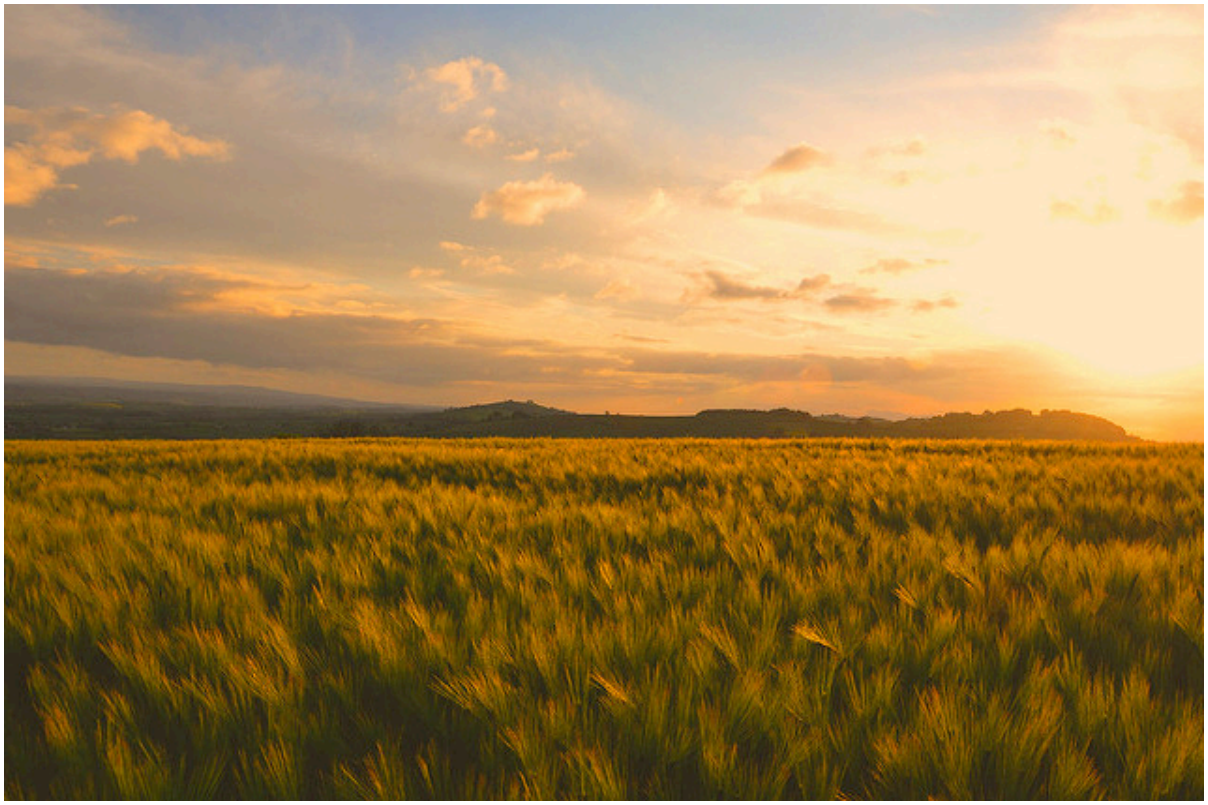
Barley Genetics Newsletter

Volume 45 - 2015



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<<Information about the Barley Genetics Newsletter>>

The Barley Genetics Newsletter is published electronically at
http://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, and the newsletter in its current form has become of limited use to the barley genetics community. At the 12th International Barley Genetics Symposium, held in Minneapolis, Minnesota, USA June 26-30, 2016, the fate of BGN was discussed. It was decided to discontinue the coordinators reports, but that continuing with certain aspects of BGN, and adding new aspects that would foster informal communication, was desirable. There was no significant support for informal research reports, a fact that is reflected on the near-absence of submissions for the last few years. Those with interest in re-developing BGN to enable it to once again to serve the barley genetics community were asked to submit ideas and encouragement to the technical editor, Phil Bregitzer. The number of people who responded to this call: one.

Therefore, volume 45 will be the last of the traditional, yearly "paper" volumes. GrainGenes will continue to host past issues of BGN in electronic format, and will serve as a platform for disseminating announcements, memoria, and significant compilations of data of interest to the community (for instance, additional genetic stock descriptions). Such contributions can be handled on a case-by-case basis by contacting Phil Bregitzer (phil.bregitzer @ars.usda.gov). However, there are no plans for coordinator's reports and informal research reports to be published.

This is the situation as of August, 2016. However, beyond hosting past content and occasional new content, GrainGenes is capable and enthusiastic about hosting additional content and exploring new ways of presenting and fostering discussions and results among researchers and stakeholders within the barley community. Thus, BGN can be reborn in a new form, as long as there is interest within the community.

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.

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Barley Genetics Newsletter, Volume 45, 2015

Robert A. (Bob) Nilan in memoriam, 1923-2015.

Roland von Bothmer and Udda Lundqvist

Robert A. (Bob) Nilan passed away in Pullman, Washington State, USA, October 7th, 2015 and with him USA and the whole barley community has lost a pioneer within plant breeding and plant genetic research.

Bob Nilan was born on December 26, 1923, in New Westminster, British Columbia, Canada. He was the son of Phyllis and Jack Nilan. Hiking and fishing in the Canadian wilderness with his father inspired him very early and then he founded a love for the natural world and plant sciences. His early school-days in Burquitlam and New Westminster launched a life-long passion for education. From University of British Columbia in Vancouver he completed a Bachelors degree in General Botanical Studies in 1944, and a Masters Degree in Plant Science in 1946. After that he moved to USA where he received a PhD in Genetics at the University of Wisconsin in Madison in 1951. During his studies at the University of British Columbia he met the love of his life, Winona Ross, and they married in Victoria, British Colombia, in 1948. After their time in Madison they moved to Pullman and Washington College for what Bob thought would be only a few years but he made a long career there, not less than 41 years. The State College soon became Washington State University, and during the first time here his focus was corn genetics. However, he soon became interested in the crops grown on Palouse Hills in the surroundings of Pullman. Here the large and life-long passion for barley breeding, barley genetics and a career at Washington State University started.

In Pullman Bob Nilan assisted to create the Genetics Department and served as department head for nine years. In 1979 he became appointed Dean of the College of Science, a position he held for twelve years until his retirement in 1992. During his years in the 'deanery' as he lovingly called it, Bob conducted the development of numerous programs, including statistics, environmental sciences, regional planning and plant physiology. He also supported the development of two essential and widely used Laboratories of Bioanalysis and Biotechnology, the Electron Microscopy Center, and the Nuclear Magnetic Resonance Center. He had a great interest in teaching and he established new education programs. During his long career he published more than 100 science research articles, authored two books and trained 60 students for their MSc- and PhD degrees.

In his research career Bob Nilan was mostly interested in the induction of mutations in barley with different mutagenic substances, but he also initiated phenotyping barley characters and its cytology. During his sabbatical year in Svalöv, Sweden, in 1960, he wrote his comprehensive work "The cytology and genetics of barley, 1951-1962" as a follow-up of his progenitor Luther Smith's publication in 1951. He summarized in this book all known and probably identified barley genes with their name, symbols, phenotypes, chromosome locations and reference publications. This work is the basic publication for all present large-scale descriptions of barley mutants and stands out as a real encyclopedia. With his research in developing the induction of mutation he discovered the inorganic substance, sodium azide (NaN_3). He detected that this substance was much more effective than many other tested mutagens up to that time. Sodium azide has an especially high mutation frequency in optimal concentrations and at a particular pH value. It has frequently been used in plant breeding programs.

One of Bob's proudest achievements during his long career was the establishment of the International Barley Genetics Symposia (IBGS) that are still taking place. Intensive discussions started at his sabbatical leave 1960 in Svalöv, Sweden, together with his Swedish host Arne Hagberg and Evald Favret, the latter also a visiting guest researcher (from Argentina) at the same time. The first symposium was organized 1963, in Wageningen, the Netherlands, but the second IBGS, Bob had the pleasure and opportunity to organize himself in Pullman 1969. In 1991 the symposium arrived in Sweden where Bob and Arne Hagberg were guests of honor. He could participate in 10 of the symposia, but unhappily he was not able to participate in the eleventh in China, 2012, because of health troubles.

At the fourth IBGS in Edinburgh, Scotland, 1981, Bob got the commission to update all gene names and gene symbols which he successfully carried out during some sabbatical months at the Carlsberg Laboratory in Copenhagen, Denmark. This immense work is published in Barley Genetics Newsletter (BGN), which he greatly contributed to establish. The first issue appeared in 1971 and with this issue BGN has been published for 45 years. At the 7th IBGS in Saskatoon, Canada, 1996, he put forward a motion recommending symbols for gene loci by utilizing a three-letter code for barley genes to the organizing committee. He was also involved in the numbering of barley chromosomes and chromosome arms based on the Triticeae system. Both systems were approved at the business meeting of IBGS on August 5th, 1996.

Bob Nilan worked with colleagues around the world to create different important programs in barley breeding and genetics. He visited barley research centers on nearly every continent and he spent sabbatical leaves in Italy, Sweden, Denmark, Germany and England. He was deeply engaged in IAEA/FAO programs on mutation genetics and agriculture and attended their symposia many times.

During his long and distinguished career he won several awards and honors, including appointment to the Danish Academy of Science, the Nilan Distinguished Professorship in Barley Research and Education, the Washington State University Foundation Outstanding Service Award, the College of Sciences Legacy of Excellence Award, most recently the establishment of the Robert A. Nilan Endowed Chair, and a honorary member of the Swedish Seed Association, Svalöv, Sweden. He once expressed about his beloved Washington State University: "I can think of no other institution where I would have had such a rewarding and satisfying career".

By his retirement he procured a wonderful house in southern part of California near Palm Springs, east of Los Angeles where he spent the warm winter months to escape the cold and unfriendly Pullman. Bob Nilan is survived by three children, Judith, Gregor and Patricia, five grandchildren and a great grandson. With the death of Robert A. Nilan the whole barley community has lost a prominent researcher in genetics and plant breeding. All of us who had the opportunity to meet and work together with Bob for many years are very grateful for all his wonderful discussions. We all miss him very much.

The picture of Bob Nilan together with Udda Lundqvist is taken at the 9th International Barley Genetics Symposium in Brno, Czeck Republic, 2004, in connection with the publication of the new book "Diversity in Barley (*Hordeum vulgare L.*)" where both were contributors (Photo Roland von Bothmer).

REPORTS OF THE COORDINATORS

Overall coordinator's report

Udda Lundqvist

Nordic Genetic Resource Center
P.O. Box 41, SE 230 53 Alnarp, Sweden

e-mail: **udda.lundqvist@nordgen.org**

First of all I have to inform the barley community the sad news that our dear friend Robert (Bob) Nilan passed away in Pullman, Washington State, USA, October 7th, 2015, with him USA and the whole barley community has lost a pioneer within plant breeding and plant genetic research especially barley. One of his proudest achievements during his long career was the establishment of the International Barley Genetics Symposia (IBGS) that are still taking place. The first symposium was organized 1963, in Wageningen, the Netherlands, but the second IBGS, Bob had the pleasure and opportunity to organize himself in Pullman, USA, 1969. He could participate in 10 of the symposia, but unhappily he was not able to make it to the eleventh in China, 2012, because of health troubles. He greatly contributed to establish the Barley Genetics Newsletter where the first issue appeared in 1971 and with this issue BGN has been published for 45 years. You can read more in the memorium written in this BGN 45:1-3.

In a few weeks the 12th International Barley Genetic Symposium will take place in Minneapolis, in the midwest of the United States, June 26-30, 2016. I do hope that many of the barley community people have the possibility to participate in this important event. Like in the last symposium in Hangzhou, China, 2012, a workshop on "Barley Genetic stocks, there Use and Potential" will be organized Tuesday evening, June 28th. Several important topics will be discussed, i.e. Developmental Mutants in Barley, Characterization and Use. The future of publishing Barley Genetics Newsletter will be a very important discussion topic. There will not be a special workshop for the coordination for several important barley mutant collections as we had in previous meetings, these discussions will get included in the above mentioned workshop as a special topic.

Since the last overall coordinator's report in BGN 44 not too many exciting news have happened. Again, no research report has been received for this issue. Once again I want to stress the importance of publishing short research notes after having been published in high level journals. The barley community should gain very much what different barley research groups are working on and receiving new results to investigate the whole barley genome.

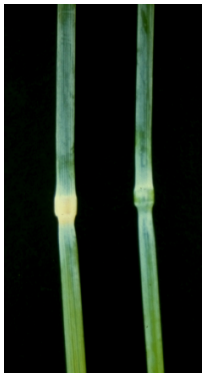
In this volume, BGN 45, again one hundred and twenty-two stock descriptions are described, revised or updated with latest research results and citied literature. They are listed in table 1, additionally also tables 2 and 3, with BGS numbers in order (table 2) and in alphabetic order of the recommended locus names and symbols (table3) are again published to make it easy for barley researchers to find gene descriptions. The construction of the 'International Database for Barley Genes and Barley Genetic Stocks' is happily proceeding fast and will be presented in a modern and easy to handle version. Hopefully it will be ready for demonstration at the IBGS in June 2016..

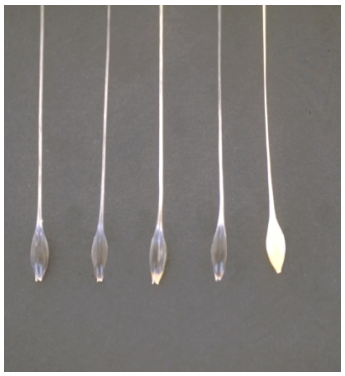
Some different barley genetic stock characters.










List of Barley Coordinators

Barley Genetics Stock Center: Harold Bockelman, USDA-ARS, National Small Grains Germplasm Research Facility, 1691 S. 2700 W., Aberdeen, ID 83210, USA. FAX: +1 208 397 4165; e-mail: <nsgchb@ars-grin.gov>

Trisomic and aneuploid stocks: Harold Bockelman, USDA-ARS, National Small Grains Germplasm Research Facility, 1691 S. 2700 W., Aberdeen, ID 83210, USA. FAX: +1 208 397 4165; e-mail: <nsgchb@ars-grin.gov >

Translocations and balanced tertiary trisomics: Andreas Houben, Institute of Plant Genetics and Crop Plant Research, Corrensstrasse 3, DE-06466 Stadt Seeland, OT. Gatersleben, Germany. FAX: +49 39482 5137; e-mail: <houben@ipk-gatersleben.de>

Desynaptic genes: Andreas Houben, Institute of Plant Genetics and Crop Plant Research, Corrensstrasse 3, DE-06466 Stadt Seeland, OT Gatersleben, Germany. FAX: +49 39482 5137; e-mail: <houben@ipk-gatersleben.de>

Autotetraploids: Wolfgang Friedt, Institute of Crop Science and Plant Breeding, Justus-Liebig-University, Heinrich-Buff-Ring 26-32, DE-35392 Giessen, Germany. FAX: +49 641 9937429; e-mail: <wolfgang.friedt@agrar.uni-giessen.de>

Disease and pest resistance genes: Frank Ordon, Julius Kühn Institute (JKI), Institute for Resistance Research and Stress Tolerance, Erwin-Baur-Strasse 27, DE-06484 Quedlinburg, Germany. e-mail: <frank.ordon@jki.bund.de>

Eceriferum genes: Udda Lundqvist, Nordic Genetic Resource Center (NordGen), Smedjevägen 3, SE-230 53 Alnarp, Sweden; e-mail: < udda.lundqvist@nordgen.org>

Chloroplast genes: Mats Hansson, Lund University, Department of Biology, Sölvegatan 35B, SE-22362 Lund, Sweden. e-mail: <mats.hansson@biol.lu.se>

Ear morphology genes: Udda Lundqvist, Nordic Genetic Resource Center (NordGen), Smedjevägen 3, SE-230 53 Alnarp, Sweden; e-mail: < udda.lundqvist@nordgen.org>
and
Antonio Michele Stanca: Department of Agricultural and Food Science, University of Modena and Reggio Emilia, Reggio Emilia, Italy. FAX +39 0523 983750, e-mail: michele@stanca.it
and
Valeria Terzi: CRA-GPG, Genomics Research Centre, Via Protaso 302, IT-29017 Fiorenzuola d'Arda (PC), Italy. e-mail: <valeria.terzi@crea.gov.it>

Semi-dwarf genes: Jerome D. Franckowiak, Department of Agronomy and Plant Genetics, University of Minnesota Twin Cities, 411 Borlaug Hall, 1991 Upper Buford Circle, St Paul, MN 55108, USA. e-mail: <jfrancko@umn.edu>

Early maturity genes: Udda Lundqvist, Nordic Genetic Resource Center (NordGen), Smedjevägen 3, SE-230 53 Alnarp, Sweden; e-mail: <udda.lundqvist@nordgen.org>

Barley-wheat genetic stocks: A.K.M.R. Islam, Department of Plant Science, Waite Agricultural Research Institute, The University of Adelaide, Glen Osmond, S.A. 5064, Australia. FAX: +61 8 8303 7109; e-mail: <akm.islam@adelaide.edu.au>

Barley Genetic Stocks (GSHO – Genetic Stocks (*Hordeum*) in the USDA-ARS National Small Grains Collection

H.E. Bockelman

USDA-ARS-NSGC
1691 S. 2700 W.
Aberdeen, ID 83210 USA

e-mail:Harold.Bockelman@ars.usda.gov

GSHO Distributions – January 1, 2015 to March 24, 2016.
A total of 1,115 GSHO accession samples were distributed in 63 separate requests to scientists in 10 countries (Australia, China, Czech Republic, Germany, Japan, Republic of Korea, Morocco, Poland, United Kingdom, and United States).

Voucher Images
High resolution scans of kernels of most GSHO accessions have been attached to the accession records as voucher images. They are viewable on the GRIN-Global search page: https://npgsweb.ars-grin.gov/gringlobal/search.aspx

New Accessions
Dr. Andris Kleinhofs has donated additional mutant stocks and GSHO numbers have been assigned as follows.

Table 1.

GSHO Number	Mutant name	Symbol
3671	Multiovary 5.o	mov5.o
3672	Multiovary 4.m	mov4.m
3673	Multiovary.n	mov.n
3674	Short awn 6.q	lks6.q
3675	Unbranched style 5.e	ubs 5.e
3676	Unbranched style 5.f	ubs5.f
3677	Uniculme 3.m	cul3.m
3678	Low number of tillers 1.b	Int1.b
3679	Waxy spike 1.b	wxs1.b
3680	Waxy spike 1.c	wxs1.c
3681	Waxy spike 1.d	wxs1.d
3682	Albino lemma 1.d	alm1.d

Table 1 continued.

GSHO number	Mutant name	Symbol
3683	Albino lemma 1.e	alm1.e
3684	Fenoxaprop-p-ethyl reaction 1	fxp1
3685	Single internode dwarf 1.c	sid1.c
3686	Many noded dwarf 7.h	mnd7.h
3687	Ovaryless 3.c	ovl3.c
3688	Male sterile genetic.ou	msg.ou
3689	Male sterile genetic.ov	msg.ov
3690	Male sterile genetic.ow	msg.ow
3691	Male sterile genetic.ox	msg.ox
3692	Male sterile genetic.oy	msg.oy

Barley Genetics Newsletter (2015) 45:4-31

Coordinator's report: Translocations and balanced tertiary trisomics

Andreas Houben

**Leibniz Institute of Plant Genetics
and Crop Plant Research (IPK) Gatersleben
D-06466 Stadt Seeland, OT Gatersleben Germany**

e-mail: houben@ipk-gatersleben.de

The 3HS.3BL spontaneous Robertsonian translocation obtained from the progenies of wheat-barley (Chinese Spring x Betzes) hybrids backcrossed with wheat line Mv9kr1 was transferred into the modern Martonvasar wheat cultivar Mv Bodri by Tukosi *et al.* (2014). The translocation was identified with molecular cytogenetic methods. Fluorescence in situ hybridization using barley subtelomeric (HvT01) and centromere-specific [(AGGGAG)4] repetitive DNA probes confirmed that the complete barley chromosome arm was involved in the Robertsonian translocation. The wheat-specific repetitive DNA probes identified the presence of the whole wheat genome, except the short arm of the 3B chromosome. Genotypes homozygous for the centric fusion were selected, after which morphological analysis was performed on the plants and the yield components were measured in the field during two consecutive vegetative seasons. The introgression of the 3HS.3BL translocation into the modern wheat cultivar Mv Bodri significantly reduced the plant height due to the incorporation of the dwarfing allele RhtD1b. The presence of the 3HS.3BL translocation in the Mv9kr1 and Mv Bodri wheat background improved tillering and seeds per plant productivity in field experiments carried out in Martonvasar and Keszthely, Hungary.

The collection is being maintained in cold storage. To the best knowledge of the coordinator, there are no new publications dealing with balanced tertiary trisomics in barley. Limited seed samples are available any time, and requests can be made to the coordinator.

References:

Turkosi E, A. Farkas, N:R. Aranyi, B. Hoffmann, V. Toth, and M. Molnar-Lang. (2014) Improvement of the agronomic traits of a wheat-barley centric fusion by introgressing the 3HS.3BL translocation into a modern wheat cultivar. Genome 57 (11-12):601-607.

Barley Genetics Newsletter (2015) 45:4-31

Coordinator's Report: Desynaptic Genes

Andreas Houben

**Leibniz Institute of Plant Genetics
and Crop Plant Research (IPK) Gatersleben
D-06466 Stadt Seeland, OT Gaterslebem, Germany**

e-mail: houben@ipk-gatersleben.de

The status of this genetic stock collection described in BGN 42 did not change.
No work was published describing the application of one of the desynaptic mutants.

However, a novel method suitable to quantify recombination events in barley was described by Dreissig *et al.* (2015). The authors investigated the feasibility of using flow-sorted haploid nuclei, Phi29 DNA polymerase-based whole-genome-amplification (WGA) and multi-locus KASP-genotyping to measure meiotic crossovers in individual barley pollen grains. To demonstrate the proof of concept, 24 gene-based physically mapped single nucleotide polymorphisms were used to genotype the WGA products of 50 single pollen nuclei. The number of crossovers per chromosome, recombination frequencies along chromosome 3H and segregation distortion were analysed and compared to a doubled haploid (DH) population of the same genotype. The number of crossovers and chromosome wide recombination frequencies show that this approach is able to produce results that resemble those obtained from other methods in a biologically meaningful way. Only the segregation distortion was found to be lower in the pollen population than in DH plants.

In many cereal crops, meiotic crossovers predominantly occur toward the ends of chromosomes and 30 to 50% of genes rarely recombine. This limits the exploitation of genetic variation by plant breeding. Previous reports demonstrate that chiasma frequency can be manipulated in plants by depletion of the synaptonemal complex protein ZIPPER1 (ZYP1) but conflict as to the direction of change, with fewer chiasmata reported in Arabidopsis thaliana and more crossovers reported for rice. Barakate *et al.* (2014) used RNA interference (RNAi) to reduce the amount of ZYP1 in barley to only 2 to 17% of normal zygotene levels. In the ZYP1(RNAi) lines, fewer than half of the chromosome pairs formed bivalents at metaphase and many univalents were observed, leading to chromosome nondisjunction and semi-sterility. The number of chiasmata per cell was reduced from 14 in control plants to three to four in the ZYP1-depleted lines, although the localization of residual chiasmata was not affected. DNA double-strand break formation appeared normal, but the recombination pathway was defective at later stages. A meiotic time course revealed a 12-h delay in prophase I progression to the first labeled tetrads. Barley ZYP1 appears to function similarly to ZIP1/ZYP1 in yeast and Arabidopsis, with an opposite effect on crossover number to ZEP1 in rice, another member of the Poaceae.

The process of meiosis results in the formation of haploid daughter cells, each of which inherit a half of the diploid parental cells' genetic material. The ordered association of homologues (identical chromosomes) is a critical prerequisite for a successful outcome of meiosis. Homologue recognition and pairing are initiated at the chromosome ends, which comprise the telomere dominated by generic repetitive sequences, and the adjacent subtelomeric region, which harbours chromosome-specific sequences. In many organisms telomeres are responsible for bringing the ends of the chromosomes close together during early meiosis, but little is known regarding the role of the subtelomeric region sequence during meiosis. Calderon Medel *et al.* (2014) report the

observation of homologue pairing between a pair of *Hordeum chilense* chromosomes lacking the subtelomeric region on one chromosome arm indicates that the subtelomeric region is important for the process of homologous chromosome recognition and pairing.

Phillips *et al.* (2015) work examines whether crossovers can be shifted to more proximal regions simply by elevating growth temperature. We utilised a genome-wide marker set for linkage analysis combined with cytological mapping of crossover events to examine the recombination landscape of plants grown at different temperatures. We found that barley shows heterochiasmy, that is, differences between female and male recombination frequencies. In addition, we found that elevated temperature significantly changes patterns of recombination in male meiosis only, with a repositioning of Class I crossovers determined by cytological mapping of HvMLH3 foci. We show that the length of synaptonemal complexes in male meiocytes increases in response to temperature. The results demonstrate that the distribution of crossover events are malleable and can be shifted to proximal regions by altering the growth temperature. The shift in recombination is the result of altering the distribution of Class I crossovers, but the higher recombination at elevated temperatures is potentially not the result of an increase in Class I events (Phillips *et al* 2015).

References:

Barakate A, J.D. Higgins, S. Vivera, J. Stephens, R.M. Perry, L. Ramsay, I. Colas, H. Oakey, R. Waugh, F. C.Franklin, S.J. Armstrong, and C. Halpin. **2014**. The synaptonemal complex protein ZYP1 is required for imposition of meiotic crossovers in barley. Plant Cell 26 (2):729-740. doi:10.1105/tpc.113.121269.

Calderon Mdel C, M. D. Rey, A. Cabrera, and P. Prieto. 2014. The subtelomeric region is important for chromosome recognition and pairing during meiosis. Scientific reports 4:6488. doi:10.1038/srep06488.

Dreissig S, J. Fuchs, P. Capal, N. Kettles, E. Byrne, and A. Houben. 2015. Measuring Meiotic Crossovers via Multi-Locus Genotyping of Single Pollen Grains in Barley. Plos One 10 (9). doi:ARTN e0137677.

