
| ant6 | | 597 | | Anthocyanin-deficient 6 | 29: 85 | Foma |
| Table 3. (continued) | | | | | | |

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr. vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| ant13 | | 598 | 6HL | Proanthocyanidin-free 13 | 29: 86 | Foma |
| ant17 | | 599 | 3HS | Proanthocyanidin-free 17 | 46:128 | Nordal |
| ant18 | | 600 | 3H | Proanthocyanidin-free 18 | 45:221 | Nordal |
| ant19 | | 601 | | Proanthocyanidin-free 19 | 29: 92 | Alf |
| ant20 | | 602 | | Anthocyanidin-rich 20 | 29: 93 | Foma |
| ant21 | | 603 | 6H | Proanthocyanidin-free 21 | 29: 94 | Georgie |
| ant22 | | 604 | 2HL | Proanthocyanidin-free 22 | 41:191 | Hege 802 |
| ant25 | | 605 | | Proanthocyanidin-free 25 | 29: 96 | Secobra 18193 |
| ant26 | | 606 | | Proanthocyanidin-free 26 | 29: 97 | Grit |
| ant27 | | 607 | | Proanthocyanidin-free 27 | 29: 98 | Zebit |
| ant28 | | 608 | 3HL | Proanthocyanidin-free 28 | 46:131 | Grit |
| ant29 | | 609 | | Proanthocyanidin-free 29 | 29:100 | Ca 708912 |
| ant30 | | 610 | | Proanthocyanidin-free 30 | 29:101 | Gunhild |
| ari-a | ari-1 | 132 | 3HS | Breviaristatum-a | 41:106 | Bonus |
| ari-b | ari-11 | 550 | | Breviaristatum-b | 44:185 | Bonus |
| ari-e | lk9,<br>GPert | 328 | 5HL | Breviaristatum-e | 47:121 | Bonus |
| ari-f | ari-21 | 551 | 7H | Breviaristatum-f | 41:182 | Bonus |
| ari-g | lk10 | 89 | 2H | Breviaristatum-g | 47: 66 | Bonus |
| ari-h | lk11 | 329 | 5HL | Breviaristatum-h | 26:277 | Foma |
| ari-j | ari-32 | 552 | | Breviaristatum-j | 44:186 | Bonus |
| ari-k | ari-504 | 553 | 3H | Breviaristatum-k | 44:187 | Bonus |
| ari-m | brh1 | 554 | 7HS | Breviaristatum-m | 47:175 | Bonus |
| ari-n | ari-45 | 555 | 7H | Breviaristatum-n | 41:185 | Bonus |
| ari-o | ert-u,<br>ert-zd | 556 | 7HL | Breviaristatum-o | 45:200 | Bonus |
| ari-p | ari-27 | 557 | | Breviaristatum-p | 46:120 | Foma |
| ari-q | ari-271 | 558 | 4H | Breviaristatum-q | 44:188 | Kristina |
| ari-r | ari-14 | 559 | 5H | Breviaristatum-r | 41:187 | Bonus |
| Ari-s | ari-265 | 630 | 5H/7H | Breviaristatum-s | 41:197 | Kristina |
| ari-t | ari-25 | 238 | 1H | Breviaristatum-t | 47:104 | Bonus |
| ari-u | ert-t | 678 | 2HS | Breviaristatum-u | 45:100 | Foma |
| ari-v | ari-137 | 680 | 5HS | Breviaristatum-v | 41:202 | Foma |
| ari-w | ari-153 | 721 | 7H | Breviaristatum-w | 43:216 | Foma |

Table 3. (continued)

| Locus symbol* | | BGS no. | Chr. Loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| ari-x | ari-22 | 274 | 6H | Breviaristatum-x | 43:124 | Bonus |
| ari-y | ari-9 | 722 | 5H | Breviaristatum-y | 43:217 | Bonus |
| asp1 | | 649 | | Aborted spike 1 | 43:172 | Steptoe |
| blf1 | bb | 326 | 5HL | Broad leaf 1 | 46: 90 | Bonus |
| blf2 | bb2, nlh | 337 | 5HL | Broad leaf 2 | 41:137 | Hannchen |
| Blp1 | B | 203 | 1HL | Black lemma and pericarp 1 | 46: 67 | Nigrinudum |
| blx1 | bl | 15 | 4HL | Non-blue aleurone xenia 1 | 26: 60 | Goldfoil |
| blx2 | bl2 | 19 | 7HS | Non-blue aleurone xenia 2 | 26: 65 | Nepal |
| blx3 | bl3 | 173 | 4HL | Non-blue aleurone xenia 3 | 26:198 | Blx |
| blx4 | bl4 | 174 | 4HL | Non-blue (pink) aleurone xenia 4 | 26:199 | Ab 6 |
| blx5 | bl5 | 454 | 7HL | Non-blue aleurone xenia 5 | 26:404 | BGM 122 |
| bra-a | | 619 | 7H | Bracteatum-a | 44:196 | Bonus |
| bra-d | | 586 | 1HL | Bracteatum-d | 40:139 | Foma |
| brc1 | brc-5, com2 | 613 | 2HS | Branched 1 | 45:224 | BGRC 13145 |
| brh1 | br | 1 | 7HS | Brachytic 1 | 47: 50 | Himalaya |
| brh2 | br2 | 157 | 4HL | Brachytic 2 | 47: 84 | Svanhals |
| brh3 | brh.g, ert-t | 631 | 2HS | Brachytic 3 | 45:229 | Birgitta |
| brh4 | brh.j | 349 | 2HL | Brachytic 4 | 42:407 | Birgitta |
| brh5 | brh.m | 185 | 4HS | Brachytic 5 | 44:110 | Birgitta |
| brh6 | brh.s | 350 | 5HL | Brachytic 6 | 42:408 | Akashinriki |
| brh7 | brh.w | 41 | 7H | Brachytic 7 | 42: 98 | Volla |
| brh8 | brh.ad | 142 | 3HL | Brachytic 8 | 42:232 | Birgitta |
| brh9 | brh.k | 187 | 4HL | Brachytic 9 | 43: 99 | Birgitta |
| brh10 | brh.l | 653 | 2HS | Brachytic 10 | 45:231 | Birgitta |
| brh11 | brh.n | 654 | 5HS | Brachytic 11 | 45:232 | Birgitta |
| brh12 | brh.o | 655 | 5HS | Brachytic 12 | 45:233 | Birgitta |
| brh13 | brh.p | 656 | 5HS | Brachytic 13 | 45:234 | Birgitta |
| brh14 | ari-o | 148 | 7HL | Brachytic 14 | 45:111 | Akashinriki |
| brh15 | brh.u | 657 | 2HL | Brachytic 15 | 44:205 | Julia |
| brh16 | brh.v | 44 | 7HL | Brachytic 16 | 45: 89 | Korál |
| brh17 | brh.ab | 658 | 5HS | Brachytic 17 | 45:236 | Morex |
| Table 3. (continued) | | | | | | |

| Locus symbol* | | BGS no. | Chr. Loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| brh18 | brh13 | 659 | 5HS | Brachytic 18 | 45:237 | Triumph |
| bsp1 | | 645 | | Bushy spike 1 | 43:168 | Morex |
| btr1 | bt1 | 115 | 3HS | Non-brittle rachis 1 | 43: 78 | A 222 |
| btr2 | bt2 | 116 | 3HS | Non-brittle rachis 2 | 43: 80 | Sakigoke |
| cal-b | | 620 | 5HL | Calcaroides-b | 44:197 | Bonus |
| Cal-c | | 621 | 5HL | Calcaroides-c | 41:195 | Bonus |
| cal-d | | 146 | 3H | Calcaroides-d | 40: 58 | Foma |
| cal-e | | 622 | 5HS | Calcaroides-e | 32:123 | Semira |
| cer-d | cer-5 | 399 | 5HL | Eceriferum-d + ++ ++ | 41:153 | Bonus |
| cer-e | cer-8 | 400 | 1HL | Eceriferum-e -/+ ++ ++ | 40:102 | Bonus |
| cer-f | cer-9 | 401 | 1H | Eceriferum-f + + ++ | 40:104 | Bonus |
| cer-g | cer-10 | 402 | 2HL | Eceriferum-g + + ++ | 47:131 | Bonus |
| cer-h | cer-13 | 403 | 4HS | Eceriferum-h - ++ ++ | 41:157 | Bonus |
| cer-i | cer-16 | 404 | 5HL | Eceriferum-i - ++ ++ | 41:158 | Bonus |
| cer-k | cer-39 | 405 | 4HL | Eceriferum-k + ++ ++ | 41:160 | Bonus |
| cer-l | cer-14 | 406 | 3HL | Eceriferum-l + ++ ++ | 44:142 | Bonus |
| cer-m | cer-15 | 407 | 1H/3H | Eceriferum-m +/++ + ++ | 41:161 | Bonus |
| cer-n | gs9,cer-20 | 408 | 2HL | Eceriferum-n - - ++ & - +/- ++ | 44:143 | Bonus |
| cer-o | cer-28 | 409 | 1HL | Eceriferum-o -/+ ++ ++ | 40:106 | Bonus |
| cer-p | cer-37 | 410 | 7HL | Eceriferum-p ++ ++ + | 41:162 | Bonus |
| cer-r | cer-19 | 411 | 3HL | Eceriferum-r +/- + ++ | 45:168 | Bonus |
| cer-t | cer-22 | 412 | 5HL | Eceriferum-t +/- ++ ++ | 41;164 | Bonus |
| cer-v | cer-49 | 414 | 2HS | Eceriferum-v +/- ++ ++ | 44:147 | Bonus |
| cer-w | cer-48 | 415 | 5HL | Eceriferum-w +/- ++ ++ | 41:166 | Bonus |
| cer-xa | cer-585 | 538 | 2HL/4H/5HL | Eceriferum-xa ++ ++ - | 44:174 | Foma |
| cer-xb | cer-943 | 539 | 4H | Eceriferum-xb - ++ ++ | 44:175 | Bonus |
| cer-xc | cer-1371 | 540 | 1H | Eceriferum-xc + + ++ | 44:176 | Bonus |
| cer-xd | cer-1455 | 541 | 4H/5HL | Eceriferum-xd + + ++ | 44:177 | Bonus |
| cer-y | cer-72 | 417 | 1HS | Eceriferum-y + +/++ ++ | 44:149 | Bonus |
| cer-ya | cer-180 | 444 | 3HS | Eceriferum-ya ++ ++ - | 26:396 | Bonus |
| cer-yb | cer-200 | 445 | 2HL | Eceriferum-yb ++ ++ - | 41:171 | Bonus |

Table 3. (continued)

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| cer-yc | cer-135 | 446 | 6H/<br>7HS | Eceriferum-yc - ++ ++ | 41:172 | Bonus |
| cer-yd | cer-139 | 447 | 3HS | Eceriferum-yd - ++ ++ | 26:399 | Bonus |
| cer-ye | cer-267 | 448 | 4H | Eceriferum-ye ++ ++ - | 43:149 | Foma |
| cer-yf | cer-652 | 449 | 7H | Eceriferum-yf ++ ++ + | 44:160 | Bonus |
| cer-yg | cer-1014 | 450 | 7HS | Eceriferum-yg - - - | 44:161 | Carlsberg II |
| cer-yh | cer-116 | 451 | 3HS | Eceriferum-yh - ++ ++ | 26:403 | Bonus |
| cer-yi | cer-254 | 522 | 2H | Eceriferum-yi ++ ++ - | 41:180 | Foma |
| cer-yj | cer-667 | 523 | 1HS | Eceriferum-yj ++ ++ - | 40:124 | Bonus |
| cer-yk | cer-627 | 524 | 7HL | Eceriferum-yk + + ++ | 44:167 | Bonus |
| cer-yl | cer-187 | 525 | 4HL | Eceriferum-yl - - ++ | 47:171 | Bonus |
| cer-ym | cer-753 | 526 | 4HL | Eceriferum-ym - - - | 47:173 | Bonus |
| cer-yn | cer-1112 | 527 | 1H | Eceriferum-yn + + ++ | 40:125 | Kristina |
| cer-yo | cer-647 | 528 | 4HS | Eceriferum-yo ++ ++ + | 44:168 | Bonus |
| cer-yp | cer-949 | 529 | 5HS | Eceriferum-yp ++ ++ + | 44:169 | Bonus |
| cer-yq | cer-1246 | 530 | 5H | Eceriferum-yq ++ ++ - | 44:170 | Kristina |
| cer-yr | cer-492 | 531 | 5HL | Eceriferum-yr -/+ + ++ | 44:171 | Foma |
| cer-ys | cer-680 | 532 | 2HL | Eceriferum-ys ++ ++ - | 44:172 | Bonus |
| cer-yt | cer-758 | 533 | 1H/5H | Eceriferum-yt - ++ ++ | 40:126 | Bonus |
| cer-yu | cer-158 | 534 | 1H | Eceriferum-yu ++ ++ - | 40:127 | Bonus |
| cer-yx | cer-421 | 535 | 1H/3H<br>/5H | Eceriferum-yx + + ++ | 40:128 | Foma |
| Cer-yy | Gle1 | 536 | 1HS | Eceriferum-yy - ++ ++ | 40:129 | Bonus |
| cer-yz | cer-1452 | 537 | 1H/5H | Eceriferum-yz + + ++ | 44:173 | Bonus |
| cer-z | cer-52 | 418 | 7HS | Eceriferum-z - - ++ | 44:150 | Bonus |
| cer-za | cer-126 | 419 | 5HL | Eceriferum-za ++ ++ - | 43:144 | Foma |
| cer-zb | cer-38 | 420 | 5HS | Eceriferum-zb - ++ ++ | 42:508 | Bonus |
| cer-zc | ccer-65 | 421 | 4HL/<br>2HS | Eceriferum-zc +/- ++ ++ | 42:510 | Bonus |
| cer-zd | cer-67 | 422 | 3HL | Eceriferum-zd ++ ++ - | 40:110 | Bonus |
| cer-ze | gl5 | 423 | 7HS | Eceriferum-ze ++ ++ - | 44:152 | Bonus |
| cer-zf | cer-70 | 424 | 3H/<br>7HS | Eceriferum-zf ++ ++ + | 42:516 | Bonus |
| cer-zg | cer-214 | 425 | 4HL | Eceriferum-zg ++ ++ + | 26:377 | Foma |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | BGS | | Locus name or phenotype | | Parental cultivar |

| Rec. | Prev. | no. | Chr. loc.† | | Descr.vol. p. | |
|---|---|---|---|---|---|---|
| | | | | | | |
| cer-zi | cer-68 | 427 | 1HL | Eceriferum-zi + + ++ | 41:168 | Bonus |
| cer-zj | cer-78 | 428 | 5HL | Eceriferum-zj ++ ++ - | 42:520 | Bonus |
| cer-zk | cer-85 | 429 | 2H | Eceriferum-zk + + +/- | 26:381 | Bonus |
| cer-zl | cer-17 | 430 | | Eceriferum-zl - - ++ | 26:382 | Bonus |
| cer-zn | cer-244 | 431 | 1H | Eceriferum-zn +/- ++ ++ | 40:112 | Foma |
| cer-zo | cer-229 | 432 | 3HS | Eceriferum-zo - ++ ++ | 44:154 | Foma |
| cer-zp | cer-313 | 433 | 5HL | Eceriferum-zp ++ ++ - | 26:385 | Bonus |
| cer-zq | cer-248 | 434 | | Eceriferum-zq ++ ++ - | 26:386 | Foma |
| cer-zr | cer-260 | 435 | 5HL | Eceriferum-zr +/- ++ ++ | 44:155 | Foma |
| cer-zs | cer-467 | 436 | | Eceriferum-zs + ++ ++ | 44:156 | Foma |
| cer-zt | cer-389 | 437 | 2HS | Eceriferum-zt + ++ ++ | 44:157 | Foma |
| cer-zu | cer-122 | 438 | 1HS | Eceriferum-zu - + ++ | 41:170 | Foma |
| cer-zv | cer-268 | 439 | 4HL | Eceriferum-zv - - - | 47:133 | Foma |
| cer-zw | cer-286 | 440 | | Eceriferum-zw + + ++ | 26:392 | Foma |
| cer-zx | cer-100 | 441 | 3H | Eceriferum-zx + + ++ | 46:111 | Bonus |
| cer-zy | cer-118 | 442 | 1HS | Eceriferum-zy ++ ++ + | 40:116 | Bonus |
| cer-zz | cer-615 | 443 | | Eceriferum-zz ++ ++ - | 44:159 | Bonus |
| clh1 | clh | 225 | 7H/5H | Curled leaf dwarf 1 | 40: 76 | Hannchen |
| com1 | lax-270,<br>bir1 | 473 | 5HL | Compositum 1 | 47:135 | Foma |
| com2 | bir2 | 71 | 2HS | Compositum 2 | 45: 95 | CIMMYT freak |
| crl1 | cl | 325 | 6H | Curly lateral 1 | 41:129 | Montcalm |
| crm1 | cm | 305 | 5HL | Cream seedling 1 | 26:256 | Black Hulless |
| cst1 | cs | 673 | 5HL | Corn stalk | 41:199 | Husky |
| cud1 | cud | 324 | 5HL | Curly dwarf 1 | 26:272 | Akashinriki |
| cud2 | | 229 | 1HL | Curly dwarf 2 | 47:103 | Akashinriki |
| cul2 | uc2 | 253 | 6HL | Uniculm 2 | 43:112 | Kindred |
| cul3 | cul3 | 616 | 3HL | Uniculme 3 | 43:161 | Donaria |
| cul4 | uc-5 | 617 | 3HL | Uniculme 4 | 46:132 | Bonus |
| cur1 | cu1 | 262 | 3HL | Curly 1 | 46: 81 | 48-cr cr-17 |
| cur2 | cu2 | 114 | 3HL | Curly 2 | 44: 82 | Choshiro |
| cur3 | cu3 | 263 | 6HL | Curly 3 | 41:125 | Akashinriki |
| cur4 | glo-d | 460 | 2HL | Curly 4 | 45:172 | Asahi 5 |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | BGS | | Locus name or phenotype | | Parental cultivar |

| Rec. | Prev. | no. | Chr. loc.† | | Descr.vol. p. | |
|---|---|---|---|---|---|---|
| | | | | | | |
| cur5 | cu5 | 231 | 2HS | Curly 5 | 41:120 | Glenn |
| ddt1 | ddt | 317 | 5HS | Reaction to DDT 1 | 26:266 | Spartan |
| des1 | lc | 12 | 7H | Desynapsis 1 | 42: 58 | Mars |
| des2 | ds | 119 | 3H | Desynapsis 2 | 43: 84 | Husky |
| des3 | | 386 | 2H/ 5HL | Desynapsis 3 | 43:140 | Betzes |
| des4 | | 13 | 7H | Desynapsis 4 | 44: 54 | Betzes |
| des5 | | 14 | 7HL | Desynapsis 5 | 44: 56 | Betzes |
| des6 | | 215 | 1HL | Desynapsis 6 | 43:106 | Betzes |
| des7 | | 64 | 3H | Desynapsis 7 | 43: 67 | Betzes |
| des8 | | 387 | 3H | Desynapsis 8 | 41:151 | Betzes |
| des9 | | 388 | 7HL | Desynapsis 9 | 44:131 | Betzes |
| des10 | | 389 | 3HL | Desynapsis 10 | 41:152 | Betzes |
| des11 | | 390 | 3HL | Desynapsis 11 | 44:132 | Betzes |
| des12 | | 391 | 3H | Desynapsis 12 | 44:133 | Betzes |
| des13 | | 392 | 3H | Desynapsis 13 | 44:134 | Betzes |
| des14 | | 393 | 7H | Desynapsis 14 | 44:135 | Betzes |
| des15 | | 394 | 3HL | Desynapsis 15 | 44:136 | Ingrid |
| dex1 | sex2 | 311 | 5HS | Defective endosperm xenia 1 | 26:260 | BTT 63-j-18-17 |
| dsk1 | dsk | 322 | 5HL | Dusky 1 | 41:128 | Chikurin-Ibaraki 1 |
| dsk2 | | 729 | 7HL | Dusky 2 | 44:208 | Betzes |
| dsp1 | l | 9 | 7HS | Dense spike 1 | 43: 50 | Honen 6 |
| dsp9 | l9, ert-e | 258 | 6HL | Dense spike 9 | 47:107 | Akashinriki |
| dsp10 | $l_c$ | 111 | 3HS | Dense spike 10 | 41: 99 | Club Mariout |
| dsp11 | dsp | 244 | 1HL | Dense spike 11 | 41:121 | Akashinriki |
| dub1 | | 661 | 6HL | Double seed 1 | 37:301 | Bonus |
| Dwf2 | | 542 | | Dominant dwarf 2 | 24:170 | Klages / Mata |
| Eam1 | Ea, Ppd-H1 | 65 | 2HS | Early maturity 1 | 47: 54 | Estate |
| Eam5 | HvPhyC-e | 348 | 5HL | Early maturity 5 | 45:123 | Higuerilla*2/ Gobernadora |
| Eam6 | Ea6, Ea, HvCEN | 98 | 2HS | Early maturity 6 | 46: 57 | Morex |
| eam7 | HvCO7 | 252 | 6HS | Early maturity 7 | 45:118 | California Mariout |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | BGS | | Locus name or phenotype | | Parental cultivar |

| Rec. | Prev. | no. | Chr. loc.† | | Descr.vol. p. | |
|---|---|---|---|---|---|---|
| | | | | | | |
| eam8 | ea$_{k}$,<br>mat-a | 214 | 1HL | Early maturity 8 | 46: 69 | Kinai 5 |
| eam9 | ea,,c | 181 | 4HL | Early maturity 9 | 26:204 | Tayeh 8 |
| eam10 | ea$_{sp}$ | 130 | 3HL | Early maturity 10 | 44: 86 | Super Precoz |
| eli-a | lig-a | 623 | | Eligulum-a | 44:199 | Foma |
| eog 1 | e | 57 | 2HL | Elongated outer glume 1 | 43: 64 | Triple Bearded Club Mariout |
| ert-a | ert-6 | 28 | 7HS | Erectoides-a | 41: 76 | Gull |
| ert-b | ert-2 | 224 | 1HL | Erectoides-b | 40: 74 | Gull |
| ert-c | ert-1 | 134 | 3HL | Erectoides-c | 41:108 | Gull |
| ert-d | ert-7 | 29 | 7HS | Erectoides-d | 42: 82 | Gull |
| ert-e | l9, dsp9 | 266 | 6HL | Erectoides-e | 47:109 | Bonus |
| ert-f | ert-18 | 560 | 1H | Erectoides-f | 40:133 | Bonus |
| ert-g | ert-g | 330 | 1HL | Erectoides-g | 41:133 | Bonus |
| ert-h | ert-25 | 561 | 5HL | Erectoides-h | 44:189 | Bonus |
| ert-ii | uzu1 | 135 | 3HL | Erectoides-ii | 45:109 | Bonus |
| ert-j | ert-31 | 90 | 2H | Erectoides-j | 43: 70 | Bonus |
| ert-k | ert-32 | 562 | 6H | Erectoides-k | 46:121 | Bonus |
| ert-l | ert-12 | 563 | | Erectoides-l | 26:489 | Maja |
| ert-m | ert-34 | 30 | 7HS | Erectoides-m | 46: 47 | Bonus |
| ert-n | ert-51 | 331 | 5HL | Erectoides-n | 44:120 | Bonus |
| ert-p | ert-44 | 564 | | Erectoides-p | 26:490 | Bonus |
| ert-q | ert-101 | 91 | 6H | Erectoides-q | 43: 71 | Bonus |
| Ert-r | Ert-52 | 332 | 2HL | Erectoides-r | 47:123 | Bonus |
| ert-s | ert-50 | 565 | | Erectoides-s | 26:491 | Bonus |
| ert-t | brh3 | 566 | 2HS | Erectoides-t | 45:203 | Bonus |
| ert-u | ari-o | 92 | 7HL | Erectoides-u | 45:100 | Bonus |
| ert-v | ert-57 | 567 | 6H | Erectoides-v | 41:188 | Bonus |
| ert-x | ert-58 | 568 | 1H/7H | Erectoides-x | 40:136 | Bonus |
| ert-y | ert-69 | 569 | | Erectoides-y | 26:495 | Bonus |
| ert-z | ert-71 | 570 | | Erectoides-z | 26:496 | Bonus |
| ert-za | ert-102 | 571 | 5H | Erectoides-za | 44:189 | Bonus |
| ert-zb | ert-132 | 572 | 7HL | Erectoides-zb | 45:205 | Bonus |
| ert-zc | ert-149 | 573 | 7HS | Erectoides-zc | 45:206 | Bonus |

Table 3. (continued)

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| ert-zd | ari-o | 93 | 7HL | Erectoides-zd | 45:102 | Bonus |
| ert-ze | ert-105 | 574 | 5HS | Erectoides-ze | 45:207 | Bonus |
| fch1 | f, lg | 55 | 2HS | Chlorina seedling 1 | 40: 49 | Minn 84-7 |
| fch2 | f2, lg5 | 117 | 3HL | Chlorina seedling 2 | 46: 63 | 28-3398 |
| fch3 | f3 | 220 | 1HS | Chlorina seedling 3 | 40: 71 | Minn 89-4 |
| fch4 | f4 | 17 | 7HL | Chlorina seedling 4 | 43: 54 | Montcalm |
| fch5 | f5 | 18 | 7HS | Chlorina seedling 5 | 43: 56 | Gateway |
| fch6 | f6 | 313 | 5HL | Chlorina seedling 6 | 44:116 | Himalaya |
| fch7 | f7 | 201 | 1HL | Chlorina seedling 7 | 41:113 | Smyrna |
| fch8 | f8 | 5 | 7HS | Chlorina seedling 8 | 41: 62 | Comfort |
| fch9 | f9 | 151 | 4HS | Chlorina seedling 9 | 44: 92 | Ko A |
| fch10 | | 177 | 4H | Chlorina seedling 10 | 43: 95 | Unknown cultivar |
| fch11 | f11 | 260 | 6HL | Chlorina seedling 11 | 45:207 | Himalaya |
| fch12 | $f_c$ | 2 | 7HS | Chlorina seedling 12 | 41:60 | Colsess |
| fch13 | f13 | 86 | 5HL | Chlorina seedling 13 | 44: 77 | Nigrinudum |
| fch14 | f14 | 87 | 2HL | Chlorina seedling 14 | 44: 78 | Shyri |
| fch15 | or | 52 | 2HS | Chlorina seedling 15 | 40: 48 | Trebi IV |
| fch16 | clo.117 | 676 | 2HS | Chlorina seedling 16 | 40:144 | Bonus |
| fch17 | vy | 191 | 1H/3H | Chlorina seedling 17 | 40: 68 | Himalaya / Ingrescens |
| fer1 | | 453 | | Few roots 1 | 46:112 | Bomi Abed |
| flo-a | | 182 | 6HL | Extra floret-a | 45:116 | Foma |
| flo-b | flo-a | 327 | 6HL | Extra floret-b | 45:121 | Foma |
| flo-c | flo-a | 74 | 6HL | Extra floret-c | 45: 97 | Foma |
| fol-a | | 73 | 2HL | Angustifolium-a | 43: 69 | Proctor |
| Fol-b | Ang | 548 | 1HS | Angustifolium-b | 40:131 | Unknown |
| fst1 | fs | 301 | 5HL | Fragile stem 1 | 26:252 | Kamairazu |
| fst2 | fs2 | 208 | 1HL | Fragile stem 2 | 41:114 | Oshichi |
| fst3 | fs3 | 24 | 7HS | Fragile stem 3 | 41: 74 | Kobinkatagi 4 |
| fxp1 | | 728 | | Fenoxaprop-p-ethyl reaction 1 | 43:223 | Morex |
| gig1 | gig | 463 | 2H | Gigas 1 | 44:164 | Tochigi Golden Melon |
| gig2 | | 612 | 4HL | Gigas 2 | 44:191 | ND12463 |

Table 3. (continued)

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| glf1 | gl, cer-zh | 155 | 4HL | Glossy leaf 1 ++ ++ - | 47: 81 | Himalaya |
| glf3 | gl3, cer-j | 165 | 4HL | Glossy leaf 3 ++ ++ - | 47: 86 | Goseshikoku |
| glo-a | | 168 | 4H | Globosum-a | 45:115 | Proctor |
| glo-b | | 336 | 5HL | Globosum-b | 26:284 | Villa |
| glo-c | glo-c | 72 | 2H | Globosum-c | 43: 68 | Villa |
| glo-e | | 230 | 1HL | Globosum-e | 45:117 | Foma |
| glo-f | | 342 | 5HL | Globosum-f | 26:291 | Damazy |
| gpa1 | gp | 59 | 2HL | Grandpa 1 | 45: 91 | Lyallpur |
| gra-a | gran-a | 131 | 7H | Granum-a | 47: 79 | Donaria |
| gsh1 | gs1, cer-q | 351 | 2HS | Glossy sheath 1 - - ++ | 46: 94 | PI 195285 |
| gsh2 | gs2, cer-b | 352 | 3HL | Glossy sheath 2 - - ++ | 47:125 | Atlas |
| gsh3 | gs3, cer-a | 353 | 7HS | Glossy sheath 3 - - ++ | 41:143 | Mars |
| gsh4 | gs4, cer-x | 354 | 6HL | Glossy sheath 4 - - ++ | 41:146 | Gateway |
| gsh5 | gs5, cer-s | 355 | 2HL | Glossy sheath 5 + - ++ | 47:128 | Jotun |
| gsh6 | gs6, cer-c | 356 | 2HS | Glossy sheath 6 - - ++ | 46:101 | Betzes |
| gsh7 | gs7 | 81 | 1H/2H/5H | Glossy sheath 7 - - ++ | 40: 55 | Akashinriki |
| gsh8 | gs8, cer-u | 413 | 2HS | Glossy sheath 8 + + ++ | 46:105 | Akashinriki |
| Gth1 | G | 69 | 2HL | Toothed lemma 1 | 47: 59 | Machine (Wexelsen) |
| hcm1 | h | 77 | 2HL | Short culm 1 | 26:115 | Morex |
| Hln1 | Hn | 164 | 4HL | Hairs on lemma nerves 1 | 44: 99 | Kogane-mugi |
| Hsh1 | Hs | 179 | 4HL | Hairy leaf sheath 1 | 44:107 | Kimugi |
| ibl1 | ibl1 | 716 | 5HL | Intense blue aleurone 1 | 46:136 | Ethiopian 637 |
| int-b | vrs2 | 320 | 5HL | Intermedium spike-b | 47:118 | Bonus |
| int-c | i, vrs5, HvTB1 | 178 | 4HS | Intermedium spike-c | 47: 92 | Gamma 4 |
| int-f | int-20 | 543 | 2HS/3HL | Intermedium spike-f | 44:178 | Foma |
| int-h | int-42 | 544 | 5H | Intermedium spike-h | 44:179 | Kristina |
| int-i | int-39 | 545 | 2HS | Intermedium spike-i | 41:181 | Kristina |
| int-k | int-47 | 546 | 7H | Intermedium spike-k | 44:180 | Kristina |
| int-m | int-85 | 547 | 5HL | Intermedium spike-m | 44:181 | Bonus |
| Kap1 | K | 152 | 4HS | Hooded lemma 1 | 26:179 | Colsess |