Phillips D, G. Jenkins, M. Macaulay, C. Nibau, J. Wnetrzak, D. Fallding, I. Colas, H. Oakey, R. Waugh, and L. Ramsay. 2015. The effect of temperature on the male and female recombination landscape of barley. New Phytol 208 (2):421-429. doi:10.1111/nph.13548.

Coordinator's report: *Eceriferum* genes

Udda Lundqvist

Nordic Genetic Resource Center (Nordgen)
P.O. Box 41, SE-230 53 Alnarp, Sweden

e-mail: udda.lundqvist@nordgen.org

Presence of wax coating and its composition is an important feature of the barley plant. It reduces evaporation of water from the plant and helps protect it against pathogens. The waxless *Eceriferum* and glossy mutants affect the presence and type of epicuticular waxes on the different organs. Many different surface wax mutants have been isolated as induced or spontaneous mutants and much research has been done during the last century both genetically and biochemically. All 79 defined loci are published as descriptions in Barley Genetics Newsletter (BGN) 42, later issues and some of them also updated in this volume. All descriptions are valid and up-to-date.

One allele of all the 79 gene loci have been backcrossed to a common genetic background the cultivar 'Bowman' by J.D. Franckowiak, USA. They are available as Near Isogenic Lines (NIL) at the Nordic Genetic Resource Centre (NordGen), Sweden, www.nordgen.org and at the Small Grain Germplasm Research Facility (USDA–ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov. But be aware of that many of the lines are a more advanced backcross derived line incorporated at NordGen than those at the Small Grain Research Facility in Aberdeen. The material in Sweden is well phenotyped and gets regenerated continuously.

Since the 1970s three with the highest numbers of alleles in the *Eceriferum* genes, *cer-c*, *cer-q* and *cer-u* with 215, 167 and 160 alleles, respectively, located in chromosome 2HS, very tightly linked, are discussed intensively. These genes affect the epicuticular wax coating on the spike and leaf sheath. They have been of large interest all the time. Intensive discussions were going on if it is one cluster gene, *cer-cqu*, or three different ones. Among all allele tested mutants in this region 13 were found to be multiple ones, among them 7 triple mutants. Mutations reverting in one step to wax formation have also occurred.

Schneider *et al*. (2016) report that recently developed genomic resources and mapping populations in barley defined the cluster gene *cer-cqu* to a small region on chromosome arm 2HS. Sequencing more than 50 independent mutants for each gene confirmed their identification. *Cer-c* is a chalcone synthase-like polyketide synthase, designated diketone synthase. *Cer-q* is a chalcone/carboxyl transferase and *Cer-u* is a P450 enzyme. A physical map revealed the order *Cer-c*, *Cer-u* and *Cer-q* with the flanking genes 101kb apart, confirming that they are a gene cluster, *Cer-cqu*. Homology-based modeling suggests that many of the mutant alleles affect overall protein structure or specific active site residues. By constructing several F2 mapping populations between the Near Isogenic Lines (NIL) BW 409 (*gsh6.s* allele, a mutation in the *cer-c* gene), BW 404 (*gsh1.a*, an allele in the *cer-q* gene) and BW 411 (*gsh8.ag*, an allele in the *cer-u* gene) and several cultivars defined in this SNP marker analyses the location of *Cer-c, Cer-q* and *Cer-u* to an interval flanked by distal marker 1_0718 and proximal marker 1_1059. After selecting candidate genes all results provide strong evidence that

MLOC_59804, *MLOC_13397* and *AK373499* encode *CER-C, -Q* and *U*, respectively. Thus the *cer-c* mutants that are caused by mutations in the CHS-like synthase encoded *MLOC_59804*, analysis of the mutants across the *MLOC_13397* model supports that *cer-q* encodes a lipase, and finally analysis supports the conclusion that *AK373499* (*Cer-u*) encodes a cytochrome *P450*. Finally the conclusion stated that *cer-c, cer-q* and *cer-u* are three different independent gene loci but very closely linked.

Li, Chao et al. (2015) reported on the characterization of epicuticular wax coating and genetic mapping of the *eceriferum-ym* (*cer-ym*) locus. The *cer-ym* mutant showed abnormally strong glossy spikes, sheaths and leaf blades. The mutant leaves showed a substantial reduction in the amounts of the major cutin monomers and a high increase in the main wax component. It is a semi-dwarf phenotype, a cutin defective mutant and is similar to the phenotype of Bowman-Near Isogenic line carrying the *cer-zv.268* allele, known as a cuticular recessive mutant. Analysis of Bowman-Near isogenic line BW 144 (*cer-ym.753*) compared with its wild barley accession 'OUH602' mapped the gene to chromosome 4H, co-segregated with AK364461 which is a marker that co-segregates with *cer-zv* in the pericentromeric region. *Cer-ym* was mapped within a 0.8 cm interval between EST marker AK370363 and AK251484. In conclusion *cer-ym* is located on chromosome 4H in the pericentromeric region which is very important for cuticle development.

Li, C. *et al*. (2012) reports on cuticle-associated genes that are protected by a cuticle against abiotic and biotic stresses. A better understanding of the determination of cuticle formation and function has the potential to contribute to the breeding of more drought tolerant and disease resistant crop cultivars. It was suggested by microarray analysis that some barley homologs have expression in epidermis of elongation zone of leaves where wax synthesis happens. The research demonstrates to facilitate the cloning of such genes. They found a case of complete linkage between an *eceriferum* (*cer*) locus and a known cuticle-associated gene: *HvCER6* of *Arabidopsis thaliana* and *eceriferum-zg* (*cer-zg*). This gene is affecting the epiticular wax coating on the leaf blades but reduced and only on the three upper leaves. It is located on chromosome 4H. *CER6* encodes an elongase condensing enzyme involved in the synthesis of very long chain fatty acid precursors. The data show therefore suggestive that *CER-ZG* might be the homolog of *AtCER6*. The phenotypes of *atcer6* and *cer-zg* mutants were similar to one another, therefore they suggest that *HvCER6* is the candidate gene of *CER-ZG*.

References:

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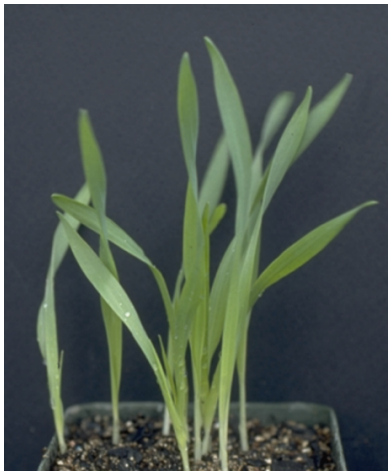
Li, Chao, Ch. Liu, X. Ma, A. Wang, R. Duan, Ch. Nawrath, T. Komatsuda, and G. Chen. 2015. Characterization and genetic mapping of *eceriferum-ym (cer-ym)*, a cutin deficient barley mutant with impaired leaf water retention capacity. Breeding Science 65:327-332.

Schneider, L M., N. M. Adamski, C.E. Christensen, D. B. Stuart, S. Vautrin, M. Hansson, C. Uauy, and P. von Wettstein-Knowles. 2016. The Cer-cqu gene cluster determines three players in a β-diketone synthase polyketyde pathway synthesizing aliphatics in epicuticular waxes. Journal of Experimental Botany Advance Access. Doi:10.1093/jxb/erw105.

BW404 (*gsh1.a*) mutant to the left compared with cultivar Bowman

BW409 (*gsh6.s*) to the left compared with cultivar Bowman

Eceriferum-zg (*cer-zg*) leaf blade to the left compared with cultivar Bowman



BW 144 (*cer-ym.753*) mutant to the left compared with cultivar Bowman, showing water drops on seedlings

Coordinator´s Report: Disease and Pest resistance genes

Caroline Breidenbach and Frank Ordon

Julius Kühn-Institute (JKI)
Institute for Resistance Research and Stress Tolerance
Erwin-Baur-Str. 27
D-06484 Quedlinburg, Germany

e-mail: frank.ordon@jki.bund.de

In the table below you will find papers published in 2015 extending last year´s list of information available on molecular markers for major resistance genes in barley published in Barley Genetics Newsletter 44.

List of papers published on mapped major resistance genes in barley updated until December 21, 2015

Resistance gene	Chromsomal location	Reference(s)
Puccinia graminis		
Rpg5	5H	Dracatos et al. 2015b, Mamo et al. 2015
rpg4	5H	Mamo et al. 2015
Puccinia hordei		
Rph3	7H	Gutiérrez et al. 2015
Rph20	5H	Dracatos et al. 2015a
Rph22	2H	Johnston et al. 2015
Rph23	7H	Singh et al. 2015, Dracatos et al. 2015a
Rynchosporium commune		
Rrs1	3H	Looseley et al. 2015
Pyrenophora teres		
Rpt4	7H	Tamang et al. 2015
Rpt6	5H	Tamang et al. 2015
Rpt7		Tamang et al. 2015
Ustilago nuda		
Un8	1H	Zang et al. 2015
Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV)		
Rym16^{Hb}	2H	Johnston et al. 2015

References:

Dracatos, P., D. Singh, U. Bansal, and R.F. Park, 2015a. Identification of new sources of adult plant resistance to *Puccinia hordei* in international barley (*Hordeum vulgare* L.) germplasm. Eur J Plant Pathol 141: 463-476.

Dracatos, P., D. Singh, T. Fetch, and R. Park, 2015b. Resistance to *Puccinia graminis f.sp avenae* in barley is associated with the Rpg5 Locus. Phytopathology105: 490-494.

Gutiérrez, L., S. Germán, P.M. Hayes, C.A. Pérez, F. Capettini, A. Locatelli, N.A. Berberian, E.E. Falconi, R. Estrada, D. Fros, V. Gonza, H. Altamirano, J. Huerto-Espino, E. Neyra, G. Orjeda, S. Sandoval-Islas, R. Singh, K. Turkington, and A.J. Castro, 2015. Multi-environment multi-QTL association mapping identifies disease resistance QTL in barley germplasm from Latin America. Theor. Appl Genet 128: 501-516.

Johnston, P.A., V. Meiyalaghan, M.E. Forbes, A. Habekuss, R.C. Butler, and R. Pickering, 2015. Marker assisted separation of resistance genes *Rph22* and *Rym16^{Hb}* from an associated yield penalty in a barley: *Hordeum bulbosum* introgression line. Theor Appl Genet 128: 1137-1149.

Looseley, M.E., R. Keith, D. Guy, G. Barral-Baron, A. Thirugnanasabandam, D. Harrap, P. Werner, and A.C. Newton, 2015. Genetic mapping of resistance to Rhynchosporium commune and characterization of early infection in a winter barley mapping population. Euphytica 203: 337-347.

Mamo, B.E., K.E. Smith, R.S. Brueggeman, and B.J. Steffenson, 2015. Genetic characterization of resistance to wheat stemm rust race TTKSK in landrace and wild barley accessions identifies the rpg4/Rpg5 locus. Phytopathology 105: 99-109.

Singh, D., P. Dracatos, L. Derevnina, M. Zhou, and R.F. Park, 2015. *Rph23*: A new designated additive adult plant resistance gene to leaf rust in barley on chromosome 7H. Plant Breeding 134: 62-69.

Tamang, P., A. Neupane, S. Mamidi, T. Friesen, and R. Brueggeman, 2015. Association mapping of seedling resistance to spot form net blotch in a world wide collection of barley. Phytopathology 105: 500-508.

Zang, W., P.E. Eckstein, M. Colin, D. Voth, A. Himmelbach, S. Beier, N. Stein, G.J. Scoles, and A.D. Beattie, 2015. Fine mapping and identification of a candidate gene for the barley Un8 true loose smut resistance gene. Theor Appl Genet 128: 1343-1357.

Coordinator's report: Nuclear genes affecting the chloroplast

Mats Hansson

Lund University,
Department of Biology,
Sölvegatan 35B,
SE-22362 Lund,
Sweden

E-mail: mats.hansson@biol.lu.se

Barley chlorophyll mutants have been named *albina*, *xantha*, *viridis*, *chlorina*, *tigrina* and *striata* depending on their colour and colour pattern. In the *albina* mutants the leaves are completely white due to lack of both chlorophyll and carotene pigments. The *xantha* mutants are yellow and produce carotene, but no chlorophyll. The *chlorina* and *viridis* mutants are both pale green, but differ in *chlorina* being viable. The *tigrina* and *striata* mutants are stripped transverse and along the leaves, respectively.

The fifth ring of the chlorophyll molecule is formed by the cyclase, which is the least known enzyme in the chlorophyll biosynthetic pathway. So far, only one subunit has been identified, encoded by *Xantha-l* in barley. Staccanella et al. (2015) used Arabidopsis mutants as well as the barley mutants *viridis-k.23*, *viridis-k.170*, *viridis-zb.63* and *xantha-l.35* to suggest that plastoquinol might function as an electron donor for the cyclase reaction.

Barley mutant *chlorina-f.104* was explored in a study concerning a chloroplastic protein with an NmrA domain, cpNrp (Brestic *et al*. 2015). The NmrA domain serves as a receptor for oxidized NAD^+/$NADP^+$ and the ability to discriminate between their oxidized and reduced forms may be linked to a possible role in redox sensing. The mutant *chlorina-f.104* shows a modified structure of the light-harvesting antennae and offered a useful system to examine the factors that determine the photosynthetic performance in leaves (Brestic *et al*. 2015). It was suggested that cpNrp is a member of a new protein family and can serve as a chloroplastic redox receptor.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found in Barley Genetics Newsletter issue 37 (2007): 37-43. Seeds of most mutants listed can be obtained from Mats Hansson (http://www.biology.lu.se/mats-hansson).

New references:

Brestic, M., M. Zivcak, M. Datko, K. Olsovska, O. Sytar and H. Shao. 2015. Novel resistance mechanism of barley chlorina f104 antenna mutant against photoinhibition: possible role of new identified chloroplasticn cpNrp protein. Theor. Exp. Plant Physiol. 27: 75-85.

Steccanella, V., M. Hansson and P. E. Jensen. 2015. Linking chlorophyll biosynthesis to a dynamic plastoquinone pool. Plant Physiol. Biochem. 97: 207-216.

Barley Genetics Newsletter (2015) 45:4-31

Coordinator's report: Early maturity and Praematurum genes

Udda Lundqvist

Nordic Genetic Resource Center (NordGen)
Smedjevägen 3
SE-23 053 Alnarp, Sweden

e-mail: udda.lundqvist@nordgen.org

The demand for early maturity in barley has become an important goal for plant breeding during the last century. Time of flowering has an important impact on yield and has been a key trait in the domestication of crop plants worldwide. Early maturity material has been collected in different geographic regions and climate conditions, today a critical issue in times of global warming. Many different *early maturity* and *Praematurum* mutants are isolated in many different cultivars, and they are stored in Gene banks in several parts of the world. Only in Scandinavia about 1250 different mutants have been isolated, their phenotypes described, analysed genetically and used in plant breeding worldwide. The *Praematurum* mutants are grouped into three categories according to their heading and maturity time with a variation between one and ten days: (1) drastically altered earliness; (2) medium increase of earliness; (3) slightly modified earliness. Long term studies made it possible to identify 10 early maturity (*eam*) and 9 *Praematurum* (*mat*) loci, among them also day-length neutral ones. All identified gene loci are incorporated into a common background, the barley cultivar 'Bowman' by J.D. Franckowiak, USA, and he established Bowman backcross derived lines (Near Isogenic Lines, 'NIL'). All these early maturity lines are well phenotyped, documentated and long-time stored in NordGen, Alnarp, Sweden. They are very important and useful for intensive molecular studies, cloning genes and understanding the barley genome.

Cultivated barley (*Hordeum vulgare L. subsp. vulgare*), like most temperate cereal crops, is a long day plant with two growth types, spring and winter. The growth habit is determined by the interaction of two genes; *Vrn-H2*, a strong inhibitor of flowering under long day conditions and *Vrn-H1* (also known as *HvVRN1*). Phytochromes play an important role in light signalling and photoperiodic control of flowering time in plants. Pankin *et al.* (2014) reported mapping and sequencing a candidate gene for the *Early maturity 5* (*Eam5*) locus. The Bowman Near-Isogenic Line having the *Eam5* allele is early flowering under both short and long day conditions, and the genetic interaction with the major barley photoperiod response gene *Ppd-H1* were analysed. The *Eam5* gene was originally located on chromosome 5H and originated from an ICARDA/CYMMIT selection. They suggested that the red/far-red light photoreceptor HvPhytochrome C (*HvPHYC*) is a candidate underlying the *early maturity 5* locus. They fine mapped the gene using a mapping-by-sequencing approach applied on the whole-exome capture data from bulked early flowering segregates derived from the backcrossed-derived Bowman line. They show that the *Eam5* gene disrupts circadian expression of clock genes, it also interacts with the major photoperiod response gene *Ppd-H1* to accelerate flowering under non-inductive short days. They suggest that *HvPHYC* participates in transmission of light signals to the circadian clock and thus modulates light-dependent processes such as photoperiodic regulation of flowering.. It also showed that *HvPHYC* carried a nonsynonymous mutation in the NIL Bowman line for *Eam5* which causes the missense substitution that leads to a change of the hydrophobic phenylalanine to the hydrophilic serine (mutation F380S).

Therefore they proposed that *HvPHYC* as the candidate gene for *Eam5*. They also found according to their segregation analysis that both *Vrn-H1* and *HvPHYC* were tightly linked to the early flowering phenotype.

Nishida *et al.* (2013) reported on different flowering time genes. The spring-type near isogenic line (NIL) of the winter-type barley (*Hordeum vulgare ssp. vulgare*) var. Hayakiso 2 (HK2) was developed by introducing *VERNALIZATION-H1 (Vrn-H1*) for spring growth habit from a spring-type var. Indo Omugi. Contrary to expectations, the spring-type NIL line flowered later than winter-type HK2. They stated that this phenotype difference was controlled by a single gene, which co-segregated only with *phytochromeC (HvPhyC*) which is one of the candidates around the *Vrn-H1* region (*Vrn-H1, HvPhycC and CASEIN KINASE IIα*). That indicated that *HvPhyC* was the most likely candidate gene for flowering time. Compared with the late flowering allele *HvPhyC-l* from NIL, the early-flowering allele *HvPhyC-e* from HK2 had a single nucleotide polymorphism T1139C in exon 1, which caused a nonsynonymous amino acid substitution of phenylalanine at position 380 by serine in the functionally essential GAF domain. Functional assay using a rice (*Oryza sativa*) *PhyA phyC* double mutant line showed that both of the *HvPhyC* alleles are functional, but *HvPhyC-e* have a hyperfunction. Expression analyses using NILs carrying *HvPhyC-e* and *HvPhyC-l*, respectively, showed that *HvPhyC-e* up-regulated only the flowering promoter *FLOWERING LOCUS T1* by bypassing the circadian clock genes and flowering integrator *CONSTANS1* under a long photoperiod. There were no apparent differences in *HvPhyC* expression between NIL (*HvPhyC-e*) and NIL (*HvPhyC-l*), despite their allelic differences. In both of the NILs, *HvPHyC* was expressed all day and seemed to show diurnal fluctuation under both long and short photoperiod conditions with the trend that it was up-regulated around dusk and down-regulated during the day. They also stressed in addition to the above mentioned genes, novel gene resources for early flowering will be important to elucidate the genetic mechanism of the flowering time and future breeding programs. Recent comparative studies in genetic pathways for flowering revealed that temperate grass species share a similar gene set with dicot species *Arabidopsis*, especially for photoperiodic pathways.

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Pankin, A., C. Campoli, X. Dong, B. Kilian, R. Sharma, A. Himmelbach, R. Saini, S.J. Davis, N. Stein, K. Schneeberger, and M. von Korff. 2014. Mapping-by-sequencing Identifies *HvPHYTOCHROME C* as a candidate gene for the *early maturity 5* Locus modulating the circadian clock and photoperiodic flowering in barley. Genetics 198:383-396.

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Coordinator's report: ear morphology genes

Michele Stanca

Department of Life Science, UNIMORE - Reggio Emilia, Italy
michele@stanca.it

Valeria Terzi

CREA-GPG, Genomics Research Centre, Fiorenzuola d'Arda, Italy
valeria.terzi@ crea.gov.it

Barley today ranks fourth behind wheat, rice and maize among the world's cereals for the importance of its contribution, whether direct or indirect, to the production of food. The global production is estimated in 2015 in 135 millions of metric tons (Mt) in a harvested area of 50 millions of hectares with an average grain yield of 2.7 t/ha.

Barley spike is one of the important source of food for humans and it has been estimated that barley production needs to increase to meet demand of increasing population. This means that the grain number of the barley spike must be improved in the near future, together with the biomass increase. As reported in previous Barley Genetic Newsletter (BGN) reports, grain number enhancement can be theoretically obtained through modifications of the spike fertility and morphology. Due to the implications in grain production and yield, the genetic dissection of the developmental plan of this storage sink is therefore of outstanding relevance to design the barley for the future in which innovative traits can be implemented through pre-breeding strategies.

Barley developmental mutants can be a Mendelian solution to identify genes controlling key steps in the establishment of the spike morphology. Large collections of natural and induced mutants have been developed since the 1920s, with the aim of understanding developmental and physiological processes and exploiting mutation breeding in crop improvement. The collections are comprehensive not only of single Mendelian spike mutants, but even of double and triple mutants obtained by intercrossing simple mutants. In recent years the integration of the most advanced omic technologies with the historical mutation-genetics research helped in the isolation and validation of some of the genes involved in spike development. Interestingly, some genes known from long time to be responsible for mutant phenotype have been recently cloned and functionally characters. Several of these genes are involved in mutations that, selected by ancient farmers, transformed wild plants in domesticated ones, giving a major contribution to the development of early agrarian societies. The most important trait selected by humans during the barley domestication process and related to the evolution of barley spike is the transformation of brittle into non-brittle spike. Loss of the natural mode of grain dispersal was perhaps the most important single event in this process. At maturity, the spike in wild (i.e. ancestral) barley forms ‘‘constriction grooves’’ and disarticulates at each rachis node, allowing mature grain to disperse freely. This phenotype is referred to as ‘‘brittle rachis.’’ Classical genetic studies have established that a mutation in either of two complementary and tightly linked genes on barley chromosome 3HS, Non-brittle rachis 1 (*btr1*) or Non-brittle rachis 2 *(btr2*), converts the brittle rachis into a non-brittle type. Pourkheirandish *et al*. (2015) identify *Btr1 and Btr2* genes and elucidate the mechanism underlying disarticulation of the wild-type barley spike. Independent recessive mutations in each of these genes caused cell wall thickening in a highly specific grain ‘disarticulation zone’, converting the brittle floral axis (the rachis) of the wild-type into a tough, non-brittle form that promoted grain retention.

The authors hypothize that anthropogenic selection operated in favor of mutations in two adjacent complementary dominant genes, the products of which are suggestive of a signal transducing receptor and its protein ligand. The two genes products, BRT1 and BRT2, act together to control the cell wall thickening in the disarticulation zone of the rachis node through a molecular mechanism using comparative DNA sequence information and archaeo botanical data. The authors demonstrated independent origin of barley domestication. Two ‘‘transition zones’’ were found, where major frequency changes between *btr1*- and *btr2*-types occur: the region between Iran and Afghanistan and the Levant and the southern part of the Mediterranean Sea. Besides these two transition zones, *btr1*-types were found to predominate in India and Ethiopia. While possible that *btr1*- and *btr2*-type barleys may be better adapted to different eco-climatic zones, an alternative scenario is that their current distribution is a direct result of human migration.

Figure 1 Spike of a barley plant derived from the small caryopsis “seeded in hood”. It is evident the large size of the hood in which fertile organs are well developed.

Figure 2 Reproductive organs in the Hood and developing grain "Seeded in Hood"

***Laxatum* (*lax*) and *Cleistogami* (*cly1*).**

Reduction or increase of the rachis internode length results in different spike density. Classical genetic studies have identified several loci involved in modulation of spike density, such as dense spike, zeocriton and laxatum. Spike density in barley is under the control of several major genes, as documented previously by genetic analysis of a number of morphological mutants.
The recessive mutation laxatum-a (*lax-a*) in barley, which causes pleiotropic changes in spike development resulting in:
(i) extended rachis internodes conferring a more relaxed (lax) inflorescence.
(ii) broadened base of the lemma awns.
(iii) thinner grains that are largely exposed due to reduced marginal-growth of the palea and lemma.
(iv) and homeotic conversion of lodicules into two stamenoid structures.

Map-based-cloning enforced by mapping-by-sequencing of the mutant *lax-a* locus enabled the identification of a homolog of BLADE-ON-PETIOLE1 and 2 (BOP1 and 2) as the causal gene. Cloning of the *laxatum*-a gene might open future perspectives in plant breeding, provide that adverse phenotypic effects can be moderated or eliminated. *Laxatum* florets can open without impetus force of lodicules, which were previously reported to be essential for open flowering in barley. Since the wild-type structure of lemma and palea help keeping barley flowers closed during anthesis, the open flowering *laxatum-a* phenotype may help to achieve open flowering independent of lodicules to facilitate hybrid breeding in barley. Furthermore and similarly to the effect of the *nud* gene, the mostly hulless *lax-a* seeds should be preferred for human food supply. The relaxed spike architecture should be beneficial in humid growing conditions to unfavor fungal growth and to achieve robust dry seeds for mechanical harvest. (Jost *et al*. 2016).

The closed floret habit (cleistogamy) is under the control of *cly1*, a gene that operates by inhibiting the development of the lodicule. In non-cleistogamous cultivars, *cly1* mRNA is degraded by miR172-directed cleavage, allowing the lodicules to swell; however, in cultivars carrying the recessive allele *cly1.b*, a single-nucleotide substitution destroys the miR172 target site preventing mRNA cleavage. Barley cv. SV235 is cleistogamous; its *cly1* coding sequence is identical to that of *cly1.b*, but its lodicules develop, although insufficiently to produce a non-cleistogamous flower. In this cultivar, the downregulation of *cly1* is unrelated to miR172-directed mRNA degradation, but rather caused by an epiallele that represses transcription. Allelic relationships between known *cly1* alleles were explored by the quantification of lodicule vascularization and an assessment of the response of the spike to the supply of exogenous auxin. The SV235 phenotype can be manipulated by a pre-anthesis application of 2,4-D, a feature that could be of interest in the context of hybrid barley grain production based on cleistogamy. The application of 2,4-D to spikes of *cly1.b2* carriers induced floret gaping and anther extrusion, thereby offering the possibility of manipulating flower type by the simple expedient of spraying with 2,4-D. In the context of F_1-hybrid grain production, fully open flowering is necessary for both pollen dispersal and cross-pollination. The *cly1.b2* allele offers a practical means of controlling flowering type in F_1-hybrids involving two carriers of *cly1.b2*. A 2,4-D application supplied prior to anthesis should encourage the non-cleistogamy needed for F_1-hybrid grain production, while the F_1-hybrid plants themselves are cultivated normally and so remain cleistogamous. Closed flowering is advantageous as it limits the entry of certain pathogens (in particular Fusarium head blight fungus) and inhibits pollen-derived gene flow (important in the context of genetically modified varieties). (Wang e*t al*.2015).

Florigen is a systematic signal that is produced in leaves in response to the stimulus of inductive day length and is transported to the shoot apex to induce flowering. Li *et al*. (2015) have studied the FLOWERING LOCUS T (FT) protein as central component of a mobile flowering signal (florigen) that is transported from leaves to the shoot apical meristem (SAM). Two FT monomers and two DNA-binding bZIP transcription factors interact with a dimeric 14-3-3 protein bridge to form a hexameric protein complex. This complex, designated as the 'florigen activation complex' (FAC), plays a critical role in flowering. The wheat homologue of FT, designated FT1 (= VRN3), activates expression of *VRN1* in the leaves and the SAM, promoting flowering under inductive long days. The authors show that FT1, other FT-like proteins, and different FD-like proteins, can interact with multiple wheat and barley 14-3-3 proteins, and they also identify the critical amino acid residues in FT1 and FD-like proteins required for their interactions, and demonstrate that 14-3-3 proteins are necessary bridges to mediate the FT1–TaFDL2 interaction. Using *in vivo* bimolecular fluorescent complementation (BiFC) assays, it has been demonstrated that the interaction between FT1 and 14-3-3 occurs in the cytoplasm, and that this complex is then translocated to the nucleus, where it interacts with TaFDL2 to form a FAC. In addition the authors demonstrate that a FAC including FT1, TaFDL2 and Ta14-3-3C can bind to the *VRN1* promoter *in vitro* and finally, they show that relative transcript levels of *FD-like* and *14-3-3* genes vary among tissues and developmental stages. Since FD-like proteins determine the DNA specificity of the FACs, variation in *FD-like* gene expression can result in spatial and temporal modulation of the effects of mobile FT-like signals.

Compositum Barley

Canonical barley spike has a branchless shape. However, mutants characterized by branched spikes have been described as naturally occurring since ancient times. Poly-row-and-branched spike (*prbs*) mutation has been described as involved in the inflorescence differentiation from a panicle into a spike. This mutation in fact can alter the inflorescence morphology in two ways: a) determining the conversion of the rudimentary lateral spikelets specific of two-rowed genotypes into fertile spikelets, b) determining the development of additional spikelets in the middle of the spike, resulting in a branched spike. In mutant *prbs*, new meristems initiated at the flanks of lateral spikelets and middle spikelet meristems were converted to branch meristems, developing branched spike. *Prbs* gene has been mapped on chromosome 3H and demonstrated that this gene is not allelic to *Vrs4*. *Vrs4* has been found involved even in another mutant phenotype derived from a particular development of the node.

'Compositum-Barley' and tetraploid 'Miracle-Wheat' (*T. Turgidum* convar. *compositum* (L.f.) Filat.) display non-canonical spike-branching in which spikelets are replaced by lateral branch-like structures resembling small-sized secondary spikes. As a result of this branch formation 'Miracle-Wheat' produces significantly more grains per spike, leading to higher spike yield. Poursarebani *et al*. (2015) investigated the genetic and molecular basis of "true spike-branching" in 'Compositum-Barley' and tetraploid 'Miracle-Wheat'

The gene *com2* was positional cloned on barley chromosome 2HS, and found that it is orthologous to *bht* that regulates spike-branching in 'Miracle-Wheat'. Both genes possess orthologs with similar functions in maize *BRANCHED SILKLESS 1* [(*BD1*); rice *FRIZZY PANICLE/BRANCHED FLORETLESS 1* [(*FZP/BFL1*); and *Brachypodium distachyon MORE SPIKELETS 1* (*MOS1*)]. This candidate gene represents a putative transcription factor consisting of a single exon, encoding a protein of 307 amino acids containing an ethylene-responsive element DNA binding factor (i.e. AP2/ERF). mRNA *in situ* hybridization, microarray experiments, and independent qRT-PCR validation analyses revealed that the branch repression pathway in barley is governed through the spike architecture gene *Six-rowed spike 4* regulating *COM2* expression, while *HvIDS1* (barley ortholog of maize *INDETERMINATE SPIKELET 1*) is a putative down-stream target of *COM2*. These findings provide new insights into the genetic basis of spike architecture in *Triticeae*, and have disclosed new targets for genetic manipulations aiming at boosting yield potential.

Liller *et al*. (2015) recently evidenciated that mutation in barley row type genes have pleiotropic effect on shoot branching. They suggest that the same genes or regulatory modules can regulate both inflorescence branching and tillering, and they studied pleiotropic effects of row type genes on seed size, seed number per spike, thousand grain weight and tillering in barley to better understand the genetic correlations between individual yield components. Allelic mutants of nine different row type loci (36 mutants), in the original spring barley cultivars Barke, Bonus, Foma and introgressed in the spring barley cultivar Bowman, were phenotyped under greenhouse and outdoor conditions. Two main mutant groups were identified and characterized by their relationships between seed and tillering parameters. The first group comprises all mutants with an increased number of seeds and significant change in tiller number at early development (group 1a) or reduced tillering only at full maturity (group 1b). Mutants in the second group are characterized by a reduction in seeds per spike and tiller number, thus exhibiting positive correlations between seed and tiller number. Reduced tillering at full maturity (group 1b) is likely due to resource limitations. In contrast, altered tillering at early development (groups 1a and 2) suggests that the same genes or regulatory modules affect inflorescence and shoot branching. Genes involved in development of the branched inflorescence architecture of the grasses also control seed size and shoot branching. These results indicate that correlations between shoot and spike architecture are due to a) competition between different sink organs for limited assimilates or b) the direct involvement of row type genes in the initiation and growth control of different plant organs, seeds and tillers. The authors thus speculate that the same regulatory genes or modules may control the development of different meristematic structures

andorgans in plants. Understanding how these genes are regulated and in turn control downstream targets in different plant organs is important to improve yield by modifying shoot and spike architecture. Understanding the genetic bases of the trade-offs between these traits is important for the genetic manipulation of individual yield components.

Double Mutants

Double mutants *Hv-Hd/tw*$_2$, formed by hybridization, are characterized by inherited phenotypic instability and by several new features, such as bract/leaf-like structures, long naked gaps in the spike, and a wide spectrum of variations in the basic and ectopic flowers which are absent in single mutants. Several of these features resemble those of mutations in auxin distribution, and thus the aim of this study was to determine whether auxin imbalances are related to phenotypic variations and instability. The effects of auxin inhibitors and 2,4-D (2,4-dichlorophenoxyacetic acid) on variation in basic and ectopic flowers were therefore examined, together with the effects of 2,4-D on spike structure. The occurrences of various malformations of spike structure, including leaf/bract-like structures, also demonstrate the existence of other developmental trends. Consequently, phenotypically unstable barley double mutants are a highly promising genetic system for the investigation of gene expression modules and trend rodersi. (Šiukšta *et al*. 2015)

The *erectoides-m anthocyanin-less 1* (*ert-m ant1*) double mutants are among the very few examples of induced double mutants in barley. From phenotypic observations of mutant plants it is known that the *Ert-m* gene product regulates plant architecture whereas the *Ant1* gene product is involved in anthocyanin biosynthesis. Zakhrabekova *et al*. (2015) used a near-isogenic line of the cultivar Bowman, BW316 (*ert-m.34*), to create four F_2-mapping populations by crosses to the barley cultivars Barke, Morex, Bowman and Quench. They phenotyped and genotyped 460 plants, allowing the *ert-m* mutation to be mapped to an interval of 4.7 cM on the short arm of barley chromosome 7H. Bioinformatic searches identified 21 candidate gene models in the mapped region. One gene was orthologous to a regulator of *Arabidopsis thaliana* plant architecture, *ERECTA,* encoding a leucine-rich repeat receptor-like kinase. Sequencing of *HvERECTA* in barley, *ert-m* mutant accessions identified severe DNA changes in 15 mutants, including full gene deletions in *ert-m.40* and *ert-m.64.* Both deletions, additionally causing anthocyanin deficiency, were found to stretch over a large region including two putative candidate genes for the anthocyanin biosynthesis locus *Ant1*. Analyses of *ert-m* and *ant1* single- and double-deletion mutants suggest *Ant1* as a closely linked gene encoding a R2R3 myeloblastosis transcription factor.

The *mirEX 2.0* portal provides the plant research community with easily accessible data and powerful tools for application in multi-conditioned analyses of miRNA expression from important plant species in different biological and developmental backgrounds. Zielenzinnski *et al*. (2015) demonstrate that the mirEX 2.0 portal is dedicated to researchers working on specific microRNA functions and expression profiles of entire microRNA family members during a particular organ/developmental stage or on microRNA biogenesis and evolution. The mirEX 2.0 web-based portal is a one-stop solution for the exploration of plant microRNA expression data covering mutants and three plant species representing scientifically (*Arabidopsis thaliana*), economically (*Hordeum vulgare*), and evolutionarily (*Pellia endiviifolia*) attractive research models. The provided user-friendly tools allow to explore expression data in any combination of species, tissues and developmental stages, thus leading to the rapid discovery and hypothesis-building of underlying relations and regulatory mechanisms. The developed technology also allows for unlimited further expansion of the data content and provides an environment for the design of novel tools following the needs of the plant community involved in the exploration of microRNA biology.

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Coordinator's report: Semidwarf genes

Jerry D. Franckowiak

Department of Agronomy and Plant Genetics
University of Minnesota Twin Cities
411 Borlaug Hall
1991 Upper Buford Circle
St Paul, MN 55108, USA

e-mail: jfrancko@umn.edu

Yield losses and quality reductions caused by lodging are a frequent production problem in barley (*Hordeum vulgare* L.) Minimizing such losses has been a goal of barley growers since the crop was domesticated. The strategy most frequently employed to minimize losses is a genetic reduction of plant height. However, lodging is a complex trait in which can be expressed from around heading time until harvest. Lodging about heading is often the most frequent cause of losses, but post-ripe straw breakage or crinkling of straw prior to mechanical harvest causes losses also.

Plant height genes - Mutant genes that reduced plant height or elongation of culm internodes are often the focus of breeding efforts. The most commonly used genes for height reduction in barley have involved specific alleles at three loci: the *uzu1.a* allele at the uzu 1 locus, the *sdw1.c* (denso) allele at the semidwarf 1 locus, and *ari-e.GP* (Golden Promise) allele at the breviaristatum-e locus. The *uzu1.a* gene was widely used in winter barleys developed in East Asia (Chono *et al*., 2003; Dockter *et al*., 2014). The *sdw1.c* gene has been widely deployed in Europe and is used in some other barley growing regions of the world (Jia *et al*., 2011; Malosetti *et al*., 2011). The *ari-e.GP* has been used to a limited extent in England and Australia (Ellis *et al*., 2002; Malosetti *et al*., 2011; Walia *et al*., 2007). More recently the *sdw4.ad* allele at the semidwarf 4 locus has found favor in winter grown spring barley cultivars developed for China and Japan (Sameri *et al.,* 2009; Yu *et al*., 2010). Despite their favorable effects on plant height, worldwide deployment of these semi-dwarfing genes in barley improvement is restricted because their origin in genetic background poorly adapted to the target production area and the semidwarf genes have pleiotropic effects on other agronomic characteristics. Most notable are the sensitivity of the *uzu1*.a mutant to high temperatures (Dockter *et al*., 2014) and delayed maturity associated with *sdw1.c* and other mutants at that locus (Jia *et al*., 2011).

Haploblock identification - The characterized semidwarf genes do not explain all the observed variation in plant height (Pasum *et al*., 2012). The advent of relatively dense molecular maps for barley has facilitated further dissection of qualitative trait loci (QTL) associated with specific traits. Using identity by descent and allele associated haplotypes, or preferably a haploblock of adjacent molecular markers, presence or absence of specific height genes can be determined in breeding materials and historic cultivars. Using procedures for DArTseq marker identification (Diversity Arrays Technology, Yarralumla, ACT 2600, Australia; http://www.diversityarrays.com), over 10,000 polymorphic SNP markers with assigned chromosomal positions were characterized for an array of Australian breeding lines, cultivars, and historic accessions (Wang *et al*., 2015). Visual realignment of markers based on breakpoints in a doubled-haploid population (NRB091087/NRB091047) and closely related breeding lines increased the number of positioned markers to

over 17,000. The relative positions of the realigned markers were used to identify haploblocks associated with specific plant height genes (Table 1).

Additional plant height genes – Haploblocks associated with semidwarf genes should be present in short stature breeding lines; however, this association was not observed in all Australian semidwarf cultivars. Likewise in a worldwide collection of barley cultivars, Pasum *et al*. (2012) reported that QTL distributed across the barley genome are associated with variation in plant height. Hence, additional semidwarf loci may exit in cultivated barley. One candidate group is the semidwarf accessions that originated from the International Center for Agricultural Research in the Dry Areas (ICARDA) barley breeding program at the International Maize and Wheat Improvement Center (CIMMYT) in Mexico. Negeri (2009) identified a plant height QTL in the short arm of chromosome 6H in the Chinese cultivar Shenmai 3 (Gobernadora/Humai 10), which was selected at CIMMYT from a cross to Gobernadora (OC640/Mari//Pioneer/3/Maris Concord). A unique haploblock was found in 6HS in Canela (Maris Canon/Laurel//Aleli) and several other ICARDA lines from Mexico (Table 1). This haploblock is near the 6HS position was identified by Pasum *et al*. (2012) as having a large effect on plant height. The recommended locus symbol for this QTL is *sdw5* and the recommended allele symbol is *sdw5.be*. The haploblock associated with the *sdw5.be* allele is present in several Australian cultivars. These include Commander (Keel/Sloop//Galaxy) and Keel (CPI18197/Clipper//WI2645).

The semidwarf genes are considered here because their deployment of various combinations can further reduce plant height and may reduce losses caused by lodging. The presence of various haploblocks associated with plant height genes suggests that several Australian cultivars already have two or more semidwarf genes. Hindmarsh (Chariot/VB9409) has the haploblocks associated with the *ari-e.GP* and *sdw1.c* genes. Commander has the haploblocks associated with *sdw1.c* and *sdw5.be*. Since other relatively short stature cultivars have one or no identified semidwarf gene, additional semidwarf genes in cultivated barley are still to be identified.

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Table 1. A partial list of plant height genes involved in adaptation of barley to specific production areas including origin, chromosomal position, and phenotypic effects.

Locus name	Chromosome position		DArTseq marker / phase	Marker position	Gene or mutant source	Probable trait origin	Notes
Plant height genes							
sdw1.c (denso)	Semidwarf 1	3H bin12	3264976 - 3663177 - 3397429 +	124.00	Abed Denso Triumph	Europe	Reduced height, delayed heading and smaller kernels
sdw4.ba	Semidwarf 4	7H bin11	3661780 - 3265446 + 3396373 -	118.24	Zhenongda 7	China	China / Japan semidwarf, short basal culm internodes
Table 1 continued							
sdw5.be (q6HT4)	Semidwarf 5	6H bin05	3985790 + 4189414 + 3931643 +	35.98	Canela Keel	Mexico Australia	Semidwarf gene in CIMMYT-ICARDA cultivars
ari-e.GP	Breviaristatum-e	5H bin06	4186599 + 3273517 + 3273238 +	50.00	Golden Promise	England	Short awned semidwarf mutant from Maythorpe
uzu1.a (HvBRI1)	Uzu 1	3H bin06	Gene not present		Winter six-rowed	China	Degree of dwarfing is temperature sensitive, short awns

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Coordinator's report: Wheat-barley genetic stocks

A.K.M.R. Islam

Faculty of Agriculture, Food & Wine
The University of Adelaide, Waite Campus,
Glen Osmond, SA 5064, Australia

e-mail: akm.islam@adelaide.edu.au

It has been possible to produce five disomic addition lines (2H,3H,4H,6H,7H) of six-rowed Ukrainian winter barley cultivar 'Manas' to 'Asakazi' wheat (Marta Molnar- Lang et al 2012). Furthermore, new wheat x barley hybrids (wheat Mr9kr1 x barley Igri; wheat Mr9kr1 x barley Betzes; wheat Asakaze komugi x barley Manas have been produced by (M.Molnar-Lang et al 2000, E.Szakacs et al 2007, I. Molnar et al 2007) Partial sets of addition, substitution and translocation lines were then developed from these hybrids. Tatyana et al (2013) reported the production of ditelosomic 7HL(7D) and monotelosomic 7HL(7A) and 7HL(7B) substitution lines of *Hordeum marinum ssp gassoneanum* to common wheat cv. Saratovskaya.

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Szakas,E. and M. Molnar-Lang. 2007. Development and Molecular Cytogenetic Identification of New Winter Wheat/Winter Barley (Martonvasari 9 kr1/Igri) Disomic Addition Lines. Genome, Vol. 50, No. 1, pp. 43-50.

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Descriptions of barley genetic stocks for 2015

Jerome D. Franckowiak[1], Andy Kleinhofs[2] and Udda Lundqvist[3]

[1] Department of Agronomy and Plant Genetics
University of Minnesota Twin Cities
411 Borlaug Hall
1991 Upper Buford Circle
St Paul, MN 55108, USA
[2]Department of Crop and Soil Sciences
Washington State University
Pullman, WA 99164-6420
[3]Nordic Genetic Resource Center (NordGen)
P.O. Box 41, SE-230 53 Alnarp, Sweden

e-mail: jfrancko@umn.edu
andyk@wsu.edu
udda.lundqvist@nordgen.org

In this volume of the Barley Genetics Newsletter, one hundred and twenty-two 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

Table 1. A listing of new and revised Barley Genetic Stock (BGS) descriptions published in volume 45 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.				
10	lks2	lk2, lk4	7HL	Short awn 2	45:80	566
11	ubs4	lks2, ari-d	7HL	Unbranched style 4	45:84	567
31	sex6	ssIIa	7HS	Shrunken endosperm xenia 6	45:86	2476
34	msg50	msg,,hm	7HL	Male sterile genetic 50	45:88	2404
44	brh16	brh.v, ari-o	7HL	Brachytic 16	45:89	1686
59	gpa1	gp, gp2	2HL	Grandpa 1	45:91	519
60	lig1	li, aur-a	2HL	Liguleless 1	45:93	6
71	com2	bir2	2HS	Compositum2	45:95	1700
74	flo-c	flo-a	6HL	Extra floret-c	45:97	1743
80	ant2	pr, rub	2HL	Anthocyanin-less 2	45:98	1632
92	ert-u	br5, ari-o	7HL	Erectoides-u	45:100	496
93	ert-zd	br7, ari-o	7HL	Erectoides-zd	45:102	504
102	uzu1	u, *HvBRI1*	2HL	Uzu1, Semi-brachytic 1	45:104	1300
133	sdw2	sdw-b	3HL	Semidwarf 2	45:108	2466
135	ert-ii	uzu1	3HL	Erectoides-ii	45:109	483
148	brh14	brh.q, ari-o	7HL	Brachytic 14	45:111	1682
166	msg25	msg,,r	4HL	Male sterile genetic 25	45:113	744
168	glo-a	glo-a	4H	Globosum-a	45:115	1328
182	flo-a	flo-a	6HL	Extra floret-a	45:116	1741
230	glo-e		3HL	Globosum-e	45:117	1755
252	eam7	ea7, HvCO7	6HS	Early matyrity 7	45:118	579
260	fch11	f11	6HL	Chlorina seedling 11	45:120	1738
327	flo-b	flo-a	6HL	Extra floret-b	45:121	1742
335	msg49	msg,,jw	5HL	Male sterile genetic 49	45:122	2402
348	Eam5	HvPhyC-e	5HL	Early maturity 5	45:123	
357	msg1	ms, ms1	1HL	Male sterile genetic 1	45:126	1810
358	msg2	ms2	2HL	Male sterile genetic 2	45:128	
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	1842

Table 1 continued

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	ms20	4H	Male sterile genetic 20	45:156	2372
376	msg21	ms21	1HL	Male sterile genetic 21	45:157	2373
377	seg1	se1	5H	Shrunken endosperm genetic 1	45:158	750
379	seg3	se3, ant17	3HS	Shrunken endosperm genetic 3	45:160	752
383	msg22	ms22	7H	Male sterile genetic 22	45:162	741, 2374
384	msg23	ms23	5H	Male sterile genetic 23	45:163	2375
385	msg24	ms24	4HL	Male sterile genetic 24	45:164	2376
395	msg26	msg,,u	7HS	Male sterile genetic 26	45:166	2378
411	cer-r	cer-r	3HL	Eceriferum-r	45:168	439
455	seg8	se8	7H	Shrunken endosperm genetic 8	45:170	2469
460	cur4	cu4, glo-d	2HL	Curly 4	45:172	1708
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
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	2394
505	msg42	msg,,db	3H	Male sterile genetic 42	45:193	2395

Table 1 continued

BGS no.	Locus Symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
506	msg43	msg,,br	2HL	Male sterile genetic 43	45:194	2396
507	msg44	msg,,cx	5HL	Male sterile genetic 44	45:195	2397
508	msg45	msg,,dp	5HL/ 7HS	Male sterile genetic 45	45:196	2398
509	msg46	msg,,ec	2H/6H	Male sterile genetic 46	45:197	2399
510	msg 47	msg,,ep	3HS/ 7HS	Male sterile genetic 47	45:198	2400
520	msg48	msg,,jt	1H	Male sterile genetic 48	45:199	2401
556	ari-o	ari-o	7HL	Breviaristatum-o	45:200	1663
566	ert-t	ert-t, brh3	2HS	Erectoides-t	45:203	494
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
580	mat-d	mat-d	4HL/6HL	Praematurum-d	45:208	1790
582	mat-f	mat-f	1H	Praematurum-f	45:210	1792
584	mat-h	mat-h	4HL	Praematurum-h	45:212	1794
585	mat-i	mat-i	7HL	Praematurum-i	45:214	1795
592	yhd2	yh2		Yellow head 2	45:215	757
595	ant4	ant4	4H	Anthocyanin-deficient 4	45:216	1642
599	ant17		3HS	Proanthocyanidin-free 17	45:218	1628
600	ant18		3H	Proanthocyanidin-free 18	45:221	1630
613	brc1	brc-5, com2	2HS	Branched 1	45:224	
624	ops1	op-3	7HS	Opposite spikelets 1	45:226	2427
627	viv-a	viv-5	2H	Viviparoides-a	45:227	2498
629	mtt6	mtt6	7HS	Mottled leaf 6	45:228	2411
631	brh3	brh.g, ert-t	2HS	Brachytic 3	45:229	1672
653	brh10	brh.l	2HS	Brachytic 10	45:231	1677
654	brh11	brh.n	5HS	Brachytic 11	45:232	1679
655	brh12	brh.o	5HS	Brachytic 12	45:233	1680
656	brh13	brh.p	5HS	Brachytic 13	45:234	1681
658	brh17	brh.ab	5HS	Brachytic 17	45:236	1669
659	brh18	brh.ac, brh13	5HS	Brachytic 18	45:237	1670
678	ari-u	ert-t	2HS	Breviaristatum-u	45:239	
716	ibl1	ibl1		Intense blue aleurone 1	45:241	
730	lab1		5HL	Labile 1	45:243	
731	rpr2	γ08-118; R43-22#1		Required for *Puccinia graminis* resistance 2	45:245	3693
732	rpr3	γ08-112; R12-31#3		Required for *Puccinia graminis* resistance 3	45:244	3696

Table 1 continued

BGS no.	Locus Symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
733	rpr4	γ08-114; R36-37#1		Required for *Puccinia graminis* resistance 4	45:245	3697
734	rpr5	γ08-117; R42-33#5		Required for *Puccinia graminis* resistance 5	45:246	3699
735	rpr6	γ08-119; R47-23#1		Required for *Puccinia graminis* resistance 6	45:247	3700
736	rpr7	γ08-115; R3-18#3		Required for *Puccinia graminis* resistance 7	45:248	3701
737	rcr1	γ08-122; R4-29		Required for resistance to *Cochliobolus sativus* 1	45:249	3702
738	rcr2	γ08-123; R4-40		Required for resistance to *Cochliobolus sativus* 2	45:250	3703
739	rcr3	γ08-124		Required for resistance to *Cochliobolus sativus* 3	45:251	3704

* 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 (2015).

Jerome D. Franckowiak[1] and Udda Lundqvist[2]

[1] Department of Agronomy and Plant Genetics
University of Minnesota Twin Cities
411 Borlaug Hall, 1991 Upper Buford Circle
St Paul, MN 55108, USA
[2]Nordic Genetic Resource Center (NordGen)
Smedjevägen 3, SE-230 53 Alnarp, Sweden

e-mail: jfrancko@umn.edu
udda.lundqvist@nordgen.org

In this section of the Barley Genetics Newsletter, 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 recent issues of the Barley Genetics Newsletter with chromosome location information, recommended locus symbols, locus names, 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 chromosomal locations, recommended locus names, 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, chromosome location information, locus names, description citation, and the accession number for the genetic stock.