Table 3. (continued)

| Locus symbol* | | BGS no. | Chr. loc.[†] | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| lab1 | | 730 | 5HL | Labile 1 | 46:137 | |
| lam1 | | 651 | | Late maturity 1 | 43:174 | Steptoe |
| lax-a | lax-8 | 474 | 5HL | Laxatum-a | 46:113 | Bonus |
| lax-b | lax-1 | 268 | 6HL | Laxatum-b | 44:113 | Bonus |
| lax-c | lax-21 | 475 | 6HL | Laxatum-c | 47:137 | Bonus |
| lax-d | lax-83 | 476 | | Laxatum-d | 47:139 | Bonus |
| lax-f | lax-61 | 477 | | Laxatum-f | 47:140 | Bonus |
| lax-g | lax-25 | 478 | | Laxatum-g | 47:141 | Bonus |
| lax-h | lax-26 | 479 | 3H | Laxatum-h | 47:142 | Bonus |
| lax-i | lax-50 | 480 | | Laxatum-i | 47:144 | Bonus |
| lax-j | lax-49 | 481 | 2H | Laxatum-j | 47:145 | Bonus |
| lax-k | lax-84 | 482 | 2H/3H | Laxatum-k | 47:147 | Bonus |
| lax-l | lax-60 | 483 | 1H | Laxatum-l | 47:148 | Bonus |
| lax-m | lax-67 | 484 | | Laxatum-m | 47:149 | Bonus |
| lax-n | lax-80 | 485 | 2H/4HL/5H | Laxatum-n | 47:150 | Bonus |
| lax-o | lax-79 | 486 | | Laxatum-o | 47:152 | Bonus |
| lax-df | lax-204 | 487 | | Laxatum-df | 47:153 | Foma |
| lax-ef | lax-225 | 488 | 2H | Laxatum-ef | 47:154 | Foma |
| lax-ff | lax-216 | 489 | | Laxatum-ff | 47:156 | Foma |
| lax-gf | lax-217 | 490 | | Laxatum-gf | 47:157 | Foma |
| lax-hf | lax-244 | 491 | 2H/3HL/5H | Laxatum-hf | 47:158 | Foma |
| lax-if | lax-246 | 492 | | Laxatum-if | 47:160 | Foma |
| Lax-jf | lax-253 | 493 | 4HS | Laxatum-jf | 47:161 | Foma |
| lax-kf | lax-295 | 494 | | Laxatum-kf | 47:163 | Foma |
| lax-lf | lax-274 | 495 | | Laxatum-lf | 47:164 | Foma |
| lax-mf | lax-302 | 496 | | Laxatum-mf | 47:165 | Foma |
| lax-nf | lax-322 | 497 | 2HL/4H | Laxatum-nf | 47:166 | Foma |
| lbi1 | lb | 308 | 5HL | Long basal rachis internode 1 | 43:125 | Wisconsin Pedigree 38 |
| lbi2 | lb2 | 156 | 4HS | Long basal rachis internode 2 | 44: 92 | Montcalm |
| lbi3 | lb3 | 27 | 7HL | Long basal rachis internode 3 | 42: 79 | Montcalm |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | | | Locus name or phenotype | | Parental cultivar |

| Rec. | Prev. | BGS no. | Chr. loc.† | | Descr.vol. p. | |
|---|---|---|---|---|---|---|
| | | | | | | |
| lel1 | lel | 235 | 2H | Leafy lemma 1 | 46: 74 | G7118 |
| Lfb1 | Lfb | 343 | 5HL | Leafy bract 1 | 41:140 | Montcalm |
| lfl1 | lfl | 275 | 6HL | Leafless 1 | 47:111 | Golden Melon |
| Lga1 | Log | 549 | 7HS | Long glume awn 1 | 44:183 | Guy Mayle |
| lgn2 | lg2 | 169 | 4HS | Light green 2 | 42:264 | Minn 75 |
| lgn3 | lg3, lg7 | 170 | 1HL | Light green 3 | 44:103 | No 154 |
| lgn4 | lg4, lg1 | 171 | 4HL | Light green 4 | 44:105 | Himalaya / Ingrescens |
| lig1 | li, aur-a | 60 | 2HL | Liguleless 1 | 45: 93 | Muyoji |
| lit1 | s, rin | 99 | 2HS | Lesser internode number 1 | 41: 92 | Natural occurrence |
| Lks1 | Lk | 75 | 2HL | Awnless 1 | 41: 84 | *Hordeum inerme* |
| lks2 | lk2 | 10 | 7HL | Short awn 2 | 45: 80 | Honen 6 |
| lks5 | lk5 | 172 | 4HL | Short awn 5 | 47: 89 | CIho 5641 |
| lks6 | lks.q | 724 | 1H/5H /6H | Short awn 6 | 43:219 | Morex |
| lnt1 | rnt | 118 | 3HL | Low number of tillers 1 | 47: 74 | Mitake |
| lys1 | lys | 338 | 5HL | High lysine 1 | 26:286 | Hiproly |
| lys3 | sex3 | 339 | 5HL | High lysine 3 | 43:127 | Bomi Abed |
| Lys4 | sex5 | 232 | 1HS | High lysine 4 | 26:230 | Bomi Abed |
| lys6 | | 269 | 6H | High lysine 6 | 44:114 | Bomi Abed |
| lzd1 | dw4 | 125 | 3H | Lazy dwarf 1 | 43: 87 | Akashinriki |
| mat-b | mat-7 | 578 | 7HL | Praematurum-b | 46:123 | Bonus |
| mat-c | Eam6, HvCEN | 579 | 2H | Praematurum-c | 46:125 | Bonus |
| mat-d | mat-14 | 580 | 4HL/ 6HL | Praematurum-d | 45:208 | Bonus |
| mat-e | mat-18 | 581 | | Praematurum-e | 26:508 | Bonus |
| mat-f | mat-23 | 582 | 1H | Praematurum-f | 45:210 | Bonus |
| mat-g | mat-30 | 583 | | Praematurum-g | 26:510 | Bonus |
| mat-h | mat-36 | 584 | 4HL | Praematurum-h | 45:212 | Bonus |
| mat-i | mat-37 | 585 | 7HL | Praematurum-i | 45:214 | Bonus |
| min1 | min | 161 | 4HL | Semi-minute dwarf 1 | 44: 97 | Taisho-mugi |
| min2 | en-min | 160 | | Enhancer of minute 1 | 26:186 | Kaiyo Bozu |
| mnd1 | m | 519 | 2H | Many noded dwarf 1 | 43:154 | Mesa |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | | | Locus name or phenotype | | Parental cultivar |

| Rec. | Prev. | BGS no. | Chr. loc.[†] | | Descr.vol. p. | |
|---|---|---|---|---|---|---|
| | | | | | | |
| mnd3 | m3 | 618 | 4HS | Many noded dwarf 3 | 44:194 | Montcalm |
| mnd4 | m4 | 347 | 5HL | Many noded dwarf 4 | 44:122 | Akashinriki |
| mnd5 | | 632 | 7HL | Many noded dwarf 5 | 44:202 | C2-95-199 |
| mnd6 | den-6 | 633 | 5HL | Many noded dwarf 6 | 44:203 | Bonus |
| mnd7 | | 726 | | Many noded dwarf 7 | 43:221 | Steptoe |
| mov1 | mo5 | 43 | 7HL | Multiovary 1 | 43: 59 | Steptoe |
| mov2 | mo | 147 | 3HS | Multiovary 2 | 43: 91 | Steptoe |
| mov3 | mo-a | 234 | 1H | Multiovary 3 | 32:102 | Akashinriki |
| mov4 | mo8 | 648 | | Multiovary 4 | 43:171 | Steptoe |
| mov5 | mov.o | 723 | | Multiovary 5 | 43:218 | Morex |
| msg1 | ms, ms1 | 357 | 1HL | Male sterile genetic 1 | 45:126 | CIho 5368 |
| msg2 | ms2 | 358 | 2HL | Male sterile genetic 2 | 45:128 | Manchuria |
| msg3 | ms3 | 359 | 1HL | Male sterile genetic 3 | 45:130 | Gateway |
| msg4 | ms4 | 360 | 1H | Male sterile genetic 4 | 45:132 | Freja |
| msg5 | ms5 | 361 | 3HS | Male sterile genetic 5 | 45:133 | Carlsberg II |
| msg6 | ms6 | 362 | 6HS | Male sterile genetic 6 | 45:135 | Hanna |
| msg7 | ms7 | 363 | 5HL | Male sterile genetic 7 | 45:137 | Dekap |
| msg8 | ms8 | 364 | 5HL | Male sterile genetic 8 | 45:139 | Betzes |
| msg9 | ms9 | 365 | 2HS | Male sterile genetic 9 | 45:141 | Vantage |
| msg10 | ms10 | 366 | 7HS | Male sterile genetic 10 | 45:142 | Compana |
| msg11 | ms11 | 367 | 5HS | Male sterile genetic 11 | 45:144 | Gateway |
| msg13 | ms13 | 368 | 3HL | Male sterile genetic 13 | 45:146 | Haisa II |
| msg14 | ms14 | 369 | 7HS | Male sterile genetic 14 | 45:147 | Unitan |
| msg15 | ms15 | 370 | | Male sterile genetic 15 | 45:149 | Atlas/2*Kindred |
| msg16 | ms16 | 371 | 5HS | Male sterile genetic 16 | 45:150 | Betzes |
| msg17 | ms17 | 372 | 5HL | Male sterile genetic 17 | 45:152 | Compana |
| msg18 | ms18 | 373 | 5HL | Male sterile genetic 18 | 45:153 | Compana |
| msg19 | ms19 | 374 | 5HS | Male sterile genetic 19 | 45:155 | CIho 14393 |
| msg20 | msg,,ad | 375 | 4H | Male sterile genetic 20 | 45:156 | Hannchen |
| msg21 | ms21 | 376 | 1HL | Male sterile genetic 21 | 45:157 | Midwest Bulk |
| msg22 | ms22 | 383 | 7H | Male sterile genetic 22 | 45:162 | Glacier / Compana |
| msg23 | ms23 | 384 | 5H | Male sterile genetic 23 | 45:163 | Betzes |
| msg24 | ms24 | 385 | 4HL | Male sterile genetic 24 | 45:164 | Betzes |
| Table 3. (continued) | | | | | | |

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| msg25 | msg,,r | 166 | 2HS | Male sterile genetic 25 | 45:113 | Betzes |
| msg26 | msg,,u | 395 | 7HS | Male sterile genetic 26 | 45:166 | Unitan |
| msg27 | msg,,ae | 464 | 2HS | Male sterile genetic 27 | 45:174 | Firlbecks III |
| msg28 | msg,,as | 465 | 2HS | Male sterile genetic 28 | 45:175 | York |
| msg29 | msg,,a | 466 | 5HL | Male sterile genetic 29 | 45:176 | Ackermans MGZ |
| msg30 | msg,,c | 467 | 7HL | Male sterile genetic 30 | 45:177 | Compana |
| msg31 | msg,,d | 468 | 1HL | Male sterile genetic 31 | 45:178 | 51Ab4834 |
| msg32 | msg,,w | 469 | 7H | Male sterile genetic 32 | 45:179 | Betzes |
| msg33 | msg,,x | 470 | 2HS | Male sterile genetic 33 | 45:180 | Betzes |
| msg34 | msg,,av | 471 | 6HS/ 7HS | Male sterile genetic 34 | 45:181 | Paragon |
| msg35 | msg,,dr | 498 | 2HL | Male sterile genetic 35 | 45:183 | Karl |
| msg36 | msg,,bk | 499 | 6HS | Male sterile genetic 36 | 45:184 | Betzes |
| msg37 | msg,,hl | 500 | 3HL | Male sterile genetic 37 | 45:186 | Clermont |
| msg38 | msg,,jl | 501 | 3H | Male sterile genetic 38 | 45:187 | Ingrid |
| msg39 | msg,,dm | 502 | 3H | Male sterile genetic 39 | 45:188 | P11 |
| msg40 | msg,,ac | 503 | 6HL | Male sterile genetic 40 | 45:190 | Conquest |
| msg41 | msg,,aj | 504 | 6HS | Male sterile genetic 41 | 45:191 | Betzes |
| msg42 | msg,,db | 505 | 3H | Male sterile genetic 42 | 45:193 | Betzes |
| msg43 | msg,,br | 506 | 2HL | Male sterile genetic 43 | 45:194 | Betzes |
| msg44 | msg,,cx | 507 | 5HL | Male sterile genetic 44 | 45:195 | HA6-33-02 |
| msg45 | msg,,dp | 508 | 5HL/ 7HS | Male sterile genetic 45 | 45:196 | RPB439-71 |
| msg46 | msg,,ec | 509 | 2H/6H | Male sterile genetic 46 | 45:197 | Hector |
| msg47 | msg,,ep | 510 | 3HS/ 7HS | Male sterile genetic 47 | 45:198 | Sel12384CO |
| msg48 | msg,,jt | 520 | 1H | Male sterile genetic 48 | 45:199 | Simba |
| msg49 | msg,,jw | 335 | 5HL | Male sterile genetic 49 | 45:122 | ND7369 |
| msg50 | msg,,hm | 34 | 7HL | Male sterile genetic 50 | 45: 88 | Berac |
| mss1 | mss | 84 | 5H | Midseason stripe 1 | 44: 75 | Montcalm |
| mss2 | | 39 | 7HS | Midseason stripe 2 | 44: 59 | ND11258 |
| mtt1 | mt | 521 | 1HS | Mottled leaf 1 | 41:179 | Montcalm |
| mtt2 | mt2 | 302 | 5HL | Mottled leaf 2 | 41:127 | Montcalm |
| mtt4 | mt,,e | 78 | 2HL | Mottled leaf 4 | 41: 86 | Victorie |
| Table 3. (continued) | | | | | | |

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| mtt5 | mt,,f | 264 | 6HL | Mottled leaf 5 | 41:126 | Akashinriki |
| mtt6 | | 629 | 7HS | Mottled leaf 6 | 45:228 | ND6809 |
| mtt7 | mtt.h | 677 | 2HS | Mottled leaf 7 | 42:753 | Morex |
| mtt8 | Mut 1661 | 674 | | Mottled leaf 8 | 43:182 | Bowman Rph3.c |
| mtt9 | Mut 2721 | 675 | | Mottled leaf 9 | 44:207 | Bowman Rph3.c |
| mul2 | | 251 | 6HL | Multiflorus 2 | 26:232 | Montcalm |
| nar1 | | 637 | 6HS | NADH nitrate reductase-deficient 1 | 35:194 | Steptoe |
| nar2 | | 638 | 5HL | NADH nitrate reductase-deficient 2 | 35:196 | Steptoe |
| nar3 | | 639 | 7HS | NADH nitrate reductase-deficient 3 | 35:197 | Winer |
| nar4 | | 640 | 2HL | NADH nitrate reductase-deficient 4 | 35:198 | Steptoe |
| nar5 | | 641 | 5HL | NADH nitrate reductase-deficient 5 | 35:199 | Steptoe |
| nar6 | | 642 | 2HL | NADH nitrate reductase-deficient 6 | 35:200 | Steptoe |
| nar7 | | 643 | 6HL | NADH nitrate reductase-deficient 7 | 35:201 | Steptoe |
| nar8 | | 644 | 6HS | NADH nitrate reductase-deficient 8 | 35:202 | Steptoe |
| nec1 | sp,,b | 222 | 1HL | Necrotic leaf spot 1 | 43:108 | Carlsberg II |
| nec2 | nec2 | 261 | 6HS | Necrotic leaf spot 2 | 26:241 | Carlsberg II |
| nec3 | nec3 | 265 | 6HS | Necrotic leaf spot 3 | 43:116 | Proctor |
| nec4 | nec4 | 138 | 3H | Necrotic leaf spot 4 | 43: 88 | Proctor |
| nec5 | nec5 | 139 | 3H | Necrotic leaf spot 5 | 43: 89 | Diamant |
| Nec6 | Sp | 611 | 7HS | Necrotic leaf spot 6 | 43:159 | Awnless Atlas |
| nec7 | nec-45 | 635 | 1H/6H/7H | Necroticans 7 | 43:166 | Kristina |
| nec8 | nec.w | 671 | 5HL | Necrotic leaf spot 8 | 43:179 | Bowman Rph3.c |
| nec9 | Mut 3091 | 672 | 3HL | Necrotic leaf spot 9 | 43:181 | Bowman Rph3.c |
| nec10 | necS 1-1 | 681 | 3H | Necroticans 10 | 43:184 | Steptoe |
| nec11 | | 682 | 1H | Necroticans 11 | 43:185 | Steptoe |
| nec12 | | 683 | | Necroticans 12 | 43:186 | Steptoe |
| nec13 | | 684 | | Necroticans 13 | 43:187 | Steptoe |

Table 3. (continued)

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| nec14 | | 685 | | Necroticans 14 | 43:188 | Steptoe |
| nec15 | | 686 | | Necroticans 15 | 43:189 | Steptoe |
| nec16t | | 687 | | Necroticans 16 | 43:190 | Steptoe |
| nec17 | | 688 | | Necroticans 17 | 43:191 | Steptoe |
| nec18 | | 689 | | Necroticans 18 | 43:192 | Steptoe |
| nec19 | | 690 | | Necroticans 19 | 43:193 | Steptoe |
| nec20 | | 691 | | Necroticans 20 | 43:194 | Steptoe |
| nec21 | | 692 | | Necroticans 21 | 43:195 | Steptoe |
| Nec22 | | 693 | | Necroticans 22 | 43:196 | Steptoe |
| nec23 | | 694 | | Necroticans 23 | 43:197 | Steptoe |
| Nec24 | | 695 | | Necroticans 24 | 43:198 | Steptoe |
| nec25 | | 696 | | Necroticans 25 | 43:199 | Steptoe |
| Nec26 | | 697 | | Necroticans 26 | 43:200 | Steptoe |
| nec27 | | 698 | | Necroticans 27 | 43:201 | Steptoe |
| nec28 | | 699 | | Necroticans 28 | 43:202 | Morex |
| nec29 | | 700 | | Necroticans 29 | 43:203 | Morex |
| nec30 | | 701 | | Necroticans 30 | 43:204 | Morex |
| nec31 | | 702 | | Necroticans 31 | 43:205 | Morex |
| nec32 | | 703 | | Necroticans 32 | 43:206 | Morex |
| nec33 | | 704 | | Necroticans 33 | 43:207 | CIho 4196 |
| nec34 | nec.k | 197 | 4HS | Necroticans 34 | 43:104 | ND13917 |
| nld1 | nld | 323 | 5HL | Narrow leafed dwarf 1 | 46: 88 | Nagaoka |
| nld2 | | 660 | 5H/6H/7H | Narrow leafed dwarf 2 | 43:176 | Steptoe |
| nud1 | n, nud | 7 | 7HL | Naked caryopsis 1 | 44: 51 | Himalaya |
| ops1 | op-3 | 624 | 7HS | Opposite spikelets 1 | 45:226 | Bonus |
| ops2 | op-2 | 718 | 5HL | Opposite spikelets 2 | 43:213 | Foma |
| ops3 | op-1 | 719 | 5HS | Opposite spikelets 3 | 43:214 | Bonus |
| ovl1 | | 176 | 4H | Ovaryless 1 | 35:191 | Kanto Bansei Gold |
| ovl2 | ovl2 | 646 | | Ovaryless 2 | 43:169 | Harrington |
| ovl3 | | 725 | | Ovaryless 3 | 43:220 | Harrington |
| Pbg1 | Pbg | 740 | 7H | Pubescens on glume 1 | 47:182 | |
| pmr1 | pmr | 40 | 7HS | Premature ripe 1 | 44: 60 | Glenn |
| Table 3. (continued) | | | | | | |

| Locus symbol* | | BGS no. | Chr. loc.[†] | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| pmr2 | nec-50 | 634 | | Premature ripe 2 | 32:135 | Bonus |
| Pre2 | Re2 | 76 | 2HL | Red lemma and pericarp 2 | 46: 53 | Buckley 3277 |
| Pub1 | Pub | 127 | 3HL | Pubescent leaf blade 1 | 44: 84 | Multiple Dominant |
| Pvc1 | $P_c$ | 68 | 2HL | Purple veined lemma 1 | 44: 67 | Buckley 2223-6 |
| Pyr1 | Pyr.g | 42 | 3HL | Pyramidatum 1 | 41: 78 | Pokko/Hja80001 |
| raw1 | r | 312 | 5HL | Smooth awn 1 | 46: 84 | Lion |
| raw2 | r2 | 340 | 5HL | Smooth awn 2 | 46: 92 | Lion |
| raw5 | r,,e | 257 | 6HL | Smooth awn 5 | 44:112 | Akashinriki |
| raw6 | r6 | 334 | 5HL | Smooth awn 6 | 26:282 | Glenn |
| rcr1 | γ08-122 | 737 | | Required for resistance to *Cochliobolus sativus* 1 | 45:249 | Morex |
| rcr2 | γ08-123 | 738 | | Required for resistance to *Cochliobolus sativus* 2 | 45:250 | Morex |
| rcr3 | γ08-124 | 739 | | Required for resistance to *Cochliobolus sativus* 3 | 45:251 | Morex |
| rob1 | o | 254 | 6HS | Orange lemma 1 | 46: 78 | CIho 5649 |
| Rpc1 | | 149 | 3H | Reaction to *Puccinia coronata* var. *hordei* 1 | 37:232 | Hor 2596 |
| Rpg1 | T | 511 | 7HS | Reaction to *Puccinia graminis* 1 | 26:437 | Chevron |
| Rpg2 | T2 | 512 | | Reaction to *Puccinia graminis* 2 | 26:439 | Hietpas 5 |
| rpg4 | | 319 | 5HL | Reaction to *Puccinia graminis* 4 | 26:267 | Q21861 |
| Rph1 | Pa | 70 | 2H | Reaction to *Puccinia hordei* 1 | 26:107 | Oderbrucker |
| Rph2 | Pa2 | 88 | 5HS | Reaction to *Puccinia hordei* 2 | 37:212 | Peruvian |
| Rph3 | Pa3 | 121 | 7HL | Reaction to *Puccinia hordei* 3 | 26:156 | Estate |
| Rph4 | Pa4 | 218 | 1HS | Reaction to *Puccinia hordei* 4 | 42:302 | Gull |
| Rph5 | Pa5 | 122 | 3HS | Reaction to *Puccinia hordei* 5 | 37:224 | Magnif 102 |
| Rph6 | Pa6 | 575 | 3HS | Reaction to *Puccinia hordei* 6 | 26:501 | Bolivia |
| Rph7 | Pa7 | 136 | 3HS | Reaction to *Puccinia hordei* 7 | 37:228 | Cebada Capa |
| Rph8 | Pa8 | 576 | | Reaction to *Puccinia hordei* 8 | 26:502 | Egypt 4 |
| Rph9 | Pa9,<br>Pa12 | 32 | 5HL | Reaction to *Puccinia hordei* 9 | 37:201 | HOR 2596 |
| Rph10 | | 137 | 3HL | Reaction to *Puccinia hordei* 10 | 26:174 | Clipper C8 |
| Table 3. (continued) | | | | | | |

| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Rec. | Prev. | | | | | |
| | | | | | | |
| Rph11 | | 267 | 6HL | Reaction to *Puccinia hordei* 11 | 26:247 | Clipper C67 |
| Rph12 | Pa12,<br>Pa9 | 333 | 5HL | Reaction to *Puccinia hordei* 12 | 26:281 | Triumph |
| Rph13 | | 590 | | Reaction to *Puccinia hordei* 13 | 28: 31 | PI 531849 |
| Rph14 | | 591 | | Reaction to *Puccinia hordei* 14 | 28: 32 | PI 584760 |
| Rph15 | Rph16 | 96 | 2HL | Reaction to *Puccinia hordei* 15 | 37:214 | PI 355447 |
| rpr1 | | 707 | 4H | Required for *Puccinia graminis* resistance 1 | 42:757 | Morex |
| rpr2 | γ08-118 | 731 | 6H | Required for *Puccinia graminis* resistance 2 | 46:139 | Morex |
| rpr3 | γ08-112 | 732 | | Required for *Puccinia graminis* resistance 3 | 46:141 | Morex |
| rpr4 | γ08-114 | 733 | | Required for *Puccinia graminis* resistance 4 | 46:142 | Morex |
| rpr5 | γ08-117 | 734 | | Required for *Puccinia graminis* resistance 5 | 46:143 | Morex |
| rpr6 | γ08-119 | 735 | | Required for *Puccinia graminis* resistance 6 | 46:144 | Morex |
| rpr7 | γ08-115 | 736 | | Required for *Puccinia graminis* resistance 7 | 46:145 | Morex |
| Rpt1 | Pt | 667 | 3HL | Reaction to *Pyrenophora teres* 1 | 43:177 | Tifang |
| Rpt2 | Rpt2c | 237 | 1HS | Reaction to *Pyrenophora teres* 2 | 43:110 | CIho 9819 |
| Rpt3 | QRptts2 | 711 | 2HS | Reaction to *Pyrenophora teres* 3 | 43:208 | Tennessee Awnless D22-5 |
| Rpt4 | QRpt7 | 48 | 7HL | Reaction to *Pyrenophora teres* 4 | 43: 61 | Galleon |
| Rpt5 | Rpt$_{a}$ | 272 | 6HL | Reaction to *Pyrenophora teres* 5 | 43:120 | CIho 5791, CIho 9819 |
| Rpt6 | | 713 | 5HL | Reaction to *Pyrenophora teres* 6 | 43:210 | CIho 9819 |
| Rpt7 | Qrpts4 | 714 | 4HL | Reaction to *Pyrenophora teres* 7 | 43:211 | Halcyon |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p | Parental cultivar |
| Rec. | Prev. | | | | | |

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|---|---|---|---|---|---|---|
| Rpt8 | QRpts4 | 198 | 4HS | Reaction to *Pyrenophora teres* 8 | 43:105 | Q21861 |
| Rsg1 | Grb | 22 | 7H | Reaction to *Schizaphis graminum* 1 | 37:199 | Omugi |
| Rsg2 | | 577 | | Reaction to *Schizaphis graminum* 2 | 37:283 | PI 426756 |
| rsm1 | sm | 35 | 7HS | Reaction to BSMV 1 | 26: 84 | Modjo 1 |
| Rsp1 | Sep | 515 | | Reaction to *Septoria passerinii* 1 | 26:441 | CIho 14300 |
| Rsp2 | Sep2 | 516 | | Reaction to *Septoria passerinii* 2 | 37:275 | PI 70837 |
| Rsp3 | Sep3 | 517 | | Reaction to *Septoria passerinii* 3 | 37:276 | CIho 10644 |
| rtt1 | rt | 51 | 2HS | Rattail spike 1 | 47: 53 | Goldfoil |
| Run1 | Un | 21 | 7HS | Reaction to *Ustilago nuda* 1 | 26: 67 | Trebi |
| rvl1 | rvl | 226 | 1HL | Revoluted leaf 1 | 40: 77 | Hakata 2 |
| Ryd2 | Yd2 | 123 | 3HL | Reaction to BYDV 2 | 26:158 | CIho 2376 |
| Rym1 | Ym | 167 | 4HL | Reaction to BaYMV 1 | 32: 96 | Mokusekko 3 |
| Rym2 | Ym2 | 20 | 7HL | Reaction to BaYMV 2 | 26: 66 | Mihori Hadaka 3 |
| rym3 | ym3 | 345 | 5HS | Reaction to BaYMV 3 | 32:105 | Chikurin Ibaraki |
| rym5 | Ym | 141 | 3HL | Reaction to BaYMV 5 | 32: 90 | Mokusekko 3 |
| sbk1 | sk, cal-a | 62 | 2HS | Subjacent hood 1 | 40: 51 | Tayeh 13 |
| sca1 | sca | 128 | 3HS | Short crooked awn 1 | 44: 85 | Akashinriki |
| sci-a | sci-3 | 625 | 5H | Scirpoides-a | 44:200 | Bonus |
| sci-b | sci-4 | 239 | 1H/6H | Scirpoides-b | 46: 76 | Bonus |
| scl-a | scl-6 | 626 | 1HL | Scirpoides leaf-a | 44:201 | Foma |
| scl-b | scl-5 | 150 | 3H/6H | Scirpoides leaf-b | 40: 60 | Bonus |
| sdw1 | denso, Hv20ox$_2$ | 518 | 3HL | Semidwarf 1 | 47:168 | M21 |
| sdw2 | sdw-b | 133 | 3HL | Semidwarf 2 | 45:108 | Mg2170 |
| sdw3 | gai | 663 | 2HS | Semidwarf 3 | 46:134 | Hv287 |
| sdw4 | | 45 | 7HL | Semidwarf 4 | 46: 51 | |
| sdw6 | sdw.f | 240 | 1H/7H | Semidwarf 6 | 46: 77 | Vada |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
| Rec. | Prev. | | | | | |
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|---|---|---|---|---|---|---|
| sdw7 | sdw.u | 196 | 4HL | Semidwarf 7 | 43:103 | Glenn |
| seg1 | se1 | 377 | 7HL | Shrunken endosperm genetic 1 | 45:158 | Betzes |
| seg2 | se2 | 378 | 7HS | Shrunken endosperm genetic 2 | 26:326 | Betzes |
| seg3 | se3 | 379 | 3H | Shrunken endosperm genetic 3 | 45:160 | Compana |
| seg4 | se4 | 380 | 7HL | Shrunken endosperm genetic 4 | 37:267 | Compana |
| seg5 | se5 | 381 | 7HS | Shrunken endosperm genetic 5 | 26:329 | Sermo / 7*Glacier |
| seg6 | se6 | 396 | 3HL | Shrunken endosperm genetic 6 | 44:138 | Ingrid |
| seg7 | se7 | 397 | | Shrunken endosperm genetic 7 | 37:269 | Ingrid |
| sex7 | sex.i | 628 | 5HL | Shrunken endosperm xenia 7 | 32:129 | I90-374 |
| sex8 | sex.j | 143 | 3HS | Shrunken endosperm xenia 8 | 43: 90 | I89-633-1 |
| sex9 | sex.1 | 195 | 4HL | Shrunken endosperm xenia 9 | 43:102 | Alf |
| sgh1 | sh1 | 163 | 4HL | Spring growth habit 1 | 26:188 | Iwate Mensury C |
| Sgh2 | Sh2 | 309 | 5HL | Spring growth habit 2 | 26:259 | Indian Barley |
| Sgh3 | Sh3 | 213 | 1HL | Spring growth habit 3 | 26:212 | Tammi / Hayakiso 2 |
| sid1 | nls | 180 | 4HL | Single internode dwarf 1 | 43: 97 | Akashinriki |
| Sil1 | Sil | 228 | 1H | Subcrown internode length 1 | 40: 79 | NE 62203 |
| sld1 | dw-1 | 126 | 3HL | Slender dwarf 1 | 41:103 | Akashinriki |
| sld2 | | 83 | 2HS | Slender dwarf 2 | 44: 74 | Akashinriki |
| sld3 | ant-567 | 186 | 4HS | Slender dwarf 3 | 40: 63 | Manker |
| sld4 | sld.d | 100 | 2HS | Slender dwarf 4 | 43: 72 | Glacier |
| sld5 | | 144 | 3HS | Slender dwarf 5 | 44: 90 | Indian Dwarf |
| sld6 | sld.gs | 242 | 1H | Slender dwarf 6 | 40: 87 | Glenn |
| sld7 | sld.f | 194 | 4HL | Slender dwarf 7 | 43:101 | Glenn |
| sld8 | sld.i | 49 | 7HS/ 4HL | Slender dwarf 8 | 43: 63 | Wisconsin Pedigree 38 |
| sls1 | sls | 227 | 1HS | Small lateral spikelet 1 | 40: 78 | Morex |
| smn1 | smn | 38 | 3H/5 H | Seminudoides 1 | 43: 58 | Haisa |
| snb1 | sb | 26 | 7HS | Subnodal bract 1 | 26: 72 | L50-200 |
| srh1 | S, l | 321 | 5HL | Short rachilla hair 1 | 46: 86 | Lion |
| stb1 | stb | 741 | | Stubble 1 | 47:183 | |
| sun1 | sun1 | 650 | | Sensitivity to *Ustilago nuda* 1 | 43:173 | Steptoe |
| tfm1 | | 190 | 1HL | Thick filament 1 | 40: 67 | Volla |
| Table 3. (continued) | | | | | | |
| Locus symbol* | | BGS no. | Chr. loc.† | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
| Rec. | Prev. | | | | | |
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|---|---|---|---|---|---|---|
| trd1 | t, bra-c | 202 | 1HL | Third outer glume 1 | 46: 65 | Valki |
| trp1 | tr | 61 | 4HL | Triple awned lemma 1 | 41: 82 | CIho 6630 |
| tst1 | tst1 | 647 | 6HL | Tip sterile 1 | 43:170 | Steptoe |
| tst2 | | 636 | 4HL | Tip sterile 2 | 43:167 | Donaria |
| twk1 | tw | 743 | 7H | Tweaky spike 1 | 47:185 | |
| ubs4 | lks2, ari-d | 11 | 7HL | Unbranched style 4 | 45: 84 | Ao-Hadaka |
| ubs5 | | 727 | | Unbranched style 5 | 43:222 | Harrington |
| uzu1 | uz, *HvBRI1* | 102 | 3HL | Uzu 1 or semi brachytic 1 | 47: 70 | Baitori |
| var1 | va | 306 | 5HL | Variegated 1 | 37:259 | Montcalm |
| var2 | va2 | 344 | 5HL | Variegated 2 | 32:104 | Montcalm |
| var3 | va3 | 303 | 5HL | Variegated 3 | 44:115 | Montcalm |
| viv-a | viv-5 | 627 | 2H | Viviparoides-a | 45:227 | Foma |
| viv-b | viv-6 | 193 | 4HS | Viviparoides-b | 43:100 | Foma |
| viv-c | viv-1 | 720 | 5H | Viviparoides-c | 43:215 | Foma |
| vrs1 | v | 6 | 2HL | Six-rowed spike 1 | 37:192 | Trebi |
| vrs1 | lr | 58 | 2HL | Six-rowed spike 1 | 26: 94 | Nudihaxtoni |
| vrs1 | $V^d$ | 66 | 2HL | Two-rowed spike 1 | 26:103 | Svanhals |
| vrs1 | $V^t$ | 67 | 2HL | Deficiens 1 | 47: 57 | White Deficiens |
| vrs2 | v2, int-b | 314 | 5HL | Six-rowed spike 2 | 47:113 | Svanhals |
| vrs3 | v3, int-a | 315 | 1HL | Six-rowed spike 3 | 47:115 | Hadata 2 |
| vrs4 | v4, int-e, HvRA2 | 124 | 3HL | Six-rowed spike 4 | 47: 76 | MFB 104 |
| wax1 | wx | 16 | 7HS | Waxy endosperm 1 | 42: 65 | Oderbrucker |
| wnd1 | wnd | 23 | 4Hl | Winding dwarf 1 | 42: 74 | Kogen-mugi |
| wst1 | wst | 107 | 3HL | White streak 1 | 41: 97 | CIho 11767 |
| wst2 | wst2 | 304 | 5HL | White streak 2 | 46: 83 | Manabe |
| wst4 | | 56 | 2HL | White streak 4 | 44: 51 | Kanyo 7 |
| wst5 | wst5 | 221 | 1HL | White streak 5 | 46: 73 | Carlsberg II |
| wst6 | wst,,j | 129 | 3HL | White streak 6 | 41:105 | Akashinriki |
| wst7 | rb | 79 | 2HL | White streak 7 | 47: 61 | GS397 |
| wxs1 | wxs | 615 | 7H/ 2HL | Waxy spike 1 | 43:160 | Steptoe |

Table 3. (continued).

| Locus symbol* Rec. | Prev. | BGS no | Chr. loc.[†] | Locus name or phenotype | Descr.vol. p. | Parental cultivar |
|---|---|---|---|---|---|---|
| Xnt1 | $X_a$ | 25 | 7HL | Xantha seedling 1 | 26: 71 | Akashinriki |
| xnt2 | $x_b$ | 513 | | Xantha seedling 2 | 26:440 | Black Hulless |

| | | | | | | |
|---|---|---|---|---|---|---|
| xnt3 | $x_c$ | 105 | 3HS | Xantha seedling 3 | 26:139 | Colsess |
| xnt4 | $x_{c2}$ | 36 | 7HL | Xantha seedling 4 | 26: 85 | Coast |
| xnt5 | $x_n$ | 255 | 6HL | Xantha seedling 5 | 26:237 | Nepal |
| xnt6 | $x_s$ | 113 | 3HS | Xantha seedling 6 | 26:147 | Smyrna |
| xnt7 | xan,,g | 233 | 1HL | Xantha seedling 7 | 26:231 | Erbet |
| xnt8 | xan,,h | 140 | 3HS | Xantha seedling 8 | 26:177 | Carlsberg II |
| xnt9 | xan,,i | 37 | 7HL | Xantha seedling 9 | 26: 86 | Erbet |
| yhd1 | yh | 158 | 4HL | Yellow head 1 | 42:250 | Kimugi |
| yhd2 | yh2 | 592 | | Yellow head 2 | 45:215 | Compana |
| ylf1 | ylf1 | 652 | 7HS | Yellow leaf 1 | 43:175 | Villa |
| Ynd1 | Yn | 183 | 4HS | Yellow node 1 | 44:109 | Morex |
| yst1 | yst | 104 | 3HS | Yellow streak 1 | 42:178 | Gateway |
| yst2 | | 109 | 3HS | Yellow streak 2 | 44: 81 | Kuromugi 148 / Mensury C |
| yst3 | yst,,c | 462 | 3HS | Yellow streak 3 | 44:163 | Lion |
| yst4 | | 85 | 2HL | Yellow streak 4 | 44: 76 | Glenn |
| yst5 | yst5 | 346 | 7HS | Yellow streak 5 | 43:130 | Bowman / ant10.30 |
| yvs1 | $y_x$ | 63 | 2HS | Virescent seedling 1 | 26: 99 | Minn 71-8 |
| yvs2 | $y_c$ | 3 | 7HS | Virescent seedling 2 | 26: 46 | Coast |
| yhd2 | yh2 | 592 | | Yellow head 2 | 45:215 | Compana |
| ylf1 | ylf1 | 652 | 7HS | Yellow leaf 1 | 43:175 | Villa |
| zeb1 | zb | 120 | 3HL | Zebra stripe 1 | 43: 86 | Mars |
| zeb2 | zb2, fch10 | 461 | 4HL | Zebra stripe 2 | 43:152 | Unknown cultivar |
| zeb3 | zb3, zb | 223 | 1HL | Zebra stripe 3 | 40: 72 | Utah 41 |
| Zeo1 | Knd, Ert-r | 82 | 2HL | Zeocriton 1 | 47: 63 | Donaria |
| Zeo2 | cly1.b, HvAP2 | 614 | 2HL | Zeocriton 2 | 47:177 | 36Ab51 |
| Zeo3 | Zeo2, cly1.c | 184 | 4HL | Zeocriton 3 | 47: 95 | Morex |

* Recommended locus symbols are based on utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996.

† Chromosome numbers and arm designations are based on the Triticeae system. Utilization of this system for naming of barley chromosomes was at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 05 August 1996. The Burnham

and Hagberg (1956) designations of barley chromosomes were 1 2 3 4 5 6 and 7 while new designations based on the Triticeae system are 7H 2H 3H 4H 1H 6H and 5H, respectively.

*Barley Genetics Newsletter (2017) 47:50-187.*

# BGS 1, Brachytic 1, *brh1*

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

Previous nomenclature and gene symbolization:

Brachytic = *br* (15, 17).
Breviaristatum-i = *ari-i* (7, 12).
Breviaristatum-28 = *ari-28* (14).
Dwarf x = *dx1* (8).

Inheritance:

Monofactorial recessive (15, 17).

Located in chromosome 7HS (5); *brh1.a* is about 9.3 cM distal from the *fch12* (chlorina seedling 12) locus (17); *brh1.ae* mapped 0.8 cM distal from RFLP marker BCD129 and cosegregated with marker MWG2074B (13); *brh1.a* is about 5.0 cM from AFLP marker E4134-8 in subgroup 1 of the Proctor/Nudinka map (16); *brh1.a* is about 13.6 cM proximal from SSR marker HVM04 in 7H bin 02 (3); *brh1.a* is associated with SNP markers 2_1419 to 2_0245 (positions 0.00 to 13.19 cM) in 7H bin 01 of the Bowman backcross-derived line BW074 (4); *brh1.x* is associated with SNP markers 1_0949 to 1_1495 (positions 0.00 to 8.77 cM) in 7H bin 01 of the Bowman backcross-derived line BW079 (4); *brh1.t* is associated with SNP markers 1_1495 to 1_0025 (positions 8.77 to 26.00 cM) in 7H bins 01 to 02 of the Bowman backcross-derived line BW078 (4); an unnamed *brh1* mutant is associated with SNP markers 1_0851 to 2_0485 (positions 17.32 to 121.90 cM) in 7H bins 02 to 07 of the Bowman backcross-derived line BW872 (4); the genomic position of the *Brh1* locus at 12.74 cM in 7HS (2), in 1H bin 01 near the border with 1H bin 02.

Description:

Plants have short leaves, culms, spikes, awns, and kernels. The seedling leaf is about 2/3 normal length. A similar reduction in the size of other organs is observed, but the awns were less than 1/2 normal length (8). The mutant phenotype was easy to classify at all stages of growth. The approximately 20% reduction in kernel weight was caused primarily by a reduction in kernel length, 7.8 vs. 9.6 mm. Grain yields of the Bowman backcross-derived lines for *brh1* mutants were about 2/3 normal and lodging was greatly reduced (2, 3). Börner (1) reported that *ari-i.38* seedlings are sensitive to gibberellic acid. Powers (15) stated that the assigned gene symbol for this mutant is *br* and that L.J. Stadler selected this symbol. The *ari-m* (breviaristatum-m) mutants occur in the *Brh1* locus (2). The *brh1* mutants are deficient in the Gα subunit of a heterotrimeric G protein, which is an important regulator of culm length in barley (2, 9). The *brh1.a* mutant did not affect malt quality negatively (2).

Origin of mutant:

A spontaneous mutant in Himalaya (CIho 1312) (15, 17).

Mutational events:

*brh1.a* (GSHO 25) in Himalaya (CIho 1312) (17); *brh1.c* (GSHO 229) in Moravian (PI 539135) (18), but SNP marker patterns this mutant originated from Himalaya and is identical to the *brh1.a* mutant (2); *ari-i.38* (NGB 115888, GSHO 1657) in Bonus (NGB 14657, PI 189763) (12, 19); *brh1.e* (GSHO 1690) in Aramir (PI 467786) (19); *brh1.f* (*dx1*, GSHO 1422) in Domen (NGB 2104, CIho 9562) (8); *brh1.t* (OUM136, GSHO 1691) in

Akashinriki (PI 467400, OUJ659); *brh1.x* (7125, GSHO 1692) in Volla (PI 280423); *brh1.z* (Hja80001) in Aapo (PI 467771; *brh1.aa* (Hja80051) in a Hja80001 cross (6, 10); *brh1.ae* (FN53, GSHO 3646) in Steptoe (CIho 15229) (6, 11); an unnamed variant of *brh1* in L50-200 (Alb Acc 67A, GSHO 1217) associated with expression of the subnodal bract 1 (*snb1.a*) gene (20). The *ari-m* (breviaristatum-m) mutants were demonstrated to be alleles at the *brh1* locus (2); *ari-m.12* (NGB 115858, GSHO 1661), *-m.28* (NGB 115876) in Bonus (NGB 14657, PI 189763), *-m.141* (NGB 115951), *-m.177* (NGB 115987) in Foma (NGB 14659, CIho 11333), *-m.251* (NGB 116059) in Kristina (NGB 14661, NGB 1500) (12); *ari-m.269* (NGB 116081) in Kristina (12, 14).

Mutant used for description and seed stocks:

*brh1.a* in Himalaya (GSHO 25); *ari-i.38* (GSHO 1657, NGB 115888) in Bonus, *brh1.a* in Bowman (PI 483237)*7 (GSHO 1820, BW074, NGB 20481); *ari-i.38* in Bowman*6 (GSHO 1821, BW047, NGB 20455); *brh1.e* in Bowman*7 (GSHO 1822, BW077, NGB 20484); *brh1.t* in Bowman*7 (GSHO 1823, BW078, NGB 20485); *brh1.x* in Bowman*7 (GSHO 1824, BW079, NGB 20486); *brh1.z* in Bowman*7 (GSHO 2179, BW080, NGB 20487); *brh1.aa* in Bowman*6 (GSHO 1668, BW075, NGB 20482); *brh1.ae* in Bowman*4 (BW076, NGB 20483); an unnamed *brh1* allele in Bowman*2 (BW872, NGB 22306); *ari-m.28* (GSHO 1661, NGB 115876) in Bonus; *ari-m.28* in Bowman (PI 483237)*6 (GSHO 2161); *ari-m.28* in Bowman*8 (BW051, NGB 20459).

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

Revised:

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J.D. Franckowiak and U. Lundqvist. 2017. Barley Genet. Newsl. 47:50-52.

# BGS 51, Rattail spike 1, *rtt1*

Stock number: BGS 51
Locus name: Rattail spike 1
Locus symbol: *rtt1*

Previous nomenclature and gene symbolization:

Rattail spike = *rt* (2).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 2HS (1), *rtt1.a* is about 6.0 cM distal from the *fch15* (chlorina seedling 15) locus (1), in 2H bin 05 or 06.

Description:

Spikes are highly modified with numerous immature spikelets and complete sterility. The arrangement of bracts in the spikelets suggests that they contain numerous spikelets. Because the homozygous recessive is completely sterile, the stock must be maintained in the heterozygous condition (1). A photograph of the rattail spikes is available (4, 5). A semidominant interaction between *rtt1.a* and one version of the normal allele (*Rt'* or *Rtt1.b*) in Okaiku 3 was reported by Takahashi et al. (3).

Origin of mutant:

A spontaneous mutant in Goldfoil (PI 5975) (1).

Mutational events:

*rtt1.a* (GSHO 216) in Goldfoil (PI 5975) (1), *Rtt1.b* (*Rt'* ) in Okaiku 3 (OUL011) (3).

Mutant used for description and seed stocks:

*rtt1.a* (GSHO 216) in Goldfoil.

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:111.

Revised:

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:53.

# BGS 65, Early maturity 1, *Eam1*

| | |
|---|---|
| Stock number: | BGS 65 |
| Locus name: | Early maturity 1 |
| Locus symbol: | *Eam1* |

Previous nomenclature and gene symbolization:

Early maturity = *Ea* (8).
Early maturity 1 = *Ea1* (7).
Photoperiod response gene H1 = *Ppd-H1* (11).

Inheritance:

Monofactorial dominant (9, 13).

Located in chromosome 2HS (1, 8, 13); weakly linked to the *vrs1* (six-rowed spike 1) locus (1, 15, 19); the *Ppd-H1* (*Eam1*) locus is in the 6 cM interval between the RFLP loci XMWG858 and XpsrB9, 1 cM proximal to XM WG858 (11, 12); specific sequence tagged site (STS) markers were developed for the *Eam1* gene of Igri (3); in bin 2H-04 near RFLP marker MWG858 (13); in Azumamugi 6 cM proximal from marker ABG602 (15), *Eam1.c* is associated with SNP markers 1_0216 to 2_1338 (positions 47.48 to 66.78 cM) in 2H bins 04 to 06 of the Bowman backcross-derived line BW280 (4); *Eam1.d* is associated with SNP markers 12_1386 to 2_1261 (position 50.56 cM) in 2H bin 05 of the Bowman backcross-derived line BW281 (4); *Eam1.f* is associated with SNP markers 1_0216 to 2_1015 (positions 47.48 to 48.68 cM) in 2H bin 04 of the Bowman backcross-derived line BW282 (4), likely in 2H bin 05.

Description:

This gene controls the strong response of some cultivars to long photoperiods. The *Eam1* gene is described as a simply inherited dominant and the main factor for early maturity (1, 7, 8, 14). Under long-day condition, a near-isogenic line with *Eam1* is reported to be 7 to 8 days earlier than the *eam1* line 'ea1' (16). The early maturity gene is weakly linked to the *vrs1* (six-rowed spike 1) locus (1, 13, 19). In North Dakota, USA, progenies from crosses of Bowman to *Hordeum vulgare* subsp. *spontaneum*, California Coast and North African accessions, facultative winter barleys, far northern spring barleys (from Finland and Alaska), and winter barleys, extremely early segregates were found (6). The *Eam1* locus in barley is homoeologous to the *Ppd1*, *Ppd2*, and *Ppd3* loci in wheat, which control strong photoperiod response (11, 12). The reduced photoperiod responsiveness of the *ppd-H1* (*eam1.a*) mutant is explained by altered circadian expression of the photoperiod pathway gene CONSTANS (CO) (10, 19) and reduced expression of its downstream target, FLOWERING LOCUS T (*HvFT1*), a key regulator of flowering (2, 18). The CCT (CO, CO-like, and TOC1) domain mutation was a G-to-T change and produced a Gly-to-Trp change in the CCT domain of the barley pseudo-response regulator (PRR) gene (18). The DNA code sequence of the dominant alleles was variable among accessions while the recessive allele was not (18). Alleles at the *Eam1* locus interact with flowering time control mutants at the *eam7* (17) and *eam10* (2), but not *eam8* (5), loci to induce earlier heading under both short and long days.

Origin of mutant:

The strong photoperiod response to short nights occurs naturally in many barley cultivars and its wild relative, *Hordeum vulgare* subsp. *spontaneum*.

Mutational events:

A single dominant gene controls early maturity based on a cross to Lion (*Eam1.b*) (PI

32767, GSHO 27) (8); *Eam1.e* (GSHO 1569) was isolated from the Australian cultivar Prior (PI 221325) (9, 16); *eam1.a* is the normal allele in Manchurian six-rowed cultivars (7, 16); *eam1.a* is the allele present likely in many two-rowed cultivars from Europe origin (16).

Mutant used for description and seed stocks:

*Eam1.c* in Estate (PI 57700, GSHO 1316); *Eam1.c* from Estate in Bowman (PI 483237)*7 (GSHO 1871); *Eam1.c* from Estate in Bowman*8 (BW280, NGB 20564); *Eam1.d* from KT1031 (a winter barley from Bulgaria, GSHO 1568) in Bowman*9 (GSHO 1872, BW281, NGB 20565); *Eam1.e* from Prior in Betzes*7 (Erbet, CIho 13826) (4); *Eam1.f* from *Hordeum vulgare* subsp. *spontaneum* in Bowman*8 (GSHO 1873, BW282, NGB 20566).

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Prepared:

J.D. Franckowiak and L.W. Gallagher. 1997. Barley Genet. Newsl. 26:101-102.

Revised:

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:64-66.
J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:54-56.

# BGS 67, Six-rowed spike 1, *Vrs1.t*

| | |
|---|---|
| Stock number: | BGS 67 |
| Locus name: | Six-rowed spike 1 (deficiens spike) |
| Locus symbol: | *Vrs1.t* |

Revised locus symbol:

Historically, alleles at the six-rowed spike 1 (*vrs1*) locus were included in several Barley Genetic Stock (BGS) descriptions even though they were known to be alleles at the same locus. The most common spike type variant is the six-rowed allele (*vrs1.a*) (3, 6, 7). Other alleles at the *vrs1* locus are described in BGS 6, BGS 58, and BGS 66.

Previous nomenclature and gene symbolization:

*Hordeum deficiens* =*V* (5).

*Hordeum deficiens* =$V^t$ (11).

Renamed *Vrs1.t1* based on allelism tests (7).

Mutation in homeodomain-leucine zipper I-class homeobox = *HvHox1* (3, 6).

Inheritance:

Monofactorial incomplete dominant (6); the *Vrs1.t1* allele is the most dominant allele in the multiple allelic series at the *vrs1* (six-rowed spike 1) locus (11), but interacts as an incomplete dominant with some alleles (2, 7).

Located in chromosome 2HL (8, 10); the *vrs1* locus is about 15.4 cM distal from the Toothed lemma 1 (*Gth1*) locus (10); *vrs1.a* is about 30.5 cM distal from the *eog1* (elongated outer glume 1) locus (8); V*rs1.t1* is associated with SNP markers 2_0781 to 2_1351 (positions 135.19 to 145.80 cM) in 2H bins 09 to 10 of the Bowman backcross-derived line BW900 (1).

Description:

Plants homozygous for *Vrs1.t1* ($V^t$) allele always have a deficiens phenotype regardless of the allele present at the *int-c* (intermedium spike-c) locus in chromosome 4H. Deficiens is characterized by the extreme reduction in size of lateral spikelets (11). The *Vrs1.t1* allele in Engleawnless does not recombine with the *Lks1.a* allele at the *Lks1* (Awnless 1) locus because a short paracentric inversion is present in this stock (9). Plants in Bowman backcross line for *Vrs1.t1* (BW900) were similar to Bowman except spikes had 1 to 2 more kernels per spike and kernels were about 10% lighter (2). Expression of the *Vrs1* gene is strictly localized in the lateral-spikelet primordia of immature spikes suggesting that the VRS1 protein suppresses development of lateral spikelets (3). Re-sequencing a 2.1 kb fragment region including the *HvHox1* region of the *vrs1* locus found that the six-rowed variants (*vrs1.a1*, *vrs1.a2* and *vrs1.a3*) and the deficiens variant (*Vrs1.t1*) had isoforms different from those of wild barleys and two-rowed barleys (6). Plants with *Vrs1.t1* gene had smaller lateral spikelet meristems compared with the typical two-rowed type (7). Transcriptome analysis revealed that a number of *histone* superfamily genes were upregulated in the *deficiens* mutant suggesting that enhanced cell proliferation in the central spikelet may contribute to larger kernel size (7).

Origin of mutant:

Natural occurrence in two-rowed barleys from Ethiopia previously classified as *Hordeum deficiens* (12). Haplotype analysis revealed that barley carrying the *deficiens* allele (*Vrs1.t1)* originated from two-rowed types carrying the *Vrs1.b2* allele, which is predominantly found in germplasm from Northern Africa (7).

Mutational events:

*Vrs1.t1* ($V^t$) in White Deficiens (CIho 7316, GSHO 684) (7, 12); *Vrs1.t2* (*Deficiens 2*) (NGB 115174), *Vrs1.t3* (*Semi-deficiens 12*) (NGB 115188) in Foma (NGB 14659, CIho 11333) (4, 7).

Mutant used for description and seed stocks:

*Vrs1.t1* ($V^t$) in White Deficiens (GSHO 684); *Vrs1.t1* in Bowman (PI 483237)*8 (GSHO 1909, BW900, NGB 22332).

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Prepared:

T.E. Haus. 1975. Barley Genet. Newsl. 5:105.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:104.

J.D. Franckowiak and U. Lundqvist. 2017. Barley Genet. Newsl. 47:57-58.

# BGS 69, Toothed lemma 1, *Gth1*

| | |
|---|---|
| Stock number: | BGS 69 |
| Locus name: | Toothed lemma 1 |
| Locus symbol: | *Gth1* |

Previous nomenclature and gene symbolization:

Toothed lemma = *G* (5, 9).

Inheritance:

Monofactorial dominant (7, 8), but modifiers were reported (5, 7).

Located in chromosome 2HL (5, 9); *Gth1.a* is about 15.4 cM proximal from the *vrs1* (six-rowed spike 1) locus (2, 5, 9); *gth1.b* is associated with SNP markers 2_0528 to 1_0823 (positions 118.78 to 133.59 cM) in 2H bins 08 to 09 of the Bowman backcross-derived line BW413 (1); the association of palea trichome develop with spike type (4) suggests that alleles at *Gth1* locus also control this trait.

Description:

Large teeth or barbs are present on the upper part of lateral lemma nerves. The barbs are easiest to see on green spikelets. This trait may be difficult to study because Ubisch (8) reported three sizes of teeth, including one that could be seen only with magnification. According to Ubisch (8), one gene pair controls the presence and absence of large teeth and one or two other genes are responsible for less developed teeth. Segregation for only one pair of factors is reported by Wexelsen (9) and in subsequent studies. Other reports on inheritance of lemma teeth were summarized by Smith (6). Besides barbs on the lateral lemma veins and slight heavier kernels, no other agronomic or morphological differences were observed between Bowman and the Bowman backcross-derived line for *gth1.b*, BW413 (3). Association of trichomes with vascular bundle traces may not be limited to the lemma because similar variations in shape of trichomes were observed on the palea (4). Trichomes with a round base and a domed peak appeared predominantly on two-rowed cultivars. But most of the six-rowed cultivars featured trichomes with a similar base, but a prickle-like point that aligned with the direction of elongation of the epidermal cells (4). The palea trichomes may play a role in infection by the scab fungus, *Fusarium graminearum*, because the prickle-type trichomes functioned to trap conidia and were sites of fungal penetration (4).

Origin of mutant:

*Gth1.a* appears to be the normal allele; while the recessive allele *gth1.b* is present in many two-rowed barley cultivars of Occidental origin (4).

Mutational events:

*Gth1.a* (GSHO 309) in Machine (CIho 4982) (9); *gth1.b* is present in many two-rowed cultivars of European origin (4).

Mutant used for description and seed stocks:

*Gth1.a* (GSHO 309) in Machine; *Gth1.a* is present in Bowman (PI 483237); *gth1.b* from ND11894 (Gitane//ND4642/Robust/3/Bearpaw/4/TR218/ND7015/3/ Norbert//ND4856/ M38) in Bowman*4 (GSHO 1897); *gth1.b* in Bowman*6 (BW413, NGB 20646).

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Prepared:
T.E. Haus. 1975. Barley Genet. Newsl. 5:109.

Revised:
T.E. Haus. 1978. Barley Genet. Newsl. 8:161.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:106.
J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:68-69.
J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:59-60.

# 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* (7).
White streak-k = *wst,,k* (11).
White streak-B = *wst,,B* (9).

Inheritance:

Monofactorial recessive (2, 12).

Located in chromosome 2HL (6, 8, 9, 10); *wst7.k* is about 22.0 cM distal from the *gpa1* (grandpa 1) locus (2, 10); *wst7.k* is over 29.4 cM distal from the *lig1* (liguleless 1) locus (9); *wst7.k* is about 6.1 cM from RFLP marker MWG949A (1); *wst7.k* is associated with SNP markers 2_1346 and 1_283 (positions 233.94 and 234.63 cM) in 2H bin 14 of the Bowman backcross-derived line BW916 (3), in 2H bin 14.

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. There were no apparent affects of the *wst7.k* gene on agronomic traits in the Bowman backcross-derived line BW916 (5).

Origin of mutant:

A spontaneous mutant isolated by Robertson (7, 12).

Mutational events:

*wst7.k* (GSHO 247) in an unknown cultivar (2, 12).

Mutant used for description and seed stocks:

*wst7.k* (GSHO 247) in an unknown cultivar; *wst7.k* from R.I. Wolfe's Multiple Recessive Marker Stock (GSHO 3451) in Bowman (PI 483237)*7 (GSHO 1935, BW916, NGB 22347).

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# BGS 82, Zeocriton 1, *Zeo1*

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

Revised locus symbols:

Since the zeocriton spike phenotype was first described by Hayes and Harlan (8), *Zeo1* became the recommended locus symbol for various mutants at this locus. The semi-dominant dense spike variants at the complex *Zeo1* locus exhibit a range of phenotypes associated with restricted elongation of the rachis internodes. Based on DNA sequencing, three distinct phenotypic groups of dense spike variants are associated with the *Hordeum vulgare APELATA2* (*AP2*)-like transcription factor (*HvAP2*) locus (10, 13). The phenotypic expressions were historical assigned different locus symbols, but each group is associated with specific molecular changes in the *HvAP2* transcript (10). Alleles at this locus are assigned locus symbols: The *Zeo1* mutants exhibit the most extreme phenotypes, the *Zeo2* variants have intermediate phenotypes, and the *Zeo3* variants show a lesser degree in shortening of rachis internodes (10). Molecular markers and/or pedigree information are necessary to separate variants assigned to the *Zeo2* (BGS614) and *Zeo3* (BGS184) groups (10).

Previous nomenclature and gene symbolization:

Erectoides-52 = *ert-52* (6, 7).
Erectoides-r = *Ert-r* (12).
"Kurz und dicht" = *Knd* (15, 18).
Cleistogamy = *Cly* (9, 10, 13, 17).
*Hordeum vulgare APELATA2* (*AP2*)-like transcription factor = *HvAP2* (10).

Inheritance:

Monofactorial incomplete dominant (6, 14).

Located in chromosome 2HL (9, 11, 17); *Zeo1.a* is about 9.2 cM distal from the *lig1* (liguleless 1) locus (11); *Zeo1.a* is about 7.3 cM distal from RFLP marker cnx1 in 2H bin 13 (1); the *Ert-r.52* allele in Bowman backcross-derived line BW322 is associated with SNP markers 2_0715 to 1_0551 (positions 213.08 to 221.70 cM) in 2H bin 13 (2); the *Zeo1.a* allele in BW937 is associated with SNP markers 2_0715 to 2_1453 (positions 213.08 to 245.71 cM) in 2H bin 13/14 (2); the *Zeo1.b* allele in BW938 is associated with SNP markers 1_1486 to 2_0590 (positions 202.70 to 218.47) in 2H bin 13 (2); the *HvAP2* locus is near marker BOPA2_12_10579 (10), in 2H bin 13.

Description:

The name zeocriton (little barley) has been historically applied to cultivars with very short rachis internodes and a pyramid shape. This name and the locus symbol *Zeo1* were applied to induced mutants having a similar phenotype (18). Homozygous *Zeo1* plants have shorter culms (short peduncle), very compact spikes, large outer glumes with long awns, and reduced fertility. Plants heterozygous for the *Zeo1* mutant have short culms, compact spikes, and wide kernels. (18). Generally, the spike emerges from the side of the sheath in homozygotes (5, 18). Although the name *zeocriton* is used for this gene, this gene is not from Spratt, the dense ear type described by Engledow (3) or those described by Hayes and Harlan (8). Spikes of plants with the *Ert-r.52* mutant are compact in heterozygotes and very compact in homozygotes, with rachis internode length values from 1.4 to 1.8 mm. Homozygotes are about 2/3 normal height with excellent vigor. The glumes associated with lateral spikelets are 3 to 4 times larger than normal. Lodicule size is reduced (14). Heterozygotes are intermediate in plant height, have slightly more lax spikes, and have normal glumes in lateral spikelets (14). $GA_3$ treatment of plants as the flag leaf emerges decreases spike density (16). Plants in Bowman backcross-derived lines for *Ert-r.52* (BW322), *Zeo1.a* (BW937), and *Zeo1.b* (BW938) are about 2/3 the height of Bowman. Rachis internodes are about 1/2 normal length (2.2 vs. 4.4 mm). Mutant plants head about two days later than Bowman; they have about 2 more kernels per spike and their grain yields are about 3/4 of those of Bowman (5). The BW938 (*Zeo1.b*) averaged one more fertile rachis node than Bowman (10). DNA sequencing showed that the *Zeo1* mutants occur in a *Hordeum vulgare* APELATA2 (*AP2*)-like transcription factor, *HvAP2* (10, 13). The dense spike and cleistogamous (small lodicules) phenotypes are a consequence of a perturbed interaction between microRNA 172 (*Hv-miR172*) and its corresponding binding site on the mRNA from the *HvAP2* gene, which acts early in spike development to regulate turnover of *HvAP2* mRNA (10, 13). The *Zeo1* mutants occur in the last intron of *HvAP2*, the binding site of *Hv-miR172*, and prevent cleavage of the *HvAP2* mRNA (10, 13).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (15); a neutron induced mutant in Bonus (NGB 14657, PI 189763) (6).

Mutational events:

*Zeo1.a* (Mut 2657, GSHO 1613) in Donaria (PI 161974) (15) has haplotype 4 in the *HVAP2* gene (10); *Zeo1.b,* received as "Kurz und dicht" and placed in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614) (4, 18) has haplotype 1 (10); *Ert-r.52* (NGB 112651, GSHO 492), *-r.67* (NGB 112666) in Bonus (NGB 14657, PI 189763) (12) have haplotype 1 (10); *Ert-r.329* (NGB 112844) in Foma (NGB 14659, CIho 11333) (14) has haplotype 1 (10); *Ert-r.453* (NGB 112968) in Foma (12) has haplotype 2 (10). Other variants in the *HvAP2* gene are assigned to the *Zeo2* (BGS614) or *Zeo3* (BGS184) groups (10).

Mutant used for description and seed stocks:

*Zeo1.a* in Donaria (GSHO 1613); *Zeo1.a* in Bowman (PI 483237)*5 (GSHO 1931); *Zeo1.a* in Bowman*7 (BW937, NGB 22366); *Zeo1.b* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614) in Bowman*9 (GSHO 1932, BW938, NGB 22367); *Ert-r.52* (*Zeo1.a*) in Bonus (GSHO 492, NGB 112651); *Ert-r.52* in Bowman (PI 483237)*8 (GSHO 2123, BW322, NGB 22117).

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Revised:

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# BGS 89, Breviaristatum-g, *ari-g*

Stock number: BGS 89
Locus name: Breviaristatum-g
Locus symbol: *ari-g*

Previous nomenclature and gene symbolization:

Breviaristatum-18 = *ari-18* (4, 5).
Short awn 10 = *lk10* (7).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 2H (1, 3); *ari-g.24* is associated based on linkage drag with the *Gth1* (Toothed lemma 1) locus (1), but the association may be caused by poor expression of the *Gth1.a* allele in the Bowman backcross-derived line, BW045 (2, 3); *ari-g.24* is associated with SNP markers 1-0796 to 2_0528 (positions 95.53 to 118.78 cM) in 2H bins 07 to 08 of a heterozygous plant from the Bowman backcross-derived line BW045 (1).

Description:

Plants with the *ari-g* mutation are semidwarf and very weak. Under greenhouse conditions, plants are 1/4 to 1/3 normal height and stiff, spikes are short and small, and seed set is low. Leaf blades are very narrow, often involuted, and are white and green striped (5, 6). When grown in the field at Fargo, North Dakota, USA, plant development is very slow, the upper portion of the sheath is white as new leaf blades emerge, and spikes are seldom produced. Thus, the Bowman backcross-derived line for *ari-g.24*, BW045, is maintained as a segregating stock (2).

Origin of mutant:

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

Mutational events:

*ari-g.18* (NGB 115865) in Bonus (NGB 14657, PI 189763) (5); *ari-g.24* (NGB 115872, GSHO 1655) in Bonus (6); *ari-g.134* (NGB 115944), *-g.138* (NGB 115948), *-g.142* (NGB 115952), *-g.158* (NGB 115968), *-g.221* (NGB 116030), *-g.234* (NGB 116044), *-g.246* (NGB 116056) in Foma (NGB 14659, CIho 11333), *-g.267* (NGB 116078) in Kristina (NGB14661, NGB 1500) (5); *ari-g.303* (NGB 116127) in Kristina (6).

Mutant used for description and seed stocks:

*ari-g.24* in Bonus (NGB 115872, GSHO 1655); *ari-g.24* in Bowman*8 (BW045, NGB 20453).