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	43: 48	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	44: 57	487
31	sex6	ssIIa	7HS	Shrunken endosperm xenia 6	45: 86	2476
32	Rph9	Pa9	5HL	Reaction to *Puccinia hordei* 9	37:201	1601
33	ant1	rs, rub-a	7HS	Anthocyanin-less 1	42: 89	1620

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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	41: 80	
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	26: 87	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	Ppd-H1, Ea	2HS	Early maturity 1	44: 64	1316
66	vrs1	V^d	2HL	Two-rowed spike 1	26:103	346
67	vrs1	V^t	2HL	Deficiens 1	26:104	684
68	Pvc 1	P_c	2HL	Purple veined lemma 1	44: 67	132
69	Gth 1	G	2HL	Toothed lemma 1	44: 68	309
70	Rph1	Pa	2H	Reaction to *Puccinia hordei* 1	26:107	1313

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
71	com2	bir2	2HS	Compositum 2	45: 95	1700
72	glo-c	glo-c	2H	Globosum-c	43: 68	1329
73	fol-a	fol-a	2HL	Angustifolium-a	43: 69	1744
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	44: 70	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	41: 87	247
80	ant2	pr, rub	2HL	Anthocyanin-less 2	45: 98	1632
81	gsh7	gs7	1H/2H/5H	Glossy sheath 7	40: 55	1759
82	Zeo1	Knd, Ert-r	2HL	Zeocriton 1	41: 89	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	ari-g, lk10	2H	Breviaristatum-g	44: 79	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	2HL	Accordion rachis 1	40: 56	1617
98	Eam6	Ea6, Ea	2HS	Early maturity 6	37:216	
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
102	uzu1	u, *HvBRI1*	3HL	Uzu 1 or semi brachytic 1	45:104	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

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
106	abo6	a_c	3HS	Albino seedling 6	26:140	30
107	wst1	wst, wst3	3HL	White streak 1	41: 97	159
108	alm1	al, ebu-a	3HS	Albino lemma 1	43: 76	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	26:151	107
118	lnt1	rnt, int-l	3HL	Low number of tillers 1	43: 82	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	mul, int-e	3HL	Six-rowed spike 4	41:101	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	44: 88	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	45:109	483
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

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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,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	40: 61	98
156	lbi2	lb2, ert-i	4HS	Long basal rachis internode 2	44: 93	572
157	brh2	br2, ari-l	4HL	Brachytic 2	44: 95	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	43: 92	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	1HL	Light green 3	44:103	171
171	lgn4	lg4, lg9	4HL	Light green 4	44:105	681
172	lks5	lk5, ari-c	4HL	Short awn 5	41:110	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
179	Hsh1	Hs	4HL	Hairy leaf sheath 1	44:107	986

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
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	Zeo.h	4HL	Zeocriton 3	32: 99	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
189	Acr2	Acr, lax	4HL	Accordion rachis 2	40: 65	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	26:207	227
203	Blp1	B	1HL	Black lemma and pericarp 1	40: 69	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	41:116	765
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	26:219	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	leaf 1	40: 77	608
227	sls1	sls	1HL	Small lateral spikelet 1	40: 78	2492

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Locus symbol* Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
228	Sil1	Sil	1H	Subcrown internode length 1	40: 79	1604
229	cud2	cud2	1HL	Curly dwarf 2	44:111	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	1HL	Leafy lemma 1	32:103	1780
237	Rpt2	Rpt2c	1HS	Reaction to *Pyrenophora teres* 2	43:110	
238	ari-t	ari-25	1H	Breviaristatum-t	40: 82	
239	sci-b	sci-4	1H/6H	Scirpoides-b	40: 83	
240	sdw6	sdw.f	1H/7H	Semidwarf 6	40: 84	2449
241	Acr3	acr	1HL	Accordionrachis 3	40: 85	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 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	37:255	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	43:114	1774
260	fch11	f11	6HL	Chlorina seedling 11	45:120	1738
261	nec2	nec2	6HS	Necrotic leaf spot 2	26:241	1224
262	cur1	cu1	6HL	Curly 1	26:242	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	ert-e, dsp9	6HL	Erectoides-e	43:118	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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	
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	26:255	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	26:261	27
313	fch6	f6, yv	5HL	Chlorina seedling 6	44:116	1390
314	vrs2	v2	5HL	Six-rowed spike 2	26:263	773
315	vrs3	v3, int-a	1HL	Six-rowed spike 3	40: 90	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	int-b	5HL	Intermedium spike-b	44:118	1764
321	srh1	s, l	5HL	Short rachilla hair 1	26:269	27
322	dsk1	dsk	5HL	Dusky 1	41:128	1714
323	nld1	nld	5HL	Narrow leafed dwarf 1	26:271	769
324	cud1	cud	5HL	Curly dwarf 1	26:272	1711
325	crl1	crl, cl	6H	Curly lateral 1	41:129	1211
326	blf1	bb	2HL	Broad leaf 1	41:130	1393
327	flo-b	flo-a	6HL	Extra floret-b	45:121	1742
328	ari-e	ari-e, lk9	5HL	Breviaristatum-e	41:131	1653
329	ari-h	ari-h	5HL	Breviaristatum-h	26:277	1656
330	ert-g	ert-g, br3	1HL	Erectoides-g	41:133	479
331	ert-n	ert-n	5HL	Erectoides-n	44:120	488
332	Ert-r	Ert-r	2HL	Erectoides-r	41:135	492
333	Rph12	Rph12	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
336	glo-b	glo-b	5HL	Globosum-b	26:284	1326
337	blf2	bb2, nlh	5HL	Broad leaf 2	41:137	1667

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	26:289	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	43:131	735
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	44:124	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	44:126	739
356	gsh6	gs6, cer-c	2HS	Glossy sheath 6	43:135	740
357	msg1	ms1	1HL	Male sterile genetic 1	45:126	1810
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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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, 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
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	44:140	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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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
412	cer-t	cer-t	5HL	Eceriferum-t	41:164	441
413	gsh8	cer-u, gs8	2HS	Glossy sheath 8	43:141	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
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		Eceriferum-zv	26:391	1529

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
440	cer-zw	cer-zw		Eceriferum-zw	26:392	1530
441	cer-zx	cer-zx	3H	Eceriferum-zx	44:158	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	44:162	
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
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	bir1	5HL	Compositum 1	40:118	1702
474	lax-a	lax-a	5HL	Laxatum-a	40:120	1775
475	lax-c	lax-c	6HL	Laxatum-c	41:174	1777
498	msg35	msg,,dr	2HL	Male sterile genetic 35	45:183	2387

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	2394
505	msg42	msg,,db	3H	Male sterile genetic 42	45:193	2395
506	msg43	msg,,br	2HL	Male sterile genetic 43	45:194	2396
507	msg44	msg,,cx	5HL	Male sterile genetic 44	45:195	2397
508	msg45	msg,,dp	5HL/ 7HS	Male sterile genetic 45	45:196	2398
509	msg46	msg,,ec	2H/6H	Male sterile genetic 46	45:197	2399
510	msg47	msg,,ep	3HS/ 7HS	Male sterile genetic 47	45:198	2400
511	Rpg1	T	7HS	Reaction to *Puccinia graminis* 1	26:437	701
512	Rpg2	T2		Reaction to *Puccinia graminis* 2	26:439	187
513	xnt2	x_b		Xantha seedling 2	26:440	2
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	3HL	Semidwarf 1	41:176	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	26:452	1545
526	cer-ym	cer-ym		Eceriferum-ym	26:453	1546
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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	
543	int-f	int-f	2HS/ 3HL	Intermedium spike-f	44:178	1767
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-f	7H	Breviaristatum-f	41:182	1654
552	ari-j	ari-j		Breviaristatum-j	44:186	1658
553	ari-k	ari-k	3H	Breviaristatum-k	44:187	1659
554	ari-m	ari-m	7HS	Breviaristatum-m	41:184	1661
555	ari-n	ari-n	7H	Breviaristatum-n	41:185	1662
556	ari-o	ari-o	7HL	Breviaristatum-o	45:200	1663
557	ari-p	ari-p		Breviaristatum-p	40:132	1664
558	ari-q	ari-q	4H	Breviaristatum-q	44:188	1665
559	ari-r	ari-r	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	43:156	485
563	ert-l	ert-l		Erectoides-l	26:489	486
564	ert-p	ert-p		Erectoides-p	26:490	490

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
565	ert-s	ert-s		Erectoides-s	26:491	493
566	ert-t	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		Praematurum-b	26:584	1788
579	mat-c	mat-c		Praematurum-c	26:506	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
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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	45:218	1628
600	ant18	ant18	3H	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	29: 99	
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	Mo1, Zeo3	2HL	Zeocriton 2	41:193	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	44:192	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
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

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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
655	brh12	brh.o	5HS	Brachytic 12	45:233	1680

Table 2. (continued)

BGS no.	Locus symbol*		Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
	Rec.	Prev.				
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	
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	Mut 3091	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	41:201	
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

Table 2. (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	BGS no.
694	nec23			Necroticans 23	43:197	3628
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		Intense blue aleurone 1	45:241	
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	Labile 1	45:242	
731	rpr2	γ08-118; R43-22#1	6H	Required for *Puccinia graminis* resistance 2	45:243	3693
732	rpr3	γ08-112; R12-31#3		Required for *Puccinia graminis* resistance 3	45:244	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; R36-37#1		Required for *Puccinia graminis* resistance 4	45:245	3699
734	rpr5	γ08-117; R42-33#5		Required for *Puccinia graminis* resistance 5	45:246	3700
735	rpr6	γ08-119; R47-23#1		Required for *Puccinia graminis* resistance 6	45:247	3701
736	rpr7	γ08-115; R3-18#3		Required for *Puccinia graminis* resistance 7	45:248	3702
737	rcr1	γ08-122; (R4-29)		Required for resistance to *Cochliobolus sativus* 1	45:249	3703
738	rcr2	γ08-123; (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

* 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 chromosomal locations, recommended locus names, 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	26:140	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	97	2HL	Accordion rachis 1	40: 56	ACBV89B229
Acr2	Acr,lax	189	4HL	Accordion rachis 2	40: 65	CIho 6164
Acr3	acr	241	1HL	Accordion rachis 3	40: 85	Burma Girl
acr4	acr-3	679	2H/ 6HL	Accordion rachis 4	41:201	Bonus
adp1	adp	593	3HL	Awned palea 1	43:158	Unknown line
alm1	al	108	3HS	Albino lemma 1	43: 76	Russia 82
als1	als	101	3HL	Absent lower laterals 1	43: 74	Montcalm
ant1	rs	33	7HS	Anthocyanin-less 1	42: 89	Bonus
ant2	pr	80	2HL	Anthocyanin-less 2	44: 72	Foma
ant3		594		Anthocyanin-deficient 3	29: 82	Bonus
ant4	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	45:218	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	29: 99	Grit
ant29		609		Proanthocyanidin-free 29	29:100	Ca 708912
ant30		610		Proanthocyanidin-free 30	29:101	Gunhild
ari-a		132	3HS	Breviaristatum-a	41:106	Bonus
ari-b		550		Breviaristatum-b	44:185	Bonus
ari-e		328	5HL	Breviaristatum-e	41:131	Bonus
ari-f		551	7H	Breviaristatum-f	41:182	Bonus
ari-g		89	2H	Breviaristatum-g	44: 79	Bonus
ari-h		329	5HL	Breviaristatum-h	26:277	Foma
ari-j		552		Breviaristatum-j	44:186	Bonus
ari-k		553	3H	Breviaristatum-k	44:187	Bonus
ari-m		554	7HS	Breviaristatum-m	41:184	Bonus
ari-n		555	7H	Breviaristatum-n	41:185	Bonus
ari-o		556	7HL	Breviaristatum-o	45:200	Bonus
ari-p		557		Breviaristatum-p	40:132	Foma
ari-q		558	4H	Breviaristatum-q	44:188	Kristina
ari-r		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	40: 82	Bonus
ari-u	ert-t	678	2HS	Breviaristatum-u	45:239	Foma
ari-v	ari-137	680	5HS	Breviaristatum-v	41:202	Foma
ari-w	ari-153	721	7H	Breviaristatum-w	43:216	Foma
ari-x	ari-22	274	6H	Breviaristatum-x	43:124	Bonus
ari-y	ari-9	722	5H	Breviaristatum-y	43:217	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. Loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
asp1		649		Aborted spike 1	43:172	Steptoe
blf1	bb	326	2HL	Broad leaf 1	41:130	Bonus
blf2	bb2	337	5HL	Broad leaf 2	41:137	Hannchen
Blp1	B	203	1HL	Black lemma and pericarp 1	40: 69	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	43: 48	Himalaya
brh2	br2	157	4HL	Brachytic 2	44: 95	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
brh18	brh13	659	5HS	Brachytic 18	45:237	Triumph

Table 3. (continued)

Locus symbol*		BGS no.	Chr. Loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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		399	5HL	Eceriferum-d + ++ ++	41:153	Bonus
cer-e		400	1HL	Eceriferum-e -/+ ++ ++	40:102	Bonus
cer-f		401	1H	Eceriferum-f + + ++	40:104	Bonus
cer-g		402	2HL	Eceriferum-g + + ++	44:140	Bonus
cer-h		403	4HS	Eceriferum-h - ++ ++	41:157	Bonus
cer-i		404	5HL	Eceriferum-i - ++ ++	41:158	Bonus
cer-k		405	4HL	Eceriferum-k + ++ ++	41:160	Bonus
cer-l		406	3HL	Eceriferum-l + ++ ++	44:142	Bonus
cer-m		407	1H/3H	Eceriferum-m +/++ + ++	41:161	Bonus
cer-n	gs9	408	2HL	Eceriferum-n - - ++ & - +/- ++	44:143	Bonus
cer-o		409	1HL	Eceriferum-o -/+ ++ ++	40:106	Bonus
cer-p		410	7HL	Eceriferum-p ++ ++ +	41:162	Bonus
cer-r		411	3HL	Eceriferum-r +/- + ++	45:168	Bonus
cer-t		412	5HL	Eceriferum-t +/- ++ ++	41:164	Bonus
cer-v		414	2HS	Eceriferum-v +/- ++ ++	44:147	Bonus
cer-w		415	5HL	Eceriferum-w +/- ++ ++	41:166	Bonus
cer-xa		538	2HL/4H/5HL	Eceriferum-xa ++ ++ -	44:174	Foma
cer-xb		539	4H	Eceriferum-xb - ++ ++	44:175	Bonus
cer-xc		540	1H	Eceriferum-xc + + ++	44:176	Bonus
cer-xd		541	4H/5HL	Eceriferum-xd + + ++	44:177	Bonus
cer-y		417	1HS	Eceriferum-y + +/++ ++	44:149	Bonus
cer-ya		444	3HS	Eceriferum-ya ++ ++ -	26:396	Bonus
cer-yb		445	2HL	Eceriferum-yb ++ ++ -	41:171	Bonus
cer-yc		446	6H/7HS	Eceriferum-yc - ++ ++	41:172	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cer-yd		447	3HS	Eceriferum-yd - ++ ++	26:399	Bonus
cer-ye		448	4H	Eceriferum-ye ++ ++ -	43:149	Foma
cer-yf		449	7H	Eceriferum-yf ++ ++ +	44:160	Bonus
cer-yg		450	7HS	Eceriferum-yg - - -	44:161	Carlsberg II
cer-yh		451	3HS	Eceriferum-yh - ++ ++	26:403	Bonus
cer-yi		522	2H	Eceriferum-yi ++ ++ -	41:180	Foma
cer-yj		523	1HS	Eceriferum-yj ++ ++ -	40:124	Bonus
cer-yk		524	7HL	Eceriferum-yk + + ++	44:167	Bonus
cer-yl		525		Eceriferum-yl - - ++	26:452	Bonus
cer-ym		526		Eceriferum-ym - - -	26:453	Bonus
cer-yn		527	1H	Eceriferum-yn + + ++	40:125	Kristina
cer-yo		528	4HS	Eceriferum-yo ++ ++ +	44:168	Bonus
cer-yp		529	5HS	Eceriferum-yp ++ ++ +	44:169	Bonus
cer-yq		530	5H	Eceriferum-yq ++ ++ -	44:170	Kristina
cer-yr		531	5HL	Eceriferum-yr -/+ + ++	44:171	Foma
cer-ys		532	2HL	Eceriferum-ys ++ ++ -	44:172	Bonus
cer-yt		533	1H/5H	Eceriferum-yt - ++ ++	40:126	Bonus
cer-yu		534	1H	Eceriferum-yu ++ ++ -	40:127	Bonus
cer-yx		535	1H/3H/ 5H	Eceriferum-yx + + ++	40:128	Foma
Cer-yy	Gle1	536	1HS	Eceriferum-yy - ++ ++	40:129	Bonus
cer-yz		537	1H/5H	Eceriferum-yz + + ++	44:173	Bonus
cer-z		418	7HS	Eceriferum-z - - ++	44:150	Bonus
cer-za		419	5HL	Eceriferum-za ++ ++ -	43:144	Foma
cer-zb		420	5HS	Eceriferum-zb - ++ ++	42:508	Bonus
cer-zc		421	4HL/ 2HS	Eceriferum-zc +/- ++ ++	42:510	Bonus
cer-zd		422	3HL	Eceriferum-zd ++ ++ -	40:110	Bonus
cer-ze	gl5	423	7HS	Eceriferum-ze ++ ++ -	44:152	Bonus
cer-zf		424	3H/ 7HS	Eceriferum-zf ++ ++ +	42:516	Bonus
cer-zg		425	4HL	Eceriferum-zg ++ ++ +	26:377	Foma
cer-zi		427	1HL	Eceriferum-zi + + ++	41:168	Bonus
cer-zj		428	5HL	Eceriferum-zj ++ ++ -	42:520	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
cer-zk		429	2H	Eceriferum-zk + + +/-	26:381	Bonus
cer-zl		430		Eceriferum-zl - - ++	26:382	Bonus
cer-zn		431	1H	Eceriferum-zn +/- ++ ++	40:112	Foma
cer-zo		432	3HS	Eceriferum-zo - ++ ++	44:154	Foma
cer-zp		433	5HL	Eceriferum-zp ++ ++ -	26:385	Bonus
cer-zq		434		Eceriferum-zq ++ ++ -	26:386	Foma
cer-zr		435	5HL	Eceriferum-zr +/- ++ ++	44:155	Foma
cer-zs		436		Eceriferum-zs + ++ ++	44:156	Foma
cer-zt		437	2HS	Eceriferum-zt + ++ ++	44:157	Foma
cer-zu		438	1HS	Eceriferum-zu - + ++	41:170	Foma
cer-zv		439		Eceriferum-zv - - -	26:391	Foma
cer-zw		440		Eceriferum-zw + + ++	26:392	Foma
cer-zx		441	3H	Eceriferum-zx + + ++	44:158	Bonus
cer-zy		442	1HS	Eceriferum-zy ++ ++ +	40:116	Bonus
cer-zz		443		Eceriferum-zz ++ ++ -	44:159	Bonus
clh1	clh	225	7H/5H	Curled leaf dwarf 1	40: 76	Hannchen
com1	bir1	473	5HL	Compositum 1	40:118	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	44:111	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	44:192	Bonus
cur1	cu1	262	6HL	Curly 1	26:242	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
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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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	43:114	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	Ppd-H1, Ea	65	2HS	Early maturity 1	44: 64	Estate
Eam5	HvPhyC -e	348	5HL	Early maturity 5	45:123	Higuerilla*2/ Gobernadora
eam6	Ea6, Ea	98	2HS	Early maturity 6	37:216	Morex
eam7	HvCO7	252	6HS	Early maturity 7	45:118	California Mariout
eam8	ea_k,ert-o	214	1HL	Early maturity 8	41:116	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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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	dsp9	266	6HL	Erectoides-e	43:118	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	43:156	Bonus
ert-l	ert-12	563		Erectoides-l	26:489	Maja
ert-m	ert-34	30	7HS	Erectoides-m	44: 57	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	41:135	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
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	117	3HL	Chlorina seedling 2	26:151	28-3398
fch3	f3	220	1HS	Chlorina seedling 3	40: 71	Minn 89-4

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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	45:120	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	44:162	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
glf1	gl,cer-zh	155	4HL	Glossy leaf 1 ++ ++ -	40: 61	Himalaya
glf3	gl3,cer-j	165	4HL	Glossy leaf 3 ++ ++ -	43: 92	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

Table 3. (continued)

Locus symbol* Rec.	Prev.	BGSno.	Chr. loc.†	Locus name or phenotype	Descr. vol. p	Parental cultivar
glo-e		230	1HL	Globosum-e	45:	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	44: 88	Donaria
gsh1	gs1, cer-q	351	2HS	Glossy sheath 1 - - ++	43:131	PI 195285
gsh2	gs2	352	3HL	Glossy sheath 2 - - ++	44:124	Atlas
gsh3	gs3	353	7HS	Glossy sheath 3 - - ++	41:143	Mars
gsh4	gs4	354	6HL	Glossy sheath 4 - - ++	41:146	Gateway
gsh5	gs5	355	2HL	Glossy sheath 5 + - ++	44:126	Jotun
gsh6	cer-c, gs6	356	2HS	Glossy sheath 6 - - ++	43:135	Betzes
gsh7	gs7	81	1H/2H/5H	Glossy sheath 7 - - ++	40: 55	Akashinriki
gsh8	cer-u, gs8	413	2HS	Glossy sheath 8 + + ++	43:141	Akashinriki
Gth1	G	69	2HL	Toothed lemma 1	44: 68	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		Intense blue aleurone 1	45:241	Ethiopian 637
int-b		320	5HL	Intermedium spike-b	44:118	Bonus
int-c	i	178	4HS	Intermedium spike-c	37:237	Gamma 4
int-f		543	2HS/3HL	Intermedium spike-f	44:178	Foma
int-h		544	5H	Intermedium spike-h	44:179	Kristina
int-i		545	2HS	Intermedium spike-i	41:181	Kristina
int-k		546	7H	Intermedium spike-k	44:180	Kristina
int-m		547	5HL	Intermedium spike-m	44:181	Bonus
Kap1	K	152	4HS	Hooded lemma 1	26:179	Colsess
lab1		730	5HL	Labile 1	45:242	
lam1		651		Late maturity 1	43:174	Steptoe
lax-a		474	5HL	Laxatum-a	40:120	Bonus
lax-b		268	6HL	Laxatum-b	44:113	Bonus
lax-c		475	6HL	Laxatum-c	41:174	Bonus

Table 3. (continued)

Locus symbol*		BGSno.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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
lel1	lel	235	1HL	Leafy lemma 1	32:103	G7118
Lfb1	Lfb	343	5HL	Leafy bract 1	41:140	Montcalm
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	170	1HL	Light green 3	44:103	No 154
lgn4	lg4	171	4HL	Light green 4	44:105	Himalaya / Ingrescens
lig1	li, aur-a	60	2HL	Liguleless 1	45: 93	Muyoji
lin1	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	41:110	CIho 5641
lks6	lks.q	724	1H/5H/6H	Short awn 6	43:219	Morex
lnt1	rnt	118	3HL	Low number of tillers 1	43: 82	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		578		Praematurum-b	26:504	Bonus
mat-c		579		Praematurum-c	26:506	Bonus
mat-d		580	4HL/6HL	Praematurum-d	45:208	Bonus
mat-e		581		Praematurum-e	26:508	Bonus
mat-f		582	1H	Praematurum-f	45:210	Bonus
mat-g		583		Praematurum-g	26:510	Bonus
mat-h		584	4HL	Praematurum-h	45:212	Bonus

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
mat-i		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
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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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
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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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
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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
nec11		682	1H	Necroticans 11	43:185	Steptoe
nec12		683		Necroticans 12	43:186	Steptoe
nec13		684		Necroticans 13	43:187	Steptoe
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	26:271	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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
pmr1	pmr	40	7HS	Premature ripe 1	44: 60	Glenn
pmr2	nec-50	634		Premature ripe 2	32:135	Bonus
Pre2	Re2	76	2HL	Red lemma and pericarp 2	44: 70	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	26:261	Lion
raw2	r2	340	5HL	Smooth awn 2	26:289	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	37:255	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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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	32	5HL	Reaction to *Puccinia hordei* 9	37:201	HOR 2596
Rph10		137	3HL	Reaction to *Puccinia hordei* 10	26:174	Clipper C8
Rph11		267	6HL	Reaction to *Puccinia hordei* 11	26:247	Clipper C67
Rph12		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	45:243	Morex
rpr3	γ08-112	732		Required for *Puccinia graminis* resistance 3	45:244	Morex
rpr4	γ08-114	733		Required for *Puccinia graminis* resistance 4	45:245	Morex
rpr5	γ08-117	734		Required for *Puccinia graminis* resistance 5	45:246	Morex
rpr6	γ08-119	735		Required for *Puccinia graminis* resistance 6	45:247	Morex
rpr7	γ08-115	736		Required for *Puccinia graminis* resistance 7	45:248	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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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
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	26: 87	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	40: 83	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	sdw	518	3HL	Semidwarf 1	41:176	M21
sdw2	sdw-b	133	3HL	Semidwarf 2	45:108	Mg2170
sdw4		45	7HL	Semidwarf 4	41: 80	
sdw6	sdw.f	240	1H/7H	Semidwarf 6	40: 84	Vada

Table 3. (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p	
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
seg8	seg8	455	7H	Shrunken endosperm genetic 8	45:170	60Ab1810-53
sex1	lys5	382	6HL	Shrunken endosperm xenia 1	26:330	Compana
sex6	ssIIa	31	7HS	Shrunken endosperm xenia 6	45: 86	K6827
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

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
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/5H	Seminudoides 1	43: 58	Haisa
snb1	sb	26	7HS	Subnodal bract 1	26: 72	L50-200
srh1	s	321	5HL	Short rachilla hair 1	26:269	Lion
sun1	sun1	650		Sensitivity to *Ustilago nuda* 1	43:173	Steptoe
tfm1		190	1HL	Thick filament 1	40: 67	Volla
trd1	trd	202	1HL	Third outer glume 1	26:207	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
ubs4	lks2, ari-d	11	7HL	Unbranched style 4	45: 84	Ao-Hadaka
ubs5		727		Unbranched style 5	43:222	Harrington
uzu1	uz	102	2HL	Uzu 1 or semi brachytic 1	45:104	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	26:104	White Deficiens
vrs2	v2	314	5HL	Six-rowed spike 2	26:263	Svanhals
vrs3	v3	315	1HL	Six-rowed spike 3	40: 90	Hadata 2
vrs4	v4	124	3HL	Six-rowed spike 4	41:101	MFB 104
wax1	wx	16	7HS	Waxy endosperm 1	42: 65	Oderbrucker
wnd1	wnd	23	4Hl	Winding dwarf 1	42: 74	Kogen-mugi

Table 3. (continued)

Locus symbol*		BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Rec.	Prev.					
wst1	wst	107	3HL	White streak 1	41: 97	CIho 11767
wst2		304	5HL	White streak 2	26:255	Manabe
wst4		56	2HL	White streak 4	44: 51	Kanyo 7
wst5		221	1HL	White streak 5	26:219	Carlsberg II
wst6	wst,,j	129	3HL	White streak 6	41:105	Akashinriki
wst7	rb	79	2HL	White streak 7	41: 87	GS397
wxs1	wxs	615	7H/ 2HL	Waxy spike 1	43:160	Steptoe
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
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	82	2HL	Zeocriton 1	41: 89	Donaria

Table 3. (continued)

Locus symbol* Rec.	Prev.	BGS no.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	Parental cultivar
Zeo2	Mo1	614	2HL	Zeocriton 2	41:193	36Ab51
Zeo3	Mo1	184	4HL	Zeocriton 3	32: 99	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.