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Revised:

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# BGS 97, Accordion rachis 1, *acr1*

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| Stock number: | BGS 97 |
| Locus name: | Accordion rachis 1 |
| Locus symbol: | *acr1* |

Phenotype explanation:

The accordion rachis phenotype was developed by Robert I. Wolfe at the Beaverlodge, Alberta Station of Agriculture and Agri-Food Canada. The F2 progenies from crosses and backcrosses of Bowman to this stock, ACBV89B229, contained very few plants with the accordion rachis phenotype. Examination of the SNP molecular data for the Bowman backcross-derived line, BW009 (Bowman*7/ACBV89B229), identified three chromosomal regions that were retained from the donor parent (1). Only a region of 2HL near the centromere was not present in other BW lines with elongated rachis internodes. This region was assumed to be where the *acr1.a* allele is located. The other regions were present in BW lines showing a dominant inheritance pattern for slightly elongated rachis internodes. The locus in the retained 4HL region was named Accordion rachis 2, *Acr2*, and the locus in the 1HL region was named Accordion rachis 3, *Acr3*.

Previous nomenclature and gene symbolization:

Lax rachis internode = *ril* (2).

Accordion rachis = *acr* (5, 6).

Inheritance:

Monofactorial recessive (2, 5, 6), part of a multiple genic series involving *acr1*, *Acr2*, and *Acr3* required for expression (3).

Located in chromosome 2HL (3); *acr1.*a is near the *vrs1* (six-rowed spike 1) locus because no recombination with the *Vrs1.t* (deficiens) allele was observed (3); *acr1.*a is associated with SNP markers 1_0525 to 2_0667 (positions 65.03 to 117.73 cM) in 2H of the Bowman backcross-derived lines BW009 and BW439 (1), likely in 2H bins 06 to 08.

Description:

Rachis internodes are greatly elongated and often bent or pleaded as the spike emerges from the boot or sheath of the flag leaf (5). The line ACBV89B229, developed by R.I. Wolfe to maximize rachis internode length, exhibits extreme elongation of rachis internodes, rachis internode length values up to 7.7 mm, and occasionally trapping of the spike tip in the boot (3, 7). Elongation of the rachis internodes is associated with slightly elongated outer glumes and the deficiens (*Vrs1.t*) spike phenotype. Two dominant modifiers, *Acr2* (see BGS 189) and *Acr3* (see BGS 241), caused variable expression of the accordion trait in different genetic backgrounds. In crosses to Bowman, segregation for *acr1* fit a three gene model based on DNA segments retained in the Bowman backcross-derived lines BW009 and BW439 (1, 3). Although the *acr1* gene is apparently associated with the deficiens spike type, the large centromeric segment of 2H retained does not overlap the six-rowed spike 1 (*vrs1*) locus (1). A pericentric inversion cannot be eliminated as a possibility. Plants in the BW009 and BW439 lines were about 3/4 of normal height and peduncles were about 1/2 of normal length. The number of fertile rachis nodes was reduced by about 3 and heading was delayed by up to 4 days. Kernels appeared thinner and weighted about 10% less. Test weights were low and grain yield was about 3/4 of normal (3).

Origin of mutant:

A naturally occurring deviant (4) incorporated into several genetic stocks, *acr1.a* in

Beaverlodge stock ACBV89B229 was used to study this locus (3, 7).

Mutational events:

*acr1.a* in ACBV89B229 (GSHO 1617) and ACBV89232 (GSHO 1573) (7).

Mutant used for description and seed stocks:

*acr1.a* in ACBV89B229 (GSHO 1617); *acr1.a* in Bowman (PI 483237)*4 (GSHO 1899); *acr1.a* in Bowman*7 (BW009, NGB 20417 and BW439, NGB 20671).

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Revised:

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J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:68-69.

# BGS 102, Uzu 1, *uzu1*

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

Previous nomenclature and gene symbolization:

Normal vs uzu = *h* (28).
Uzu = *u* (15).
Uzu (semi-brachytic) = *uz* (27).
Uzu 2 = *uz2* (13, 30, 32).
Uzu 3 = *uz3* (13, 30, 32).
*Hordeum vulgare* BR-insensitive 1 = *HvBRI1* (3).
Erectoides-79 = *ert-79* (11).
Breviaristatum-256 = *ari-256* (14).
*Hordeum vulgare* DWARF = *HvDWARF* (7, 8).
Brassinosteroid deficient 1 = *brd1* (7).

Inheritance:

Monofactorial recessive (15, 23, 25, 27).

Located in chromosome 3HL (21, 22, 27); *uzu1.a* is about 17.6 cM proximal from the *alm1* (albino lemma 1) locus (26); *uzu1.a* is in bin 3H 06 near cDNA marker C1271 (3); *uzu1.a* is about 10.1 cM from AFLP marker E3733-6 in subgroup 27 of the Proctor/Nudinka map (19); *uzu1.a* is associated with SNP markers 1_0373 to 1_1314 (positions 92.55 to 107.40 cM) in 3H bins 06 to 07 of the Bowman backcross-derived line BW885 (5); *uzu1.a* with *sld1.a* (slender dwarf 1) is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman line BW912 (5); *uzu1.a* with *wst1.c* (white streak 1) is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman line BW860 (5); *ert-ii.79* is associated with SNP markers 2_0686 to 2_0931 (positions 67.01 to 104.39 cM) in 3H bins 05 to 06 of the Bowman line BW312 (5); *uzu1.256* (formerly *ari.256*) is associated with SNP markers 1_0728 to 2_1405 (positions 96.75 to 187.28 cM) in 3H bins 06 to 12 of Bowman line BW033 (5); the *ert-ii.79* allele at the *uzu1* (*HvBRI1*) locus is positioned at 57.1 cM (4) on the barley genome map (29), in 3H bin 06.

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (24, 25, 27). 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 (25, 30, 31). The temperature sensitive reduction in culm length of *uzu1.a* plants ranged from less than 15% in cool environments to over 75% in warm ones (6). The Bowman backcross-derived line for *uzu1.a*, BW885, produced plants that were 20 to 40% shorter than Bowman, awns were about 1/3 of normal length, rachis internodes were shorter, 3.0 vs.4.7 mm, and leaf blades were shorter and wider. Kernels of BW885 were shorter, 7.9 vs. 9.5 mm, and lighter, averaged 4.7 vs. 5.7 mg. Spikes of BW885 often had 2 more kernels than those of Bowman. Grain yields of BW885 ranged from 1/3 to 3/4 those of Bowman (6). Chono et al. (3) reported that the *uzu1.a* variant is caused by a mutation that changed a highly conserved residue of the kinase domain of the *HvBRI1* protein [*BRI1* (brassinosteroid insensitive 1) of *Arabidopsis*] from His-857 to Arg-857. The *uzu1* (*HvDWARF*) gene encodes for the enzyme brassinosteroid C6-oxidase, which is involved in brassinosteroid biosynthesis (7). When grown at low temperatures, the *uzu1.a* mutant was a semidwarf with 80% of wild-type culm length. The overall plant architecture is more erect, with acute leaf blade angles. Short-awned spikes are compact with dense basal spikelets, and frequently with opposite spikelets in the tip caused by irregular elongation of rachis internodes. Leaf blade margins and auricles of *uzu1.a* plants have a slightly undulating appearance (4). When grown at 26°C, *uzu1.a* plants (BW885) showed extreme dwarfing, less than 1/3 the height of Bowman plants. This extreme dwarfing caused by temperature was not observed with other mutants at the *uzu1* locus (4). In progeny from crosses to the BW885 line, tillering was reduced (1). The *uzu1.a* variant was associated with decreased incidence of crown root, *Fusarium pseudograminearum* (2). Differential phenotypic expressions and responses to heat and drought stress were observed among the *uzu1* mutants (4, 7, 12).

Origin of mutant:

Natural occurrence in some cultivars of Japanese origin (24, 25).

Mutational events:

*uzu1.a* (OUJ371, PI 182624, GSHO 1300) in East Asian cultivars with a winter growth habit (20, 25, 32); *uzu1.b* (092AR) in Aramir (PI 467781) (9, 10); *uzu1.c* 36 (Katovice 32-1-1) in the doubled-haploid line 36-H930 (4); *ert-ii.79* (NGB 112678, GSHO 483) in Bonus (NGB 14657, PI 189763) (4, 10); *uzu1.256* (formerly *ari.256*) (NGB 116065) in Kristina (NGB 14661, NGB 1500) (4, 14); 522DK (*brd1-a*) and 527DK (*brd1-b*) from Delisa (PI 315937) (7, 8); *brd1-c* and *brd1-d* from Sebastian (7).

Mutant used for description and seed stocks:

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

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# BGS 118, Low number of tillers 1, *lnt1*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (7).

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

Description:

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

Origin of mutant:

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

Mutational events:

*lnt1.a* (GSHO 833) in Mitake (OUJ408) (7); *int-l.81* (NGB 115499, GSHO 1771) in Bonus (NGB 14657, PI 189763) (3, 6); *lnt1.b* (FN468, GSHO 3678) in Steptoe (CIho 15229) may be an allele based on phenotypic similarity (5).

Mutant used for description and seed stocks:

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

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# BGS 124, Six-rowed spike 4, *vrs4*

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|---|---|
| Stock number: | BGS 124 |
| Locus name: | Six-rowed spike 4 |
| Locus symbol: | *vrs4* |

Previous nomenclature and gene symbolization:

Multiflorus = *mul* (8, 19).
Intermedium spike-e = *int-e* (6, 13).
Six-rowed spike 4 = *v4* (3).
*Hordeum vulgare RASMOSA2 = HvRA2* (10).

Inheritance:

Monofactorial recessive (3, 4, 5, 7).

Located in chromosome 3HL (5, 16, 17, 18); *vrs4.k* is about 27.5 cM from the *uzu1* (uzu 1) locus (5); *int-e.58* is associated with SNP markers 1_0672 to 2_1083 (positions 38.56 to 156.06 cM) in 3H bins 04 to 10 of the Bowman backcross-derived line BW423 (1); *mul1.a* is associated with SNP markers 1_0762 and 2_0115 (positions 38.56 and 126.83 cM) in 3H bins 04 and 08 of line BW606 (1); *vrs4.k* is associated with SNP markers 1_0863 to 1_0926 (positions 64.85 to 85.26 cM) in 3H bin 05 and with SNP markers 2_1493 to 1_1330 (positions 161.43 to 178.12 cM) in 3H bin 10 of the Bowman backcross-derived line BW903 (1); the lack of SNP marker heterogeneities in the centromeric region of the BW lines and more markers retained in 3HS indicate that the *vrs4* locus is more likely in 3H bin 05 (1, 2).

Description:

Alleles at this locus enhance the development of lateral spikelets and formation of additional spikelets to various degrees. The *int-e* mutants, which were isolated in two-rowed cultivars, have enlarged lateral spikelets that may set seed in the upper two-thirds of the spike. Kernels in lateral spikelets are smaller than those from central spikelets in *int-e* mutants. The rachilla may be deformed by partial formation of an extra spikelet. The awn size on lateral spikelets ranges from a pointed apex to 3/4 normal length (14). The *mul1.a* and *vrs4.k* alleles, which were isolated in six-rowed cultivars, may produce numerous extra spikelets at the base of the lateral spikelets and on the rachilla (4, 8). Plants of the backcross derived line BW903 with the *vrs4.k* allele and BW606 with *mul1.a* are slightly taller than Bowman, plants lodge easily, and rachis internodes are slightly longer. Kernels of BW423 with *int-e.58* had weights that range similar to those of Bowman to 10% less. Kernels of BW606 and BW903, which include small lateral ones, had average weights 20 to 40% less than those of Bowman. The kernel weights for BW606 were slightly less than those of BW093. Kernels of all BW lines with *vrs4* alleles are about 10% shorter than those of Bowman (2). Compared to Bowman, BW903 had more kernels per spike, but tiller numbers and seed weights were reduced (11). Expression analyses through mRNA in situ hybridization and microarray showed that *Vrs4* (*HvRA2*) controls the row-type pathway through *Vrs1* (Six-rowed spike 1, *Hordeum vulgare* Homeobox 1 = *HvHox1*), which is a negative regulator of lateral spikelet fertility (10). Scanning electron microscopy imaging of wild type and *vrs4* mutants at double ridge stage revealed no morphological differences. However, the appearance of two additional mounds on either side of the lateral spikelet meristems was the first visible deviation observed in *vrs4* mutant inflorescences. The additional spikelets emerging at rachis internodes were frequently fertile and developed into kernels (10).

Origin of mutant:

A gamma-ray induced mutant in MFB 104 (PI 232921) (5).

Mutational events:

*mul1.a* (Alb Acc 321, GSHO 561) in Montcalm (CIho 7149) (8, 19); *vrs4.k* (Gamma III 3B, MFB-2, GSHO 775) in MFB 104 (PI 232921), *vrs4.l* (Xc 41.5, Piro-2) in Piroline (PI 262210) (5); *vrs4.m* (X17 2497, Piro-7) in Piroline (4, 5); *int-e.4* (trans) (NGB 115423) in Bonus (NGB 14657, PI 189763), *-e.20* (trans) (NGB 115438), *-e.23* (NGB 115441), *-e.26* (NGB 115444) in Foma (NGB 14659, CIho 11333), *-e.58* (NGB 115476, GSHO 1776), *-e.66* (NGB 115484) in Kristina (NGB 14661, NGB 1500), *-e.65* (NGB 115483) in Bonus (13); *int-e.72* (NGB 115490), *-e.87* (NGB 115505) in Bonus, *-e.89* (NGB 115507), *-e.90* (NGB 115508), *-e.91* (NGB 115509), *-e.92* (NGB 115510), *-e.101* (NGB 115519) in Hege (NGB 13692) (12); *hex-v.46* (NGB 115583), *hex-v.47* (NGB 115584), *hex-v.48* (NGB 115585) in Bonus (9, 12).

Mutant used for description and seed stocks:

*vrs4.k* (Gamma III 3B, GSHO 775) in MFB 104; *int-e.58* in Kristina (GSHO 1776, NGB 115476); *mul1.a* in Bowman (PI 483237)*6 (GSHO 1985); *mul1.a* in Bowman*7 (BW606, NGB 22172); *vrs4.k* in Bowman*6 (GSHO 1986); *vrs4.k* in Bowman*7 (BW903, NGB 22335); *int-e.58* in Bowman*6 (GSHO 1987); *int-e.58* in Bowman*7 (BW423, NGB 20656).

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## BGS 131, Granum-a, *gra-a*

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| Stock number: | BGS 131 |
| Locus name: | Granum-a |
| Locus symbol: | *gra-a* |

Previous nomenclature and gene symbolization:

Many-noded and nodal-branched with no gene symbol (8).

Granum-a = *gran-a* (3).

Inheritance:

Monofactorial recessive (3, 7, 8).

Located in chromosome 7H (2); *gra-a.1* is associated with SNP markers 1_0861 to 1_0078 (positions 183.90 to 187.83 cM) in 7H bin 11 of the Bowman backcross-derived line BW398 (2); *gra-a.2* is associated with SNP markers 1_0078 to 1_0547 (position 187.83 to 231.00 cM) in 7H bins 11 to 13 of the Bowman backcross-derived line BW399 (2), likely in 7H bin 11. Previously the *gra-a.1* mutant was reported to be in chromosome 3HL (3, 7).

Description:

Plants have numerous, thin tillers with narrow leaves and short internodes (1/2 normal plant height). Spikes are less than half normal length and seeds are thin and small (3, 7). Spikes emerge from the sheath of the flag leaf prematurely, 4 to 7 days before anthesis (5). Compared to Bowman plants of Bowman, backcross-derived lines for *gra-a.1* (BW398) and *gra-a.2* (BW399) were about half of normal height and peduncles were about 1/3 normal length (4). Awns and rachis internodes of the BW398 spikes were slightly shorter than those of Bowman (1, 4). The tip of the spike has a fascinated appearance because spikelets are very close together (1, 4). The number of kernels per spike for BW398 and BW399 were often 4 to 7 less than the number for Bowman. Kernel weights were about 25% less (45 vs. 59 mg) than those of Bowman, but grain yields were almost normal (4). Combining the *gra-a.1* and *cul2.b* (uniculm 2) mutants produced short plants that occasionally produced two tillers (1).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (3, 7).

Mutational events:

*gra-a.1* (GSHO 1757) in Donaria (PI 161974) (3; 7); *gra-a.2* (GSHO 1758) from a Tokak (PI 178421) mutant in OR-SS-2 (5, 6, 9); *gra-a.3* (DWS1176) in HE2816 (likely from HE-MN-C 292) from Milan Váša (5, 6); many noded and nodal branched mutants in C. 167 (8).

Mutant used for description and seed stocks:

*gra-a.1* (GSHO 1757) in Donaria; *gra-a.1* in Bowman (PI 483237)*7 (GSHO 1980, BW398, NGB 20635); *gra-a.2* in Bowman*7 (GSHO 1981, BW 399, NGB 20636).

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## 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* (16).
Glossy = *gl* (14).
Glossy leaves = *gl* (21).
Glossy leaf = *gl* (20).
Glossy seedling *2* = *gl2* (6, 14).
Eceriferum-zh = *cer-zh* (9).

Inheritance:

Monofactorial recessive (14).

Located in chromosome 4HL (5, 14, 17, 19); *glf1.a* is about 1.5 cM distal from the *lbi2* (long basal rachis internode 2) locus (2, 6, 7); *glf1.a* is about 1.2 cM proximal from the *Mlg (Reg2,* reaction to *Erysiphe graminis* 2) locus (2, 6); *glf1.a* is associated with SNP markers 2_0820 to 1_0606 (positions 89.78 to 95.92 cM) in 4HL of the Bowman backcross-derived line BW385 (1); *glf1.a* co-segregated with molecular markers AK361226 and AK362558 (8), in 4H bin 06.

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 ++ ++ -) (9). Plants are semidwarf, relatively weak, and late in heading. The stock in the Bonus is highly sterile (9), but the Bowman backcross-derived line has nearly complete fertility (3). The lack of surface waxes reduces the ability of growing germ tube of certain fungi to find the stomata openings (15). Plants of Bowman backcross-derived line BW385 were 5 to 15% shorter than Bowman and headed about 2 days later. Kernel weights were about 20% lower and grain yields were approximately 3/4 of normal (3). Seedling leaf waxes in the *cer-zh.54* mutant showed a 76% decrease in total wax load due to marked decreases of all wax classes except the esters (8). The gene mutated in *cer-zh.54* was identified an elongase component, *β*-ketoacyl-CoA synthase (CER-ZH/*Hv*KCS1) (8).

Origin of mutant:

A radiation induced mutant in Himalaya (CIho 1312) (14, 18), an X-ray induced mutant in Bonus (NGB 14657, PI 189763) (9).

Mutational events:

*glf1.a* (GSHO 98)*, glf1.b (gl2*, GSHO 22) in Himalaya (CIho 1312) (18); *glf1.f* in 34-119-1, *glf1.g* in II-34-199-7-2 (GSHO 89) (4); *cer-zh.54* (NGB 110938, GSHO 455) in Bonus (NGB 14657, PI 189763) (9, 10); *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) in Foma (NGB 14659, CIho 11333) (10, 13); *cer-zh.325* (NGB 111212) in Foma (10); *cer-zh.373* (NGB 111260) in Foma (11); *cer-zh.865* (NGB 111753) in Bonus (12); *glf1.h* (MXM137) in Morex (CIho 15773) based on phenotype and SNP markers retained in the Bowman backcross-derived line BW384 (1, 3).

Mutant used for description and seed stocks:

*glf1.a* (GSHO 98) in Himalaya; *cer-zh.54* (NGB 110938, GSHO 455) in Bonus was used for allelism tests; *glf1.a* via R.I. Wolfe's chromosome 4 multiple recessive marker stock in Bowman (PI 483237)*8 (BW385, NGB 20623, GSHO 2015); *cer-zh.54* in Bowman*3 (BW164, NGB 21996); *glf1.h* in Bowman*5 (BW384, NGB 22146).

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# BGS 157, Brachytic 2, *brh2*

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

Previous nomenclature and gene symbolization:

Brachytic 2 = *br2* (11).

Breviaristatum-l = *ari-l* (6, 7).

Inheritance:

Monofactorial recessive (10).

Located in chromosome 4HL (10); *brh2.b* is about 1.5 cM proximal from the *glf3* (glossy leaf 3) locus (4, 10); *brh2.b* is over 22.8 cM proximal from the *Kap1* (Hooded lemma 1) locus (10); *brh2.b* is near AFLP marker E4140-7 in subgroup 38-40 of the Proctor/Nudinka map (9), *brh2.b* is about 15.9 cM distal from SSR marker Bmag0353 near the boundary between 4H bins 06 and 07 (2); *brh2.b* is associated with SNP markers 2_0012 to 1_1319 (positions 57.19 to 110.93 cM) in 4H bins 05 to 07 of the Bowman backcrossed-derived line BW090 (3); *ari-l.3* is associated with SNP markers 2_1374 to 2_1332 (positions 41.13 to 112.64 cM) in 4H bins 04 to 08 of the Bowman backcrossed-derived line BW050 (3), likely in 4H bin 06.

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 (11). 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-l.3* allele at the *brh2* locus is sensitive to gibberellic acid treatment (1). The Bowman backcross-derived for *brh2.b*, BW090, and *ari-l.3*, BW050, were morphologically similar to each other, shorter than Bowman, 65 vs. 90 cm. They also had short awns, 2.5 vs. 12 cm beyond the tip of the spike and small kernels. Compared to Bowman, kernels were shorter, 7.5 vs. 9.8 mm, and thinner, 3.61 vs.3.83 mm, and weighed less, 40 vs. 56 mg. Grain yields for BW050 and BW090 were 1/2 to 2/3 of those produced by Bowman (5).

Origin of mutant:

An X-ray induced mutant in Svanhals (NGB 1482, PI 5474) (11).

Mutational events:

*brh2.b* (Kmut 28, OUM283, GSHO 573) in Svanhals (NGB 1482, PI 5474) (10); *ari-l.3* (NGB 115848) in Bonus (NGB14657, PI 189763) (7); *ari-l.132* (NGB 115942) in Foma (NGB 14659, CIho 11333) (8); *ari-l.135* (NGB 115945), *-l.145* (NGB 115956), *-l.214* (NGB 116023), *-l.237* (NGB 116047) in Foma, *-l.257* (NGB 116066) in Kristina (NGB 14661, NGB 1500) (7).

Mutant used for description and seed stocks:

*brh2.b* (GSHO 573) in Svanhals; *ari-l.3* (GSHO 1660) in Bonus; *brh2.b* in Bowman (PI 483237)*7 (GSHO 2016, BW090, NGB 20496); *ari-l.3* in Bowman*7 (GSHO 2017, BW050, NGB 20458).

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# BGS 165, Glossy leaf 3, *glf3*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (17, 19).

Located in chromosome 4HL (2, 7, 17); *glf3.c* is about 1.5 cM distal from the *brh2* (brachytic 2) locus (6); *glf3.c* is about 13.7 cM from the *sid1* (single elongated internode 1) locus (6); *glf3.d* is associated with SNP markers 1_1180 to 1_1513 (positions 58.13 to 101.44 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW386 (1); *cer-j.59* is associated with SNP markers 2_1122 to 2_1332 (positions 47.80 to 112.64 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW114 (1); likely in 4H bin 06.

Description:

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

Origin of mutant:

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

Mutational events:

*glf3.c* (Goseshikoku-hen, OUL032, GSHO 577) in Goseshikoku (OUJ128) (18); *glf3.d (gl4*, GSHO 1376*)* in Gateway (CIho 10072) (22); *cer-j.59* (NGB 110943, GSHO 431), -*j.62* (NGB 110946) in Bonus (NGB 14657, PI 189763) (8, 9); *cer-j.71* (NGB 110955), -*j.142* (NGB 111028)*, -j.148* (NGB 111034) in Bonus, *-j.274* (NGB 111161)*, -j.288* (NGB 111175)*, -j.301* (NGB 111188)*, -j.311* (NGB 111198)*, -j.340* (NGB 111227)*, -j.346* (NGB 111233)*, -j.349* (NGB 111236), *-j.358* (NGB 111245), *-j.370* (NGB 111257), *-j.390* (NGB 111277)*, -j.429* (NGB 111317), *-j.447* (NGB 111335)*, -j.470* (NGB 111358) in Foma (NGB 14659, CIho 11333) (9, 16); *cer-j.183* (NGB 111069), *-j.184* (NGB 111070)*, -j.696* (NGB 111584) in Bonus, *-j.275* (NGB 111162)*, -j.399* (NGB 111286)*, -j.517* (NGB 111405)*, -j.521* (NGB 111409)*, -j.558* (NGB 111446) in Foma, *-j.1024* (NGB 111912)*,* -*j.1081* (NGB 111969) in Carlsberg II (NGB 5085, CIho 10114) (11); *cer-j.458* (NGB 111346) in Foma, *-j.780* (NGB 111668)*, -j.797* (NGB 111685)*, -j.832* (NGB 111720) in Bonus, *-j.1090* (NGB 111978)*, -j.1102* (NGB 111990) in Kristina (NGB 14661, NGB 1500) (12); *cer-j.909* (NGB 111797) in Bonus, *-j.1152* (NGB 112040) in Kristina (11); *cer-j.1204* (NGB 112092)*, -j.1231* (NGB 112119)*, -j.1233* (NGB 112121)*, -j.1239* (NGB 112127)*, -j.1251* (NGB 112139) in Kristina (12); *cer-j.997* (NGB 111885)*, -j.1331* (NGB

112219), *-j.1361* (NGB 112249), *-j.1388* (NGB 112276), *-j.1405* (NGB 112293), *-j.1433* (NGB 112321), *-j.1469* (NGB 112357) in Bonus (12); *cer-j.1712* (NGB 112525), *-j.1744* (NGB 112558), *-j.1761* (NGB 112576), *-j.1803* (NGB 117351), *-j.1808* (NGB 117356) in Bonus (12); *cer-j.1827* (NGB 117375) in Bonus, *-j.1831* (NGB 117379), *-j.1835* (NGB 117383), *-j.1839* (NGB 117387), *-j.1841* (NGB 117389), *-j.1843* (NGB 117391), *-j.1844* (NGB 117392), *-j.1847* (NGB 117395), *-j.1850* (NGB 117398), *-j.1852* (NGB 117400), *-j.1857* (NGB 117405), *-j.1858* (NGB 117406), *-j.1859* (NGB 117407), *-j.1860* (NGB 117408), *-j.1861* (NGB 117409), *-j.1862* (NGB 117410) in Sv 79353 (15).

Mutant used for description and seed stocks:

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

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# BGS 172, Short awn 5, *lks5*

| | |
|---|---|
| Stock number: | BGS 172 |
| Locus name: | Short awn 5 |
| Locus symbol: | *lks5* |

Previous nomenclature and gene symbolization:

Short awn 5 = *lk5* (7).
Breviaristatum-2 = *ari-2* (5, 6).
Breviaristatum-c = *ari-c.2* (6, 13, 14).

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 4HL (15); *lks5.f* is about 6.9 cM distal from the *Kap1* (Hooded lemma 1) locus (7, 9); *lks5.f* is near AFLP marker E4143-5 in subgroup 38 of the Proctor/Nudinka map (10); *lks5.f* is associated with SNP markers 1_0262 to 2_0072 (positions 76.26 to 95.92 cM) in 4H bin 06 of the Bowman backcrossed-derived line BW493 (2); *ari-c.2* is associated with SNP markers 2_0289 to 2_1322 (positions 69.62 to 112.64 cM) in 4H bins 05 to 08 of the Bowman backcrossed-derived line BW040 (2), in 4H bin 06; *lks5.p* was isolated in genetic stocks BW474 and BW475 from the *lel1* (leafy lemma 1) stock, G7118, *lks5.p* is associated with SNP markers 2_1122 to 1_1019 (positions 47.80 to 183.54) in 4H bins 05 to 13 of the Bowman backcrossed-derived line BW474 (2); *lks5.p* is associated with SNP markers 2_0422 to 2_0072 (positions 38.41 to 95.92 cM) in 4H bins 04 to 06 of the Bowman backcrossed-derived line BW475 (2); in 4H bin 06.

Description:

Awns on both central and lateral spikelets are reduced to 1/4 or less of normal length in six-rowed cultivars (7). Only the central spikelets exhibit reduced awn length in two-rowed cultivars (3, 6). The rachilla is often modified, and in extreme cases the rachilla may develop as a malformed additional floret (7). Awns are thin and brittle (6). Plants of the Bowman backcross-derived line for *lks5.f*, BW493, had awns that extended 3 to 4 cm beyond the tip of the spike, while those of Bowman were 12 to 13 cm beyond the tip. Kernels of BW493 were slightly shorter, narrower (3.4 vs. 3.9 mm), and lighter (4.6 vs. 5.5 mg). BW493 plants were slightly taller than Bowman and grain yields were slightly reduced (4). Presence of the mutant allele *lks5.p* is needed for expression of the leafy lemma 1 (*lel1.a*) gene (4, 10).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (7).

Mutational events:

*lks5.f* (GSHO 1297) in CIho 5641 (7, 13); *lks5.g* (Kmut 218) in Asahi 5 (OUJ509) (13); *ari-c.2* (NGB 115847, GSHO 1651), *-c.59* (NGB 115913) in Bonus (NGB 14657, PI 189763), *-c.103* (NGB 115915) in Foma (NGB 14659, CIho 11333) (3); *ari-c.106* (NGB 115918) in Foma (5); *ari-c.109* (NGB 115921), *-c.110* (NGB 115922), *-c.111* (NGB 115923), *-c.112* (NGB 115924), *-c.120* (NGB 115932), *-c.139* (NGB 115949), *-c.157* (NGB 115967), *-c.159* (NGB 115969), *-c.179* (NGB 115989), *-c.180* (NGB 115990), *-c.199* (NGB 116008), *-c.201* (NGB 116010), *-c.203* (NGB 116012), *-c.204* (NGB 116013), *-c.206* (NGB 116014), *-c.210a* (NGB 116018), *-c.210b* (NGB 116019) *-c.229* (NGB 116039) in Foma, *-c.259* (NGB 116068), *-c.262* (NGB 116071), *-c.272* (NGB 116084), *-c.276* (NGB 116089), *-c.289* (NGB 116107), *-c.291* (NGB 116111) in Kristina

(NGB 14661, NGB 1500) (6); *ari-c.307* (NGB 116135) in Kristina (8); two possible additional alleles have been reported, *lks5.h* (*lk,,f*) in two-rowed Glacier (3); and a mutant in Morex (CIho 15773) (12); *lks5.p* in G7118 (leafy lemma, GSHO 1780) mutant stock (1, 3, 4, 11).

Mutant used for description and seed stocks:

*lks5.f* (GSHO 1297) in CIho 5641; *ari-c.2* (NGB 115847, GSHO 1651) in Bonus; *lks5.f* in Bowman (PI 483237)*6 (GSHO 2014); *lks5.f* in Bowman*7 (BW493, NGB 20721); *ari-c.2* in Bowman*7 (GSHO 2013, BW040, NGB 20448); *lks5.p* from G7118 in Bowman*4 with *lel1.a* (BW474, NGB 20704); *lks5.p* from G7118 in Bowman*5 (BW475, NGB 20705).

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

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

Previous nomenclature and gene symbolization:

Intensifier for *Z* = *W* (25).
Infertile intermedium = *i* (14, 23, 24).
Allelic series *$I^h$, I, i* (14, 26).
Intermedium spike-c = *int-c* (8, 9, 19, 20).
Six-rowed spike 5 = *v5* (*vrs5*) (27).
*Hordeum vulgare TEOSINTE BRANCHED 1 = HvTB1* (22).

Inheritance:

Monofactorial recessive (6, 7, 20, 24, 27).

Located in chromosome 4HS (5, 7, 20, 24, 27); *Int-c.a* is about 13.1 cM proximal from the *fch9* (chlorina seedling 9) locus (3, 5, 6, 7, 13); *Int-c.a* is about 14.5 cM distal from the *Kap1* (Hooded lemma 1) locus (3, 5, 6, 7, 13); *Int-c.a* is about 3.5 cM from AFLP marker E4143-5 in subgroup 8 of the Proctor/Nudinka map (21); *int-c.5* is associated with SNP markers 1_0113 to 2_1122 (positions 26.58 to 47.80 cM) in 4H bins 02 to 05 of the Bowman backcross-derived line BW421 (2); *Int-c.a* is associated with SNP markers 1_0312 to 2_1374 (positions 38.41 to 41.13 cM) in 4H bins 03 to 04 of the Bowman backcross-derived line BW911, with SNP markers 1_0409 to 2_1122 (positions 5.24 to 47.80 cM) in 4H bins 01 to 05 of the Bowman backcross-derived line BW889 and with SNP markers 1_0132 to 2_0109 (positions 38.41 to 39.48 cM) in 4H bins 03 to 04 of the Bowman backcross-derived line BW624 (2); near SNP marker 2_0302 (22), in 4H bin 04.