BGS 10, Short awn 2, lks2

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (11, 12, 13, 22, 25).
Located in chromosome 7HL (11, 13, 14, 24, 25); position estimates for the *lks2* locus ranged from 7.9 to 10.5 cM distal from the *nud1* (naked caryopsis 1) locus (4, 22, 24); *lks2.b* is about 2.8 cM distal from molecular marker WG541 in 7H bin 05 (15); *lks2.b* is 3.6 cM from AFLP marker E4138-3 in subgroup 6 of the Proctor/Nudinka map (16); *lks2.b* is about 8.6 cM proximal from RFLP marker WG380B in 7H bin 08 (1); *lks2.b* is located in the long arm of 7H and flanked by EST-based markers k04151 and k06123 (co-segregation with Bmac64) (27, 31); *lks2.b* is associated with SNP markers 2_0790 to 2_0060 (positions 73.96 to 97.66 cM) in 7H bins 06 to 07 of the Bowman backcross-derived line BW492 (2); *ubs4.d* is about 8.0 cM distal from the *nud1* (naked caryopsis 1) locus (25); *ubs4.d* is associated with SNP markers 2_0103 to 1_0563 (positions 139.96 to 154.35 cM) in 7H bins 08 to 09 of the Bowman backcross-derived line BW884 (2); *ari-d.15* is associated with SNP marker 1_0169 (position 142.66 cM) in 7H bin 08 of the Bowman backcross-derived line BW041 (1*); ari-d.44* is associated with SNP markers 1_0056 to 2_0092 (positions 51.93 to 152.29 cM) in 7H bins 04 to 09 of the Bowman backcross-derived line BW035 (2), likely in 7H bin 07. The Lks2 gene has been cloned (31).

Description:

Awns of both central and lateral spikelets of lks2.b spikes are reduced to about 3/5 that of the long awned type. Texture of the short awn is finer and more flexible than that of the long awn, especially in non-uzu genotypes (24, 26, 31). Kernel weights of lks2 plants were slightly reduced and kernels per spike were slightly increased, but other traits remained unchanged (23). The Atlas near-isogenic lines for *lks2* (half awn) were found to respond better to environmental and genetic stress than the normal lines (20, 21). The awn length of heterozygotes in some crosses was shorter that of the normal parent. Awns, as measured from the tip of the last fertile spikelet on the spike to the tip of the awn, of BW492 were about 1/2 as long as Bowman awns, 5 to 6 vs. 11 to 12 cm (5). The number of longitudinal parenchyma cells in the Bowman backcross-derived line BW492 awns was about half that of Bowman awns (31). Kernels of BW492 plants were slightly lighter than those of Bowman and kernel widths averaged slightly less (5). Allelism tests demonstrated that *lks2.b* gene in BW492 is allelic and dominant to *ubs4.d* gene in BW884 and to the *ari-d.15* gene in BW041 (31). All 25 accessions identified as mutants at the lks2 locus had lesions in the Lks2 candidate gene (31). Among accessions with

the lks2 phenotype, three variants were found: *lks2.b1* and *lks2.b2* in accessions from China, Japan, and Korea and *lks2.b3* in accessions from Tibet (31). Stigmas of *ari-d* and ubs4 mutants have only a few very short branches, which prevents normal pollen reception and reduces seed set to 13 to 30% in uzu type plants. Both the *uzu1.a* and *srh1.a* (short rachilla hair 1) genes interact with ubs4.d to further reduce in seed set (25). The stigmas have very few stigma hairs (31). Pollen fertility is normal (25). Awn length is about 1/4 normal (4, 31). Seed set for plants of the Bowman backcross-derived lines for *ari-d.15* and *ubs4.d*, BW041 and BW884, respectively, varied from about 10% for plants grown in greenhouses to nearly 50% for plants grown at Aberdeen, Idaho, USA (5). Grain yields of BW041 and BW884 ranged from 1/4 to 1/2 those of Bowman. Compared to Bowman, kernel weights of BW041 and BW884 varied from slightly less to slightly more. Other morphological traits of BW041, BW492, and BW884 were similar to those of Bowman (5).

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Revised:

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BGS 11, Unbranched style 4, ubs4

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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

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Revised:

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U. Lundqvist and J.D. Franckowiak 2015. Barley Genet. Newsl. 45:84-85.

BGS 31, Shrunken endosperm xenia 6, sex6

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

Previous nomenclature and gene symbolization:
starch synthase IIa = ssIIa (6).

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

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

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

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

Mutant used for description and seed stocks:
sex6.h (GSHO 2476) in K6827, *sex6.h* in Bowman (PI 483237)*6 (GSHO 3425); *sex6.h* in Bowman*7 (BW846, NGB 22283); *sex6.h* in NFC Tipple (Syngenta Seeds Ltd., Market Rasen, UK)*3 (4).

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Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl.26:80.

Revised:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:86-87.

BGS 34, Male sterile genetic 50, *msg50*

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

Previous nomenclature and gene symbolization:
Male sterile genetic gh = *msg,,gh* (4).
Male sterile genetic hm = *msg,,hm* (4).

Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 7HL (2); *msg50.gh* is about 18.9 cM from the *lks2* (short awn 2) locus (2); *msg50.hm* is about 8.7 cM from the *lks2* locus (2); *msg50.hm* is associated with SNP markers 2_1270 to 2_1229 (positions 93.97 to 176.37 cM) in 7H bins 06 to 10 in a heterozygous plant from Bowman backcross-derived line BW588 (1); *msg50.gh* is associated with SNP markers 2_1270 to 1_1440 (positions 93.97 to 198.70 cM) in 7H bins 06 to 12 in a heterozygous plant from Bowman backcross-derived line BW972 (1).

Description:
Selfing - 0% is reported (4), but occasionally 5 to 10% selfed seed set is observed.
Outcrossing - complete female fertility (4).
Stamens - anthers slightly smaller than fertile sib with filament elongation and stomium (4).

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

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

Mutant used for description and seed stocks:
msg50.gh (MSS435) in Maris Mink; *msg50.gh* from Maris Mink in Bowman*4 (BW972, NGB 23467); *msg50.hm* (GSHO 2404) in Berac; *msg50.hm* in Bowman (PI 483237)*7 (GSHO 1861, BW588, NGB 23448).

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Prepared:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:83.

Revised:
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:57.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:88.

BGS 44, Brachytic 16, *brh16*

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 5).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Revised:

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

BGS 59, Grandpa 1, *gpa1*

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

Previous nomenclature and gene symbolization:
Grandpa = *gp* (3).
Grandpa 2 = *gp2* (7, 8).

Inheritance:
Monofactorial recessive (3).
Located in chromosome 2HL (6, 7); *gp a1.a* is about 24.5 cM distal from the *lig1* (liguleless 1) locus (5); *gpa1.a* is associated with SNP markers 2_0069 to 10085 (positions 179.99 to 247.86 cM) in 2H bins 11 to 14 of the Bowman backcross-derived line BW397 (1).

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

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

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

Mutant used for description and seed stocks:
gpa1.b (GSHO 1379) in Montcalm; *gpa1.a* in Bowman (PI 483237)*7 (GSHO 1934, BW397, NGB 22147).

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Prepared:
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Revised:

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BGS 60, Liguleless 1, *lig1*

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

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

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

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

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

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

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

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Prepared:

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Revised:

J.D. Franckowiak, U. Lundqvist, T. Konishi. 1997. Barley Genet. Newsl. 26:96.
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BGS 71, Compositum 2, *com2*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (4, 12).
Located in chromosome 2HS (2, 4, 5); *com2.g* is linked to *Eam1* (early maturity 1) (4); *brc1.5* maps in 2H subgroup 17 at about 55 cM, near markers MWG2067 and CDO665 (2); BLASTn association of *brh1.5* with rice gene *FUZZY PANICLE* (*FZP*) (10); *com2.g* is associated with SNP markers 1_0525 to 1_0325 (positions 65.03 to 90.54 cM) in 2H bins 04 to 06 of the Bowman backcross-derived line BW192 (3); *com2.k* is associated with markers 1_0943 to 1_1015 (positions 34.31 to 91.62 cM) in 2H bins 04 to 07 of the Bowman backcross-derived line BW187 (3); the Bowman backcross-derived line BW191 for *com2.f*, BW191, did not contain any donor parent SNP markers (3), likely in 2H bin 06.

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

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

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

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

BGS 80, Anthocyanin-less 2, *ant2*

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

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

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

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

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

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

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

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Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:118.

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

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

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (6).
Located in chromosome 7HL (1, 2); *ert-u.56* is associated with SNP marker 1_0547 (about position 228 cM) in 7H bin 13 of the Bowman backcross-derived line BW325 (2); *ert-u.56* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (1) in the barley genome map (9). The *ert-u.56* mutant was previously associated with chromosome 2H based on linkage drag with the *Gth1* (toothed lemma 1) locus (4).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

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

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (6).
Located in chromosome 7HL (1, 2); *ert-zd.159* is associated with SNP marker 1_0547 (about position 228 cM) in 7H bin 13 of the Bowman backcross-derived line BW333 (2). *ert-u.56* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (1) in the barley genome map (7). Previously located in chromosome 2H, based on linkage drag with the *Gth1* (toothed lemma 1) locus (4).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Revised:

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BGS 102, Uzu 1, *uzu1*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (12, 20, 22, 24).
Located in chromosome 3HL (18, 19, 24); *uzu1.a* is about 17.6 cM proximal from the *alm1* (albino lemma 1) locus (23); *uzu1.a* is in bin 3H 06 near cDNA marker C1271 (3); *uzu1.a* is about 10.1 cM from AFLP marker E3733-6 in subgroup 27 of the Proctor/Nudinka map (16); *uzu1.a* is associated with SNP markers 1_0373 to 1_1314 (positions 92.55 to 107.40 cM) in 3H bins 06 to 07 of the Bowman backcross-derived line BW885 (5); *uzu1.a* with *sld1.a* (slender dwarf 1) is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman line BW860 (5); *uzu1.a* with *wst1.c* (white streak 1) is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman line BW912 (5); *ert-ii.79* is associated with SNP markers 2_0686 to 2_0931 (positions 67.01 to 104.39 cM) in 3H bins 05 to 06 of the Bowman line BW312 (5); *uzu1.256* (formerly *ari.256*) is associated with SNP markers 1_0728 to 2_1405 (positions 96.75 to 187.28 cM) in 3H bins 06 to 12 of Bowman line BW033 (5); the *ert-ii.79* allele at the *uzu1* (*HvBRI1*) locus is positioned at 57.1 cM (4) on the barley genome map (26), in 3H bin 06.

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (21, 22, 24). These organs are often reduced in length and increased in width. Changes in organ length are temperature sensitive, but heading date and maturity are unaltered. The coleoptile of uzu plants shows a prominent projection or hook near the apex. Sometimes the coleoptile of the mutant shows a V-shaped notch on the side opposite from the projection. Thus, the apex of the coleoptile has two notches, one on each side (22, 27, 28). The temperature sensitive reduction in culm length of *uzu1.a* plants ranged from less than 15% in cool environments to over 75% in warm ones (6). The Bowman backcross-derived line for *uzu1.a*, BW885, produced plants that were 20 to 40% shorter than Bowman, awns were about 1/3 of normal length, rachis internodes were shorter, 3.0 vs.4.7 mm, and leaf blades were shorter and wider. Kernels of BW885 were shorter, 7.9 vs. 9.5 mm, and lighter, averaged 4.7 vs. 5.7 mg. Spikes of BW885 often had 2 more kernels than those of Bowman. Grain yields of BW885 ranged from 1/3 to 3/4 those of Bowman (6). Chono et al. (3) reported that the *uzu1.a* variant is caused by a mutation that changed a highly conserved residue of the kinase domain of the *HvBRI1* protein [*BRI1* (brassinosteroid insensitive 1) of *Arabidopsis*] from His-857 to Arg-857. When grown at low temperatures, the *uzu1.a* mutant was a semidwarf with 80% of wild-type culm length. The overall plant architecture

is more erect, with acute leaf blade angles. Short-awned spikes are compact with dense basal spikelets, and frequently with opposite spikelets in the tip caused by irregular elongation of rachis internodes. Leaf blade margins and auricles of *uzu1.a* plants have a slightly undulating appearance (4). When grown at 26°C, *uzu1.a* plants (BW885) showed extreme dwarfing, less than 1/3 the height of Bowman plants. This extreme dwarfing caused by temperature was not observed with other mutants at the *uzu1* locus (4). In progeny from crosses to the BW885 line, tillering was reduced (1). The *uzu1.a* variant was associated with decreased incidence of crown root, *Fusarium pseudograminearum* (2).

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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BGS 133, Semidwarf 2, *sdw2*

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

Previous nomenclature and gene symbolization:
Semidwarf-b = *sdw-b* (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 3HL (3); *sdw2.b* is over 34.5 cM distal from the *sld1* (slender dwarf 1) locus (3); *sdw2.b* is associated with SNP markers 2_0650 to 2_0612 (positions 192.0 to 198.33 cM) in 3H bins 12 to 13 of the Bowman backcross-derived line BW829 (1).
Description:
Plants are about 3/4 normal height; culms are thin with narrow, short, erect leaves. The flag leaf is narrow and short. The peduncle is short, the collar has a small leaf-like bract, and the basal rachis internode is elongated (3). Compared to Bowman, plants of the Bowman backcross-derived line for *sdw2.b*, BW829, were shorter 10 to 20% shorter, peduncles were 1/2 to 2/3 as long, rachis internodes were 10 to 20% shorter, and leaf blades were about 2/3 normal length and width. BW829 plants headed 1 to 3 days earlier than Bowman and they yielded about 2/3 as much. Kernels were shorter and thinner and weighed about 20% less, 4.6 vs 5.6 mg (2).
Origin of mutant:
An N-methyl-N-nitrosourea induced mutant in Mg4170 (3).
Mutational events:
sdw2.b (267MK, later called 437MK, GSHO 2466) in Mg4170 (3).
Mutant used for description and seed stocks:
sdw2.b (GSHO 2466) in Mg4170; *sdw2.b* in Bowman (PI 483237)*7 (GSHO 1965, BW829, NGB 22266).
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Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:108.

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

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (5, 6).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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Revised:

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

BGS 148, Brachytic 14, *brh14*

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (5, 9).
Located in chromosome 7HL (3, 4); *brh14.q* is associated with SNP marker 1_0387 (position 229.65 cM) in 7H bin 13 of the Bowman backcross-derived line BW085 (4); *brh14.af* is associated SNP markers 1_0174 to 1_0378 (position 229.66 cM) in 7H bin 13 of Bowman backcross-derived line BW072 (4); *brh14.q* and *brh14.af* are alleles at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (3) in the barley genome map (11). Previously located approximately 24.9 cM proximal from SSR marker Bmac0029 in 3H bin 15 (2).

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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

Prepared:

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

Revised:

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

BGS 166, Male sterile genetic 25, *msg25*

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

Previous nomenclature and gene symbolization:
Male sterile = *msg,,r* (8).

Inheritance:
Monofactorial recessive (3, 8).
Located in chromosome 4HL (2, 7); *msg25.r* is near the centromere and proximal from the *Blx1* (Blue aleurone xenia 1) locus (7, 10); the Bowman backcross-derived line for *msg25.r,* BW560, did not retain any donor parent SNP marker polymorphisms compared to Bowman (1).

Description:
Selfing - 0.7% for *msg25.r* (7), 2.6% for *msg25.dz* (4).
Outcrossing - complete female fertility (7).
Stamens - anthers smaller than fertile sib, but some have stomium. Some filament elongation may occur (7).

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

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

Mutant used for description and seed stocks:
msg25.r (GSHO 744) in Betzes; *msg25.r* in Bowman (PI 483237)*7 (GSHO 2020, BW560, NGB 23428).

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Prepared:

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Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:192.

J.D. Franckowiak. 2014. Barley Genet. Newsl. 44:101-102.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:113-114.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (2).
Located in chromosome 4H (2, 5); *glo-a.1003* is associated with chromosome 4H based on crosses to a translocation set (2, 5); *glo-a.1003* is associated with SNP markers 3_0554 and 1_0510 (positions 140.93 and 149.26 cM) in 4H bin 10 of Bowman backcross-derived line BW392 (1).
Description:
Fertile spikelets are shortened and the resulting kernels are nearly round or globe-shaped. Sterile lateral spikelets are 1/2 normal length and twisted (3). In the Bowman backcross-derived line for *glo-a.1003*, BW392, kernel length was much reduced and other spike tissues were reduced in length. Kernel weights were very low, 4.2 vs. 5.6 mg, and so were test weights. Compared to Bowman, BW392 plants were 10% shorter and peduncles were about 20% shorter. Awn length varied 1/3 to 2/3 of that for Bowman. The grain yield of BW392 averaged about 15% lower than that of Bowman (3).
Origin of mutant:
An X-ray induced mutant in Proctor (PI 280420) (1, 3).
Mutational events:
glo-a.1003 (1343/63, GSHO 1328) in Proctor (PI 280420) (1, 2, 3).
Mutant used for description and seed stocks:
glo-a.1003 (GSHO 1328) in Proctor; *glo-a.1003* in Bowman (PI 483237)*7 (GSHO 2006, BW392, NGB 20630).
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Prepared:
G. Fischbeck. 1978. Barley Genet. Newsl. 8:152.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:194.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:115.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (3, 4).
Location in chromosome 6HL (1); *flo-a.1* is associated with SNP markers 1_0539 to 1_0040 (positions 76.05 to 107.26 cM) in 6H bins 06 to 07 of the Bowman backcross-derived line BW367 (1); *flo-a.3* is associated with SNP markers 2_0746 to 1_1246 (positions 125.86 to 134.55 cM) in 6H bin 08 of the Bowman backcross-derived line BW368 (1); *flo-a.5* is associated with SNP markers 1_0061 to 1_1246 (positions 70.15 to 134.55 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW369 (1), likely in 6H bin 07.
Description:
Extra floral bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra floral bracts is most common in the central portion of the spike, but rarely will the floral bracts form another spikelet (2, 4). Except for the occasional development of a floral bract below the central spikelet, the Bowman backcross-derived lines for mutants at the *flo-a* locus, BW367, BW368, and BW369 were similar to Bowman (2).
Origin of mutant:
An ethylene imine induced mutant in Foma (CIho 11333, NGB 14659) (4).
Mutational events:
flo-a.1 (NGB 114271, GSHO 1741) in Foma (CIho 11333, NGB 14659) (4); *flo-a.3* (NGB 114273, GSHO 1742), previously named *flo-b.3*, in Foma (4); *flo-a.5* (NGB 114275, GSHO 1743), previously named *flo-c.5*, in Foma (4).
Mutant used for description and seed stocks:
flo-a.1 (GSHO 1741, NGB 114271) in Foma; *flo-a.3* (GSHO 1742, NGB 114273) in Foma; *flo-a.5* (GSHO 1743, NGB 114275) in Foma; *flo-a.1* in Bowman (PI 483237)*5 (GSHO 2005), in Bowman*7 (BW367, NGB 20606); *flo-a.3* in Bowman (PI 483237)*6 (GSHO 2128, BW368, NGB 20607); *flo-a.5* in Bowman (PI 483237)*7 (GSHO 1877, BW369, NGB 20608).
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Prepared:
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Revised:
J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:112.
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:116.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1).
Located in chromosome 3HL or 1HS (1); *glo-e.15* is associated with SNP markers 1_0646 to 1_0694 (positions 239.73 to 248.51 cM) in 3H bin 15 and with SNP markers 2_0373 to 2_1067 (positions 0.10 to 3.18 cM) in 1H bin 01 in Bowman backcross-derived line BW396 (1).
Description:
Plants appear normal, but kernels are larger and more rounded than those of normal sibs (3). No morphological differences were noted between Bowman and the Bowman backcross-derived line for *glo-e.15*, BW396, except kernels seemed a little wider (2).
Origin of mutant:
A neutron induced mutant in Foma (CIho 11333, NGB 14659) (4).
Mutational events:
glo-e.15 (*glo-e.1010,* NGB 115633, GSHO 1755) in Foma (CIho 11333, NGB 14659) (3, 4).
Mutant used for description and seed stocks:
glo-e.15 (NGB 115633, GSHO 1755) in Foma; *glo-e.15* in Bowman (PI 483237)*7 (GSHO 2050, BW396, NGB 20634).
References:
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Prepared:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:228.
Revised:
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:117.

BGS 252, Early maturity 7, *eam7*

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

Previous nomenclature and gene symbolization:
Early heading = *ec* (9).
Early maturity 7 = *ea7* (8).

Inheritance:
Monofactorial recessive (5, 8).
Located in chromosome 6HS (9); *eam7.g* is about 0.5 cM from the *rob1* (orange lemma 1) locus (8); *eam7.g* is about 3.0 cM from the centromere (7); *eam7.g* is near the centromere and between markers mwg2264 and mwg916 (10); *eam7.g* is associated with SNP markers 2_0886 to 1_0978 (positions 3.28 to 156.09 cM) in 6H bins 01 to 06 of the Bowman backcross-derived line BW288 (1); *eam7.g* is associated with homozygous SNP markers 2_0886 to 2_0291 (positions 3.28 to 81.35 cM) in 6H bins 01 to 06 of the Bowman backcross-derived line BW287 (1), likely in 6H bin 05.

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

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

Mutational events:
eam7.g in BC_6 California Mariout (GBC326, GSHO 579) (4, 8); *eam7.n* (Ea1), *eam7.o* (Ea2), *eam7.p* (Ea3) in Chikurin Ibaraki 1 (OUJ069, CIho 7370) (11).

Mutant used for description and seed stocks:
eam7.g in BC_6 California Mariout (GSHO 579); *eam7.g* in Bowman (PI 483237)*3 (GSHO 2068, BW288, NGB 20572), *eam7.g* in Bowman*2 (BW287, NGB 20571).

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Prepared:

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

Revised:

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

BGS 260, Chlorina seedling 11, *fch11*

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

Previous nomenclature and gene symbolization:
Pale green = *pg* 3).
Chlorina seedling 11 = *f11* (1).

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

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

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

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

Mutant used for description and seed stocks:
fch11.t (GSHO 1738) in Himalaya; *fch11.t* in Bowman (PI 483237)*6 (GSHO 2082); *fch11.t* in Bowman*7 (BW353, NGB 20592).

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

Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:240.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:120.

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

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (3, 4).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

BGS 335, Male sterile genetic 49, *msg49*

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

Previous nomenclature and gene symbolization:
Male sterile genetic jw = *msg,,jw* (4).
Inheritance:
Monofactorial recessive (2, 3, 4).
Located in chromosome 5HL (2); *msg49.jw* is about 10.4 cM from the *raw1* (smooth awn 1) locus (2); *msg49.jw* is associated with SNP markers 2_1150 to 2_0629 (positions 145.57 to 187.37 cM) in 5H bins 09 to 10 in a homozygous male sterile plant from Bowman backcross-derived line BW586 (1).
Description:
Selfing - none (4).
Outcrossing - Complete female fertility (4).
Stamens - anthers rudimentary, no stomium or filament elongation (4).
Origin of mutant:
A spontaneous mutant in ND7369, a six-rowed selection from North Dakota State University, Fargo, North Dakota, USA (4).
Mutational events:
msg49.jw (MSS528, GSHO 2402) in ND7369 (3, 4).
Mutant used for description and seed stocks:
msg49.jw (GSHO 2402) in ND7369; *msg49.jw* in Bowman (PI 483237)*8 (GSHO 2141, BW586, NGB 24137).
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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:283.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:122.

BGS 348, Early maturity 5, *Eam5*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

Description:

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

al. (8) and Pankin et al. (9) may be caused by the presence of the *Eam6.h* (early maturity 6) or *eps-2S* (earliness per se 2S) allele in the Bowman backcross-derived lines (3).