Description:

Alleles at the *int-c* (*vrs5*) locus alter the size of lateral spikelets (1, 6, 22). The lemma apex of lateral kernels is rounded or weakly pointed, awnless or short-awned (1, 11, 18). Lower lateral spikelets may develop poorly in some *int-c* mutants (6), while seed development may occur in all lateral spikelets of others (8, 17). 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 (11, 25). The *int-c.5* mutant in Bonus produces fertile stamens in lateral spikelets (11). In the presence of the *Int-c.h* (formerly *$I^h$*) allele of Mortoni, lateral spikelets are male fertile and may occasionally set seed (10, 14). Spikes of *vrs5.n* 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 (5, 6). The *Int-c* (*HvTB1*) gene is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1* (*TB1*) (22). Seventeen barley mutations in the coding region for *HvTB1* were correlated with lateral spikelet fertility phenotypes (22).Compared to Bowman the backcross-derived lines for *int-c.5*, BW421, had slightly smaller leaf blades and smaller, lighter kernels, 4.2 vs.5.6 mg. In spite of more kernels per spike (lateral spikelet fertility), the grain yields of BW421 were slightly lower than those of Bowman. (4) Compared to Bowman, tillering was increased in BW421 (22) The increased size of sterile lateral spikelets in Bowman backcross-derived lines for *Int-c.a*, BW421 and BW889, seems to be associated with a slight increase in leaf blade size (4).

Origin of mutant:

The dominant allele, *Int-c.a*, is present in six-rowed barley (22) and wild barley (28); the recessive allele, *int-c.b*, is present in many two-rowed cultivars (22, 28); an X-ray induced mutant in Gamma 4 (5, 7).

Mutational events:

*int-c.b* (*i*) in many two-rowed barleys (26); *Int-c.h* ($I^{h}$) in Mortoni (CIho 2210, GSHO 72) (10, 14); *vrs5.n* (*v5*) (38X-197, OUM338, GSHO 776) in Gamma 4 (5, 7, 16); *int-c.5* (NGB 115423, GSHO 1765) in Bonus (NGB 14657, PI 189763) (17, 20); *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 (NGB 14659, 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 (NGB14661, 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) (15).

Mutant used for description and seed stocks:

*vrs5.n* (GSHO 776, OUM338) in Gamma 4; *int-c.b* in *Hordeum distichon* var. *nigrinudum* (GSHO 988); *int-c.5* (GSHO 1765) in Bonus; *int-c.b* from Compana (CIho 5438) in Bonneville (CIho 7248)*6 (CIho 16176) (10); *vrs5.n* from Manabe Island (OUL067, GSHO 766) in Bowman (PI 483237)*5 (GSHO 2102, BW904, NGB 20788); *int-c.5* in Bowman*6 (GSHO 2003); *int-c.5* in Bowman*7 (BW421, NGB 20654); *Int-c.a* from SEN “sib” from CIMMYT.in Bowman*4 (GSHO 2363); *Int-c.a* from SEN ‘sib” in Bowman*7 (BW889, NGB22322). Note that based on SNP markers the Bowman backcross-derived lines from Manabe (GSHO 2002, BW904, NGB 20788); do not have the *vrn5,n* gene.

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Revised:

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:237-239.
U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:92-94.

# BGS 184, Zeocriton 3, *Zeo3*

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|---|---|
| Stock number: | BGS 184 |
| Locus name: | Zeocriton 3 |
| Locus symbol: | *Zeo3* |

Revised locus symbol:

Since the zeocriton spike phenotype was studied by Hayes and Harlan (8), the recommended locus name is Zeocriton 1 (*Zeo1*). The semi-dominant dense spike variants at the complex *Zeo1* locus exhibit a range of phenotypes associated with restricted elongation of the rachis internodes. Based on DNA sequencing, three distinct phenotypic groups of dense spike variants are associated with the *Hordeum vulgare APELATA2* (*AP2*)-like transcription factor (*HvAP2*) locus (10, 11). The phenotypic expressions were historical assigned different locus symbols, but each group is now associated with specific molecular changes in the *HvAP2* transcript (10). Alleles at this locus are assigned locus symbols: the *Zeo1* (BGS 082) mutants exhibit the most extreme phenotypes; the *Zeo2* variants have intermediate phenotypes; and the *Zeo3* variants may show a lesser degree in shortening of rachis internodes (10). Molecular markers and/or pedigree information are necessary to separate variants assigned to the *Zeo2* (BGS 614) and Zeo3 (BGS 184) groups (10).

Previous nomenclature and gene symbolization:

Zeocriton with no gene symbol (4, 8).
Semidwarf mutant in Morex = Mo1 (15).
Zeocriton 2 = *Zeo2* (6).
Cleistogamy 1 = *cly1.c* (10, 11, 14).
*Hordeum vulgare APELATA2* (*AP2*)-like transcription factor = *HvAP2* (10, 11).

Inheritance:

Monofactorial semi-dominant (9, 13).

Located in chromosome 2HL (2, 13); *Zeo3.d* is associated with SNP markers 1_1118 to 2_0494 (positions 180.85 to 221.70 cM) in 2HL bins 11 to 14 of Bowman backcross-derived line BW933; *Zeo3.h* is associated with SNP markers 2_1125 to 2_0943 (positions 206.17 to 237.13 cM) in 2HL bins 13 to 14 of the Bowman backcross-derived line BW940; *Zeo3.j* is associated with SNP markers 2_1370 to 1_1023 (positions 199.54 to 224.35 cM) in 2HL bins 12 to 14 of the Bowman backcross-derived line BW936; *Zeo3.av* (formerly named *dsp.av*) is associated with SNP markers 1_1236 to 2_0561 (positions 184.46 to 247.96 cM) in 2HL bins 11 to 15 of the Bowman backcross-derived line BW369 (2); the *HvAP2* locus is near marker BOPA2_12_10579 and these Bowman lines have the same single base pair change in the microRNA172 binding site (9), in 2H bin 13. Bowman backcross-derived lines BW660 (*Zeo3.g*) and BW661(*Zeo3.i*) have the same change at the microRNA172 binding site (9) and SNP markers associated with dense spike mutants *ert-c.1* and *ert-d.7* in chromosomes 3HL and 7HS, respectively (2).

Description:

Hayes and Harlan (8) reported that three genes controlled rachis internode length in their cross to Zeocriton. One of these genes produced strap-shaped spikes with shortened rachis (8). Identification of Bowman backcross-derived lines with the *Zeo3* gene was based on DNA sequencing of the *HvAP2* gene (10). A similar degree of rachis internode shortening was observed in Bowman backcross-derived lines with either the *Zeo2* or the *Zeo3* sequence changes in the *HvAP2* gene (6, 10). Mutants at *Zeo3* are apparently in some cultivars identified as having small lodicules (closed flowering or cleistogamy) (9, 13). The original *Zeo3.h* (Mo1) mutant differed from the parental cultivar Morex (CIho 15773) in plant height, tiller number, grain yield, and grain quality (12). The Bowman backcrossed lines for *Zeo2* and *Zeo3* have similar rachis internode lengths, but variability among cultivars with the same genes was observed (10). The rachis internode length of plants in Bowman backcross-derived lines for *Zeo3* alleles averaged 3.3 mm compared to 4.5 mm for Bowman. In some test environments, the BW lines with the *Zeo3* genes had 1 to 2 more kernels per spike than Bowman, and kernel weights were slightly lower. No effects of the *Zeo3* gene on plant height and grain yield were observed (5). DNA sequencing showed that the *Zeo1* mutants occur in a *Hordeum vulgare* APELATA2 (*AP2*)-like transcription factor, *HvAP2*. The dense spike and cleistogamous (small lodicules) phenotypes are a consequence of a perturbed interaction between microRNA 172 (*Hv-miR172*) and its corresponding binding site on the mRNA from the *HvAP2* gene, which acts early in spike development to regulate turnover of *HvAP2* mRNA (10, 11).

Origin of mutant:

A naturally and induced mutants occurring variant in the fourth exon of the *HvAP2* locus (10, 11). A sodium azide induced mutant in Morex (CIho 15773) (15).

Mutational events:

Based on haplotypes similarity for in the *HvAP2* gene, the potential *Zeo3* alleles can be placed in one group (10, 11). The *Zeo3* mutant is present in Tammi (OUU059, PI 175505) and a few other cultivars (11) and in Harry (NGB 2666, PI 491575) and in several other cultivars (10). *Zeo3.d* was isolated from line with a male sterile mutant in P11 (CIho 15836) from Finland (1). The Bowman backcross-derived stocks with *Zeo3.g*, *Zeo3.i*, and *Zeo3.av* were isolated from Finnish cultivars Aapo (PI 467771) and Pokko (PI 467770) (2). *Zeo3.h* (WA11094-81, GSHO 1611) identified as Mo1 from Morex (CIho 15773) (7, 15), and *Zeo3.j* (SA121-4-5, GSHO 1612) from Glenn (CIho 15769) (4) were isolated as spike density variants from North American six-rowed cultivars. The SNP markers retained in Bowman backcross-derived lines, BW936 with *Zeo3.h* and BW940 with *Zeo3.j*, suggest that these two variants originated independent of the Bowman backcrose-derived lines having Finish cultivars as donor parents (2, 5).

Mutant used for description and seed stocks:

*Zeo3.d* from P11 (CIho 15836) in Bowman*7 (BW933, NGB 22362); *Zeo3.av* from Aapo (PI 467771) via Pokko (PI 467770) in Bowman*4 (BW269, NGB 22094); *Zeo3.g* and *Zeo3.i*, both with another dense spike gene, from Aapo (PI 467771) via Pokko (PI 467770) in Bowman*7 (BW660, NGB 22225; and BW661, NGB 22226), respectively; *Zeo3.h* (Mo1, Wa11094-81, GSHO 1611) (formerly listed as *Zeo2.h*) in Morex (CIho 15773); *Zeo3.h* in in Bowman*5 (GSHO 1999); *Zeo3.h* from Morex in Bowman*8 (BW940, NGB 22369); *Zeo3.j* (SA121-4-5, GSHO 1612) from Glenn (CIho 15769) in Bowman*7 (GSHO 1882, BW936, NGB 22365).

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Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:99.

Revised:

J.D. Franckowiak and U. Lundqvist. 2017. Barley Genet. Newsl. 47:95-97.

# BGS 188, Aluminum tolerance 1, *Alp1*

Stock number: BGS 188
Locus name: Aluminum tolerance 1
Locus symbol: *Alp1*

Previous nomenclature and gene symbolization:

Aluminum tolerance (4, 17).
Aluminum tolerance = *Alp* (15).
pH tolerance = *Pht* (18).
Aluminum tolerance = *Alt* (14).
*Hordeum vulgare* Al-activated citrate transporter 1 = *HvAACT1* (7).

Inheritance:

Incomplete dominant with inheritance pattern dependent on Al concentration (15, 16).
Location in chromosome 4HL (13, 18); *Alp1.a* is about 25 cM from the *Kap1* (Hooded awn 1) locus (18); *Alp1.a* is 2.1 cM proximal to the marker *Xbcd1117* and 2.1 cM distal to the markers *Xwg464* and *Xcdo1395* (19); the *Alp1* locus is flanked by SSR markers Bmag353 and HVM68 (21); *Alp1.*a is flanked by microsatellite markers Bmac310 and Bmag353 (9); the 4H QTL for Al-tolerance is 0.8 cM from DArT marker bPb-6949 (3).

Description:

Better performance in acid or aluminum-toxic soils was observed among spring (10, 11, 17) and winter (4, 15, 16) barley cultivars. An association between root and shoot yields in greenhouse studies and grain yield in field studies was reported (16). Recommended screening conditions in nutrient solutions with 4 ppm aluminum (Al) and adjusted twice daily to pH 4.8 (5, 15). Retarded root elongation was observed in 4 to 5 days with roots thickened and more branched. Al-tolerant cultivars tended to raise the pH while the opposite tend was reported for Al-sensitive cultivars (5). Aluminum sensitivity of cultivars was determined by staining seedling roots after aluminum treatment with a hematoxylin staining solution (12). An Al-tolerant cultivar secreted citrate from the roots in response to Al treatment (9, 22) The differential acid soil response caused by alleles at the *Alp1* locus was associated with the *HvAACT1* (*Hordeum vulgare* Al-activated citrate transporter 1) gene (7; 21). Increased expression of the *HvAACT1* gene in East Asian cultivars was associated with the presence of a 1023-bp transposable-element like insertion in the 5' untranslated region (6).

Origin of mutant:

Natural occurrence in Dayton (PI 539129) from Composite Cross X (CIho 6625) (4, 15) and in Charlottetown 80 (CIho 2732) (10, 11).

Mutational events:15

*Alp1.a* in Dayton (PI 539129) (15); *Alp1.a* in Murasakimochi (6, 9); *Alp1.a* in Svanhals (NGB 1482, PI 5474) (2); *Alp1.a* in Honen (PI 307495) (21); Al-tolerance is present in Tibetan wild barley at the *Alp1* locus (3); *Alp1.a* in Cevada BR2 (1); a new allele (*Alp1.c*) at the *Alp1* locus was identified in Chinese barley CXHKSL (8).

Mutant used for description and seed stocks:

*Alp1.a* in Dayton; *Alp1.a* in Svanhals; *Alp1.a* in Murasakimochi; *Alp1.c* in CXHKSL.

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Prepared:

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:98-100.

# BGS 189, Accordion rachis 2, *Acr2*

| | |
|---|---|
| Stock number: | BGS 189 |
| Locus name: | Accordion rachis 2 |
| Locus symbol: | *Acr2* |

Previous nomenclature and gene symbolization:

Lax spike = lax (4, 9, 11).
Accordion rachis = *acr* (7, 9, 12).
Accordion rachis 1 = *acr1.a* (6).
Accordion rachis b and c = *acr.b*, *acr.c* (3, 5).
Laxatum spike stocks = *Lax.aa*, *Lax.ab*, *Lax.am*, *lax.ao*, (5, 12).

Inheritance:

Monofactorial incomplete dominant for lax spike, one of three factors required for expression of accordion rachis trait (5, 12).

Located in chromosome 4HL (3); *Acr2.ab* is associated with SNP markers 1_0123 to 2_1018 (positions 158.82 to 183.54 cM) in 4HL of the Bowman backcross-derived line BW445; Bowman backcross-derived lines BW007, BW008, BW009, BW439, BW444, and BW456 have identical heterogeneous SNP markers in 4HL, but their segments from the donor parent are longer (3), in 4H bins 11 or 12.

Description:

Rachis internodes are elongated and kernels appear longer than normal. The *Acr2* gene is in the second of three chromosomal regions associated with expression of the accordion rachis trait in Bowman backcross-derived lines BW009 and BW439. The long rachis internode trait was specifically added to the original accordion rachis stock by R.I. Wolfe (12). Characteristics associated with variants at the *Acr2* locus are difficult to determine because only the Bowman backcross-derived line BW444 (*Lax.aa* or *Acr2.aa*) did not have more than one chromosome segment from its donor parent (3). Rachis internodes of BW444 plants were about 30% longer, 5.7 vs. 4.4 mm, than those of Bowman. Leaf blades were slightly longer and wider. Kernels were slightly longer and heavier, 61 vs. 58 mg. Grain yields were equal or slightly more than those of Bowman. The donor parent (FN280) of the BW444 line traces to lines developed by Mary L. Martini and Harry V. Harlan (8) in Idaho via crosses to six-rowed barley made by D.C. Rasmusson (10). The Bowman backcross-derived lines BW007 (*Acr2.b2*) and BW008 (*Acr2.c2*) had the identical segment of chromosome 4HL plus a 1H segment retained from their donor parents; however, the 1H segments in these lines differed for SNP marker patterns (3). The Bowman lines BW007 and BW008 are 10 to 15% taller than Bowman. The rachis internodes of BW007 are about 25% longer than those of Bowman, 4.7 vs. 3.7 mm., Burma Girl (GSHO 1071, *Acr2.b2*), the original stock for BW007, has several sterile rachis nodes at the base of the spike before spikelet development is initiated (4). BW007 had kernel weights that varied across experiments from smaller to slightly larger than those of Bowman. The rachis internodes of BW008 were nearly twice as long as those of Bowman, 8.2 vs. 4.5 mm, but they did not show the accordion-like bending associated with the accordion phenotype. Kernels of the BW008 line were slightly longer and heavier than those of Bowman (5). Two other Bowman backcross-derived lines, BW439 and BW456, have the 4HL SNP pattern associated with the *Acr2* locus. Both originate from the same donor stock AB1398 (GSHO 1115) from Aberdeen, Idaho and are assigned the gene symbol *Acr2.am*. BW456 was selected based on lax spikes while BW439 was selected based on tall plants (5).

Origin of mutant:

A naturally occurring deviant possibly in Long Rachis Internode (CIho 6164), developed by M.L. Martini and H.V. Harlan (8), or Burma Girl (CIho 14831), donated to the USDA Small Grains Collection by G.A. Wiebe. The *Acr2* gene has been incorporated into several genetic stocks from that source.

Mutational events:

*Acr2.b2* in Burma Girl (CIho 14831, GSHO 1071) (5, 12); *Acr2.aa* in FN280 (GSHO 1572) (5, 10); *Acr2.ab* in ACBV89B229 (GSHO 1617) and ACBV89B232 (GSHO 1573) (12); *Acr2.c2* in T188 (GSHO 1480) from R.W. Woodward (2); *Acr2.am* in AB 1398 [GSHO 1115, likely CIho 14785 from G.A. Wiebe (1)]; all alleles may have been derived from one stock (3, 5).

Mutant used for description and seed stocks:

*Acr2.aa* in FN280 (GSHO 1572); *Acr2.b2* in Burma Girl (GSHO 1071); *Acr2.a2* in ACBV89B229 (GSHO 1617); *Acr2.c2* in T188 (GSHO 1480); *Acr2.am* in AB 1398 (GSHO 1115); *Acr2.a2* from ACBV89229 in Bowman*4 (GSHO 1899); *Acr2.a2* in Bowman*7 (BW009, NGB 20417 and BW439, NGB 20671); *Acr2.aa* from FN280 in Bowman*4 (GSHO 2276); *Acr2.aa* in Bowman*5 (BW444, NGB 20676); *Acr2.ab* from ACBV89B232 (GSHO 1573) in Bowman*4 (GSHO 2277); *Acr2.ab* in Bowman*6 (BW445, NGB 20677); *Acr2.b2* from Burma Girl in Bowman *2 (GSHO 1898); *Acr2.b2* in Bowman*5 (BW007, NGB 20415); *Acr2.c2* from T188 in Bowman*6 (BW008, NGB 20416); *Acr2.am* from AB 1398 in Bowman*4 (BW456, NGB 20688).

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Prepared:

J.D. Franckowiak 2010. Barley Genet. Newsl. 40:65-66.

Revised:

J.D. Franckowiak 2017. Barley Genet. Newsl. 47:101-102.

# BGS 229, Curly dwarf 2, *cud2*

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|---|---|
| Stock number: | BGS 229 |
| Locus name: | Curly dwarf 2 |
| Locus symbol: | *cud2* |

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3).

Located in chromosome 1HL (3); *cud2.b* is about 14.6 cM proximal from the *Blp1* (Black lemma and pericarp 1) locus (3, 4); no SNP markers different than those of Bowman were retained in the Bowman backcross-derived line BW199 for *cud2.b* (1).

Description:

Lemmas and awns are curly or strongly twisted, and stem internodes are curved. Culms are short (1/2 normal), spikes are semi-compact, awns are short (2/3 normal length), and kernels are globe-shaped. Most leaves are short and slightly twisted (3). In the Bowman backcross-derived line for *cud2.b*, BW199, plants were short (3/5 of Bowman), the twisted leaf blades were slightly shorter, peduncles were coiled and about 1/2 normal length, rachis internodes were slightly shorter, and awns were twisted and 2/3 normal length. Compared to Bowman, kernels were short (80% as long) and slightly wider and were about 3/4 normal weight (4.2 vs. 5.5 mg) and test weights were about 25% lower. Grain yields of BW199 were 1/4 to 1/2 of those for Bowman (2).

Origin of mutant:

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

Mutational events:

*cud2.b* (OUM112, GSHO 1712) in Akashinriki (OUJ659, PI 467400) (3).

Mutant used for description and seed stocks:

*cud2.b* (OUM112, GSHO 1712) in Akashinriki; *cud2.b* in Bowman (PI 483237)*2 (GSHO 2062); *cud2.b* in Bowman*7 (BW199, NGB 22031).

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Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:227.

Revised:

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:111.

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:103.

# BGS 238, Breviaristatum-t, *ari-t*

| | |
|---|---|
| Stock number: | BGS 238 |
| Locus name: | Breviaristatum-t |
| Locus symbol: | *ari-t* |

Previous nomenclature and gene symbolization:

Breviaristatum-25 = *ari-25* (3).

Inheritance:

Monofactorial recessive (2, 4).

Located in chromosome 1H (1); *ari-t.25* is associated with SNP markers between 1_0744 to 1_1326 (positions 39.84 to 82.35 cM) in 1H of the Bowman backcross-derived line BW032 (1), in 1H bins 05 to 08.

Description:

The awns of *ari-t* plants are 2/3 of normal length and slightly curly. Peduncles are coiled and less than half normal length and plants are 1/2 to 2/3 of normal height (4, 5). In the Bowman backcross-derived line for *ari-t.25*, BW032, leaf blades were shorter and narrower than those of Bowman. Kernels of BW032 were shorter and narrower, seed weights were about 20% lower, and seed yields were about 1/4 of normal (2). A new locus name was assigned based on the unique phenotype and lack of other breviaristatum mutants located in 1H.

Origin of mutant:

An ethylene oxide induced mutant in Bonus (NGB 14657, PI 189763) (4, 5).

Mutational events:

*ari-t.25* (NGB 115873) in Bonus (NGB 14657, PI 189763) (5).

Mutant used for description and seed stocks:

*ari-t.25* in Bonus (NGB 115873); *ari-t.25* in Bowman (PI 483237)*5 (BW032, NGB 20440).

References:

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

J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:82.

Revised:

J.D. Franckowiak and U. Lundqvist. 2017. Barley Genet. Newsl. 47:104.

# BGS 241, Accordion rachis 3, *Acr3*

| | |
|---|---|
| Stock number: | BGS 241 |
| Locus name: | Accordion rachis 3 |
| Locus symbol: | *Acr3* |

Previous nomenclature and gene symbolization:

Lax spike = Lax (7, 8)
Accordion rachis = *acr* (6).
Accordion rachis c = *acr.c* (4).
Accordion rachis 1 = *acr1.a* (5).

Inheritance:

Monofactorial incomplete dominant for lax spike, the third factor required for expression of accordion rachis 1 (*acr1*) trait (3, 4).

Located in chromosome 1HL (3); *Acr3.a3* is associated with SNP markers 2_1357 to 2_0997 (positions 76.96 to 94.86 cM) in 1HL of the Bowman backcross-derived lines BW009 and BW439 (3), likely in 1H bin 08. Bowman backcross-derived lines BW007 with *Acr3.b3*, BW009 with *Acr3.a3*, BW438 with *Acr3.a*, and BW456 with *Acr3.am3* contain overlapping segments of variable length and SNP marker patterns in 1H from their donor parents (3).

Description:

Mutant plants have slightly elongated rachis internodes (1). The *Acr3* gene is in the third chromosomal region associated with expression of the accordion rachis trait in Bowman backcross derived lines BW009 and BW439. The contribution of the 1HL region to characteristics of the accordion phenotype is unknown. Only the line BW438 (*Lax.an* or *Acr3.an*) has a 1HL donor chromosome segment in a line lacking both the 2H and 4HL segments identified as containing the *acr1* (see BGS 097) and *Acr2* (see BGS 189) genes, respectively. Plants of the Bowman derived line BW438 lines were ranged from slightly shorter to slightly taller than Bowman and had slightly longer rachis internodes (4). Kernels of BW438 were slightly longer than those of Bowman, but weighed slightly less (5.3 vs. 6.0 mg). Grain yield of BW003 was about 2/3 that of Bowman (4).

Origin of mutant:

A naturally occurring deviant for lax spike from several sources (3, 4).

Mutational events:

*Acr3.a3* in ACBV89B229 (GSHO 1617) and ACBV89B232 (GSHO 1573) (3, 9); *Acr3.b3* in Burma Girl (CIho 14831, GSHO 1071) (4, 9); *Acr2.am2* and *Acr3.an* in AB 1398 [GSHO 1115, likely CIho 14785 from G.A. Wiebe (1)]. *Acr3.c3* in T188 (GSHO 1480) from R.W. Woodward (2).

Mutant used for description and seed stocks:

*Acr3.a3* in ACBV89B229 (GSHO 1617); *Acr3.b3* in Burma Girl (GSHO 1071); *Acr2.am2* and *Acr3.an* in AB 1398 (CIho 14785); *Acr3.an* from AB 1398 in Bowman*5 (BW438, NGB 20670); *Acr3.b3* from Burma Girl in Bowman *2 (GSHO 1898); *Acr3.b3* in Bowman*5 (BW007, NGB 20415); *Acr3.am3* from AB 1398 in Bowman*4 (BW456, NGB 20688); *Acr3.a3* plus *acr1.a* and *Acr2.a2* in Bowman*7 (BW009, NGB 20417 and BW439, NGB 20671); *Acr3.c3* in T188 (GSHO 1480); *Acr3.c3* from T188 in Bowman*6 (BW008, NGB 20416).

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Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:85-86.

Revised:

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:105-106.

# BGS 258, Dense spike 9, *dsp9*

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (3).

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

Description:

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

Origin of mutant:

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

Mutational events:

*dsp9.i* (OUM113, GSHO 1774) in Akashinriki (OUJ659, PI 467400) (3); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118) in Akashinriki (5).

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

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

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:107-108.

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

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

Previous nomenclature and gene symbolization:

Erectoides-17 = *ert-17* (3).
Dense spike = *la* (5).
Dense spike 9 = *l9* (5).
Dense spike 9 = *dsp9* (8).

Inheritance:

Monofactorial recessive (3, 5, 10).

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

Description:

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

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (3); an ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (5).

Mutational events:

*ert-e.17* (GSHO 477, NGB112619), *-e.65* (NGB 112664) in Bonus (NGB 14657, PI 189763) (2); *ert-e.94* (NGB 112693), *-e.143* (NGB 112742) in Bonus, *-e.331* (NGB112846), *-e.396* (NGB 114150) in Foma (NGB 14659, CIho 11333) (11); *dsp9.i* (OUM113) in Akashinriki (OUJ659, PI 467400) (5); *dsp9.j* (OUM106), *dsp9.k* (OUM107), *dsp9.l* (OUM115), *dsp9.m* (OUM118, GSHO 1774) in Akashinriki (7).

Mutant used for description and seed stocks:

*ert-e.17* (GSHO 477, NGB 112619) in Bonus; *ert-e.17* in Bowman (PI 483237)*6 (GSHO 2091); *ert-e.17* in Bowman*7 (BW307, NGB 22103); *dsp9.i* (GSHO 1774) in Akashinriki; *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090, BW279, NGB 20563).

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Prepared:

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Revised as BGS 258:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 2007. Barley Genet. Newsl. 37:257-258.
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:118-119.
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# BGS 275, Leafless 1, *lfl*

Stock number: BGS 275
Locus name: Leafless 1
Locus symbol: *lfl1*

Previous nomenclature:

Leafless = *lfl* (3).
Leafless 1.a = *lfs1.a* (1).
Leafless 2.b = *lfs2.b* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosomes 6HL (1, 2); *lfl1.b* is associated with SNP markers 1_0297 to 1_0128 (positions 85.71 to 180.85 cM) in 2H bins 07 to 11, with SNP markers 1_0676 to 1_1534 (positions 44.96 to 180.69 cM) in 6H bins 03 to 11, and with SNP markers 2_0247 to 2_1223 (positions 159.73 to 198.70 cM) in 7H bins 09 to 12 of the Bowman backcross-derived line BW477 (1); the $F_2$-derived line for *lfl1.a* (BW476) contains many markers from GSHO 609, but donor parents SNP markers were retained in both BW lines only in the long arm of chromosome 6H (1, 2).

Description:

The leafless 1 mutants are characterized by a reduction in the size of leaf blades. Leaf blades on lower culm phytomers are normal while those associated with upper phytomers of the culm are gradually shortened until the blade of the flag leaf is commonly less than 2 to 3 cm in length. Other morphological traits appear unaffected by the *lfl1* mutant (2, 4). The original leafless mutant (GSHO 609) showed a much stronger reduction in leaf blade development with only a few partially developed leaf blades on lower culm leaf sheathes. The nearly complete loss of leaf blades was associated with numerous tillers of which only a few elongating and producing spikes (2). The second leafless mutant *lfl1.b* could be an allele based on phenotypic in the BW lines, but allelism tests have not been conducted (2).

Origin of mutant:

An induced mutant (KM 255, GSHO 609) in Kanto Bansei Gall [this cultivar likely is Golden Melon (OUJ818, CIho 958)] based on notes from T. Tsuchiya (3).

Mutational events:

*lfl1.a* in Golden Melon (OUJ818, CIho 958) from Okayama University, Kurashiki, Japan (3); *lfl1.b* in an unidentified breeding line, which likely originated from KM 255, from the Institute of Plant Science and Resources, Okayama University, Kurashiki, Japan (4).

Mutant used for description and seed stocks:

*lfl1.a* (KM 255, GSHO 609) in Golden Melon (OUJ818, CIho 958); *lfl1.b* in an unidentified breeding line; *lfl1.a* from GSHO 609 in Bowman (PI 483237)*1 (BW 476, NGB 22155); *lfl1.b* from an unidentified breeding line in Bowman*2 (BW 477, NGB 22156).

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4. Takeda, K. (Personal communications).

Prepared:

J.D. Franckowiak 2017. Barley Genet. Newsl. 47:111-112.

# BGS 314, Six-rowed spike 2, *vrs2*

| | |
|---|---|
| Stock number: | BGS 314 |
| Locus name | Six-rowed spike 2 |
| Locus symbol: | *vrs2* |

Previous nomenclature and gene symbolization:

Six-rowed spike 2 = *v2* (10).

Intermedium-b = *int-b* (6, 7, 13).

Inheritance:

Monofactorial recessive (4, 5, 6, 8, 12).

Located in chromosome 5HL (10, 11); *vrs2.e* is over 19.0 cM proximal from the *srh1* (short rachilla hair 1) locus (10, 11, 12); *vrs2.e* is associated with SNP markers 2_1421 to 1_0477 (positions 159.51 to 173.49 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW901 (1); *int-b.3* is near the *raw1* (smooth awn 1) locus based on linkage drag (3); *int-b.3* is associated with SNP markers 2_0134 to 2_1355 (positions 163.29 to 234.98 cM) in 5H bins 10 to 13 of the Bowman backcross-derived line BW420 (1), likely in 5H bin 10. A high-resolution genetic map of the *vrs2* locus was developed using recombinants and barley BACs (13).

Description:

The spike appears similar to the ordinary six-rowed spike, but the lateral spikelets on the upper and lower portion of the spike are reduced in size, less fertile, and more or less pedicellated. Lateral spikelets are pointed with reduced awn length or awnless (4, 11, 12). Kernels of the Bowman backcross-derived line for *vrs2.e*, BW901, were 15 to 20% lighter than kernels of Bowman. BW901 plants exhibited reduced tillering and grain yield was about half that of Bowman (2). Plants of the backcross derived line for *int-b.3*, BW420, headed 2 to 3 days earlier than Bowman, but more lodging was observed. The BW420 kernels were slightly longer, but weighed less, 52 vs. 58 mg, compared to those of Bowman. Grain yields of BW420 were 10 to 30% of those recorded for Bowman (3). Late heading and prolonged development of BW901 was reported in Germany (13), but this was not observed in field tests in Australia, England, New Zealand, or the USA (3). During barley inflorescence and shoot development, the gene at the *Vrs2* locus encodes for a SHORT INTERNODES (SHI) transcriptional regulator (13).

Origin of mutant:

*vrs2.e* is an X-ray induced mutant in Svanhals (PI 5474, GSHO 784, OUU032) (10, 12); *int-b.3* is a neutron induced mutant in Bonus (NGB 14657, PI 189763) (9).

Mutational events:

*vrs2.e* (Kmut 27, OUM284, GSHO 773) in Svanhals (PI 5474, GSHO 784, OUU032) (12); *int-b.3* (NGB 115421, GSHO 1764)*, -b.6* (NGB 115424) in Bonus (NGB 14657, PI 189763) (6, 8); *int-b.75* (NGB 115493) in Bonus (8); HOR19366 in the Genebank of the Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany. (isolated as spontaneous mutant in a cultivated landrace collection from USA) (13).