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

BGS 357, Male sterile genetic 1, *msg1*

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

Previous nomenclature and gene symbolization:
Male sterile = *ms* (14).
Male sterile 1 = *ms1* (5).
Inheritance:
Monofactorial recessive (16).
Located in chromosome 1HL (13); *msg1.ca* is near the centromere (8); *msg1.ca* is about 10.0 cM proximal from the *nec1* (necrotic leaf spot 1) locus (11, 14); probably proximal from the small lateral spikelet 1 (*sls1*) gene which also originated from MSS005 (2); *msg1.ca* is associated with SNP markers 1_0933 to 1_0324 (positions 82.35 to 87.19 cM) in 1H bin 08 of a heterozygous plant from the Bowman backcross-derived line BW545 (1), in 1H bin 08.
Description:
Selfing - none (7).
Outcrossing - complete female fertility (7).
Stamens - anthers smaller than fertile sib, no stromium or filament elongation (15).
Pollen - microspores degenerate at or before the free microspore stage (12); non-staining, shrunken, and devoid of cytoplasm (15).
Cytology - normal development and differentiation of anthers until completion of meiosis (12). SNP markers in the plant studied as *msg1.ca* of Bowman backcross-derived line BW145 were identical to those of Bowman (1).
Origin of mutant:
A spontaneous mutant in the Composite Cross line CIho 5368 (16).
Mutational events:
msg1.ca (GSHO 1810) from CIho 5368 in Betzes (PI 129430)*11 (MSS005) (12, 16); *msg1.i* (MSS077) in 80TT25 (CIho 13638), *msg1.t* (MSS042) in Trophy (CIho 10647), *msg1.ai* (MSS100) in Betzes (PI 129430) (9, 10); *msg1.ar* (MSS310) in Glossy Brachytic (CIho 15246), *msg1.bp* (MSS330) in Betzes (3, 10); *msg1.cz* (MSS348) in Betzes (4, 10); *msg1.gb* (MSS429) in Maris Mink (5); *msg1.jv* (MSS527) in a Harrington outcross (6).
Mutant used for description and seed stocks:
msg1.ca in Betzes*11 (GSHO 1810); *msg1.ca* in Bowman (PI 483237)*8 (GSHO 2042, BW545, NGB 24128).
References:
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Prepared:

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

Revised:

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

BGS 358, Male sterile genetic 2, *msg2*

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

Previous nomenclature and gene symbolization:
Male sterile 2 = c_2(1).
Male sterile 2 = *ms2* (4).
Inheritance:
Monofactorial recessive (1).
Located in chromosome 2HL (1, 11); *msg2.cb* is about 2.4 cM proximal from the *eog1* (elongated outer glume 1) locus (7); *msg2.cb* is less than 1 cM from the T2-7a translocation breakpoint and about 3 cM from the *eog1* locus (8); *msg2.cb* is associated with SNP markers 2_0674 to 2-0585 (positions 85.71 to 103.71 cM) in 2H bins 07 to 08 of a heterozygous plant from Bowman backcross-derived line BW554 (2).
Description:
Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (10).
Pollen - non-staining, shrunken, and no normal grains (10).
Origin of mutant:
A spontaneous mutant in the F_2 progeny of Manchuria (CIho 2330) X CIho 4363 (4).
Mutational events:
msg2.cb (MSS046) in F_2 of Manchuria/CIho 4363 (4, 6); *msg2.ax* (MSS045) in Compana (PI 539111) (5, 6); *msg2.ed* (MSS379) in Ingrid (CIho 10083, NGB 2671) (3, 9).
Mutant used for description and seed stocks:
msg2.cb in Herta*10 (GSHO 2371, NGB 2664); *msg2.cb* in Manchuria*19 (MSS047); *msg2.cb* in Ogalitsu*14 (MSS048); *msg2.cb* in Trebi*19 (MSS050) (5); *msg2.cb* from Herta*10 in Bowman (PI 483237)*7 (GSHO 1890, BW554, NGB 23423).
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Prepared:

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

Revised:

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

BGS 359, Male sterile genetic 3, *msg3*

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

Previous nomenclature and gene symbolization:
Male sterile 10 = *ms10* (3, 8).
Male sterile 3 = *ms3* (3, 5).
Inheritance:
Monofactorial recessive (5).
Located in chromosome 2HS (5); *msg3.cc* is about 4.6 cM distal from the *eog1* (elongated outer glume 1) locus (5); *msg3.cc* is 0.6 cM distal from the *fch1* (chlorina seedling 1) locus (5); *msg3.cc* is associated with SNP markers 1_1493 to 1_1046 (positions 76.05 to 96.47 cM) in 2H bins 06 to 07 of a heterozygous plant from the Bowman backcross-derived line BW565 and with small regions of 1H and 3H (1, 2).
Description:
Selfing - none (3, 5).
Outcrossing - complete female fertility (3, 5).
Stamens - anthers much smaller than fertile sib (3), no stomium or filament elongation (6).
Pollen - non-staining, no free pollen grains (7).
The male sterile plants are also about 1/3 normal size with short, wide leaves (3, 5). Spikes are dense and spikelets are small and malformed, awns are 1/3 normal length, and double or triple pistils (fasciation) occur in some spikelets (5). The fused double and triple kernels, which developed after pollination of male sterile plants, were likely caused by failure of rachilla abortion and partial fusion of adjacent florets (2). Partial fertility was observed in mutant plants of the BW565 stock when they were grown in Lund, Sweden in 2013 and 2014 (6).
Origin of mutant:
An acetone induced mutant in Gateway (CIho 10072) (5).
Mutational events:
msg3.cc (MSS051, GSHO 1130) in Gateway (CIho 10072) (4, 5).
Mutant used for description and seed stocks:
msg3.cc (GSHO 1130) in Gateway; *msg3.cc* from Gateway in Bowman (PI 483237)*7 (GSHO 1885); *msg3.cc* in Bowman*8 (BW565, NGB 24806).
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linkage studies in cultivated barley, *Hordeum* species: Supplement III. 1954-1963. Crop Sci. 5:33-43.

Prepared:

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

Revised:

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

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

BGS 360, Male sterile genetic 4, *msg4*

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

Previous nomenclature and gene symbolization:
Male sterile 4 = *ms4* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 1H (3); *msg4.cd* is near the centromere (3); *msg4.cd* is associated with SNP markers 2_0617 to 1_0552 (positions 50.96 to 88.33 cM) in 1H bins 05 to 08 of a heterozygous plant from the Bowman backcross-derived stock BW576 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (5).
Pollen - non-staining, shrunken, and no normal grains (5).
Origin of mutant:
A spontaneous mutant in Freja (CIho 7130, NGB 1485) (5).
Mutational events:
msg4.cd (MSS052, GSHO 2392) in Freja (CIho 7130, NGB 1485) (2, 4).
Mutant used for description and seed stocks:
msg4.cd (GSHO 2392) in Freja; *msg4.cd* in Bowman (PI 483237)*7 (GSHO 2043, BW576, NGB 23438.
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
4. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
5. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:177-178.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:308.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:100.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:132.

BGS 361, Male sterile genetic 5, *msg5*

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

Previous nomenclature and gene symbolization:
Male sterile 5 = *ms5* (6).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 3HS (7); *msg5.ce* is about 13.1 cM proximal from the *uzu1* (uzu 1) locus (2); *msg5.ce* is about 6.8 cM proximal from the *alm1* (albino lemma 1) locus (2); *msg5.ce* is associated with SNP marker 1_1191 (position 98.41 cM) in 3H bin 6 in a heterozygous plant from Bowman backcross-derived line BW587 (1); *msg5.ie* is associated with SNP markers 1_0926 to 2_0326 (positions 85.26 to 119.10 cM) in 3H bins 05 to 07 in a heterozygous plant from Bowman backcross-derived line BW971 (1).
Description:
Selfing - none (6).
Outcrossing - complete female fertility (6).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (9).
Pollen - non-staining, some normal-appearing grains (9).
Origin of mutant:
A spontaneous mutant in Carlsberg II (CIho 10114, NGB 5085) (6).
Mutational events:
msg5.ce (MSS053, GSHO 2403) in Carlsberg II (CIho 10114, NGB 5085) (6, 8); *msg5.s* (MSS087) in Schweigers Erika (CIho 11501) (4, 8); *msg5.fr* (MSS419) in Midas (PI 343078) (5); *msg5.ie* (MSS 484) in Universe (PI 410864) (3, 5).
Mutant used for description and seed stocks:
msg5.ce (GSHO 2403) in Carlsberg II; *msg5.ce* in Bowman (PI 483237)*7 (GSHO 1954, BW587, NGB 23447); *msg5.ie* in Bowman*6 (BW971. NGB 23466).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F., and W.L. McProud. 1974. Positioning of the male sterile 5 (*msg5*) on chromosome 3. Barley Genet. Newsl. 4:16-23.
3. Franckowiak, J.D. (Unpublished).
4. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. Barley Genet. Newsl. 2:139-144.
5. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:178.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:309.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:133-134.

BGS 362, Male sterile genetic 6, *msg6*

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

Previous nomenclature and gene symbolization:
Male sterile 6 = *ms6* (6).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 6HS (5); *msg.cf* is near the centromere (4, 8); *msg6.cf* is about 1.0 cM distal from the *rob1* (orange lemma 1) locus (4); *msg6.cf* is associated with SNP markers 1_0061 to 1_0040 (positions 70.15 to 107.26 cM) in 6H bins 05 to 07 in a heterozygous plant from Bowman backcross-derived line BW589 (3), likely in 6H bin 06..
Description:
Selfing - none, but occasionally a few selfed seeds occur (4).
Outcrossing - complete female fertility (4).
Stamens - equal in size to normal anthers (4); stomium present, filament elongation (9).
Pollen - nearly normal stained in both field and greenhouse plants, most grains appear normal (9). The *msg6.cf* pollen grains are non-functional because aperture development is abnormal (1, 2). This mutant can be classified as a pollen sterile (3).
Cytology - normal development and differentiation of anthers (9, 10).
Origin of mutant:
A spontaneous mutant in Heines Hanna (PI 539131) (6, 7).
Mutational events:
msg6.cf (MSS054, GSHO 2405) in Heines Hanna (PI 539131) (6, 7).
Mutant used for description and seed stocks:
msg6.cf (GSHO 2405) in Heines Hanna; *msg6.cf* in Bowman (PI 483237)*7 (GSHO 2078, BW589, NGB 23449).
References:
1. Ahokas, H. 1975. Male sterile mutants of barley. I. Inaperturate pollen of the *msg6cf* mutant. Ann. Bot. Fenn. 12:17-21.
2. Ahokas, H. 1975. Male sterile mutants of barley. II. Cytochemistry of non-mutant and *msg6cf* microspores and pollen. Hereditas 81:33-45.
3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
4. Eslick, R.F., R.T. Ramage, and D.R. Clark. 1974. Two genetic male steriles, *msg6* and *msg,,bk*, assigned to chromosome 6. Barley Genet. Newsl. 4:11-15.
5. Falk, D.E. 1994. Creation of a marked telo 6S trisomic for chromosome 6. Barley Genet. Newsl. 23:32.
6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Lehmann, L., and P. Hagberg. 1978. Linkage studies of msg6 using four translocations involving chromosomes 5 and 6. Barley Genet. Newsl. 8:73-74.
9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
10. Roath, W.W., and E.A. Hockett. 1971. Pollen development in genetic male-sterile barley. p. 308-315. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet.

Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:178-179.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:310.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:135-136.

BGS 363, Male sterile genetic 7, *msg7*

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

Previous nomenclature and gene symbolization:
Male sterile 7 = *ms7* (6).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 5HL (2); *msg7.cg* is about 5.5 cM from the *raw1* (smooth awn 1) locus (2); the plant of the Bowman backcross-derived line for *msg7.cg* stock, BW590, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (2).
Description:
Selfing - none (6).
Outcrossing - complete female fertility (6).
Stamens - anthers much smaller than fertile sibs, no stomium or filament elongation (8).
Pollen - microspores degenerate before the free microspore stage, non-staining, no free grains (8, 9).
Cytology - normal development and differentiation of anthers until completion of meiosis, but degeneration of tapetal tissue at the tetrad stage (9).
Origin of mutant:
A spontaneous mutant in Dekap (CIho 3351) (5).
Mutational events:
msg7.cg (MSS055, GSHO 2406) in Dekap (CIho 3351) (3, 5); *msg7.ah* (MSS099) in HB 421/78 (CIho 13641) (3, 7); *msg7.fx* (MSS425) in Proctor (PI 269153) (4, 5).
Mutant used for description and seed stocks:
msg7.cg (GSHO 2406) in Dekap; *msg7.cg* in Bowman (PI 483237)*7 (GSHO 2109, BW590. NGB 24811).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Hockett, E.A. 1976. The genetic male sterile collection. Barley Genet. Newsl. 6:108.
4. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl.14:70-75.
5. Hockett, E.A. 1991. The identification of eight new loci and allelism of 14 additional mutants. Barley Genet. Newsl. 20:37-40.
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7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
9. Roath, W.W., and E.A. Hockett. 1971. Pollen development in genetic male-sterile barley. p. 308-315. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:179-180.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:311.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:137-138.

BGS 364, Male sterile genetic 8, *msg8*

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

Previous nomenclature and gene symbolization:
Male sterile 8 = *ms8* (5).

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

Description:
Selfing - none (5).
Outcrossing - complete female fertility (5).
Stamens - anthers smaller than fertile sibs (5), stomium present, and filament elongation (1, 8).
Pollen - reduced staining (6.9% stains with 2,3,5-triphenyltetrazolium, 20.7% stains with acetocarmine), some grains appear normal (8, 9).
Cytology - normal development and differentiation of microspores up to the free microspore stage (9). Pollen grains are undeveloped, have a stainable ring at the apertural annulus without any actual pore; the exine staining with Fast Blue B is darker than in normal grains (1).

Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (5).

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

Mutant used for description and seed stocks:
msg8.ch (GSHO 2407) in Betzes; *msg8.ch* in Bowman (PI 483237)*6 (GSHO 2110, BW591, NGB 23450).

References:
1. Ahokas, H. 1976. Male sterile mutants of barley. III. Additional inaperturate mutants. Barley Genet. Newsl. 6:4-6.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
4. Hockett, E.A. 1975. The genetic male sterile collection. Barley Genet. Newsl. 5:84-86.
5. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
6. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

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

Prepared:

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

Revised:

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

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

BGS 365, Male sterile genetic 9, *msg9*

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

Previous nomenclature and gene symbolization:
Male sterile 9 = *ms9* (4).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 2HS (2, 4); *msg9.ci* is about 6 cM from the T2-7a translocation point (4); *msg9.ci* is over 18.7 cM distal from the *eog1* (elongated outer glume 1) locus (2); *msg9.ci* is associated with adjacent SNP markers 1_0786 to 2_1242 (position 133.59 cM) in 2H bin 09 in a plant from Bowman backcross-derived line BW592 (1). The position of the *msg9* locus based on SNP data does not correspond to the linkage based map distances.
Description:
Selfing - 10% at Bozeman, Montana and 24% at Tucson, Arizona, USA (4).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sib (4), stomium present and filament elongation occurs (5).
Pollen - stained in plants grown in the field and in the greenhouse, in some samples the grains appear normal (5).
Origin of mutant:
A spontaneous mutant in Vantage (CIho 7324) (4).
Mutational events:
msg9.ci (MSS057, GSHO 2408) in Vantage (CIho 7324) (4).
Mutant used for description and seed stocks:
msg9.ci (GSHO 2408) in Vantage; *msg9.ci* in Bowman (PI 483237)*7 (GSHO 1883, BW592, NGB 24138).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
4. Ramage, R.T., and R.F. Eslick. 1975. Translocation linkage tests – T2-7a x male sterile. Barley Genet. Newsl. 5:46-48.
5. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:181.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:313.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:141.

BGS 366, Male sterile genetic 10, *msg10*

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

Previous nomenclature and gene symbolization:
Male sterile 3 = *ms3* (6).
Male sterile 10 = *ms10* (4).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 7HS (2, 5); *msg10.ay* is about 7.2 cM distal from the *nud1* (naked caryopsis 1) locus (3, 8); *msg10.ay* is about 14.1 cM from the *lks2* (short awn 2) locus (3); *msg10.ay* is about 2.0 cM from the *msg14* (male sterile genetic 14) locus (3); *msg10.ay* is associated with SNP markers 1_0056 to 2_0485 (positions 51.93 to 84.97 cM) in 7H bins 4 to 7 in a homozygous male sterile plant from Bowman backcross-derived line BW546 (1).
Description:
Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (9).
Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (9).
Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (6).
Mutational events:
msg10.ay (MSS058, GSHO 1811) in Compana (PI 539111) (6, 7); *msg10.cy* (MSS059) in Manchuria (CIho 2330)*9 (4, 7).
Mutant used for description and seed stocks:
msg10.ay (GSHO 1811) in Compana; *msg10.ay* in Bowman (PI 483237)*7 (GSHO 1835, BW546, NGB 23471).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
3. Eslick, R.F., and E.A. Hockett. 1972. Recombination values of four genes on chromosome 1. Barley Genet. Newsl. 2:123-126.
4. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
5. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
6. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
8. Jarvi, A.J., and R.F. Eslick. 1975. Shrunken endosperm mutants in barley. Crop Sci.

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

Prepared:

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

Revised:

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

BGS 367, Male sterile genetic 11, *msg11*

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

Previous nomenclature and gene symbolization:
Male sterile 10 = *ms10* (2, 3, 4, 5, 7, 8).
Male sterile 11 = *ms11* (2, 9).
Male sterile 12 = *msg12* (2).
Inheritance:
Monofactorial recessive (2, 9).
Located in chromosome 5HS (1); *msg11.az* is associated with adjacent SNP markers 2_0206 to 2_0010 (positions 9.61 to 28.11 cM) in 5H bin 01 in a heterozygous plant from Bowman backcross-derived line BW547 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (6).
Pollen - no staining in *msg11.ck* plants, but very low staining in *msg11.a*z plants, no normal-appearing grains (6).
Origin of mutant:
A spontaneous mutant in Gateway (CIho 10072) (5).
Mutational events:
msg11.ck (MSS060, GSHO 1812) in Gateway (CIho 10072) (4, 5); *msg11.az* (MSS061) in Svalöf 50-109 (CIho 10524) (2, 4).
Mutant used for description and seed stocks:
msg11.az (GSHO 1812) in Svalöf 50-109; *msg11.az* in Bowman (PI 483237)*7 (GSHO 2299, BW547, NGB 23419).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
4. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
5. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. Can. J. Genet. Cytol. 2:397-415.
6. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
7. Robertson, D.W., G.A. Wiebe, R.G. Shands, and A. Hagberg. 1965. A summary of linkage studies in cultivated barley, *Hordeum* species: Supplement III. 1954-1963. Crop Sci. 5:33-43.
8. Walker, G.W.R., J. Dietrich, R. Miller, and K. Kasha. 1963. Recent barley mutants and their linkages II. Genetic data for further mutants. Can. J. Genet. Cytol. 5:200-219.
9. Walker, G.W.R., K. Kasha, and R.A. Miller. 1958. Recombination studies in barley. Proc. Genet. Soc. Can. 3:41-43.
Prepared:

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

Revised:

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

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

BGS 368, Male sterile genetic 13, *msg13*

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

Previous nomenclature and gene symbolization:
Male sterile 13 = *ms13* (2).
Inheritance:
Monofactorial recessive (1).
Located in chromosome 3HL (1); *msg13.cl* is associated with adjacent SNP markers 2_0063 to 2_1277 (positions 133.92 to 173.82 cM) in 3H bins 08 to 11 in a homozygous male sterile plant from Bowman backcross-derived line BW548 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than those of fertile sibs, no stomium or filament elongation (4).
Pollen - no staining, shrunken, no normal-appearing grains (4).
Origin of mutant:
A spontaneous mutant in Haisa II (CIho 10420) (2).
Mutational events:
msg13.cl (MSS062, GSHO 1813) in Haisa II (CIho 10420) (2, 3).
Mutant used for description and seed stocks:
msg13.cl (GSHO 1813) in Haisa II; *msg13.cl* in Bowman (PI 483237)*7 (GSHO 2300, BW548, NGB 23420).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
4. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:183.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:316.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:146.

1

BGS 369, Male sterile genetic 14, *msg14*

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

Previous nomenclature and gene symbolization:
Male sterile 14 = *ms14* (6).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 7HS (2, 7); *msg14.cm* is about 2.0 cM from the *msg10* (male sterile genetic 10) locus (3); *msg14.cm* is associated with SNP markers 1_0983 to 2_0880 (positions 74.81 to 82.16 cM) in 7H bin 07 in a homozygous male sterile plant from Bowman backcross-derived line BW549 (1).
Description:
Selfing - none (6).
Outcrossing - complete female fertility (6).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (9).
Pollen - less than 1% staining with 2,3,5-triphenyltetrazolium, about 9% with acetocarmine, some normal-appearing grains (9).
Origin of mutant:
A spontaneous mutant in Unitan (CIho 10421) (6).
Mutational events:
msg14.cm (MSS063, GSHO 1814) in Unitan (CIho 10421) (6, 8); *msg14.da* (MSS349) in Betzes (PI 129430) (4, 8); *msg14.dl* (MSS360) in Hector (CIho 15514) (5, 8).
Mutant used for description and seed stocks:
msg14.cm (GSHO 1814) in Unitan; *msg14.cm* in Bowman (PI 483237)*7 (GSHO 1836, BW549, NGB 23472).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
3. Eslick, R.F., and E.A. Hockett. 1972. Recombination values of four genes on chromosome 1. Barley Genet. Newsl. 2:123-126.
4. Hockett, E.A. 1975. The genetic male sterile collection. Barley Genet. Newsl. 5:84-86.
5. Hockett, E.A. 1979. The genetic male sterile collection. Barley Genet. Newsl. 9:124-128.
6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.

Prepared:

E.A. Hockett. 1971. Barley Genet. Newsl. 1:184.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:317.

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:147-148.

BGS 370, Male sterile genetic 15, *msg15*

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

Previous nomenclature and gene symbolization:
Male sterile 15 = *ms15* (2).
Inheritance:
Monofactorial recessive (2).
Location is unknown.
Description:
Selfing - early tillers have 7.7% and late tillers have 46.2% at Bozeman, Montana, USA (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sibs (2).
The phenotype of *msg15.cn* plants differ from other male sterile genetic mutants because late tillers are fertile (2). Anthesis is delayed in relationship to spike emergence from the flag leaf (1). Only fully fertile plants were recovered from the attempt to develop a Bowman backcross-derived line for *msg15.cn* (1).
Origin of mutant:
A spontaneous mutant in a selection from the cross Atlas/2*Kindred (CIho 13446) (2).
Mutational events:
msg15.cn (MSS064, GSHO 1815) in Atlas/2*Kindred (CIho 13446) (2, 3).
Mutant used for description and seed stocks:
msg15.cn (GSHO 1815) in Atlas/2*Kindred.
References:
1. Franckowiak, J.D. (Unpublished).
2. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:184-185.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:318.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:149.

BGS 371, Male sterile genetic 16, *msg16*

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

Previous nomenclature and gene symbolization:
Male sterile 16 = *ms16* (7).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 5HS (3, 7); *msg16.co* is 8.0 to 15.0 cM distal from the breakpoint in translocation stock T2-7a (10, 11); the plant of the Bowman backcross-derived line for *msg16.co* stock, BW550, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (2).
Description:
Selfing - none (4, 6).
Outcrossing - complete female fertility (6).
Stamens - anthers are almost equal in size to fertile sibs, stomium present, and filament elongation (6, 12).
Pollen - partial staining (15 to 35%) from plants grown under both field and greenhouse conditions, normal-appearing grains occur in some samples (12). Pollen appears immature based on staining with Fast Blue B, grains lack a pore or aperture, the exine is thinner, not distinctly two-layered, and bears fewer spicules than normal pollen (1).
Tapetal tissue degeneration was observed at the free microspore stage (9).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (6).
Mutational events:
msg16.co (MSS065, GSHO 1816) in Betzes (PI 129430) (6, 8); *msg16.bi* (MSS323) in Betzes (4, 5, 8).
Mutant used for description and seed stocks:
msg16.co (GSHO 1816) in Betzes; *msg16.co* in Bowman (PI 483237)*7 (GSHO 2116, BW550, NGB 24129.
References:
1. Ahokas, H. 1976. Male sterile mutants of barley. III. Additional inaperturate mutants. Barley Genet. Newsl. 6:4-6.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Hayes, J.D., and M.S. Rana. 1966. Investigations on genetic resistance to chemicals in spring barley. p. 47-48. Welsh Plant Breed. Station, Aberystwyth, Report for 1965.
4. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. Barley Genet. Newsl. 2:139-144.
5. Hockett, E.A. 1975. The genetic male sterile collection. Barley Genet. Newsl. 5:84-86.
6. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
7. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Mian, H.R., J. Kuspira, G.W.R. Walker, and N. Muntjewerff. 1981. Macromolecular

changes and submicroscopic structure in the differentiation of *msg16* male-sterile barley anthers. p. 804-813. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.) Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp., Edinburgh. Edinburgh Univ. Press, Edinburgh.

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

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

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

Prepared:

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

Revised:

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

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

BGS 372, Male sterile genetic 17, *msg17*

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

Previous nomenclature and gene symbolization:
Male sterile 17 = *ms17* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 5HL (1); *msg17.cp* is associated with SNP markers 2_0134 to 2_0388 (positions 163.29 to 230.08 cM) in 5H bins 10 to 12 in a heterozygous plant from Bowman backcross-derived line BW551 (1).
Description:
Selfing - 1% at Bozeman, Montana and 3% at Tucson, Arizona, USA (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (4).
Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (4).
Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (2).
Mutational events:
msg17.cp (MSS066, GSHO 1817) in Compana (PI 539111) (2, 3).
Mutant used for description and seed stocks:
msg17.cp (GSHO 1817) in Compana; *msg17.cp* in Bowman (PI 483237)*7 (GSHO 2301, BW551, NGB 23421).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
3. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
4. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:186.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:320.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:152.

BGS 373, Male sterile genetic 18, *msg18*

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

Previous nomenclature and gene symbolization:
Male sterile 18 = *ms18* (5).
Inheritance:
Monofactorial recessive (5).
Located in chromosome 5HL (2); *msg18.cq* is over 37.0 cM distal from the T2-7a translocation breakpoint (7); the plant of the Bowman backcross-derived line for *msg18.cq* stock, BW552, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (1).
Description:
Selfing - none (5).
Outcrossing - complete female fertility (5).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (8).
Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (8).
Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (5).
Mutational events:
msg18.cq (MSS067, GSHO 1818) in Compana (PI 539111) (5, 6); *msg18.z* (MSS093) in Betzes (PI 129430) (4, 6); *msg18.am* (MSS304) in Betzes (3, 6).
Mutant used for description and seed stocks:
msg18.cq (GSHO 1818) in Compana; *msg18.cq* in Bowman (PI 483237)*7 (GSHO 2117, BW552. NGB24130).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
3. Hockett, E.A. 1976. The genetic male sterile collection. Barley Genet. Newsl. 6:108.
4. Hockett, E.A. 1977. The genetic male sterile collection. Barley Genet. Newsl. 7:97-100.
5. Hockett, E.A., and R.F. Eslick. 1968. Genetic male sterility in barley. I. Nonallelic genes. Crop Sci. 8:218-220.
6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
7. Ramage, R.T., and R.F. Eslick. 1975. Translocation linkage tests – T2-7a x male sterile genes. Barley Genet. Newsl. 5:46-48.
8. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:186-187.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:321.