Mutant used for description and seed stocks:

*vrs2.e* (Kmut 27, GSHO 773, OUM284) in Svanhals; *vrs2.e* in Bowman (PI 483237)*4 (GSHO 2111), *vrs2.e* in Bowman*6 (BW901, NGB 22333); *int-b.3* (NGB 115421, GSHO 1764) in Bonus; *int-b.3* in Bowman (PI 483237)*6 (GSHO 2129); *int-b.3* in Bowman*7 (BW420, NGB 20653).

References:

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Prepared:

T. Fukuyama. 1983. Barley Genet. Newsl. 13:112.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:263.

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:113-114.

# BGS 315, Six-rowed spike 3, *vrs3*

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|---|---|
| Stock number: | BGS 315 |
| Locus name: | Six-rowed spike 3 |
| Locus symbol: | *vrs3* |

Previous nomenclature and gene symbolization:

Six-rowed spike 3 = *v3* (5).
Intermedium spike-a = *int-a* (8, 9, 12, 17).
Intermedium spike-g = *int-g* (8, 9, 14).

Inheritance:

Monofactorial recessive (5, 7, 8, 12, 14).

Located in chromosome 1HL (6, 10, 18); *int-a.2* is near the centromere and proximal from the *ert-b* (erectoides-b) locus (10, 18); *int-a.1* is associated with SNP markers 2_0619 to 1_1361 (positions 50.96 to 82.35 cM) in 1H of the Bowman backcross-derived line BW419 (2); *vrs3.f* is associated with SNP markers 1_0575 to 1_0075 (positions 37.21 to 82.35 cM) in 1H of the Bowman backcross-derived line BW902 (2); *int-a*.1 is located between molecular markers 1_0520 and 2_1217 [82.35 to 81.26 cM based on the scale in (2)] in 1H bin 08 (1); only one gene, MLOC_69611.1 located at 47.52 cM, carried a unique mutation in both BW419 (*int-a.1*) and BW902 (*vrs3.f*) (1, 3).

Description:

The upper half of the spike appears six-rowed, but lateral spikelets in the lower half are reduced in size. The basal portion of the spike appears two-rowed. Awns on the lateral spikelets range from normal near the top, to awnletted or pointed in the middle, to awnless at the base of the spike. Seeds may develop in lateral spikelets of only the upper two-thirds of the spike. Lateral spikelets may be pedicellated in some stocks. Central spikelets often have double awns, one on the lemma and one on the palea. The rachilla may be deformed (5, 6, 7, 8, 14, 16). In Bowman backcross-derived lines for *int-a.1* and *vrs3.f*, BW419 and BW902 respectively, plants were often slightly shorter, rachis internodes were slightly longer, and kernels were thinner than those of Bowman. Kernel weights for BW419 ranged from 70 to 85% of normal compared to only 60 to 75% for those of BW902. Grain yields of Bowman lines BW419 and BW902 were often lower than those of Bowman (4). Compared to Bowman, BW419 and BW902 had more kernels per spike, but tiller numbers and seed weights were reduced (11). The VRS3 gene encodes a putative histone Lys demethylase with a conserved zinc finger and Jumonji C and N domain (1, 3). Comparative transcriptome analysis of the row-type mutants at the *Vrs3*, *Vrs4*, and *Int-c* (*Vrs5*) loci confirmed that all three genes act as transcriptional activators of *Vrs1* variants and produce quantitative variation in the expression levels of VRS1 and differences in the number of developed lateral spikelets (3). The naturally occurring variants *Vrs3.w* (Haplotype 45) and *Vrs3.x* (Haplotype 46) were identified as present predominantly in two-rowed spring barleys and six-rowed winter barleys, respectively (1), and could explain the row-type associations with winter and spring growth habit (1, 15, 19). Combining a *vrs3* mutant allele (*int-a.1* or *vrs3.f*) with natural six-rowed alleles of *vrs1* and *vrs5* (*int-c*) loci leads to increased lateral grain size and greater grain uniformity (1).

Origin of mutant:

A gamma-ray induced mutant in Hakata 2 (OUJ807, PI 263407) (5, 7); an X-ray induced mutant in Bonus (NGB 14657, PI 189763) (12).

Mutational events:

*vrs3.f* (Kmut 213, OUM292, GSHO 774) in Hakata 2 (OUJ807, PI 263407), *vrs3.g* (Xb 388.8, Piro-1), *vrs3.h* (Xd 160.46, Piro-3), *vrs3.i* (X15 1463, Piro-5), *vrs3.j* (X17 3555, Piro-8) in Piroline (PI 539132) (7); *int-a.1* (NGB 115419) in Bonus (NGB 14657, PI 189763) (13); *int-a.2* (NGB 115420) in Bonus (14, 17); *int-a*.8 (NGB 115426)*,-a.9* (NGB 115427)*, -a.10* (NGB  115328)*, -a.64* (NGB 115482) in Bonus, *-a.14* (NGB 115432)*, -a.17* (NGB 115435)*, -a.21* (NGB 115439)*, -a.27* (NGB 115445)*, -a.30* (NGB 115448)*, -a.31* (NGB 115449)*, -a.32* (NGB 115450)*, -a.34* (NGB 115452)*, -a.35* (NGB 115453)*, -a.37* (NGB 115455) in Foma (NGB 14659, CIho 11333), *-a.46* (NGB 115464)*, -a.51* (NGB 115469)*, -a.52* (NGB 115470)*, -a.54* (NGB 115472)*, -a.55* (NGB 15473)*, -a.59* (NGB 115477)*, -a.61* (NGB 115479) in Kristina (NGB14661, NGB 1500) (14); *int-a.71* (NGB 115489)*, -a.74* (NGB 115492)*, -a.77* (NGB 115495)*, -a.79* (NGB 115497)*, -a.86* (NGB 115504)*, -a.88* (NGB 115506) in Bonus, *-a.102* (NGB 115529)*, -a.103* (NGB 115521) in Hege (NGB 13692) (13); wildtype alleles *Vrs3.w* [Haplotype 45 in Morex (CIho 15773)] and *Vrs3.x* [Haplotype 46 in Bowman (PI 483237)] were present predominantly in two-rowed spring barleys and six-rowed winter barleys, respectively (1).

Mutant used for description and seed stocks:

*vrs3.f* (GSHO 774) in Hakata 2; *int-a.1* (GSHO 170, NGB 115419) in Bonus; *vrs3.f* in Bowman (PI 483237)*7 (GSHO 2056, BW902, NGB 22334); *int-a.1* in Bowman*5 (GSHO 2055); *int-a.1* in Bowman*7 (BW419, NGB 20652).

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# BGS 320, Intermedium spike-b, *int-b*

| | |
|---|---|
| Stock number: | BGS 320 |
| Locus name: | Intermedium spike-b |
| Locus symbol: | *int-b* |

Revised locus symbol:

The *int-b* mutants are alleles at the *vrs2* (six-rowed spike 2) locus based on DNA sequencing (9). Although phenotypic expression of spike type is somewhat between *int-b* and *vrs2* in Bowman backcross-derived lines BW420 and BW901, respectively (4), SNP molecular marker are retained in the same region of 5HL in both lines (3). See BGS 314 for more information about the alleles at the *vrs2* locus.

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (6, 7).

Located in chromosome 5HL (5); *int-b.3* is near the *raw1* (smooth awn 1) locus based on linkage drag (5); *int-b.3* is associated with SNP markers 2_0134 to 2_1355 (positions 163.29 to 234.98 cM) in 5H bins 10 to 13 of the Bowman backcross-derived line BW420 (3), likely in 5H bin 10.

Description:

The spike appears similar to the six-rowed spike, but developmental irregularities occur commonly in the lower portion of the spike. All lateral spikelets are reduced in size, and their lemma awns are short or reduced to a pointed tip. Commonly, only lateral spikelets in the middle of the spike set seed (6, 9). Plants of the Bowman backcross-derived line for *int-b.3*, BW420, showed reduced vigor and tillering (1). Plants of BW420 headed 2 to 3 days earlier than Bowman, and more lodging was observed. The BW420 kernels were slightly longer, but weighed less, 52 vs. 58 mg, compared to those of Bowman. Grain yields of BW420 were 10 to 30% of those recorded for Bowman (4). Combining the *int-b.3* and *cul2.b* (uniculm 2) mutants produced uniculm plants having spikes without spikelets (1). The double mutant combination, *int-b.3* and low number of tillers 1 (*lnt1.a*), produced uniculm plants (2). The *Vrs2* (*Int-b*) locus encodes for a SHORT INTERNODES (SHI) transcriptional regulator during barley inflorescence and shoot development (10).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (9).

Mutational events:

*int-b.3* (NGB 115421, GSHO 1764), *-b.6* (NGB 115424) in Bonus (NGB 14657, PI 189763) (6, 9); *int-b.75* (NGB 115493) in Bonus (8).

Mutant used for description and seed stocks:

*int-b.3* (NGB 115421, GSHO 1764) in Bonus; *int-b.3* in Bowman (PI 483237)*6 (GSHO 2129); *int-b.3* in Bowman*7 (BW420, NGB 20653).

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# BGS 328, Breviaristatum-e, *ari-e*

Stock number: BGS 328
Locus name: Breviaristatum-e
Locus symbol: *ari-e*

Previous nomenclature and gene symbolization:

Breviaristatum-1 = *ari-1* (6, 7).
Short awn 9 = *lk9* (20).
Golden Promise erectoides = *GPert* (19).
*Hordeum vulgare* dense and erect panicle 1 = *Hvdep1* (21).

Inheritance:

Monofactorial recessive (6).

Located in chromosome 5HL (12, 13, 14, 15, 19); *ari-e.1* is about 5.6 cM proximal from the *cer-zj* (eceriferum-zj) locus (17, 18); *ari-e.GP* is near SSR molecular marker Bmag337 (3); *ari-e.GP* is close to SNP marker 2_1239 (11); *ari-e.1* is associated with SNP markers 2_1480 and 3_0285 (position 137.96 cM) in 5H bin 08 of the Bowman backcross-derived line BW042 (1); *ari-e.GP* is associated with SNP markers 1_1198 to 2_0449 (positions 73.70 to 154.37 cM) in 5H bins 02 to 09 of the Bowman backcross-derived line BW043 (1), in 5H bin 06. The *ari-e* locus is positioned at 52.30 cM on the barley physical map (9. 22). The *ari-e.GP* gene was fine mapped to a 0.58 Mb interval on the POPSEQ physical map (7).

Description:

Awns are about 2/3 normal length, plants are 3/4 to 5/6 normal height, and kernels are smaller (8, 19). Awns and spikes are more erect than those of normal sibs (4). Mutant alleles at the *ari-e* locus are associated with salt tolerance, lower accumulation of $Na^+$ (2, 3, 12), and show relative insensitivity to $GA_3$ (12). The *ari-e.GP* mutant is described as an elongation (*elo*) type of semidwarf mutant based on cell size reduction in leaf blades (2). Plants of the Bowman backcross-derived lines for *ari-e.1* (BW042) and *ari-e.GP* (BW043) are about 3/4 as tall as Bowman and have awns that are about half as long. Rachis internodes and leaf blades are slightly shorter. Kernels of BW042 and BW043 were about 10% shorter than those of Bowman and weighed about 10% less. Grain yields of BW042 and BW043 were often less than those of Bowman (5). The *ari-e.GP* mutant compared to Maythorpe headed 1.5 days earlier. The effect of the *ari-e.GP* mutant on grain yield per plant was greater in Bowman genetic background than in Maythorpe background (22). The *ari-e* mutants are loss-of-function mutations in the *Hordeum vulgare* dense and erect panicle 1 (*HvDep1*) gene, an Arabidopsis heterotrimeric G protein (AGG3)-type γ-subunit encoding gene that regulates culm elongation and seed size (22). The *HvDep1* coding sequence consists of five exons and four introns (22).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (8).

Mutational events:

*ari-e.1* (NGB 115846, GSHO 1653) in Bonus (NGB 14657, PI 189763) (8); *ari-e.30* (NGB 115879), *-e.39* (NGB 115889) in Bonus (10); *ari-e.119* (NGB 115931), *-e.156* (NGB 115966) in Foma (NGB 14659, CIho 11333) (8); *ari-e.166* (NGB 115976), *-e.178* (NGB 115988), *-e.222* (NGB 116301) in Foma (10); *ari-e.228* (NGB 116038) in Foma (8); *ari-e.GP* (Golden Promise, PI 343079, GSHO 1733) in Maythorpe (PI 260893) (3, 4, 16), but PI 260893 has three genomic regions that differ from Golden Promise (21). Based on DNA sequencing of the *HvDep1* gene, the *ari-e.178*, *ari-e.222*, and *ari-e.228* mutants could not be confirmed as being *ari-e* mutants (22).

Mutant used for description and seed stocks:

*ari-e.1* (NGB 115846, GSHO 1653) in Bonus; *ari-e.GP* in Maythorpe (GSHO 1733); *ari-e.1* in Bowman (PI 483237)*7 (GSHO 2104, BW042, NGB 20450); *ari-e.GP* from Golden Promise in Bowman*7 (GSHO 2105, BW043, NGB 20451).

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Revised:

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:131-132.
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# BGS 332, Erectoides-r, *Ert-r*

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|---|---|
| Stock number: | BGS 332 |
| Locus name: | Erectoides-r |
| Locus symbol: | *Ert-r* |

Revised locus symbol:

The *Ert-r.52* mutant is an allele at the *Zeo1* (Zeocriton 1) locus based on phenotypic expression and retained SNP markers in 2HL of the Bowman backcross-derived lines BW 322 with *Ert-r.52*, the BW937 line with *Zeo1.a*, and the BW938 line with *Zeo1.b* (1) and DNA sequencing of the *HvAP2* gene (5). Historically, the recommended locus symbol is *Zeo1* based on descriptions by Hayes and Harlan (4). See BGS 082 for more information the alleles at the *Zeo1* locus.

Previous nomenclature and gene symbolization:

Erectoides-52 = *ert-52* (2).

*Hordeum vulgare APELATA2* (*AP2*)-like transcription factor = *HvAP2* (5).

Inheritance:

Monofactorial incomplete dominant (3).

Located in chromosome 2HL (1); *Ert-r.52* is associated with SNP markers 2_0715 to 1_0551 (positions 213.08 to 221.70 cM) in 2HL of the Bowman backcross-derived line BW322, in 2H bin 13 (1).

Description:

Spikes are compact in heterozygotes and very compact in homozygotes, with rachis internode length values from 1.4 to 1.8 mm. Homozygotes are about 2/3 normal height with excellent vigor. The glumes associated with lateral spikelets are 3 to 4 times larger than normal. Lodicule size is reduced (8). Heterozygotes are intermediate in plant height, have slightly more lax spikes, and have normal glumes in lateral spikelets (8). $GA_3$ treatment of plants as the flag leaf emerges decreases spike density (9). DNA sequencing showed that the *Zeo1* mutants occur in a *Hordeum vulgare* APELATA2 (*AP2*)-like transcription factor, *HvAP2*. The dense spike and cleistogamous (small lodicules) phenotypes are a consequence of a perturbed interaction between microRNA 172 (*Hv-miR172*) and its corresponding binding site on the mRNA from the *HvAP2* gene, which acts early in spike development to regulate turnover of *HvAP2* mRNA (5, 7).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (2).

Mutational events:

*Ert-r.52* (NGB 112651, GSHO 492), *-r.67* (NGB 112666) in Bonus (NGB 14657, PI 189763), *-r.329* (NGB 112844) in Foma (NGB 14659, CIho 11333) (8); *Ert-r.453* (NGB 112968) in Foma (6). *Ert-r.52* and *Ert-r.67* have the same basepair change in the *HvAP*2 locus and are identified as *Zeo1.b* mutants (5).

Mutant used for description and seed stocks:

*Ert-r.52* (GSHO 492, NGB 112651) in Bonus; *Ert-r.52* in Bowman (PI 483237)*8 (GSHO 2123, BW322, NGB 22117).

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Revised:

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:135-136.
U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:123-124.

# BGS 352, Glossy sheath 2, *gsh2*

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|---|---|
| Stock number: | BGS 352 |
| Locus name: | Glossy sheath 2 |
| Locus symbol: | *gsh2* |

Previous nomenclature and gene symbolization:

Glossy sheath 2 = *gs2* (21, 23).

Eceriferum-b = *cer-b* (9, 23).

Inheritance:

Monofactorial recessive (9, 20).

Located in chromosome 3HL (2, 4, 22); *gsh2.f* is about 5.1 cM proximal from the *als1* (absent lower laterals 1) locus (5, 6); *gsh2.f* is over 32.5 cM distal from the *uzu1* (uzu 1) locus (2, 5, 6); *gsh2.f* is associated with SNP markers 2_1161 to 1_0584 (positions 169.94 to 178.12 cM) in 3H bin 11 of the Bowman backcross-derived line BW405; *cer-b.2* is associated with SNP markers 22_1513 to 1_1172 (positions 190.97 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW107 (1); *gsh2* variants mapped at position 96.6 cM in 3H (19) in the POPSEQ map (17); the *cer-b.2* mutant mapped to a 1.3-cM interval flanked by SNP markers MLOC_10972 and MLOC_69561 (24), in 3H bin 11.

Description:

Surface wax coating appears absent on the spike, leaf sheath, and stem (wax code - - ++) (9, 20). The nodes of mutant plants are covered with surface wax (7). The Bowman backcross-derived lines for the *gsh2* mutants, BW107 with *cer-b.2* and BW405 with *gsh2.f*, had agronomic traits similar to those of Bowman, but grain yields were slightly lower (3). The *cer-b.2* mutant caused major changes in the composition of surface waxes on the leaf sheath and deficiency in the cuticular wax component 14,16-hentriacontanedione (24).

Origin of mutant:

Spontaneous occurrence in Vantage (CIho 7324) (18); an X-ray induced mutant in Maja Abed (NGB 8815, PI 184884) (9).

Mutational events:

*gsh2.d* in Vantage (CIho 7324), *gsh2.e* in Ymer (NGB 14860. CIho 7275), *gsh2.f* (GSHO 736), *gsh2.g* in Atlas (CIho 4118), *gsh2.h* in Klargrin (18); *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja Abed (NGB 8815, PI 184884) (7, 8, 9, 22); *cer-b.4* (NGB 110888 ), *-b.64* (NGB 110948), *-b.66* (NGB 110950), *-b.109* (NGB 110994 in Bonus (NGB 14657, PI 189763) (9, 10); *cer-b.79* (NGB 110963), *-b.94* (NGB 110978), *-b.96* (NGB 110980) in Bonus, *-b.209* (NGB 111096), *-b.222* (NGB 111109), *-b.319* (NGB 111206), *-b.336* (NGB 111223), *-b.337* (NGB 111224), *-b.377* (NGB 111264), *-b.418* (NGB 111306), *-b.424* (NGB 111312), *-b.427* (NGB 111315) in Foma (NGB 14659, CIho 11333) (10, 16); *cer-b.169* (NGB 111055), *-b.193* (NGB 111079) in Bonus, *-b.412* (NGB 111300), *-b.531* (NGB 111419), *-b.549* (NGB 111437) in Foma, *-b.1037* (NGB111925), *-b.1059* (NGB 111947) in Carlsberg II (NGB 5085, CIho 10114) (10); *cer-b.751* (NGB 111639), *-b.769* (NGB 111657), *-b.791* (NGB 111679), *-b.799* (NGB 111687), *-b.800* (NGB 111688) in Bonus, *-b.1129* (NGB 112017) in Kristina (NGB 1500, NGB 14661) (10); *cer-b.910* (NGB 111798) in Bonus (12); *cer-b.932* (NGB 111820) in Bonus (13); *cer-b.147* (NGB 111033), *-b.182* (NGB 111068), *-b.623* (NGB 111511) in Bonus, *-b.1099* (NGB 111987), *-b.1267* (NGB 112155), *-b.1269* (NGB 112157) in Kristina (14);

*cer-b.1699* (NGB 119343) in Bonus (15); *gsh2.ab* (OUM019), *gsh2.ah* (OUM025) in Akashinriki (OUJ659, PI 467400) (4, 6); *gsh2.bb* in the cross NDB112/Fr926-77 (3); *gsh2.bd* in Ms13551 and *gsh2.be* in PI 282610 both in *Hordeum vulgare* subsp. *spontaneum* (1, 3); *gsh2* variants in *H. vulgare* ssp. *spontaneum* accessions WBDC032, WBDC035, and WBDC348 (19).

Mutant used for description and seed stocks:

*gsh2.f* (GSHO 736) in Atlas; *cer-b.2* (NGB 110886, GSHO 434; GSHO 1081) in Maja Abed (NGB 8815, PI 184884); *gsh2.f* in Bowman (PI 483237)*7 (GSHO 1988); *gsh2.f* in Bowman*8 (BW405, NGB 20678); *cer-b.2* in Bowman*6 (GSHO 1989); *cer-b.2* in Bowman*7 (BW107, NGB 20513): *gsh2.bd* from Ms13551in Bowman*4 (BW402, NGB 22150); *gsh2.be* from PI 282610 in Bowman*7 (BW403, NGB 22151).

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# BGS 355, Glossy sheath 5, *gsh5*

| | |
|---|---|
| Stock number: | BGS 355 |
| Locus name: | Glossy sheath 5 |
| Locus symbol: | *gsh5* |

Previous nomenclature and gene symbolization:

Glossy sheath 5 = *gs5* (15).
Eceriferum-s = *cer-s* (5, 13).
Glossy sheath 8 = *gs8* (17).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 2HL (15, 16, 17, 19); *gsh5.m* is located in the centromeric region about 2.5 cM proximal from the *eog1* (elongated outer glume 1) locus (15, 17); *gsh5.m* is about 32.0 cM proximal from the *vrs1* (six-rowed spike 1) locus (15, 17); *gsh5.m* is associated with SNP markers 1_0851 to 2_1437 (positions 81.43 to 113.28 cM) in 2H bins 06 to 08 of the Bowman backcross-derived line BW408 (2); *cer-s.31* is associated with SNP markers 1_0796 to 2_0528 (positions 95.53 to 118.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW122 (2), in 2H bin 07.

Description:

Mutants have a reduced surface wax covering on the spikes and stems, and a bright glossy green color on all leaf sheaths (15) (wax code + - ++) (5). The nodes appear to have an excessive wax covering (4). The Bowman backcross-derived line with the *cer-s.31* allele, BW122, headed 2 to 4 days later than BW408 with the *gsh5.m* allele and Bowman (4). BW122 also had 3 to 6 more kernels per spike. Kernels of BW122 and BW408 were about 10% lighter than those of Bowman. The grain yields of BW408 were often slightly lower than those of Bowman or BW408 (4). The differences in maturity and number of kernels per spike between BW122 and BW408 were attributed to close linkage between alleles at the *gsh5* locus and those at the *Eam6* [Early maturity 6, Earliness per se 2S (*eps2S*), Praematurum-c (*mat-c*), or *Hordeum vulgare CENTRORADIALIS* (*HvCEN*)**]** locus (1, 4).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (5); a radiation induced mutant in Jotun (PI 467357) (15); a spontaneous mutant in Okaiku 3 (OUL011) (18).

Mutational events:

*cer-s.24* (NGB 110908) in Bonus (NGB 14657, PI 189763) (5); *cer-s.31* (NGB 110915, GSHO 440) in Bonus (3, 5); *cer-s.41* (NGB 110925) in Bonus (5); *cer-s.287* (NGB 111174), *-s.303* (NGB 111190), *-s.372* (NGB 111259), *-s.444* (NGB 111332) in Foma (NGB 14659, CIho 11333) (13); *cer-s.1047* (NGB 111935) in Carlsberg II (NGB 5085, CIho 10114) (6); *cer-s.137* (NGB 111022) in Bonus, *-s.591* (NGB 111479) in Foma, *-s.803* (NGB 111691) in Bonus, *-s.1132* (NGB 112020) in Kristina (NGB 14661, NGB 1500) (7); *cer-s.914* (NGB 111802) in Bonus (8); *cer-s.622* (NGB 111510) in Bonus, *-s.1054* (NGB 111942) in Carlsberg II, *-s.1153* (NGB 117264) in Kristina (9); *cer-s.1323* (NGB 112211) in Bonus (10); *cer-s.1134* (NGB 112022) in Kristina (11); *cer-s.1754* (NGB 112568) in Bonus (12); *gsh5.m* (GSHO 739) in Jotun (PI 467357) (15); *gsh5.n* (GSHO 832) in Okaiku 3 (OUL011) (14, 18).

Mutant used for description and seed stocks:

*gsh5.m* (GSHO 739) in Jotun; *cer-s.31* (NGB 110915, GSHO 440) in Bonus; *cer-s.31* in

Bowman (PI 483237)*5 (GSHO 1888); *cer-s.31* in Bowman*8 (BW122, NGB 20528); *gsh5.m* in Bowman*8 (GSHO 1889, BW408, NGB 20641).

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# BGS 402, Eceriferum-g, *cer-g*

| | |
|---|---|
| Stock number: | BGS 402 |
| Locus name: | Eceriferum-g |
| Locus symbol: | *cer-g* |

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HL (2, 14); *cer-g.10* is about 15.9 cM distal from the *vrs1* (six-rowed spike 1) locus (14, 15); *cer-g.10* is associated with SNP markers 1_0317 to 2_0374 (positions 98.35 to 104.81 cM) in 2H bin 08 and SNP markers 1_0619 to 1_0533 (positions 133.59 to 141.56 cM) in 2H bin 09 of the Bowman backcross-derived line BW111 (1), in 2H bin 08.

Description:

Mutants have reduced surface wax coating on spike, leaf sheath, and stem (wax code + + ++) with the wax coating of the leaf sheath and stem wax present in broad horizontal bands (4). Double and triple stomatal complexes are produced during stomatal development (4, 16). All *cer-g* mutants have globe-shaped or globosum kernels (4). Plants of the Bowman backcross-derived line for *cer-g.10*, BW111, headed 1 to 2 days later than Bowman and were about 10% shorter. Kernels of BW111 were shorter (8.2 vs. 9.5 mm), narrower (3.5 vs. 3.8 mm) and weighed 15 to 20% less. Grain yields of BW111 were 2/3 to 3/4 of those for Bowman (3).

Origin of mutant:

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

Mutational events:

*cer-g.10* (NGB 110894, GSHO 428), *-g.11* (NGB 110895), *-g.23* (NGB 110907), *-g.47* (NGB 110931), *-g.55* (NGB 110939) in Bonus (NGB 14657, PI 189763) (4); *cer-g.106* (NGB 110991) in Bonus, *-g.202* (NGB 111089), *-g.208* (NGB 111095), *-g.210* (NGB 111097), *-g.494* (NGB 111382) in Foma (NGB 14659, CIho 11333) (13); *cer-g.166* (NGB 111052) in Bonus, *-g.553* (NGB 111441), *-g.568* (NGB 111456), *-g.700* (NGB 111588), *-g.709* (NGB 111597), *-g.710* (NGB 111598) in Foma, *-g.1026* (NGB 111914) in Carlsberg II (NGB 5085, CIho 10114) (5); *cer-g.746* (NGB 111634), *-g.818* (NGB 111706), *-g.875* (NGB 111763) in Bonus, *-g.1033* (NGB 111921), *-g.1071* (NGB 111959) in Carlsberg II, *-g.1097* (NGB 111985), *-g.1116* (NGB 112004) in Kristina (NGB 14661, NGB 1500) (6); *cer-g.893* (NGB 111781), *-g.976* (NGB 111864) in Bonus, *-g.1172* (NGB 112060) in Kristina (7); *cer-g.1161* (NGB 117265), *-g.1169* (NGB 112057) in Kristina (8); *cer-g.1038* (NGB 111926) in Carlsberg II, -*g.1289* (NGB 112177) in Kristina, *-g.1332* (NGB 112220) in Bonus (9); *cer-g.1410* (NGB 112298), *-g.1451* (NGB 112339), *-g.1454* (NGB 112342) in Bonus (10); *cer-g.1495* (NGB 112383) in Bonus, *-g.1510* (NGB 112398) in Nordal (NGB 13680, NGB 4704), *-g.1736* (NGB 112549), *-g.1740* (NGB 112553), *-g.1741* (NGB 112554) in Bonus (11); *cer–g.1573* (NGB 112461) in Nordal (12).

Mutant used for description and seed stocks:

*cer-g.10* (NGB 110894, GSHO 428) in Bonus; *cer-g.10* in Bowman (PI 483237)*6 (GSHO 1906); *cer-g.10* in Bowman*7 (BW111, NGB 20517).

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## BGS 439, Eceriferum-zv, *cer-zv*

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|---|---|
| Stock number: | BGS 439 |
| Locus name: | Eceriferum-zv |
| Locus symbol: | *cer-zv* |

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (6).

Located in chromosome 4HL (1, 3, 4); *cer-zv.268* is associated with SNP markers 2_1122 to 1_0568 (positions 47.80 to 78.18 cM) in 4H bins 05 to 06 of the Bowman backcross-derived line BW177 (1); *cer-ym.753*, a possible allele (4), is associated with SNP markers 2_0289 to 1_1513 (positions 69.62 to 101.44 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW144 (1); *cer-zv.268* and *cer-ym.753* are in a 0.8 cM interval between EST markers AK370363 and AK251484 in pericentromeric region of 4H (3, 4).

Description:

Surface wax coating on the spike, the leaf sheath and stem, and the leaf blade appears absent (wax code - - -) (6). Plants are semidwarf, very weak, and head late, and the hull is poorly attached to the kernel. The Bowman backcross-derived line for *cer-zv.268*, BW177, is a semidwarf (2/3 normal height) with a kinked upper peduncle and a strong wax coating on the nodes (2). Compared to Bowman, BW177 plants headed 2 to 10 days later in various environments. Plant height, peduncle length, and leaf blade length measurements were 1/2 to 2/3 those for Bowman. Awns were slightly shorter, but rachis internodes were slightly longer. Kernels of BW177 were shorter and thinner and weighed less, 3.5 vs. 5.8 mg, compared to Bowman kernels. Grain yields of BW177 averaged 10% those of Bowman (2). The *cer-ym.753* plants are weak, culms have a kinked peduncle, nodes are wax covered, and kernels are small, globe shaped, and nearly hulless (2, 5). Plants of the Bowman backcross-derived line for *cer-ym.753*, BW144, were phenotypically similar to BW177 plants, but they were more vigorous (2, 3, 4). Detached leaves of the mutant *cer-ym.753* lost 41.8% of their initial weight after 1 hour of dehydration under laboratory conditions, while that of the wild type Bowman plants lost only 7.1%. Stomata function was not affected by the mutation, but the mutant leaves showed increased cuticular permeability to water, suggesting a defective leaf cuticle, which was confirmed by toluidine blue staining. The *cer-ym.753* leaf blades showed a substantial reduction in the amounts of the major cutin monomers and a slight increase in the main wax component, suggesting that the enhanced cuticle permeability was a consequence of cutin deficiency (3, 4). Allelism tests demonstrated that mutants at the *cer-zv* and *cer-ym* loci are not alleles (5).

Origin of mutant:

An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (5).

Mutational events:

*cer-zv.268* (NGB 111155, GSHO 1529), *-zv.342* (NGB 111229), *-zv.576* (NGB 111464) in Foma (NGB 14659, CIho 11333) (6); *cer-zv.1256* (NGB 112144) in Kristina (NGB 14661, NGB 1500) (8); and based on location possibly *cer-ym.130,* (NGB 111015, GSHO 1546), *-ym.753* (NGB 111641) in Bonus (NGB 14657, PI 189763) (7).

Mutant for description and seed stocks:

*cer-zv.268* (NGB 111155, GSHO 1529) in Foma; *cer-zv.268* in Bowman (PI 483237)*5 (GSHO 2207); *cer-zv.268* in Bowman *7 (BW177, NGB 22009); *cer-ym.753* (NGB 111641, GSHO 1546) in Bonus; *cer-ym.753* in Bowman (PI 483237)*5 (GSHO 2217); *cer-ym.753* in Bowman*7 (BW144, NGB 20550).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Li, C., C. Liu, X. Ma, A. Wang, R. Duan, C. Nawrath, T. Komatsuda, and G. Chen. 2015. Characterization and genetic mapping of *eceriferum-ym* (*cer-ym*), a cutin deficient barley mutant with impaired leaf water retention capacity. Breed. Sci. 65:327-332.
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7. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. Barley Genet. Newsl. 7:92-96.
8. Lundqvist, U., and D. von Wettstein. 1979. Stock list for the eceriferum mutants V. Barley Genet. Newsl. 9:135-137.

Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:157.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:391.
U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:109-110.
U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:133-134.

# BGS 473, Compositum 1, *com1*

| | |
|---|---|
| Stock number: | BGS 473 |
| Locus name: | Compositum 1 |
| Locus symbol: | *com1* |

Previous nomenclature and gene symbolization:

Laxatum-270 = *lax-270* (5, 7, 9).

Short-haired, inflorescent rachilla = $s^i$ (7).

Branching, inflorescent rachilla = *bir1a* (8).

Compositum = *com1a* (9, 10, 11).

Inheritance:

Monofactorial recessive (7, 8, 9).

Located in chromosome 5HL (11, 12); *com1.a* is near the *srh1* (short rachilla hair 1) locus (12); *com1.a* is between the *ert-n* (erectoides-n) and the *lax-a* (laxatum-a) loci (11), but widely different estimates of their distance from the *srh1* (short rachilla hair 1) locus are reported (6, 11); *com1.a* is associated with SNP markers 1_0974 to 1_0641 (positions 41.99 to 108.33 cM) in 5H of the Bowman backcross-derived line BW189 (1); *com1.l* is associated with SNP markers 3_0745 to 1_0641 (positions 99.51 to 108.33 cM) in 5HL of the Bowman backcross-derived line BW605 (1), likely in 5H bin 06.

Description:

The spike is branched from the rachis of the bottom 1 to 10 spikelets. Awns, which vary from normal to thread-like and protruding branches, are bent in various directions because of "packing" problems in the boot (7). More spike branches develop from rachis nodes under favorable environmental conditions. Plants of Bowman backcross-derived lines BW189, BW190, and BW605 had slightly lower kernel weight and test weights compared to Bowman. The average kernel width was slightly reduced (3).

Origin of mutant:

An ethyl methanesulfonate and neutron induced mutant in Foma (NGB 14659, CIho 11333) (2, 7).

Mutational events:

*com1.a* (*lax.270*, NGB 116495, GSHO 1702), *com1.b* (*lax.271*, NGB 116496), *com1*.c (*lax.27*2, NGB 116497), *com1.d* (*lax.206*, NGB 116433), *com1.e* (*lax.213*, NGB 116442) in Foma (NGB 14659, CIho 11333) (9); *com1.i* (lax.296, NGB 116520, GSHO 1699) in Foma (3, 9); *com1.l* (*mul.c*, Mut. 2227, GSHO 2412) in Donaria (PI 161974) (3, 13).

Mutant used for description and seed stocks:

*com1.a* (NGB 116495, GSHO 1702) in Foma; *com1.a* in Bowman (PI 483237)*6 (GSHO 2098); *com1.a* in Bowman*7 (BW189, NGB 22021); *com1.i* (NGB 116520, GSHO 1699) in Foma; *com1.i* in Bowman*3 (GSHO 2232); *com1.i* in Bowman*5 (BW190, NGB 22022); *com1.l* (*mul.c*) in Donaria (GSHO 2412); *com1.l* in Bowman*6 (GSHO 2312); *com1.l* in Bowman*7 (BW605, NGB 22171).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
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10. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
11. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. Hereditas 103:269-279.
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Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:56.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:420.
U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:118-119.
U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:135-136.

## BGS 475, Laxatum-c, *lax-c*

| | |
|---|---|
| Stock number: | BGS 475 |
| Locus name: | Laxatum-c |
| Locus symbol: | *lax-c* |

Previous nomenclature and gene symbolization:

Laxatum-21 = *lax-21* (3, 4, 5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 6HL (6); *lax-c.21* is linked to a translocation breakpoint in chromosome 6HL (6); *lax-c.21* is over 27.3 cM distal from the *lax-b* (laxatum-b) locus (6); *lax-c.21* is associated with SNP markers 1_0015 to 1_1534 (positions 160.38 to 180.69 cM) in 6H bin 11 of the Bowman backcross-derived line BW460 (1); *lax-c.231* (*sld.l*) is associated with SNP markers 2_0783 to 1_1534 (positions 146.43 to 180.69 cM) in 6H bins 09 to 11 of the Bowman backcross-derived line BW858 (1).

Description:

The grain is thin and angular and caryopses are exposed between the lemma and palea. The awn has a very wide base. Rachis internodes are about 7% longer than normal. In the original Bonus stock, the tip of the spike is frequently sterile, and the tiller number is reduced (4). Plants of the Bowman backcross-derived line for *lax-c.21*, BW460, were 3/4 the height of Bowman. Rachis internodes of BW460 were slightly longer in some trials. The awns and peduncles of BW460 were slightly shorter than those of Bowman. Kernels were about 10% shorter and thinner and their weights were about 20% lighter, 4.8 mg vs. 5.7 mg, than those of Bowman. Grain yields were about 3/4 of those for Bowman (2). Plants of the Bowman backcross-derived line for *lax-c.231* (*sld.l*), BW858, were similar to those of BW460, except they had more pronounced spiral coiling of the neck and occasionally formed small branches on the awn (2).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4, 7).

Mutational events:

*lax-c.21* (NGB 116355, GSHO 1777)*, -c.23* (NGB 116358) in Bonus (NGB 14657, PI 189763) (4, 5); *lax.231* (*sld.l*, NGB 116459, GSHO 2478) in Foma (NGB 14659, CIho 11333) may be an allele based on phenotype and SNP markers retained in 6HL of its Bowman backcross- derived line, BW858 (NGB 22295) (1, 2)

Mutant used for description and seed stocks:

*lax-c.21* (NGB 116355, GSHO 1777) in Bonus; *lax-c.21* in Bowman (PI 483237)*6 (GSHO 2086); *lax-c.21* in Bowman*7 (BW460, NGB 20691); *lax-c.231* (*sld.l*) from Foma in Bowman*3 (GSHO 2359); *lax-c.231* in Bowman*6 (BW858, NGB 22295).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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5 Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.

6. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. Hereditas 103:269-279.

7. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:58.

Revised:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:423.

U. Lundqvist and J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:174.

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:137-138.

# BGS 476, Laxatum-d, *lax-d*

| | |
|---|---|
| Stock number: | BGS 476 |
| Locus name: | Laxatum-d |
| Locus symbol: | *lax-d* |

Previous nomenclature and gene symbolization:

Laxatum-83 = *lax-83* (3, 4).

Inheritance:

Monofactorial incomplete dominant (5).

Location is unknown.

Description:

Rachis internodes of *lax-d.83* were about 6% longer than those of Bonus (4). Plants were taller and relatively vigorous; and the kernels were comparatively long (4).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

*lax-d.2* (NGB 116336), *-d.27* (NGB 116362), *-d.83* (NGB 116415) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6, 7).

Mutant used for description and seed stocks:

*lax-d.2* (NGB 116336) and *lax-d.83* (NGB 116415) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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.
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Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:59.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:139.

# BGS 477, Laxatum-f, *lax-f*

| | |
|---|---|
| Stock number: | BGS 477 |
| Locus name: | Laxatum-f |
| Locus symbol: | *lax-f* |

Previous nomenclature and gene symbolization:

Laxatum-61 = *lax-61* (3, 4).

Inheritance:

Monofactorial dominant (5).

Location is unknown.

Description:

Rachis internodes of *lax-f.61* were about 14% longer than those of Bonus, and the mutants had lower kernel weights (4).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

*lax-f.7* (NGB 116341), *-f.61* (NGB 116395), in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6, 7).

Mutant used for description and seed stocks:

*lax-f.7* (NGB 116341) and *lax-f.61* (NGB 116395) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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4. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).
7. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:60.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:140.

# BGS 478, Laxatum-g, *lax-g*

Stock number: BGS 478
Locus name: Laxatum-g
Locus symbol: *lax-g*

Previous nomenclature and gene symbolization:

Laxatum-25 = *lax-25* (3, 4).

Inheritance:

Monofactorial incomplete dominant (5).

Location is unknown.

Description:

Rachis internodes of *lax-g.25* were about 8% longer than those of Bonus; and mutant plants exhibited tip sterility and reduced tiller numbers (4).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

*lax-g.25* (NGB 116360), *-g.59* (NGB 116393) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6, 7).

Mutant used for description and seed stocks:

*lax-g.25* (NGB 116360) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).
7. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. Hereditas 58:359-384.

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:61.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:141.

# BGS 479, Laxatum-h, *lax-h*

| | |
|---|---|
| Stock number: | BGS 479 |
| Locus name: | Laxatum-h |
| Locus symbol: | *lax-h* |

Previous nomenclature and gene symbolization:

Laxatum-26 = *lax-26* (5, 6).

Inheritance:

Monofactorial recessive (7).

Located possibly likely in chromosome 3H (1); *lax-h.26* is associated with SNP markers 2_1398 to 1_1172 (positions 13.67 to 190.87 cM) in 3H bins 01 to 12, with SNP markers 1_1061 to 1_1205 (positions 70.15 to 81.35 cM in 6H bins 05 to 06, and with SNP markers 2_1241to 2_0320 positions 159.51 to 166.29 cM) in 5H bins 09 to 10 of the Bowman backcross-derived line BW463 (1). The original *lax-h.26* mutant was previously associated with translocation testers involving chromosome arms 5HS and 6HL (8, 10).

Description:

Rachis internodes of *lax-h.26* were about 20% longer than those of Bonus (6). Spikes had some sterile spikelets; and kernels were relatively thin and angular (6). Plants of the Bowman backcross-derived line for *lax-h.26*, BW463, had rachis internodes that averaged 20% longer (5.4 vs. 4.5 mm). Compared to Bowman, BW463 had one to two more kernels per spike, and leaf blades were shorter and narrower. Kernels were longer (12.0 vs. 9.3 mm), wider (4.0 vs. 3.8 mm), and weighted about the same, but the test weight was much lower (5). Grain yields of BW463 were less than 1/4 those of Bowman (5).

Origin of mutant:

An X-ray induced mutant in Bonus (NGB 14657, PI 189763) (6, 9).

Mutational events:

*lax-h.26* (NGB 116361)*, -h.38* (NGB 116373) in Bonus (NGB 14657, PI 189763) (2, 3, 6, 7).

Mutant used for description and seed stocks:

*lax-h.26* (NGB 116361) in Bonus; *lax-h.26* in Bowman (PI 483237)*3 (BW463, NGB20693).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
4. Franckowiak, J.D. (Unpublished).
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
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7. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.

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Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:62.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:142-143.

# BGS 480, Laxatum-i, *lax-i*

| | |
|---|---|
| Stock number: | BGS 480 |
| Locus name: | Laxatum-i |
| Locus symbol: | *lax-i* |

Previous nomenclature and gene symbolization:

Laxatum-50 = *lax-50* (3, 4).

Inheritance:

Monofactorial recessive (5).

Location is unknown.

Description:

Rachis internodes of *lax-i.50* were about 18% longer than those of Bonus. The *lax-i.50* plants showed partial sterility, had coiled awns, and had small angular kernels (4).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

*lax-i.28* (NGB 116363), *-i.50* (NGB 116384) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-i.50* (NGB 116363) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:63.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:144.

# BGS 481, Laxatum-j, *lax-j*

Stock number: BGS 481
Locus name: Laxatum-j
Locus symbol: *lax-j*

Previous nomenclature and gene symbolization:

Laxatum-49 = *lax-49* (6, 7).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 2H (2); *lax-j.49* is associated with SNP markers 1_0399 to 2_0887 (positions 66.78 to 103.73 cM) in 2H bins 05 to 08 and a small segment of 3HL between markers 2_0944 and 1_1172 (positions 185.12 and 190.87 cM) in 3H bin 12 of the Bowman backcross-derived line BW465 (2).

Description:

Rachis internodes of *lax-j.49* were about 24% longer than those of Bonus (7). Plants produced few tillers, awns were slightly twisted, seed set was reduced, and kernels were angular (7). Plants of the Bowman backcross-derived line for *lax-j.49*, BW465, headed eight days later than Bowman and had rachis internodes that were about 30% longer (6.0 vs. 4.6 mm). Compared to Bowman, BW465 plants were slightly shorter, had slightly shorter awns and peduncles, had slightly longer and wider leaf blades, and had about three more kernels per spike (5). Kernels were long (10.3 vs. 9.2 mm), thin (3.4 vs. 3.9 mm), and weighed less (5.1 vs. 6.0 mg). The caryopsis was partially exposed between the lemma and palea. Grain yields of BW465 were about 1/3 those of Bowman (5). A portion of the delayed heading of BW465 could be attributed to the late allele at the Early maturity 6 (*Eam6*) or Praematurum-c (*mat-c*) locus, which was retained in the 2H segment from the donor parent Bonus (1, 2).

Origin of mutant:

An ethylene oxide induced mutant in Bonus (NGB 14657, PI 189763) (7, 9).

Mutational events:

*lax-j.29* (NGB 116364)*, -j 33* (NGB 116368), *-j.49* (NGB 116383) in Bonus (NGB 14657, PI 189763) (3, 4, 7, 8).

Mutant used for description and seed stocks:

*lax-j.49* (NGB 116383) in Bonus; *lax-j.49* in Bowman (PI 483237)*3 (BW465, NGB20695).

References:

1. Comadran, J., B. Kilian, J. Russell, L. Ramsay, N. Stein, M. Ganal, P. Shaw, M. Bayer, W. Thomas, D. Marshall, P. Hedley, A. Tondelli, N. Pecchioni, E. Francia, V. Korzun, A. Walther, and R. Waugh. 2012. Natural variation in a homolog of *Antirrhinum CENTRORADIALIS* contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genet. 44:1388-1392.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
4. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.

5. Franckowiak, J.D. (Unpublished).
6. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
7. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
8. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
9. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:64.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:145-146.

# BGS 482, Laxatum-k, *lax-k*

Stock number: BGS 482
Locus name: Laxatum-k
Locus symbol: *lax-k*

Previous nomenclature and gene symbolization:

Laxatum-84 = *lax-84* (3, 4).

Inheritance:

Monofactorial incomplete dominant (5).

Located in chromosomes 2H or 3H (6); *lax-k.84* is linked to the translocation breakpoint in translocation stock T2-3f (6).

Description:

Rachis internodes of *lax-k.84* were about 4% longer than those of Bonus. The *lax-k.84* plants had narrow, dark green leaf blades and very thin kernels (4).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB 14657, PI 189763) (4, 7).

Mutational events:

*lax-k.42* (NGB 116376), *-k.44* (NGB 116378), *k.84* (NGB 116416) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 7).

Mutant used for description and seed stocks:

*lax-k.84* (NGB 116416) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. Hereditas 103:269-279.
7. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:65.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:147.

# BGS 483, Laxatum-l, *lax-l*

Stock number: BGS 483
Locus name: Laxatum-l
Locus symbol: *lax-l*

Previous nomenclature and gene symbolization:

Laxatum-60 = *lax-60* (5, 6).

Inheritance:

Monofactorial recessive (7).

Located likely in chromosome 1H (1); *lax-l.60* is associated with SNP markers 1_0744 to 2_1126 (positions 39.84 to 110.10 cM) in 1H bins 03 to 10 and with small groups of SNP markers in chromosome arms 3HL and 7HS of the Bowman backcross-derived line BW468 (1).

Description:

Rachis internodes of *lax-l.60* were about 23% longer than those of Bonus (6). Spikes exhibited tip sterility, awns were slightly twisted, leaf blades were relatively broad, and kernels were large and angular (6). Plants of the Bowman backcross-derived line for *lax-l.60*, BW468, had visually longer rachis internodes (4).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (6, 8).

Mutational events:

*lax-l.60* (NGB 116394)*, -l.78* (NGB 116411) in Bonus (NGB 14657, PI 189763) (2, 3, 6).

Mutant used for description and seed stocks:

*lax-l.60* (NGB 116394) in Bonus; *lax-l.60* in Bowman (PI 483237)*2 (BW468, NGB 20698).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
4. Franckowiak, J.D. (Unpublished).
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
6. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
7. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
8. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:66.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:148.

# BGS 484, Laxatum-m, *lax-m*

| | |
|---|---|
| Stock number: | BGS 484 |
| Locus name: | Laxatum-m |
| Locus symbol: | *lax-m* |

Previous nomenclature and gene symbolization:

Laxatum-80 = *lax-80* (3, 4).

Inheritance:

Monofactorial recessive (5).

Location is unknown.

Description:

Rachis internodes of *lax-m.80* were about 16% longer than those of Bonus. The *lax-m.80* plants had light-green leaf blades, slightly coiled awns, and reduced kernel weights (4).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

*lax-m.65* (NGB 116398), *-m.80* (NGB 116413) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-m.80* (NGB 116413) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:67.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:149.

# BGS 485, Laxatum-n, *lax-n*

| | |
|---|---|
| Stock number: | BGS 485 |
| Locus name: | Laxatum-n |
| Locus symbol: | *lax-n* |

Previous nomenclature and gene symbolization:

Laxatum-67 = *lax-67* (6, 7).

Inheritance:

Monofactorial recessive (8).

Located in chromosomes 2H, 4HL, or 5H (2); *lax-n.67* is associated with SNP markers 2_1187 to 2_0887 (positions 51.62 to 103.73 cM) in 2H bins 05 to 08, with SNP markers 2_0496 to 2_11332 (positions 72.70 to 112.64 cM in 4H bins 05 to 07, and with SNP markers 2_0010 to 2_1244 (positions 28.11 to 91.91 cM) in 5H bins 02 to 05 of the Bowman backcross-derived line BW469 (2).

Description:

Rachis internodes of *lax-n.67* were about 4% longer than those of Bonus, the awns were coiled, leaf blades were narrow, and kernel weights were low (7). Plants of the Bowman backcross-derived line for *lax-n.67*, BW469, headed about three days later than Bowman and had rachis internodes that were slightly longer (4.8 vs. 4.5 mm). Compared to Bowman, BW469 plants had slightly shorter awns and had two to four more kernels per spike (5). Kernels weighed slightly less than those of Bowman (5.5 vs. 6.0 mg). The awns of BW469 plants were slightly twisted (5). The delayed heading of BW469 and greater number of fertile rachis could be caused by the presence of the late allele at the Early maturity 6 (*Eam6*) or Praematurum-c (*mat-c*) locus, which was retained in the 2H segment from the donor parent Bonus (1, 2).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (7, 9).

Mutational events:

*lax-n.67* (NGB 116400)*, -n.68* (NGB 116401) in Bonus (NGB 14657, PI 189763) (7, 8).

Mutant used for description and seed stocks:

*lax-n.67* (NGB 116400) in Bonus; *lax-n.67* in Bowman (PI 483237)*3 (BW469, NGB20699).

References:

1. Comadran, J., B. Kilian, J. Russell, L. Ramsay, N. Stein, M. Ganal, P. Shaw, M. Bayer, W. Thomas, D. Marshall, P. Hedley, A. Tondelli, N. Pecchioni, E. Francia, V. Korzun, A. Walther, and R. Waugh. 2012. Natural variation in a homolog of *Antirrhinum CENTRORADIALIS* contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genet. 44:1388-1392.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155*:*617-627.
3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
4. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
5. Franckowiak, J.D. (Unpublished).
6. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system

of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.

7. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.

8. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.

9. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:68.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:150-151.

*Barley Genetics Newsletter (2017): 46:50-187.*

# BGS 486, Laxatum-o, *lax-o*

| | |
|---|---|
| Stock number: | BGS 486 |
| Locus name: | Laxatum-o |
| Locus symbol: | *lax-o* |

Previous nomenclature and gene symbolization:

Laxatum-79 = *lax-79* (3, 4).

Inheritance:

Monofactorial recessive (5).
Location is unknown.

Description:

Rachis internodes of *lax-o.79* were about 14% longer than those of Bonus (4). Plants were relatively vigorous, rachis nodes in the upper part of the spike had enlarged sterile lateral spikelets, some sterile spikelets were observed, awn length was reduced, and kernels were relatively long (4).

Origin of mutant:

An ethylene imine induced mutant in Bonus (NGB 14657, PI 189763) (4, 6).

Mutational events:

*lax-o.79* (NGB 116412), *-o.88* (NGB 116421) in Bonus (NGB 14657, PI 189763) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-o.79* (NGB 116412) in Bonus.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:69.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:152.

# BGS 487, Laxatum-df, *lax-df*

| | |
|---|---|
| Stock number: | BGS 487 |
| Locus name: | Laxatum-df |
| Locus symbol: | *lax-df* |

Previous nomenclature and gene symbolization:

Laxatum-204 = *lax-204* (3, 4).

Inheritance:

Monofactorial recessive (5).

Location is unknown.

Description:

Rachis internodes of *lax-df.204* were about 2% longer than those of Foma. Plants were somewhat earlier, had relatively good vigor and leaf blades were darker green (4).

Origin of mutant:

A glycidol induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-df.204* (NGB 116431), *-df.241* (NGB 116471) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-df.204* (NGB 115431) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:70.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:153.

# BGS 488, Laxatum-ef, *lax-ef*

| | |
|---|---|
| Stock number: | BGS 488 |
| Locus name: | Laxatum-ef |
| Locus symbol: | *lax-ef* |

Previous nomenclature and gene symbolization:

Laxatum-225 = *lax-225* (6, 7).
Laxatum-238 = *lax-238* (6, 7).

Inheritance:

Monofactorial recessive (5).

Located likely in chromosome 2H (2); *lax-ef.225* is associated with SNP markers 2_1187 to 2_0528 (positions 51.62 to 118.78 cM) in chromosome 2H bins 05 to 08 and with small segments of chromosomes 3HS, 5HS, 5HL, and 6HS of the Bowman backcross-derived line BW462 (2).

Description:

Rachis internodes of *lax-ef.238* spikes were about 23% longer than those of Bonus (7). Leaf blades were relatively wide and darker green; spikes had more fertile rachis nodes, and the straw was very weak when dry (7). Plants of the Bowman backcross-derived line for *lax-ef.225*, BW462, headed three days later than Bowman and had rachis internodes that were nearly 30% longer (5.7 vs. 4.4 mm). Compared to Bowman, BW462 plants had slightly shorter peduncles and awns; and spikes had about 4 to 6 more kernels (5). Kernels were slightly longer and thinner and weighed less (5.3 vs. 6.0 mg). Grain yields of BW462 were 10 to 20% lower than those of Bowman (5). The delayed heading of BW462 could be attributed to the late allele at the Early maturity 6 (*Eam6*) or Praematurum-c (*mat-c*) locus, which was retained in the 2H segment from the donor parent Foma (1, 2).

Origin of mutant:

*lax-ef.225* is a glycidol induced mutant in Foma (NGB 14659, CIho 11333) (2, 9); *lax-ef.238* is an ethylene imine induced mutant in Foma (7, 9).

Mutational events:

*lax-ef.205* (NGB 116432), *-ef.225* (NGB 116453), *-ef.236* (NGB 116463), *-ef.237* (NGB 116466), *-ef.238* (NGB 116467), *-ef.263* (NGB 116488), *-ef.287* (NGB 116512), *-ef.290* (NGB 116514), *-ef.292* (NGB 116516), *-ef.309* (NGB 116532) in Foma (NGB 14659, CIho 11333) (3, 4, 7, 8).

Mutant used for description and seed stocks:

*lax-ef.225* (NGB 116453) in Foma; *lax-ef.225* in Bowman (PI 483237)*3 (BW462, NGB20692).

References:

1. Comadran, J., B. Kilian, J. Russell, L. Ramsay, N. Stein, M. Ganal, P. Shaw, M. Bayer, W. Thomas, D. Marshall, P. Hedley, A. Tondelli, N. Pecchioni, E. Francia, V. Korzun, A. Walther, and R. Waugh. 2012. Natural variation in a homolog of *Antirrhinum CENTRORADIALIS* contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genet. 44:1388-1392.

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

3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of

ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.

4. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.

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

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

7. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.

8. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.

9. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:71.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:154-155.

*Barley Genetics Newsletter (2017): 46:50-187.*

# BGS 489, Laxatum-ff, *lax-ff*

| | |
|---|---|
| Stock number: | BGS 489 |
| Locus name: | Laxatum-ff |
| Locus symbol: | *lax-ff* |

Previous nomenclature and gene symbolization:

Laxatum-216 = *lax-216* (3, 4).

Inheritance:

Monofactorial recessive (5).

Location is unknown.

Description:

Rachis internodes of *lax-ff.216* were about equal to those of Foma at normal sowing distances, but rachis internodes were a little longer at lower sowing densities (4). Kernels were relatively round and weighed about 25% less than Foma kernels (4).

Origin of mutant:

An ethyle neimine induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-ff.216* (NGB 116444), *-ff.233* (NGB 116461) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-ff.216* (NGB 116444) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:72.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:156.

# BGS 490, Laxatum-gf, *lax-gf*

| | |
|---|---|
| Stock number: | BGS 490 |
| Locus name: | Laxatum-gf |
| Locus symbol: | *lax-gf* |

Previous nomenclature and gene symbolization:

Laxatum-217 = *lax-217* (3, 4).

Inheritance:

Monofactorial recessive (5).

Location is unknown.

Description:

Rachis internodes of *lax-gf.217* were 22% longer than those of Foma (4). Plants were relatively vigorous, spikes exhibited irregular rachis internode elongation, and sterile lateral spikelets were enlarged (4).

Origin of mutant:

An ethylene imine induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-gf.217* (NGB 116445), *-gf.288* (NGB 116512) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6,).

Mutant used for description and seed stocks:

*lax-gf.217* (NGB 116445) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:73.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:157.

# BGS 491, Laxatum-hf, *lax-hf*

| | |
|---|---|
| Stock number: | BGS 491 |
| Locus name: | Laxatum-hf |
| Locus symbol: | *lax-hf* |

Previous nomenclature and gene symbolization:

Laxatum-244 = *lax-244* (6, 7).

Inheritance:

Monofactorial recessive (5).

Located in chromosomes 2H, 3HL or 5H (2); partially sterile F1 plants indicated that a translocation was present in *lax-hf.244 (6); lax-hf.244* is associated with SNP markers 2_1338 to 2_1242 (positions 74.97 to 133.59 cM) in chromosome 2H bins 05 to 08, with SNP markers 2_0931 to 2_0009 (positions 104.39 to 164.68 cM) in chromosome 3H bins 07 to 11, and with SNP markers 1_1381 to 2_0392 (positions 11.26 to 109.27 cM) in chromosome 5H bins 01 to 06 of the Bowman backcross-derived line BW464 (2). Based on translocation testers, *lax-hf.244* was previously associated with chromosome 5HL (9).

Description:

Rachis internodes of *lax-hf.244* plants were about 21% longer than those of Bonus (7). Leaf blades were relatively narrow and darker green; spikes were long, and kernels were relatively thin (7). A translocation could be present in the original *lax-hf.244* stock based on semisterility of the F1s following a cross to Foma (8). Plants of the Bowman backcross-derived line for *lax-hf.244*, BW464, headed two to three days later than Bowman and had rachis internodes that were about 15% longer (5.2 vs. 4.5 mm). Compared to Bowman, BW464 plants had slightly shorter peduncles and awns and had about four more kernels per spike (5). Kernels were longer (10.5 vs. 9.3 mm), thinner (3.3 vs. 3.8 mm) and weighed less (5.3 vs. 6.0 mg). Grain yields of BW464 were 15 to 20% lower than those of Bowman (5). The delayed heading of BW464 could be attributed to the late allele at the Early maturity 6 (*Eam6*) or Praematurum-c (*mat-c*) locus, which was retained in the 2H segment from the donor parent Foma (1, 2).

Origin of mutant:

*lax-hf.244* is an ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (7, 10).

Mutational events:

*lax-hf.232* (NGB 116460)*, -hf.242* (NGB 116472), *-hf.244* (NGB 116474), *-hf.251* (NGB 116478) in Foma (NGB 14659, CIho 11333) (3, 4, 8, 10).

Mutant used for description and seed stocks:

*lax-hf.244* (NGB 116474) in Foma; *lax-hf.244* in Bowman (PI 483237)*4 (BW464, NGB20694).

References:

1. Comadran, J., B. Kilian, J. Russell, L. Ramsay, N. Stein, M. Ganal, P. Shaw, M. Bayer, W. Thomas, D. Marshall, P. Hedley, A. Tondelli, N. Pecchioni, E. Francia, V. Korzun, A. Walther, and R. Waugh. 2012. Natural variation in a homolog of *Antirrhinum CENTRORADIALIS* contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genet. 44:1388-1392.

2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011.

Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.

3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
4. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
5. Franckowiak, J.D. (Unpublished).
6. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
7. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
8. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
9. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. Hereditas 103:269-279.
10. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:74.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:158-159.

# BGS 492, Laxatum-if, *lax-if*

Stock number: BGS 492
Locus name: Laxatum-if
Locus symbol: *lax-if*

Previous nomenclature and gene symbolization:

Laxatum-246 = *lax-246* (3, 4).

Inheritance:

Monofactorial recessive (5), but partially sterile F1 plants indicated that a translocation was present in *lax-if.246* (5).

Location is unknown.

Description:

Rachis internodes of *lax-if.246* were about equal to those of Foma at normal sowing distances, but rachis internodes were a little longer at lower sowing densities (4). Spikes that emerged earlier had slightly longer rachis internodes than later emerging spikes (4).

Origin of mutant:

A propyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-if.246* (NGB 116475), *-if.248* (NGB 116477) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-if.246* (NGB 116475) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:75.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:160.

## BGS 493, Laxatum-jf, *Lax-jf*

Stock number: BGS 493
Locus name: Laxatum-jf
Locus symbol: *Lax-jf*

Previous nomenclature and gene symbolization:

Laxatum 253 = *Lax-253* (5, 6).
Laxatum 255 = *Lax-255.*(5, 6).

Inheritance:

Monofactorial dominant (4, 7).

Located in chromosome 4HS (1); *Lax-jf.253* is associated with SNP markers 2_0145 to 2_1558 (positions 2.58 to 5.42 cM) in chromosome 4H bin 01 of the Bowman backcross-derived line BW466 (1). Based on translocation breakpoints, *Lax-jf.255* was previously reported to have a weak linkage to chromosome 5H (8).

Description:

Rachis internodes of *Lax-jf.255* were about 12% longer than those of Bonus (6). Spikes had a few sterile spikelets and the kernels were thin and angular (6). Plants of the Bowman backcross-derived line for *Lax-jf.253*, BW466, were slightly taller and had rachis internodes that were 5 to 10% longer (4.8 vs. 4.5 mm) (4). Compared to Bowman, the *Lax-jf.253*, BW466, plants had slightly shorter peduncles and 2 to 4 more kernels per spike. Kernels of BW466 were of similar size and weight as those of Bowman. Grain yields of BW466 were on average equal to those of Bowman (4).

Origin of mutant:

*Lax-jf.255* is a propyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (6, 9). *Lax-jf.253* is an ethyl methanesulfonate induced mutant in Foma (1, 9).

Mutational events:

*Lax-jf.253* (NGB 116480, GSHO 1571)*, -jf.254* (NGB 116481), *-jf.255* (NGB 116482 in Foma (NGB 14659, CIho 11333) (2, 3, 6, 7).

Mutant used for description and seed stocks:

*Lax-jf.253* (NGB 116480, GSHO 1571) in Foma; *Lax-jf.255* (NGB 116482) in Foma; *Lax-jf.253* in Bowman (PI 483237)*3 (GSHO 2138); *Lax-jf.253* in Bowman (PI 483237)*5 (BW466, NGB20696).

References:;

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
4. Franckowiak, J.D. (Unpublished).
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
6. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
7. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.

8. Larsson, H.E.B. 1985. Linkage studies with genetic markers and some *laxatum* barley mutants. Hereditas 103:269-279.

9. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:76.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:160-162.

# BGS 494, Laxatum-kf, *lax-kf*

| | |
|---|---|
| Stock number: | BGS 494 |
| Locus name: | Laxatum-kf |
| Locus symbol: | *lax-kf* |

Previous nomenclature and gene symbolization:

Laxatum-295 = *lax-295* (3, 4).

Inheritance:

Monofactorial recessive (5), but partially sterile F1 plants indicated that a translocation was present in *lax-kf.295* (5).

Location is unknown.

Description:

Rachis internodes of *lax-kf.295* were about equal to those of Foma at normal sowing distances, but rachis internodes were a little longer at lower sowing densities (4). Spikes that emerged earlier had slightly longer rachis internodes than later emerging spikes (4).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-kf.268* (NGB 116493), *-kf.295* (NGB 116519) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-kf.295* (NGB 116493) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:77.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:163.

# BGS 495, Laxatum-lf, *lax-lf*

| | |
|---|---|
| Stock number: | BGS 495 |
| Locus name: | Laxatum-lf |
| Locus symbol: | *lax-lf* |

Previous nomenclature and gene symbolization:

Laxatum-274 = *lax-274* (3, 4).

Inheritance:

Monofactorial recessive (5).

Location is unknown.

Description:

Rachis internodes of *lax-lf.274* were about 16% longer than those of Foma (4). Compared to Foma, spikes were long and kernels were large (4).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-lf.273* (NGB 116499), *-lf.274* (NGB 116500) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-lf.274* (NGB 116500) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:78.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:164.

# BGS 496, Laxatum-mf, *lax-mf*

| | |
|---|---|
| Stock number: | BGS 496 |
| Locus name: | Laxatum-mf |
| Locus symbol: | *lax-mf* |

Previous nomenclature and gene symbolization:

Laxatum-302 = *lax-302* (3, 4).