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

BGS 374, Male sterile genetic 19, *msg19*

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

Previous nomenclature and gene symbolization:
Male sterile 19 = *ms19* (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 5HS (2, 4); *msg19.cr* is between the centromere and the breakpoint in translocation stock T2-7a (6); *msg19.cr* is associated with SNP markers 1_0983 to 2_0880 (positions 74.81 to 82.16 cM) in 5H bins 04 to 06 in a heterozygous plant from Bowman backcross-derived line BW553 (1).
Description:
Selfing - none (3).
Outcrossing - complete female fertility (3).
Stamens - anthers smaller than fertile sib, no stomium or filament elongation (7).
Pollen - no staining with 2,3,5-triphenyltetrazolium, but staining with acetocarmine, some normal-appearing grains (7).
Origin of mutant:
A spontaneous mutant in an introduction from Russia (CIho 14393) (3).
Mutational events:
msg19.cr (MSS068, GSHO 1819) in an introduction from Russia (CIho 14393) (3, 5).
Mutant used for description and seed stocks:
msg19.cr (GSHO 1819) in an introduction from Russia; *msg19.cr* in Bowman (PI 483237)*6 (GSHO 2118, BW553, NGB 23422).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid seed production. p. 292-297. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
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4. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
6. Ramage, R.T., M. Paluska, and G.A. Wiebe. 1973. Genetics and cytology of the translocation T2-7a. Barley Genet. Newsl. 3:47-49.
7. Roath, W.W., and E.A. Hockett. 1971. Genetic male sterility in barley. III. Pollen and anther characteristics. Crop Sci. 11:200-203.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:187.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:322.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:155.

BGS 375, Male sterile genetic 20, *msg20*

Stock number: BGS 375
Locus name: Male sterile genetic 20
Locus symbol: *msg20*
Previous nomenclature and gene symbolization:
Male sterile ad = *msg,,ad* (3, 4, 6).
Male sterile 20 = *ms 20* (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 4H (1); *msg20.ad* is associated with SNP markers 1_0942 to 1_1224 (positions 69.62 to 91.93 cM) in 4H bins 05 to 06 in a homozygous partially fertile plant from Bowman backcross-derived line BW555 (1). The *msg20.ad* mutant was previously associated with chromosome 1H (3).
Description:
Selfing - none (3).
Outcrossing - complete female fertility (3).
Stamens - anthers smaller than fertile sib (3). Selfed seed set in the Bowman backcross-derived line is 50 to 75% or more, but both the original stock and the Bowman backcross-derived line for *msg20.ad*, BW555, have short awns (3/4 normal length) (2).
Origin of mutant:
An X-ray induced mutant in Hannchen (CIho 531) (3).
Mutational events:
msg20.ad (MSS096, GSHO 2372) in Hannchen (CIho 531) (3, 5).
Mutant used for description and seed stocks:
msg20.ad (GSHO 2372) in Hannchen; *msg20.ad* in Bowman (PI 483237)*5 (GSHO 2059, BW555, NGB 23424). (The BW555 seed stock is maintained as homozygous for the *msg20.ad* allele.)
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
4. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
6. Robertson, D.W. 1971. Recent information of linkage and chromosome mapping. p. 220-242. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:188.
Revised:
T. Tsuchiya. 1982. Barley Genet. Newsl. 12:107.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:323.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:139.
J.D. Franckowiak. 2013. Barley Genet. Newsl. 44:130.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:156.

BGS 376, Male sterile genetic 21, *msg21*

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

Previous nomenclature and gene symbolization:
Male sterile q = *msg,,q* (3, 4, 6).
Male sterile 21 = *ms 21* (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 1HL (1*); msg21.q* is associated with SNP markers 2_0290 to 2_0780 (positions 102.33 to 154.89 cM) in 1HL bins 11 to 12 of the Bowman backcross-derived line BW556 (1).
Description:
Selfing - 3.8% at Bozeman, Montana and 2.9% at Tucson, Arizona, USA (3, 4).
Outcrossing - complete female fertility (3).
Stamens - anthers almost equal in size to fertile sibs (3). The Bowman backcross-derived line for *msg21.q*, BW556, had 70 to 85% or more selfed seed set and partially male fertile segregates were difficult to identify during backcrossing (2).
Origin of mutant:
A spontaneous mutant in a Midwest Bulk (CIho 13640) (4).
Mutational events:
msg21.q (MSS085, GSHO 2373) in CIho 13640 (CIho 13640) (3, 5).
Mutant used for description and seed stocks:
msg21.q (GSHO 2373) in CIho 13640; *msg21.q* in Bowman (PI 483237)*7 (GSHO 2302, BW556, NGB 23425). (The BW556 seed stock is maintained as homozygous for the *msg21.q* allele.)
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
4. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
5. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
6. Robertson, D.W. 1971. Recent information of linkage and chromosome mapping. p. 220-242. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
Prepared:
E.A. Hockett. 1971. Barley Genet. Newsl. 1:188-189.
Revised:
T. Tsuchiya. 1982. Barley Genet. Newsl. 12:108.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:324.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:101.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:157.

BGS 377, Shrunken endosperm genetic 1, *seg1*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se1* (6).

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

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

Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (5).

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

Mutant used for description and seed stocks:
seg1.a (GSHO 750) in Betzes; *seg1.a* in Bowman (PI 483237)*7 (GSHO 1852, BW834, NGB 22274).

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Prepared:

A.J. Jarvi and R.F. Eslick. 1971. Barley Genet. Newsl.1:190.
Revised:
R.F. Eslick. 1976. Barley Genet. Newsl. 6:135.
T. Tsuchiya. 1980. Barley Genet. Newsl. 10:124.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:325.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:264.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:158-159.

BGS 379, Shrunken endosperm genetic 3, *seg3*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se3* (6).
Proanthocyanidin-free 17 = *ant17* (4).

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

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

Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (5).

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

Mutant used for description and seed stocks:
seg3.c (GSHO 752) in Compana; *seg3.c* in Bowman (PI 483237)*7 (GSHO 1957, BW836, NGB 22273); *ant17.148* from Triumph in Bowman*4 (GSHO 1973, BW016, NGB 20424).

References:
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3. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
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Thesis. Montana State Univ., Bozeman.
6. Jarvi, A.J., and R.F. Eslick. 1971. BGS 379, Normal vs. shrunken endosperm, *se3*. Barley Genet. Newsl. 1:191.
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Prepared:

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

Revised:

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

BGS 383, Male sterile genetic 22*, msg22*

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

Previous nomenclature and gene symbolization:
Male sterile e = *msg,,e* (5, 6).
Male sterile 22 = *ms22* (2, 5).

Inheritance:
Monofactorial recessive (5).
Located in chromosome 7H (5); *msg22.e* is associated with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73 cM) in 5H bins 04 to 06 in a homozygous male sterile plant from Bowman backcross-derived line BW557 (1).

Description:
Selfing - none (5).
Outcrossing - complete female fertility (5).
Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (3).

Origin of mutant:
A spontaneous mutant in a selection from Glacier/Compana (CIho 10861) (6).

Mutational events:
msg22.e (MSS073, GSHO 741, GSHO 2374) in a selection from Glacier/Compana (CIho 10861) (6, 7); *msg22.fc* (MSS404) in Proctor (PI 280420), *msg22.fo* (MSS416) in Zephyr (PI 339815) (3, 4).

Mutant used for description and seed stocks:
msg22.e (GSHO 741, GSHO 2374) in a selection from Glacier/Compana; *msg22.e* in Bowman (PI 483237)*7 (GSHO 1857, BW557, NGB 24131).

References:
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Prepared:
E.A. Hockett. 1972. Barley Genet. Newsl. 2:178 as BGS 377, Male sterile 22, *ms22*.
E.A. Hockett. 1973. Barley Genet. Newsl. 3:121.

Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:331.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:162.

BGS 384, Male sterile genetic 23, *msg23*

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

Previous nomenclature and gene symbolization:
Male sterile b = *msg,,b* (4, 5).
Male sterile 23 = *ms23* (2, 4).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 5H (1); *msg23.b* is associated with SNP markers 1_1198 to 2_1275 (positions 73.70 to 104.73 cM) in 5H bins 04 to 06 in a heterozygous plant from Bowman backcross-derived line BW558 (1). The *msg23.b* gene was previously associated with chromosome 7HL (4).
Description:
Selfing - none in *msg23.b* and *msg23.bg* (4), but 1.9 to 13.6% in *msg23.y* (3).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (4).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (5).
Mutational events:
msg23.b (MSS071, GSHO 2375) in Betzes (PI 129430) (5, 6); *msg23.y* (MSS092) in Betzes (3, 4, 6); *msg23.bg* (MSS321) in Betzes (2, 3, 6).
Mutant used for description and seed stocks:
msg23.b (GSHO 2375) in Betzes; *msg23.b* in Bowman (PI 483237)*8 (GSHO 1867, BW558, NGB 23426).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1972. Barley Genet. Newsl. 2:179 as BGS 378, Male sterile 23, *ms23*.
E.A. Hockett. 1973. Barley Genet. Newsl. 3:122.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:332.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:163.

BGS 385, Male sterile genetic 24, *msg24*

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

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

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

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

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

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

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

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

Revised:

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

BGS 395, Male sterile genetic 26, *msg26*

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

Previous nomenclature and gene symbolization:
Male sterile u = *msg,,u* (7).
Inheritance:
Monofactorial recessive (5, 6).
Located in chromosome 7HS (3, 4); *msg26.u* is linked to the *nud1* (naked caryopsis 1) locus (3); *msg26.u* is linked to the *ant1* (anthocyanin-less 1) locus based on linkage drag (4); *msg26.u* is associated with SNP markers 2_0790 to 1_1098 (positions 73.69 to 93.97 cM) in 7H bins 05 to 06 of Bowman backcross-derived line BW561 (1).
Description:
Selfing - none (6).
Outcrossing - complete female fertility (6).
Stamens - anthers smaller than fertile sibs, no stomium or filament elongation (6).
The Bowman backcross-derived line for *msg26.u*, BW561, has adequate self-fertility so that it can be maintained as an inbred line (2).
Origin of mutant:
A spontaneous mutant in Unitan (CIho 10421) (7).
Mutational events:
msg26.u (MSS088, GSHO 745, GSHO 2378) in Unitan (CIho 10421) (5, 7, 8).
Mutant used for description and seed stocks:
msg26.u (GSHO 745, GSHO 2378) in Unitan; *msg26.u* in Bowman (PI 483237)*6 (GSHO 1858, BW561, NGB 23429).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1974. Barley Genet. Newsl. 4:136 as BGS 387, Male sterile genetic 26, *msg26*.
E.A. Hockett. 1975. Barley Genet. Newsl. 5:170.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:343.

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

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

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

Previous nomenclature and symbolization:
None.

Inheritance:
Monofactorial recessive (4).
Located in chromosome 3HL (2); *cer-r.19* is about 4.3 cM distal from the *uzu1* (uzu 1) locus (11, 12, 13, 14); *cer-r.19* is associated with SNP markers 1_0601 to 1_0047 (positions 71.29 to 119.1 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW121 (1); likely in 3H bin 06.

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

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

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

Mutant used for description and seed stocks:
cer-r.19 (GSHO 439, NGB 110903) in Bonus; *cer-r.19* in Bowman (PI 483237)*7 (GSHO 1977, BW121, NGB 20527).

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. Fester, T., and B. Søgaard. 1969. The localization of eceriferum loci in barley. Hereditas 61:327-337.
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Prepared:

U. Lundqvist. 1975. Barley Genet. Newsl. 5:129.

Revised:

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

BGS 455, Shrunken endosperm genetic 8, *seg8*

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

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (5).
Located in chromosome 7H (6); *seg8.k* in a 4.6 cM interval flanked by markers GBM1516 and Bmag341 (8); *seg8.k* is associated with SNP markers 1_0772 to 1_0169 (positions 71.81 to 142.56 cM) in 7H bins 05 to 08 of the Bowman backcross-derived line BW840 (1), likely in 7H bin 07.

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

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

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

Mutant used for description and seed stocks:
seg8.k (GSHO 2469) in 60Ab1810-53; *seg8.k* in Bowman (PI 483237)*3 (GSHO 1854); *seg8.k* in Bowman*5 (BW840, NGB 22277).

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Prepared:

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Revised:

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BGS 460, Curly 4, *cur4*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (6, 8, 12, 13).
Located in chromosome 2HL (5, 6, 9, 14); *glo-d.1006* is close to the *Gth1* (Toothed lemma 1) locus based on linkage drag (3); *cur4.f* is associated with SNP markers 1_0297 to 2_1258 (positions 85.71 to 114.96 cM) in 2H bins 07 to 08 of Bowman backcross-derived line BW223 (1); *glo-d.1006i* is associated with SNP markers 2_0674 to 2_0528 (positions 85.28 to 118.78 cM) in 2H bins 07 to 08 of Bowman backcross-derived line BW395 (1); *cur4.i* is associated with SNP markers 1_0216 to 2_0833 (positions 47.48 to 115.90 cM) in 2H bins 04 to 08 of Bowman backcross-derived line BW224 (1), in 2H bin 08.

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:
T. Tsuchiya. 1984. Barley Genet. Newsl. 14:97.
Revised:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:406.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:172-173.

BGS 464, Male sterile genetic 27, *msg27*

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

Previous nomenclature and gene symbolization:
Male sterile ae = *msg,,ae* (7).
Inheritance:
Monofactorial recessive (4, 8).
Located in chromosome 2HS (1, 2, 3); *msg27.ae* did not recombine with the *vrs1* (six-rowed spike 1) locus (2); *msg27.ae* is about 20.5 cM distal from the *vrs1* locus (3); *msg27.ae* is associated with SNP markers 2_1366 to 2_1153 (positions 50.56 to 89.09 cM) in 2H bins 05 to 06 in a heterozygous plant from Bowman backcross-derived line BW562 (1); likely in 2H bin 05.
Description:
Selfing - none (5, 7, 8).
Outcrossing - complete female fertility (8).
Stamens - anthers rudimentary, no stomium or filament elongation (5, 8).
Origin of mutant:
A spontaneous mutant in Firlbecks III (PI 223985) (8).
Mutational events:
msg27.ae (MSS097, GSHO 2379) in Firlbecks III (PI 223985) (4, 7, 8); *msg27.jr* (MSS523) in Mona (NGB 1499, PI 466726) (5, 6).
Mutant used for description and seed stocks:
msg27.ae (GSHO 2379) in Firlbecks III; *msg27.ae* in Bowman (PI 483237)*7 (GSHO 1921, BW562, NGB 24805).
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BGS 465, Male sterile genetic 28, *msg28*

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

Previous nomenclature and gene symbolization:
Male sterile as = *msg,,as* (3).
Inheritance:
Monofactorial recessive (3, 6).
Located in chromosome 2HS (1); *msg28.as* is associated with SNP markers 2_1015 to 2_0864 (positions 48.68 to 55.52 cM) in 2HS bin 05 of a plant presumed to be a heterozygous plant from the Bowman backcross-derived line BW563 (1). The *msg28.as* mutant was previously mapped in chromosome 6H near the *rob1* (orange lemma 1) locus (2).
Description:
Selfing - none (3).
Outcrossing - complete female fertility (3, 6).
Stamens - anthers rudimentary, with no stomium or filament elongation (6).
Pollen - non-staining, shrunken, and no normal-appearing grains (6).
Cytology - normal meiosis (6).
Origin of mutant:
A spontaneous mutant in York (CIho 10075) (6).
Mutational events:
msg28.as (MSS311, GSHO 2380) in York (CIho 10075) (4, 5, 6).
Mutant used for description and seed stocks:
msg28.as (GSHO 2380) in York; *msg28.as* in Bowman (PI 483237)*7 (GSHO 2079, BW563, NGB 24132).
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Prepared:
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BGS 466, Male sterile genetic 29, *msg29*

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

Previous nomenclature and gene symbolization:
Male sterile a = *msg,,a* (4).
Male sterile = 63msx1 and 63msx2 (*ms-aa*) (5).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 5HL (2); *msg29.a* is about 22.7 cM from the *raw1* (smooth awn 1) locus (2); the plant of the Bowman backcross-derived line for *msg29.a* stock, BW564, evaluated for SNP markers did not have any deviant markers in 5H from those of Bowman (1).
Description:
Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sibs, with no stomium or filament elongation (4).
Origin of mutant:
A spontaneous mutant in Ackermans MGZ (CIho 11491) (5).
Mutational events:
msg29.a (MSS069, GSHO 2381) in Ackermans MGZ (CIho 11491) (3, 6); *msg29.aa* in Ackermans MGZ (MSS070) (4, 6).
Mutant used for description and seed stocks:
msg29.a (GSHO 2381) in Ackermans MGZ; *msg29.a* in Bowman (PI 483237)*7 (GSHO 2140, BW564, NGB 24133).
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Revised:
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J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:413.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:176.

BGS 467, Male sterile genetic 30, *msg30*

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

Previous nomenclature and gene symbolization:
Male sterile c = *msg,,c* (5).
Male sterile = msx2 (*msa*) (6).
Inheritance:
Monofactorial recessive (5).
Located in chromosome 7HL (2); *msg30.c* is about 11.4 cM from the *lks2* (short awn 2) locus (2); *msg30.c* is associated with SNP markers 2_0282 to 2_0485 (positions 107.40 to 128.28 cM) in 7H bin 07 in a heterozygous plant from Bowman backcross-derived line BW566 (1), in 7H bin 07.
Description:
Selfing - 0.7% at Bozeman, Montana, USA (5).
Outcrossing - complete female fertility (5), open pollinated seed set of 15% at Bozeman, MT and 2% at Elimäki, Finland (4).
Stamens - anthers smaller than fertile sibs, stomium present and the filament elongates (4).
Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (6).
Mutational events:
msg30.c (MSS072, GSHO 2382) in Compana (PI 539111) (3, 6, 7).
Mutant used for description and seed stocks:
msg30.c (GSHO 2382) in Compana; *msg30.c* in Bowman (PI 483237)*7 (GSHO 1859, BW566, NGB 23431).
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Revised:
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J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:414.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:177.

BGS 468, Male sterile genetic 31, *msg31*

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

Previous nomenclature and gene symbolization:
Male sterile d = *msg,,d* (4).
Male sterile dwarf = *msdwf* (4).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 1HL (1); *msg31.d* is distal from the *sls1* (small lateral spikelet 1) locus (3); *msg31.d* is associated with SNP markers 1_0434 to 2_0267 (positions 127.71 to 149.80 cM) in 1HL bin 11 and with SNP markers 1_1098 to 2_1274 (positions 161.08 to 218.47 cM) in 2HL bins 11 to 13 of a heterozygous plant from the Bowman backcross-derived line BW567 (1).
Description:
Selfing - none (6).
Outcrossing - complete female fertility (6).
Stamens - anthers rudimentary, no stomium or filament elongation (5).
In addition to male sterility, mutant plants are weak and short (about 1/2 normal height), show delayed development, and appear to lack surface wax on the spike (wax code - ++ ++) (2, 4).
Origin of mutant:
A spontaneous mutant in the six-rowed line 51Ab4934 (CIho 15245) (6).
Mutational events:
msg31.d (MSS306, GSHO 2383) in 51Ab4934 (CIho 15245) (4, 6).
Mutant used for description and seed stocks:
msg31.d (GSHO 2383) in 51Ab4934; *msg31.d* in Bowman (PI 483237)*6 (GSHO 2031, BW567, NGB 23432).
References:
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6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1986. Barley Genet. Newsl. 16:51.
Revised:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:98.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:415.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:117.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:178.

BGS 469, Male sterile genetic 32, *msg32*

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

Previous nomenclature and gene symbolization:
Male sterile w = *msg,,w* (4).
Male sterile = 63msx7 (5).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 7H (2, 4); *msg32.w* is linked to the *nud1* (naked caryopsis 1) locus (2); *msg32.w* is associated with SNP markers 1_0327 to 2_0911 (positions 55.54 to 107.44 cM) in 7H bins 05 to 07 in a homozygous male sterile plant from Bowman backcross-derived line BW568 (1).
Description:
Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers smaller than fertile sibs, no stomium or filament elongation 4).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (5).
Mutational events:
msg32.w (MSS090, GSHO 2384) in Betzes (PI 129430) (3, 4, 6).
Mutant used for description and seed stocks:
msg32.w (GSHO 2384) in Betzes; *msg32.w* in Bowman (PI 483237)*7 (GSHO 1860, BW568, NGB 23433).
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6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1986. Barley Genet. Newsl. 16:52.
Revised:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:99.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:416.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:179.

BGS 470, Male sterile genetic 33, *msg33*

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

Previous nomenclature and gene symbolization:
Male sterile x = *msg,,x* (6).
Male sterile = 63msx8 (7).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 2HS (2); *msg33.x* is about 5.2 cM distal from the centromere and 25.6 cM proximal from the *vrs1* (six-rowed spike 1) locus (3); *msg33.x* is associated with SNP markers 2_0458 to 1_1250 (positions 96.47 to 161.08 cM) in 2H bins 07 to 11 in a heterozygous plant from Bowman backcross-derived line BW569 (1).
Description:
Selfing - 20% at Bozeman, Montana, 17% at Tucson, Arizona, USA, and 0% at Elimäki, Finland (5).
Outcrossing - complete female fertility (6).
Stamens - anthers smaller than fertile sibs, stomium present, and filament elongation (6).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (7).
Mutational events:
msg33.x (MSS091, GSHO 2385) in Betzes (PI 129430) (4, 6, 7, 8).
Mutant used for description and seed stocks:
msg33.x (GSHO 2385) in Betzes; *msg33.x* in Bowman (PI 483237)*7 (GSHO 1884, BW569, NGB 24807).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
3. Franckowiak, J.D. (Unpublished).
4. Hockett, E.A. 1979. The genetic male sterile barley collection. Barley Genet. Newsl. 9:124-128.
5. Hockett, E.A., and H. Ahokas. 1979. Male and female fertility levels of genetic male sterile barley grown at two different latitudes. Hereditas 91:65-71.
6. Hockett, E.A., and R.F. Eslick. 1971. Genetic male sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA. Washington State Univ. Press, Pullman.
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8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1986. Barley Genet. Newsl. 16:53.
Revised:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:100.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:417.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:180.

BGS 471, Male sterile genetic 34, *msg34*

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

Previous nomenclature and gene symbolization:
Male sterile av = *msg,,av* (4).
Male sterile = 63msy1 (4).
Inheritance:
Monofactorial recessive (4, 7, 8).
Located in chromosome 6HS or 7HS (2, 3); *msg34.av* is associated with SNP markers 1_0775 to 1_0744 (positions 26.42 to 39.34 cM) in 1H bins 03 to 05 in a homozygous plant from Bowman backcross-derived line BW570 (1). Previously recombination between *msg34.av* and the *rob1* (orange lemma 1) locus was not observed (2).
Description:
Selfing - none (4).
Outcrossing - complete female fertility (4).
Stamens - anthers rudimentary, with no stomium or filament elongation (4).
Heterozygotes show reduced fertility (75 to 85% seed set), and male sterile plants always have a Long glume awn 1 (*Lga1.a* in 7HS) gene from Paragon. Thus, the *msg34.av* mutant may involve a translocation between chromosomes 6HS and 7HS (3).
Origin of mutant:
A spontaneous mutant in Paragon (CIho 13649) (8).
Mutational events:
msg34.av (MSS314, GSHO 2386) in Paragon (CIho 13649) (5, 6).
Mutant used for description and seed stocks:
msg34.av (GSHO 2386) in Paragon; *msg34.av* in Bowman (PI 483237)*7 (GSHO 2070, BW570, NGB 24134).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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3. Franckowiak, J.D. (Unpublished).
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7. Ramage, R.T., and R.F. Eslick. 1975. Translocation linkage tests – T2-7a x male sterile genes. Barley Genet. Newsl. 5:46-48.
8. Sharma, R.K. 1970. Studies of sterility mutants in spring barley (*Hordeum vulgare* L.). Ph.D. Thesis. Univ. of Guelph, Ontario.
Prepared:
E.A. Hockett. 1986. Barley Genet. Newsl. 16:54.
Revised:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:101.
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:418.

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

BGS 498, Male sterile genetic 35, *msg35*

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

Previous nomenclature and gene symbolization:
Male sterile genetic,,dr = *msg,,dr* (3).
Male sterile = 76Y17 (3).

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

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

Origin of mutant:
A spontaneous mutant in Karl (CIho 15487) (3).

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

Mutant used for description and seed stocks:
msg35.dr (GSHO 2387) in Karl; *msg35.dr* in Bowman (PI 483237)*7 (GSHO 1933, BW571, NGB 23435).

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

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

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

BGS 499, Male sterile genetic 36, *msg36*

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

Previous nomenclature and gene symbolization:
Male sterile bk = *msg,,bk* (6).
Male sterile = 867N-89 (6).
Inheritance:
Monofactorial recessive (6).
Located in chromosome 6HS (2*); msg36.bk* is about 10.8 cM distal from the *rob1* (orange lemma 1) locus (2, 3, 9); *msg36.bk* is associated with two groups of SNP markers separated by a gap, 1_0244 to 1_0013 (positions 71.39 to 74.97) in 6H bin 06 and markers 1_1261 to 1_1246 (positions 107.28 to 134.55 cM) in 6H bins 07 to 08 in a heterozygous plant from Bowman backcross-derived line BW572 (1), likely in 6H bin 06.
Description:
Selfing - about 1.1% (6).
Outcrossing - complete female fertility (6).
Stamens - anthers nearly normal sized with stomium and filament elongation (6).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (6).
Mutational events:
msg36.bk (MSS325, GSHO 2388) in Betzes (PI 129430) (5, 6, 8); *msg36.eg* (MSS382) in Pavo P57 (4, 7).
Mutant used for description and seed stocks:
msg36.bk (GSHO 2388) in Betzes; *msg36.bk* in Bowman (PI 483237)*7 (GSHO 2067, BW 572, NGB 23436).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Eslick, R.F., R.T. Ramage, and D.R. Clark. 1974. Two genetic male steriles, *msg6* and *msg,,bk*, assigned to chromosome 6. Barley Genet. Newsl. 4:11-15.
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4. Franckowiak, J.D. (Unpublished).
5. Franckowiak, J.D., and E.A. Hockett. 1987. Allelism tests for the genetic male sterile *msg,,bk*. Barley Genet. Newsl. 17:77-78.
6. Hockett, E.A. 1972. Coordinator's report on the genetic male sterile barley collection. Barley Genet. Newsl. 2:139-144.
7. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
9. Ramage, R.T., and M. Paluska. 1975. Mapping chromosome 6. Barley Genet. Newsl. 5:49-51.
Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:103.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:425.

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

BGS 500, Male sterile genetic 37, *msg37*

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

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

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 3HL most likely (1), *msg37.jx* is associated with SNP markers 3_1220 (position 182.97 cM) in 3H bin 12 in the homozygous partially sterile Bowman backcross-derived line BW573; *msg37.hl* is associated with SNP markers 2_0797 to 1_1516 (positions 5.45 to 249.75 cM) in 3H bins 01 to 16, plus SNP markers in all other chromosomes, in a heterozygous plant from Bowman backcross-derived line BW970 (1).