Inheritance:

Monofactorial dominant (5), but partially sterile F1 plants indicated that a translocation was present in *lax-mf.302* (5).

Location is unknown.

Description:

Rachis internodes of *lax-mf.302* were about 15% longer than those of Foma (4). Plants had few tillers and matured late. Compared to Foma, spikes were short and kernels weighed less (4).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Foma (NGB 14659, CIho 11333) (4, 6).

Mutational events:

*lax-mf.300* (NGB 116524), *-mf.301* (NGB 116525), *-mf.302* (NGB 116526) in Foma (NGB 14659, CIho 11333) (1, 2, 5, 6).

Mutant used for description and seed stocks:

*lax-mf.302* (NGB 116526) in Foma.

References:

1. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
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. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
5. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas 103:255-267.
6. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:79.

Revised:

U. Lundqvist. 2017. Barley Genet. Newsl. 47:165.

# BGS 497, Laxatum-nf, *lax-nf*

| | |
|---|---|
| Stock number: | BGS 497 |
| Locus name: | Laxatum-nf |
| Locus symbol: | *lax-nf* |

Previous nomenclature and gene symbolization:

Laxatum-322 = *lax-322* (5, 6).
Laxatum-323 = *lax-323* (5, 6).

Inheritance:

Monofactorial recessive (7).

Located likely in chromosomes 2HL or 4H (1); *lax-nf.322* is associated with SNP markers 1_0786 to 2_1474 (positions 133.59 to 218.47 cM) in chromosome 2H bins 09 to 13, with SNP markers 1_0113 to 1_0568 (positions 26.58 to 78.18 cM) in chromosome 4H bins 02 to 06, and with SNP markers in small segments of chromosomes 3HL, 5HL, 6HS, and 6HL of the Bowman backcross-derived line BW470 (1).

Description:

Rachis internodes of *lax-nf.322* were about 29% longer than those of Foma (6). Kernels were relatively thin and weighed less than half those of Foma. Spikes showed tip sterility (6). Compared to Bowman the Bowman backcross-derived line for *lax-nf.322*, BW470, had rachis internodes that were about 25% longer (5.6 vs. 4.5 mm). BW470 plants were 5 to 10% taller, had slightly shorter awns, and 1 to 3 more fertile spikelets (4). Kernels were longer (10.5 vs. 9.2 mm) and thinner (3.3 vs. 3.8 mm) and weighed less (5.2 vs. 6.0 mg). Grain yields of BW470 were about 25% lower than those of Bowman (4).

Origin of mutant:

*lax-nf.322* and *lax-nf.323* are ethyl methanesulfonate induced mutants in Foma (NGB 14659, CIho 11333) (7, 8).

Mutational events:

*lax-nf.322* (NGB 116542)*, -nf.323* (NGB 116543) in Foma (NGB 14659, CIho 11333) (2, 3, 7, 8).

Mutant used for description and seed stocks:

*lax-nf.322* (NGB 116542) in Foma; *lax-nf.323* NGB 116543) in Foma; *lax-nf.322* in Bowman (PI 483237)*3 (BW470, NGB20700).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1959. The mutagenic effects of ionizing radiations and reactive ethylene derivatives in barley. Hereditas 45:351-368.
3. Ehrenberg, L., Å. Gustafsson, and U. Lundqvist. 1961. Viable mutants induced in barley by ionizing radiations and chemical mutagens. Hereditas 47:243-282.
4 Franckowiak, J.D. (Unpublished).
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
6. Larsson, H.E.B. 1985. Morphological analysis of *laxatum* barley mutants. Hereditas 103:239-253.
7. Larsson, H.E.B. 1985. Genetic analysis of *laxatum* barley mutants. Hereditas

103:255-267.

8. Lundqvist, U. (Unpublished).

Prepared:

H.E.B. Larsson and U. Lundqvist. 1986. Barley Genet. Newsl. 16:80.

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:166-167.

# BGS 518, Semidwarf 1, *sdw1*

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

Previous nomenclature and gene symbolization:

Denso dwarf = *denso* (7, 18).

*Hordeum vulgare* gibberellin 20-oxidase = *Hv20ox*$_2$ (10, 11, 21).

Inheritance:

Monofactorial recessive (7, 19); some F$_1$'s are intermediate in height (1, 13).

Location in chromosome 3HL (2, 14); *sdw1.d* is probably proximal from the *gsh2* (glossy sheath 2) locus and near RFLP marker PSR170 (14); *sdw1.d* is in bin 3H-11 (12); *sdw1.d* is near RFLP marker R1545 (22); *sdw1.d* is close to SNP marker 1_0867 (15); *sdw1.a* is associated with SNP markers 1_0044 to 2_0650 (positions about 190 to 192.00 cM) in 3H bin 12 of the Bowman backcross-derived line BW827 (4); *sdw1.d* is associated with SNP markers 2_0023 to 1_0821 (positions 169.94 to 190.87 cM) in 3H bins 11 and 12 of the Bowman backcross-derived line BW828 (4), in 3H bin 12.

Description:

Plants homozygous for the *sdw1.a* gene ranged from 10 to 30 cm shorter than normal sibs, with expression partial dependent on environment (1, 18, 20). Spike length was variable, but fully as long as normal barley. The stock used for description of the *sdw1.a* gene, M21, has the short straw and long spike of the original 'Jotun Mutant' as well as a large culm diameter from its parent 'Vantage' (1, 20). The semidwarf mutants, 'Diamant' and ‘Abed Denso’, are alleles at the *sdw1* locus (7, 16). Alleles at the *sdw1* locus are associated with semi-prostrate juvenile growth (7, 18), delayed maturity (5, 7, 8, 18, 22), smaller grain size (7), and reduced malt quality (5, 8, 18). The *sdw1* mutants are GA sensitive (3, 23). They are very likely mutants in an orthologue of the rice *sd1* gene (23), which encodes a GA-oxidase that produces lower levels of GA and reduced levels of cause the dwarf phenotype (9, 17). A gibberellin 20-oxidase gene (*Hv20ox*$_2$) was identified as the candidate gene for *sdw1* (10, 11). The reduced expression of *Hv20ox*$_2$ increased the number of effective tillers and enhanced grain yield (11, 21). The reduction in *Hv20ox*$_2$ levels was 4-fold in the *sdw1.d* mutant and 60-fold in the *sdw1.a* mutant, which causes a reduced endogenous GAs concentration and delayed heading (11). Plants of the Bowman backcross-derived line for *sdw1.a*, BW827, were 15 to 30% shorter than Bowman and heading was delayed 1 to 3 days. Plants of the Bowman backcross-derived line for *sdw1.d*, BW828, were 10 to 20% shorter than Bowman, heading was delayed 1 to 3 days, and spikes had 1 to 2 more kernels in some trials. Kernels of BW827 and BW828 were up to 10% lighter than Bowman kernels in some trials. Grain yields of BW828 were similar to those of Bowman, while those of BW827 were about 85% of the Bowman yields (6). The QTL for *sdw1.d* co-located with QTL for yield, plant height, development score, hectoliter weight and grain plumpness (11).

Origin of mutant:

An X-ray induced mutant in the Norwegian cultivar Jotun (PI 467357) isolated as Jotun 22 by Knut Mikaelsen (1, 13).

Mutational events:

*sdw1.a* (66/86, GSHO 1414) in Jotun (PI 467357) (20); *sdw1.c* in Abed Denso (PI 361639) (7); *sdw1.d* (*denso*) (Diamant, PI 330397, PI 467775) in Valticky (PI 268173)

(7); *sdw1.e* (Risø no. 9265) in Abed Bomi (NGB 5096, PI 43371) (7, 9). Some cultivars demonstrated to have the *sdw1.a* and *sdw1.d* alleles are listed in Xu et al. (21). Note that the *denso* name was original assigned to the *sdw1.c* mutant (7), but *sdw1.d* mutant from Diamant is the only allele present in cultivars described as having the *denso* semidwarf (21).

Mutant used for description and seed stocks:

*sdw1.a* in M21 (CIho 15481, GSHO 2513) from the cross Jotun Mutant/Kindred// Vantage (20); *sdw1.d* in Trumpf (Triumph, PI 548762, GSHO 2465) from Diamant; *sdw1.a* from a Jotun derivative in Bowman (PI 483237)*7 (GSHO 1978), *sdw1.a* in Bowman*8 (BW827, NGB 22264); *sdw1.d* from Trumpf in Bowman*4 (GSHO 1979), *sdw1.d* in Bowman*5 (BW828, NGB 22265).

References:

1. Ali, M.A.M., O. Okiror, and D.C. Rasmusson. 1978. Performance of semidwarf barley. Crop Sci. 18:418-422.
2. Barau, U.M., K.J. Chambers, W.T.B. Thomas, C.A. Hackett, V. Lea, P. Jack, B.P. Forster, R. Waugh, and W. Powell. 1994. Molecular mapping of genes determining height, time to heading, and growth habit in barley (*Hordeum vulgare*). Genome 36:1080-1087.
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*Barley Genetics Newsletter (2017): 46:50-187.*

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (4).

Located in chromosome 4HL (1); *cer-yl.187* is associated with SNP markers 2_0411 to 1_0062 (positions 52.11 to 91.93 cM) in 4H bins 04 to 06 of the Bowman backcross-derived line BW143 (1).

Description:

Surface wax coating on the spike, the leaf sheath, and the stem appears absent (wax code - - ++) (4). The original mutant stock produces weak plants (about 3/4 normal height) with a high level of sterility (4). Plants of the Bowman backcross-derived line for *cer-yl.187*, BW143, are semidwarf with waxy nodes, coiled peduncles, globose shaped seeds, and poor hull attachment. Reduced seed set can be caused by adverse environmental conditions (2). The BW143 plants headed 1 to 2 days later than Bowman and were shorter, 67 v. 89 cm. Peduncles and leaf blades were about 2/3 normal length. Kernels were thinner and weighed less, 4.4 vs. 5.9 mg and grain yields were 1/4 to 1/3 those of Bowman (2). Although not as extreme, the phenotypic characteristics of BW143 are similar to those of the Bowman backcross-derived lines for *cer-zv.268* (BW177) and *cer-ym.753* (BW144). Since all three loci retain donor parent markers in the same region of 4HL, they might have mutations in the same gene (1, 2). However, allelism tests demonstrated that the mutants at these loci are not alleles (3).

Origin of mutant:

A propane disulfonic acid diethyl ester induced mutant in Bonus (NGB 14657, PI 189763) (3).

Mutational events:

*cer-yl.187* (NGB 111073, GSHO 1545)*, -yl.188* (NGB 111074) in Bonus (NGB 14657, PI 189763) (4); *cer-yl.407* (NGB 111295) in Foma (NGB 14659¸ CIho 11333), *-yl.821* (NGB 111709) in Bonus (5).

Mutant used for description and seed stocks:

*cer-yl.187* (GSHO 1545, NGB 111073) in Bonus; *cer-yl.187* in Bowman (PI 483237)*6 (GSHO 2216); *cer-yl.187* in Bowman*7 (BW143, NGB 20549). GSHO 1545 and GSHO 2216 do not show the phenotype of *cer-yl.187*, but rather the phenotype of *cer-zv.268* or *cer-ym.753.* NGB 111073 and NGB 20549 have the correct phenotypes (3).

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Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:116.
U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:171-172.

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

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (7).

Located in chromosome 4HL (1, 3, 4); *cer-ym.753* is associated with SNP markers 2_0289 to 1_1513 (positions 69.62 to 101.44 cM) in 4H bins 05 to 07 of the Bowman backcross-derived line BW144 (1); *cer-zv.268*, a possible allele (4), is associated with SNP markers 2_1122 to 1_0568 (positions 47.80 to 78.18 cM) in 4H bins 05 to 06 of the Bowman backcross-derived line BW177 (1); *cer-ym.753* and *cer-zv.268* are in a 0.8 cM interval between EST markers AK370363 and AK251484 in pericentromeric region of 4H (3, 4).

Description:

Surface wax coating on the spike, the leaf sheath and stem, and the leaf blade appears absent (wax code - - -) (7). Plants are weak, culms have a kinked peduncle, nodes are wax covered, and kernels are small, globe shaped, and nearly hull-less (2, 5). Plants of the Bowman backcross-derived line for *cer-ym.753*, BW144, averaged about 2/3 the height of Bowman with peduncles and leaf blades about 2/3 normal length. Awns of BW144 were slightly shorter and kernels were smaller and lighter, 4.2 vs. 6.1 mg. The grain yields of BW144 were less than 1/3 that of Bowman. Plants of the Bowman backcross-derived line for *cer-zv.268* (BW177) were phenotypically similar to BW144 (*cer-ym.753*) plants, but they were weaker (2, 3). Detached leaves of the mutant *cer-ym.753* lost 41.8% of their initial weight after 1 hour of dehydration under laboratory conditions, while that of the wild type Bowman plants lost only 7.1%. Stomata function was not affected by the mutation, but the mutant leaves showed increased cuticular permeability to water, suggesting a defective leaf cuticle, which was confirmed by toluidine blue staining (3, 4). The *cer-ym.753* leaf blades showed a substantial reduction in the amounts of the major cutin monomers and a slight increase in the main wax component, suggesting that the enhanced cuticle permeability was a consequence of cutin deficiency (3, 4). Allelism tests demonstrated that mutants at the *cer-ym* and *cer-zv* loci are not alleles (5).

Origin of mutant:

An ethylene oxide induced mutant in Bonus (NGB 14657¸ PI 189763) (5).

Mutational events:

*cer-ym.130,* (NGB 111015, GSHO 1546), *-ym.753* (NGB 111641) in Bonus (NGB 14657, PI 189763) (7); *cer-zv.268* (NGB 111155, GSHO 1529)*, -zv.342* (NGB 111229)*, -zv.576* (NGB 111464) in Foma (NGB 14659, CIho 11333) (6); *cer-zv.1256* (NGB 112144) in Kristina (NGB 14661, NGB 1500) (8).

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2016. Barley Genet. Newsl. 46:118-119.

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:173-174.

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

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

Revised locus symbol:

The allelism based similarities in phenotypes of the Bowman-backcross-derived lines (3) and retained donor parent SNP markers (2) for the *ari-m .28* and several *brh1* mutants (2) was confirmed by Braumann et al. (1). Therefore, to find more information about this locus, see BGS 001, the barley genetic stock (BGS) description for the Brachytic 1 (*brh1*) locus.

Previous nomenclature and gene symbolization:

Brachytic = *br* (1, 8, 9).

Breviaristatum-i = *ari-i* (5, 6).

Breviaristatum-28 = *ari-28* (7).

Inheritance:

Monofactorial recessive (6).

Location in chromosome 7HS (3); *ari-m.28* is associated with SNP markers 2_0710 to 2_0307 (positions 4.74 to 9.55 cM) in 7H bin 01 of the Bowman backcrossed-derived line BW051 (3); the genomic position of the *Brh1* locus at 12.74 cM in 7HS (1), in 1H bin 01 near the border with 1H bin 02.

Description:

Plants are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (4). Kernels are globe-shaped and awns are about 1/2 normal length (4). Spikes are slightly more lax than normal (4). Plants of the Bowman backcross-derived line for *ari-m.28* (BW051) are phenotypically similar to other Bowman backcross-derives with mutant alleles at the *Brh1* (Brachytic 1) locus (1). The *ari-m* mutants occur in the *Brh1* locus and are deficient in the Gα subunit of a heterotrimeric G protein, which is an important regulator of culm length in barley (1).

Origin of mutant:

A gamma-ray induced mutant in Bonus (NGB14657, PI 189763) (6).

Mutational events:

*ari-m.12* (NGB 115858, GSHO 1661), *-m.28* (NGB 115876) in Bonus (NGB14657, PI 189763), *-m.141* (NGB 115951), *-m.177* (NGB 115987) in Foma, (NGB 14659, CIho 11333), *-m.251* (NGB 116059) in Kristina (NGB 14661, NGB 1500) (6); *ari-m.269* (NGB 116081) in Kristina (6, 7).

Mutant used for description and seed stocks:

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

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Prepared:

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Revised:

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

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# BGS 614, Zeocriton 2, *Zeo2*

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

Revised locus symbol:

Since the zeocriton spike phenotype was first described by Hayes and Harlan (7), *Zeo1* became the recommended locus symbol for various mutants at this locus. The semi-dominant dense spike variants at the complex *Zeo1* locus exhibit a range of phenotypes associated with restricted elongation of the rachis internodes. Based on DNA sequencing, three distinct phenotypic groups of dense spike variants are associated with the *Hordeum vulgare APELATA2* (*AP2*)-like transcription factor (*HvAP2*) locus (9, 10). The phenotypic expressions were historical assigned different locus symbols, but each group is associated with specific molecular changes in the *HvAP2* transcript (9). Alleles at this locus are assigned locus symbols: The *Zeo1* mutants exhibit the most extreme phenotypes, the *Zeo2* variants have intermediate phenotypes, and the *Zeo3* variants may show a lesser degree in shortening of rachis internodes (9). Molecular markers and/or pedigree information are necessary to separate variants assigned to the *Zeo1* (BGS 082) and *Zeo3* (BGS 184) groups (8). See BGS 082 for more information of the alleles at the *Zeo1* locus (9).

Previous nomenclature and gene symbolization:

Zeocriton with no gene symbol (4, 7).
Zeocriton 2 = *Zeo2* (6, 9).
Rachis internode length QTL in 2HL = *qSIL.ak-2H* (11).
Cleistogamy 1 = c*ly1.b* (8, 9, 13, 14).
*Hordeum vulgare APELATA2* (*AP2*)-like transcription factor = *HvAP2* (9. 10).

Inheritance:

Monofactorial semi-dominant (2, 11).

Located in chromosome 2HL (2, 11, 17); *Zeo2* from Haruna Nijo Is in 2H bin 13 (2); *qSIL.ak* (*Zeo2*) from Kanto Nakate Gold is near SRS marker ABG613 (11); *Zeo2* is closely to the *Cleistogamy 1* (*cly1.b*) locus (10, 13, 14); *Zeo2.c* is associated with SNP markers 1_0404 to 1_0072 (positions 186.61 to 239.78 cM) in 2HL bins 12 to 14 of the Bowman backcross-derived line BW939 (3); the dense spike traits in the *dsp1.a* stock (likely *Zeo2.c*) is associated with SNP markers 1_0376 to 2_0561 (positions 209.87 to 247.86 cM) in 2HL bins 13 to 14 of the Bowman backcross-derived line BW277 (3); *Zeo2* with the *eog1.e* gene from GSHO 285 (Ab 1380) is associated with SNP markers 1_1480 to 2_0895 (positions 173.50 to 209.91 cM) in 2HL bins 11 to 13 of the Bowman backcross derived line BW302 (3); *Zeo2.ax* (previously named *dsp.ax*) is associated with SNP markers 2_0064 to 2_0175 (positions 179.99 to 213.08 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW270 (3); *Zeo2* from Haruna Nijo in the *ant22.1508* stock is associated with SNP markers 1_1346 to 2_0895 (positions about 165 to 209.87 cM) in 2H bins 11 to 13 of the Bowman backcross-derived line BW022 (3); the *HvAP2* locus is near marker BOPA2_12_10579 (9), in 2H bin 13.

Description:

Many dense spike phenotypes with shortened rachis internodes have been described in the barley literature (12). Hayes and Harlan (7) identified a strong pyramid shaped spike with short internodes as zeocriton (little barley), but they reported that three genes controlled this trait in their cross to Zeocriton (8). Accession CIho 6238 is phenotypically to the Zeocriton cultivar. The progeny cross to the cultivar Svanhals (NGB 1482, PI 5474) best matched the inheritance pattern expected for cross segregating for the *Zeo2* gene (7). Spikes of plants with the *Zeo2* mutant are compact and remain strap-shaped because all rachis internodes are about the same length. Plants are slightly shorter and spikes contain 2 to 4 more fertile spikelets than those of normal sibs (2). Plants of the Bowman backcross-derived lines with *Zeo2* alleles in the *Zeo2.c* and *Zeo2.ax* group have small anthers (2/3 of normal length) (5) and are associated with small lodicules (closed flowering or cleistogamy) (11, 14). The rachis internode length of plants in Bowman backcross lines for *Zeo2* alleles averaged 3.3 mm compared to 4.5 mm for Bowman. In some field environments, the BW lines for *Zeo2* gene had 1 to 2 more kernels per spike than Bowman, and kernel weights were slightly lower. No effects of the *Zeo2* gene on plant height and grain yield were observed (5). Cleistogamy or closed flowering was strongly associated with a gene for reduced rachis internode length (13), which was later identified as *Zeo2* (9). The *Zeo2* region of 2HL was associated with tolerance to low temperature injury (1) and Fusarium head blight infection (10, 16. 17). Cultivars with the *Zeo2* mutant were demonstrated to have cleistogamous flowering pattern (11). The cleistogamous flower sheds its pollen before opening, forcing plants with this habit to be almost entirely autogamous. The lodicule in cleistogamous plants is atrophied (8). DNA sequencing showed that the *Zeo1* mutants occur in a *Hordeum vulgare* APELATA2 (*AP*2)-like transcription factor, *HvAP*2. The dense spike and cleistogamous (small lodicules) phenotypes are a consequence of a perturbed interaction between microRNA 172 (*Hv-miR172*) and its corresponding binding site on the mRNA from the *HvAP2* gene, which acts early in spike development to regulate turnover of *HvAP2* mRNA (9, 10). The *Zeo1* mutants occur in the last intron of *HvAP*2, the binding site of *Hv-miR172*, and prevent cleavage of the *HvAP2* mRNA (9, 10).

Origin of mutant:

A naturally occurring variant in the fourth exon of the *HvAP2* locus (9), likely of occidental origin in two-rowed barley cultivars from Europe (9, 13); this variant was likely evaluated in Svanhals (NGB 1482, PI 5474) by Hayes and Harlan (7).

Mutational events:

Phenotypically similar variants were isolated from several different accessions (2, 4, 7, 12). However, based on identical DNA haplotypes in the first exon of the *HvAP*2 gene, all of the variants have the same gene identified as *Zeo2* (9. 10). Several cultivars from Northern Europe were identified as having the Zeo2 mutant including Golden Promise (PI 343079), Imperial (OUU352, PI 61340), and Plumage (OUU351, CIho 2511) (9, 10). The variants identified initially as having different origins include *Zeo2.c* from line 36Ab51 (GSHO 637), which was called “good zeocriton” (15), and *Zeo2.ax* from CIho 6880 and Haruna Nijo (3, 9); which likely is the *Zeo2* allele from Golden Melon (OUJ808, PI 263410) as identified in Kanto Nakato Gold (OUJ 518) (8).

Mutant used for description and seed stocks:

*Zeo2.c* in 36Ab51 (GSHO 637); *Zeo2.c* in Bowman (PI 483237)*4 (GSHO 3433); *Zeo2.c* in Bowman*4 (BW939, NGB 22368); *Zeo2.ax* from CIho 6880 (Ahang/Twisted Flag//Triple-awn Lemma) in Bowman*5 (BW270, NGB 22095); *Zeo2.ax* with *ant22.1508* (Proanthocyanidin-free 22, GSHO 1635) from Haruna Nijo (NGB 13705) in Bowman*4 (GSHO 1841); *Zeo2.ax* with *ant22.1508* in Bowman*6 (BW022, NGB 20430); *Zeo2.c* from 36Ab51 (GSHO 637, ‘good zeocriton’) in Bowman*4 (GSHO 3433, BW939, NGB 22368); *Zeo2.c* from a naked two-rowed accession from China [originally identified as *dsp1.a* (3)] in Bowman*7 (GSHO 1833, BW277, NGB 20561).

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Prepared:

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

Revised:

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

J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:177-180.

# BGS 679, Accordion rachis 4, *acr4*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2, 3).

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

Description:

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

Origin of mutant:

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

Mutational events:

*acr4.3* (NGB 115043) in Bonus (NGB 14657, PI 189763) (2, 3).

Mutant used for description and seed stocks:

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

References:

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

Prepared:

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

Revised:

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:181.

# BGS 740, Pubescence on glume 1, *Pbg1*

| | |
|---|---|
| Stock number: | BGS 740 |
| Locus name: | Pubescence on outer glume 1 |
| Locus symbol: | *Pbg1* |

Previous nomenclature:

Pubescence on the outer glume = *S* (1).

Pubescence on outer glume = *Pbg* (2).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 7H (1); *pbg1.b* is about 25.3 cM from the naked caryopsis 1 (*nud1*) locus based on coupling data (1); *pdg1.b* is closer to the dense spike 1 (*dsp1*) locus than the *nud1* locus (1).

Description:

Plants with the incomplete dominant allele, *Pbg1.a*, have the outside surface of the outer glumes covered with pubescence on short hairs. Plants with the recessive allele, *pbg1.b*, pubescence restricted to a central ridge on the outer glume (1). The short rachilla hair 1 (*srh1.a*) allele reduces the length of the hairs on the outer glumes, but not their distribution (1). Other studies in which inheritance of glume hairs is more complex were reviewed by Smith (2). Wiebe and Reid (3) classified the distribution of hairs on the outer surface of glumes into four groups: fully covered, narrow band, midline only, and absent.

Origin of mutant:

Natural occurrence with naked caryopsis in line No. 154 (1); hairs confined to bands in Montcalm (CIho 7149) (3); hairs restricted to the midline in Otis (CIho 7557) (3).

Mutant used for description:

*pbg1.b* in line No. 154, possibly GSHO 173 (1).

Mutant used for description and seed stocks:

*pbg1.b* in line No. 154 and likely in a number of six-rowed cultivars from East Asia.

References:

1. Hor, K.S. 1924. Interrelations of genetic factors in barley. Genetics 9:151-180.
2. Smith, L. 1951. Cytology and genetics of barley. Bot. Rev. 17:1-51, 133-202, 285-355.
3. Wiebe, G.A., and D. A. Reid. 1961. Classification of barley varieties grown in the United States and Canada 1958. U. S. Dept. Agric. Technical Bulletin No 154. 234 pp.

Prepared:

J.D. Franckowiak 2017. Barley Genet. Newsl. 47:182.

# BGS 741, Stubble 1, *stb1*

Stock number: BGS 741
Locus name: Stubble 1
Locus symbol: *stb1*

Previous nomenclature:

Gillette (2, 4).
Stubble = *stb* (3, 4).
Short rachilla hair 2 = *srh2* (1).

Inheritance:

Monofactorial recessive (3, 4).

Location is unknown; *stb1.a* is associated with several groups of retained SNP markers in 1H (positions 61.55 to 157.02 cM in bins 06 to 12), 3H (52.41 to 119.10 cM in bins 04 to 07), and 5H (26.06 to 98.42 cM in bins 02 to 10) in the Bowman backcross-derived line BW874 (1).

Description:

Gillette or stubble 1, *stb1.a*, is expressed on the rachilla, glume, and rachis margin hairs. The effect looks as if a mower had been run over these areas leaving a “stubble” of very short hairs. This expression can readily be seen in both lines with long rachilla hair (*Srh1*) and short rachilla hair (*srh1*) (3, 4). The stubble trait cannot be scored easily in certain smooth-awned barleys where most, and sometimes all, hairs on the glumes and rachis margins are missing. In an F2 population, segregation of the stubble trait appeared independent of the short rachilla hair trait (4). The stubble trait was found in the world collection barleys from Korea and adjacent China (4). Isogenic lines with "stubble" (*stb1*) and short rachilla hair 1 (*srh1*) were selected from a Manchuria (CIho 2330) X Gillette (CIho 4485) cross (4). Both parents have rough awns (*Raw1* plus *Raw2*).

Origin of mutant:

Natural occurrence in US 85 [GSHO 656, selected from CIho 4551 (PI 69686) introduced from Jilin, China] and US 86 [GSHO 659, selected from CIho 4485 (PI 69621) from Shanxi, China] (2, 4).

Mutational events:

*stb1.a* in GSHO 659 (T12-34) selected from CIho 4485 (PI 69621) (2).

Mutant used for description and seed stocks:

*stb1.a* in GSHO 656 and GSHO 659; *stb1.a* from GSHO 656 in Bowman (PI 483237)*2 (BW874, NGB 22308). The isogenic lines for *stb1.a* were selected in the $F_{25}$ generation from a Manchuria (CIho 2330) X Gillette (CIho 4485) cross: CIho 16005 (*Srh1 Stb1*), CIho 16006 (*Srh1 stb1.a*), CIho 16007 (*srh1.a Stb1*), and CIho *srh1.a stb1.a*).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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3. Reid, D.A., and G.A. Wiebe. 1968. Taxonomy, botany, classification, and world

collection. p. 61-84. *In* Barley: Origin, Botany, Culture, Winterhardiness, Genetics, Utilization, Pests. USDA Agric. Handb. No. 338.
4. Wiebe, G.A. 1972. “Stubble” gene. Barley Genet. Newsl. 2:109.

Prepared:

J.D. Franckowiak 2017. Barley Genet. Newsl. 47:183-184.

# BGS 743, Tweaky spike 1, *twk1*

| | |
|---|---|
| Stock number: | BGS 743 |
| Locus name: | Tweaky spike 1 |
| Locus symbol: | *twk1* |

Previous nomenclature:

Tweaky = *tw* (1, 5).

Tweaked spike (3).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 7H (5).

Description:

Tweaky is a spike development abnormality in which one or more rachis internodes in the upper third of the spike are elongated and rounded in shape giving the appearance of a short stem. As a result, the spike is misshapen or twisted and appears to have missing kernels (6). Often rachis internodes just above the tweaked area are foreshortened and give a bunched appearance of spikelets. The tweaky characteristic has been reported only in the cultivar Wisconsin Barbless (CIho 5105) where it occurs in only a small percentage of the spikes (6). See Reid and Wiebe (3) for a photo of the *twk1.a* mutant. Chemically induced mutants in barley that exhibit instability in inflorescence and floral organ development have been isolated (4, 7). These mutants resemble some of the traits associated with *twk1.a* mutant. Partial rescue of specific phenotypic features of tweaky mutants following treatment with auxin inhibitors and the synthetic auxin 2,4-dichloroacetic acid (2,4-D) has been reported (4).

Origin of mutant:

Natural occurrence in Wisconsin Barbless (CIho 5105) (1, 6).

Mutational events:

*twk1.a* in Wisconsin Barbless (CIho 5105) (1, 6); a tweaky-like spike phenotype might be present in the two-rowed cultivar ND Genesis (PI 677345) (2). Chemically induced mutants in Auksiniai II have somewhat similar, but more extreme, phenotypes (4, 7); however, they have not been tested for allelism with the *twk1.a* mutant.

Mutant used for description and seed stocks:

*twk1.a* in Wisconsin Barbless.

References:

1. Åberg, E., and G.A. Wiebe. 1948. Taxonomic Value of Characters in Cultivated Barley. U. S. Dept. Agr. Tech, Bul. 942. 88 pp.
2. Franckowiak, J.D. (Unpublished).
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4. Šiukšta, R., V. Vaitkūnienė, G. Kaselytė, V. Okockytė, J. Žukauskaitė, D. Žvingila, and V. Rančelis. 2015. Inherited phenotype instability of inflorescence and floral organ development in homeotic barley double mutants and its specific modification by auxin inhibitors and 2,4-D. Ann. Bot. 115:651-663.
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Prepared:

J.D. Franckowiak 2017. Barley Genet. Newsl. 47:185-186.

## BGS 744, Accordion rachis 5, *acr5*

| | |
|---|---|
| Stock number: | BGS 744 |
| Locus name: | Accordion rachis 5 |
| Locus symbol: | *acr5* |

Previous nomenclature and gene symbolization:

Accordion rachis 2 = *acr-2* (3).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 7H (1); *acr5.2* is associated with SNP markers 1_0721 to 2_0103 (positions 82.82 to 139.96 cM) in 7H bins 06 to 08 of the Bowman backcross-derived line BW003 (1).

Description:

The *acr5.2* mutant plants exhibited low plant vigor, elongated rachis internodes, and a reduced number of kernels per spike (3). Plants of the Bowman backcross-derived line for *acr5.2*, BW003, showed reduced plant vigor (2). Compared to Bowman, rachis internodes of BW003 were slightly longer (5.1 vs. 4.3 mm), plants and awns were slightly shorter, and peduncles were slightly longer. Kernels of BW003 were elongated (11.3 vs. 9.7 mm) and thin (3.4 vs. 3.9 mm) and weighed less (3.5 vs. 5.9 mg). Grain yields of BW003 were highly variable, but never more than half those of Bowman (2).

Origin of mutant:

A neutron induced mutant in Bonus (NGB 14657, PI 189763) (1, 3).

Mutational events:

*acr5.2* (NGB 115042) in Bonus (NGB 14657, PI 189763) (2, 3).

Mutant used for description and seed stocks:

*acr5.2* (NGB 115042, GSHO 2153) in Bonus; *acr5.2* in Bowman (PI 483237)*6 (BW003, NGB 20411).

References:

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

U. Lundqvist and J.D. Franckowiak. 2017. Barley Genet. Newsl. 47:187.