Description:
Selfing - none to 6% or more (4), the degree of selfing seems sensitive to environmental conditions, favored by cool conditions (3).
Outcrossing - complete female fertility (4).
Stamens - anthers shrunken, no stomium or filament elongation (5) to nearly normal (4).
The level of self-fertility in *msg37.hl* and *msg37.jx* plants gradually increased as more backcrosses to Bowman were made. The level of self-fertility approached 80% in BW573, a selection with the *msg37.jx* allele from the sixth backcross to Bowman (3).

Origin of mutant:
A spontaneous mutant in Clermont (PI 343724) (4).

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

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

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

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

Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:426.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:186.

BGS 501, Male sterile genetic 38, *msg38*

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

Previous nomenclature and gene symbolization:
Male sterile jl = *msg,,jl* (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 3H (1); *msg38.jl* is associated with SNP markers 2_1533 to 1_0728 (positions 87.01 to 96.85 cM) in 3H bins 05 to 06 in a heterozygous plant from Bowman backcross-derived line BW574 (1).
Description:
Selfing - none (3).
Outcrossing - complete female fertility (3).
Stamens - anthers nearly normal in size, but without stomium, filament elongates (3).
Origin of mutant:
A spontaneous mutant in Ingrid (CIho 10083, NGB 2671) (3).
Mutational events:
msg38.jl (MSS51, GSHO 2390) in Ingrid (CIho 10083, NGB 2671) (2, 3).
Mutant used for description and seed stocks:
msg38.jl (GSHO 2390) in Ingrid; *msg38.jl* in Bowman (PI 483237)*7 (GSHO 2304, BW574, NGB 23437).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D., and E.A. Hockett. 1988. Identification of three new loci which control male sterility of barley. Barley Genet. Newsl. 18:11-13.
3. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:105.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:427.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:187.

BGS 502, Male sterile genetic 39, *msg39*

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

Previous nomenclature and gene symbolization:
Male sterile dm = *msg,,dm* (5).
Inheritance:
Monofactorial recessive (1, 5).
Located in chromosome 3H (2); *msg39.dm* is associated with SNP markers from 1_0312 to 1_0044 (positions 173.82 to 190.87 cM) in 3H bin 12 of a heterozygous plant from the Bowman backcross-derived stock BW575 (2), in 3H bin 12. The *msg36.dm* and *msg39.ff* mutants were previously associated with chromosome 6H, over 33.9 cM from the *rob1* (orange lemma 1) locus (3).
Description:
Selfing - about 1% in Bozeman, Montana, USA and Elimäki, Finland (1, 5).
Outcrossing - complete female fertility (1).
Stamens - anthers are the same size as fertile sibs, stomium present, and filament elongates (1, 5). Pollen shower is normal (1).
The pollen grains of the *msg39.dm* and *msg39.dn* mutants are non-functional because aperture development is abnormal. These mutants can be classified as pollen steriles (1).
Origin of mutant:
A spontaneous mutant in a Finnish six-rowed barley (P11, CIho 15836) (1, 5).
Mutational events:
msg39.dm (MSS361, GSHO 2391, GSHO 3021) in P11 (CIho 15836) (4, 7); *msg39.dn* (MSS362, GSHO 3022) in a Finnish six-rowed barley (H31, CIho 15837) (1, 4, 7); *msg39.ff* (MSS407) in Sabarlis (CIho 15484) (4, 6).
Mutant used for description and seed stocks:
msg39.dm (GSHO 2391) in P11; *msg39.dm* in Bowman (PI 483237)*7 (GSHO 2080, BW575, NGB 24135).
References:
1. Ahokas, H. 1976. Male sterile mutants of barley. III. Additional inaperturate mutants. Barley Genet. Newsl. 6:4-6.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. 1991. Association of male sterility genes with a specific chromosome using multiple marker stocks. Barley Genet. Newsl. 20:31-36.
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6. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:106.
Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:428.
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:122.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:188-189.

BGS 503, Male sterile genetic 40, *msg40*

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

Previous nomenclature and gene symbolization:
Male sterile ac = *msg,,ac* (5, 7).
Male sterile = ms-C (7).
Inheritance:
Monofactorial recessive (5).
Located in chromosome 6HL (1, 2); *msg40.ac* is over 27.8 cM from the *rob1* (orange lemma 1) locus (2); *msg40.ac* is associated with SNP markers 2_1025 to 2_0036 (positions 147.51 to 169.88 cM) in 6H bins 09 to 11 in a heterozygous plant from Bowman backcross-derived line BW577 (1).
Description:
Selfing - none (5).
Outcrossing - less than 30% in crosses and in the Bowman backcross-derived line (3, 5).
Stamens - anthers are smaller than those of fertile sibs, no stomium or filament elongation (5).
Origin of mutant:
A spontaneous mutant in Conquest (CIho 11683) (6).
Mutational events:
msg40.ac (MSS095, GSHO 2393) in Conquest (CIho 11683) (4, 5, 7).
Mutant used for description and seed stocks:
msg40.ac (GSHO 2393) in Conquest; *msg40.ac* in Bowman (PI 483237)*6 (GSHO 2081, BW577, NGB 24808).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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7. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:107.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:429.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:190.

BGS 504, Male sterile genetic 41, *msg41*

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

Previous nomenclature and gene symbolization:
Male sterile aj = *msg,,aj* (6).
Male sterile = 65msx166 (7).
Inheritance:
Monofactorial recessive (6).
Located in chromo some 6HS (1); *msg41.aj* is associated with SNP markers 1_0061 to 1_1250 (positions 70.15 to 82.43 cM) in 6H bins 05 to 06 in a heterozygous plant from Bowman backcross-derived line BW976 (1); the plant of the Bowman backcross-derived line for the *msg41.dk* stock, BW578, evaluated for SNP markers did not have any deviant markers from those of Bowman (1).
Description:
Selfing - none (4, 6).
Outcrossing - complete female fertility (6).
Stamens - anthers rudimentary, no stomium or filament elongation (4, 6).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (6).
Mutational events:
msg41.aj (MSS101, GSHO 2394) in Betzes (PI 129430) (5, 7, 8); *msg41.dk* (MSS359) in Betzes (2, 5, 8); *msg41.do* (MSS363) in Maris Baldric (PI 294512) (3, 5, 8); *msg41.ef* (MSS381) in Hector (CIho 15514), *msg41.el* (MSS387) in Sabarlis (CIho 15484), *msg41.eq* (MSS392) in Sel 12387Co; *msg41.fa* (MSS402) in Midas (PI 343078), *msg41.gl* (MSS439) in Maris Mink (PI 467824), *msg41.ij* (MSS489) in Mazurka (PI 410868) (4, 5).
Mutant used for description and seed stocks:
msg41.aj (GSHO 2394) in Betzes; *msg41.aj* in Bowman (PI 483237)*7 (BW976, NGB 23469); *msg41.dk* (MSS359) in Betzes; *msg41.dk* in Bowman*6 (GSHO 2305, BW578, NGB 23440).
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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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32. Hockett, E.A. 1977. The genetic male sterile barley collection. Barley Genet. Newsl. 7:97-100.
4. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
5. Hockett, E.A. 1991. The genetic male sterile collection. Identification of eight new loci and allelism tests of 14 additional mutants. Barley Genet. Newsl. 20:37-40.
6. Hockett, E.A., and R.F. Eslick. 1971. Genetic male sterile genes useful in hybrid barley production. p. 298-307. *In* R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
7. Hockett, E.A., R.F. Eslick, D.A. Reid, and G.A. Wiebe. 1968. Genetic male sterility in barley. II. Available spring and winter stocks. Crop Sci. 8:754-755.
8. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley

stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:108.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:430.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:191-192.

BGS 505, Male sterile genetic 42, *msg42*

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

Previous nomenclature and gene symbolization:
Male sterile db = *msg,,db* (3).
Male sterile = B68-N-109 (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 3H (2); *msg42.db* is over 18.9 cM from the *alm1* (albino lemma 1) locus (2); *msg42.db* is associated with SNP markers 1_0672 to 1_1191 (positions 58.56 to 98.41 cM) in 3H bins 04 to 06 in a heterozygous plant from Bowman backcross-derived line BW579 (1).
Description:
Selfing - none (3, 4).
Outcrossing - complete female fertility (3, 4).
Stamens - anthers rudimentary, no stomium or filament elongation (3, 4).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (3).
Mutational events:
msg42.db (MSS350, GSHO 2395) in Betzes (PI 129430) (2, 5, 6); *msg42.gt* (MSS447) in Berac (PI 355136), *msg42.hw* (MSS476) in Sel 15025Co, *msg42.iy* (MSS504) in Sv73608 (5, 6).
Mutant used for description and seed stocks:
msg42.db (GSHO 2395) in Betzes; *msg42.db* in Bowman (PI 483237)*6 (GSHO 1948, BW579, NGB 23441).
References:
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6. Hockett, E.A., and D.A. Reid. 1981. Spring and winter genetic male-sterile barley stocks. Crop Sci. 21:655-659.
Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:109.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:431.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:193.

BGS 506, Male sterile genetic 43, *msg43*

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

Previous nomenclature and gene symbolization:
Male sterile br = *msg,,br* (2).
Male sterile = B65msx38 (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 2HL (1); *msg43.br* is associated with SNP markers 2_0064 to 2_1274 (positions 179.99 to 218.47 cM) in 2H bins 11 to 13 in a heterozygous plant from Bowman backcross-derived line BW580 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers rudimentary, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (2).
Mutational events:
msg43.br (MSS332, GSHO 2396) in Betzes (PI 129430) (2, 3, 4).
Mutant used for description and seed stocks:
msg43.br (GSHO 2396) in Betzes; *msg43.br* in Bowman (PI 483237)*7 (GSHO 2306, BW580, NGB 24809).
References:
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Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:110.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:432.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:194.

BGS 507, Male sterile genetic 44, *msg44*

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

Previous nomenclature and gene symbolization:
Male sterile cx = *msg,,cx* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 5HL (1); *msg44.cx* is associated with SNP markers 1_1249 to 1_1290 (positions 109.27 to 145.57 cM) in 5H bins 06 to 09 in a heterozygous plant from Bowman backcross-derived line BW581 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers rudimentary, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in selection HA6-33-02 (CIho 15835) (2).
Mutational events:
msg44.cx (MSS346, GSHO 2397) in HA6-33-02 (CIho 15835) (2, 3, 4).
Mutant used for description and seed stocks:
msg44.cx (GSHO 2397) in HA6-33-02; *msg44.cx* in Bowman (PI 483237)*7 (GSHO 2307, BW581, NGB 23443).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:111.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:433.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:195.

BGS 508, Male sterile genetic 45, *msg45*

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

Previous nomenclature and gene symbolization:
Male sterile dp = *msg,,dp* (2).
Male sterile = 76Y2 (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 5HL or 7HS (1); *msg45.dp* is associated with SNP markers 2_1150 to 2_1168 (positions 145.57 to 168.17 cM) in 5H bins 09 to 10 and with SNP markers 1_0949 to 2_0993 (positions 0.00 to 44.83 cM) in 7H bins 01 to 03 in a heterozygous plant from Bowman backcross-derived line BW582 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers rudimentary, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in selection RPB439-71 (CIho 15838) (2).
Mutational events:
msg45.dp (MSS364, GSHO 2398) in RPB439-71 (CIho 15838) (2, 3, 4).
Mutant used for description and seed stocks:
msg45.dp (GSHO 2398) in RPB439-71; *msg45.dp* in Bowman (PI 483237)*4 (GSHO 2308, BW582, NGB 23444).
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Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:112.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:434.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:196.

BGS 509, Male sterile genetic 46, *msg46*

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

Previous nomenclature and gene symbolization:
Male sterile ec = *msg,,ec* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 2H or 6H (1); *msg46.ec* is associated with SNP markers 1_0602 to 2_0182 (positions 95.53 to 185.53 cM) in 2H bins 07 to 12 and with SNP markers 1_0061 to 1_1261 (positions 70.15 to 107.26 cM) in 6H bins 06 to 07 in a heterozygous plant from Bowman backcross-derived line BW583 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers smaller than those of fertile sibs, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in Hector (CIho 15514) (2).
Mutational events:
msg46.ec (MSS378, GSHO 2399) in Hector (CIho 15514) (2, 3, 4).
Mutant used for description and seed stocks:
msg46.ec (GSHO 2399) in Hector; *msg46.ec* in Bowman (PI 483237)*4 (GSHO 2309, BW583, NGB 23445).
References:
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Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:113.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:435.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:197.

BGS 510, Male sterile genetic 47, *msg47*

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

Previous nomenclature and gene symbolization:
Male sterile ep = *msg,,ep* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 3HS or 7HS (1); *msg47.ep* is associated with SNP markers 2_0159 to 2_0742 (positions 6.31 to 29.05 cM) in 3H bins 01 to 02 and with SNP markers 2_1270 to 1_0299 (positions 93.97 to 101.23 cM) in 7H bins 01 to 02 in a homozygous male sterile plant from Bowman backcross-derived line BW584 (1).
Description:
Selfing - none (2).
Outcrossing - complete female fertility (2).
Stamens - anthers rudimentary, no stomium or filament elongation (2).
Origin of mutant:
A spontaneous mutant in Sel 12384Co (2).
Mutational events:
msg47.ep (MSS391, GSHO 2400) in Sel 12384Co (2, 3).
Mutant used for description and seed stocks:
msg47.ep (GSHO 2400) in Sel 12384Co; *msg47.ep* in Bowman (PI 483237)*5 (GSHO 2310, BW584, NGB 24810).
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Prepared:
E.A. Hockett. 1991. Barley Genet. Newsl. 20:114.
Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:436.
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:198.

BGS 520, Male sterile genetic 48, *msg48*

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

Previous nomenclature and gene symbolization:
Male sterile genetic jt = *msg,,jt* and Msg76-5 (3).

Inheritance:
Monofactorial recessive (2, 3).
Probably located in chromosome 1H (1); *msg48.jt* is associated with SNP markers from 1_0744 to 1_0552 (positions 39.84 to 88.33 cM) in 1H bins 05 to 08 of a heterozygous plant from Bowman backcross-derived line BW585, plus small heterozygous regions in chromosomes 4HL and 7HL (1).

Description:
Selfing - 5% (2), but it may be near 50% in certain environments.
Outcrossing - Complete female fertility (2).
Stamens - anthers slightly smaller than fertile sib with filament elongation, but no stomium (2).

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

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

Mutant used for description and seed stocks:
msg48.jt (GSHO 2401) in Simba; *msg48.jt* in Bowman (PI 483237)*4 (GSHO 1925, BW585, NGB 24136).

References:
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Prepared:
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Revised:
J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:123.
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BGS 556, Breviaristatum-o, *ari-o*

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

Previous nomenclature and gene symbolization:

Breviaristatum-40 = *ari-40* (11).
Erectoides-56 = *ert-56* (7); *ert-u.56* (see BGS 092).
Brachytic 5 = *br5* (14).
Erectoides-159 = *ert-159* (12); *ert-zd.159* (see BGS 093).
Brachytic 7 = *br7* (14).
Brachytic-q = *brh.q* (4); *brh14.q* (see BGS 148) (2).
Brachytic-af = *brh.af* (2, 5); *brh14.af* (see BGS 148) (2).
Brachytic-v = *brh.v* (4); *brh16.v* (see BGS 044) (2).

Inheritance:

Monofactorial recessive (11).
Located in chromosome 7HL (3); *ari-o.40* is associated with SNP markers 1_0547 and 3_0166 (about position 232 cM) in 7H bin 14 of the Bowman backcross-derived line BW053 (3); *ari-o.40* is an allele at the *HvDIM* locus located in chromosome 7H at position 138.2 cm (2) in the barley genome map (13).

Description:

Plants of the *ari-o.40* mutant have reduced awn length (11), but they are semidwarf (2/3 normal height) and can be placed in the brachytic class of semidwarfs (4). The culm may have a short or extra internode and a leafy bract below the spike. The peduncle is often slightly coiled, and the basal rachis internode is elongated. Kernels are globe-shaped, and awns are about 3/4 normal length (11). Plants of BW053, the Bowman backcross-derived line for mutant *ari-o.40*, were about 25% shorter than Bowman, 65 vs. 90 cm, and awns were about 3 cm shorter. Rachis internode lengths and kernels were slightly shorter for BW053, but spikes had 2 to 3 more kernels. Kernels of BW053 were slightly shorter than those of Bowman. Kernel weights varied from slightly more to 20% less. Grain yields for BW053 varied from 20 to 50% of the Bowman yields (5). As with other mutants at the *ari-o* locus*, ari-o.40* shows a brassinosteroid-deficient phenotype that includes a short culm, about 70% of normal, caused largely by an extreme shortening of the second culm internode (2). Other common traits include shorter rachis internodes, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (2). The six Bowman backcross-derived lines with a mutation at the *ari-o* or *HvDIM* locus, *ari-o.40*, *brh14.af*, *brh14.q*, *brh16.v*, *ert-u.56*, and *ert-zd.159*, have retained a small, common genetic donor parent interval (2). The sequence of *HvDIM*, encoding the barley Δ^5-sterol-Δ^{24}-reductase DIMINUTO, corresponds directly to single-nucleotide polymorphism (SNP) marker 1_0547 located in the telomere on the long arm of chromosome 7H (2).

Origin of mutant:

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

Mutational events:

ari-o.40 (NGB 115890, GSHO 1663)*, -o.43* (NGB 115894) in Bonus (PI 189763, NGB 14657) (11); *ari-o.143* (NGB 115953) in Foma (CIho 11333, NGB 14659) (12); *ert-u.56* (NGB 112655, GSHO 496) in Bonus (PI 189763, NGB 14657) (2, 7); *ert-zd.159* (NGB 112758, GSHO 504) in Bonus (2, 12); *brh14.q* (OUM131, *dw-d,* DWS1035, GSHO 1682) in Akashinriki (OUJ659, PI 467400) (2, 5, 7, 9, 10); *brh14.af* (FN46, GSHO 3706) in Steptoe (CIho 15229) (2, 3, 8); *brh16.v* in HE 2816 (DWS1176, GSHO 1686) from a

cross between two semidwarf mutants (6, 15). Previously *ari-o.297* (*uzu1.297*, NGB 116118), *ari-o.301* (*uzu1.301*, NGB 116124), *ari-o.306* (*uzu1.306*, NGB 116133) in Kristina (NGB 1500, NGB 14661) were recorded as alleles at the *ari-o* locus (12), but retesting demonstrated allelism at the uzu 1 (*uzu1*) locus and the mutants were renamed (2). The *ari-o.304* (*ari-u.304*, NGB 116129) mutant in Kristina was shown to be an allele at *ert-t* (*HvBRD*) locus and renamed *ari-u.304* (2).

Mutant used for description and seed stocks:

ari-o.40 (GSHO 1663, NGB 115890) in Bonus; *ari-o.40* in Bowman (PI 483237)*6 (GSHO 2162); *ari-o.40* in Bowman*7 (BW053, NGB 20461); *ert-u.56* in Bonus (NGB 112655, GSHO 496); *ert-u.56* in Bowman (PI 483237)*8 (GSHO 1904, BW325, NGB 22120); *ert-zd.159* in Bonus (GSHO 504, NGB 112758); *ert-zd.159* in Bowman (PI 483237)*7 (GSHO 1901, BW333, NGB 22128); *brh14.q* (GSHO 1682) in Akashinriki; *brh14.q* in Bowman (PI 483237)*6 (GSHO 2175, BW085, NGB 20492); *brh14.af* (GSHO 3706) from Steptoe in Bowman*7 (BW072, NGB 20479); *brh16.v* in HE 2816/Bowman (GSHO 1686); *brh16.v* in Bowman (PI 483237)*7 (GSHO 2177, BW087, NGB 20494).

References:

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Prepared:

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Revised:

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

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

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

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

Previous nomenclature and gene symbolization:

Erectoides-55 = *ert-55* (10).
Brachytic 4 = *br4* (15).
Brachytic-g = *brh.g* (2, 5).
Brachytic-h = *brh.h* (2, 5).
Brachytic-i = *brh.i* (2, 5).
Brachytic-y = *brh.y* (2, 5).
Brachytic 3 = *brh3* (2, 6).
Breviaristatum-245 = *ari.245* (3, 11).
Breviaristatum-o.304 = *ari-o.304* (3, 13).
Hordeum vulgare brassinosteroid-6-oxidase = *HvBRD* (3).

Inheritance:

Monofactorial recessive (4, 10, 14).
Located in chromosome 2HS (2, 3, 4); *ert-t.55* is approximately 11.4 cM distal from SSR marker Bmac0134 (2), near the boundary between 2H bins 01 and 02 (2); *ert-t.55* is associated SNP markers 1_0326 to 2_0563 (positions 16.91 to 21.19) in 2H bin 02 of the Bowman backcross-derived line BW324 (4); *brh3.g* is associated with markers 2_0609 to 1_1059 (positions unmapped to 17.96) in 2H bin 02 of the Bowman backcross-derived line BW091 (4); *brh3.y* is associated with SNP markers 1_0326 to 1_0180 (positions 16.91 to 40.06) in 2H bins 02 to 04 of the Bowman backcross-derived line BW094 (4); the *brh3* mutants are in the *HvBRD* locus, which encodes for a brassinosteroid-6-oxidase, and is located in the telomeric region of 2HS (3); *ari-u.245* is associated with SNP markers 2_0609 to 2_1377 (positions about 13.0 to 20.11 cM) in 2H bin 02 of the Bowman backcrossed-derived line BW031 (4); except for *ert-t.55*, mutants at the *ert-t* locus were reported to be structural changes in the *HvBRD* locus (3); in 2H bin 02.

Description:

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

Origin of mutant:

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

Mutational events:

ert-t.55 (NGB 112654, GSHO 494) in Bonus (PI 189763, NGB14657) (10); *ert-t.437* NGB 112953) in Foma (CIho 11333, NGB 14659) (3, 13); *brh3.g* (17:10:1, GSHO 1672), *brh3.h* (17:11:3, GSHO 1673), *brh3.i* (17:12:1, GSHO 1674) in Birgitta (NSGC 1870,

NGB 1494, NGB 14667) (2, 5, 6, 12); *brh3.y* (10001, GSHO 1688) in Bido (PI 399485) (2, 5, 9); *ari-u.245* (NGB 116054) in Foma (CIho 11333, NGB 14659) (3, 11, 13); *ari-u.304* (previously named *ari-o.304*) (NGB 116129) in Kristina (NGB 1500, NGB 14661) (3. 13).

Mutant used for description and seed stocks:

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

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Prepared:

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J.D. Franckowiak. 2002. BGS 631, Brachytic 3, *brh3*. Barley Genet. Newsl. 32:132.

Revised:

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J.D. Franckowiak and U. Lundqvist. 2010. Barley Genet. Newsl. 40:134-135.
J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:203-204.

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

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

Previous nomenclature and gene symbolization:
Erectoides-132 = *ert-132* (3).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 7HL (1); *ert-zb.132* is associated with SNP markers 2_0824 to 2_1363 (positions 146.97 to 198.70 cM) in 7H bins 9 to 12 of the Bowman backcross-derived line BW331 (1).
Description:
Plants are 3/4 normal height and spikes tend to emerge prematurely (3). Compared to Bowman, plants of the backcross-derived line for *ert-zb.132*, BW331, headed 2 to 4 days later and were 15 to 20% shorter. Peduncles were 2/3 normal length and rachis internodes were about 10% shorter. Kernel weights for BW331 averaged 15% less than those of Bowman, 5.1 vs.5.8 mg, and grain yields were about 25% lower (2).
Origin of mutant:
A diepoxybutane induced mutant in Bonus (PI 189763, NGB 14657) (3).
Mutational events:
ert-zb.132 (NGB 112731, GSHO 502) in Bonus (PI 189763, NGB 14657) (3).
Mutant used for description and seed stocks:
ert-zb.132 (NGB 112731, GSHO 502) in Bonus; *ert-zb.13 2* in Bowman (PI 483237)*5 (GSHO 2262, BW331, NGB 22126).
References:
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3. Lundqvist, U. (Unpublished).
Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:498.
Revised:
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:205.

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

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

Previous nomenclature and gene symbolization:
Erectoides-149 = *ert-149* (3).
Inheritance:
Monofactorial recessive (3).
Located probably in chromosome 7HS (1); *ert-zc.149* is associated with SNP markers 2_0722 to 1_0056 (positions 23.45 to 51.93 cM) in 7H bins 2 to 4 and with SNP markers 1_1497 to 2_0545 (positions 237.41 to 244.39 cM) in 5H bin 12 of the Bowman backcross-derived line BW332 (1).
Description:
Spikes are semicompact and plants are semidwarf (3/4 normal height). The basal rachis internode is slightly elongated (3). Compared to Bowman, plants of the backcross-derived line for *ert-zc.149*, BW332, were about 10 cm shorter, peduncles were 4 to 8 cm shorter, and rachis internodes were 10 to 20% shorter. BW332 plants headed 2 to 3 days later than Bowman plants. Kernels of BW332 weighed 5 to 10% less than those of Bowman, but both lines had similar grain yields (2).
Origin of mutant:
An ethylene oxide induced mutant in Bonus (PI 189763, NGB 14657) (3).
Mutational events:
ert-zc.149 (NGB 112748, GSHO 503) in Bonus (PI 189763, NGB 14657) (3).
Mutant used for description and seed stocks:
ert-zc.149 (NGB 112748, GSHO 503) in Bonus; *ert-zc.149* in Bowman (PI 483237)*3 (GSHO 2263); *ert-zc.149* in Bowman*4 (BW332, NGB 22127).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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3. Lundqvist, U. (Unpublished).
Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:499.
Revised:
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:206.

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

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

Previous nomenclature and gene symbolization:
Erectoides-105 = *ert-105* (3).

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

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

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

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

Mutant used for description and seed stocks:
ert-ze.105 (NGB 112704, GSHO 505) in Bonus; *ert-ze.105* in Bowman (PI 483237)*5 (GSHO 2264); *ert-ze.105* in Bowman*6 (BW334, NGB 22129).

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

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

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

Previous nomenclature and gene symbolization:
Early 14 = *ea-d14* (5).
Early maturity-d = *ea-d* (10).

Inheritance:
Monofactorial incomplete dominant (5).
Located in chromosome 4HL or 6HL (2); the narrow leaf blade trait from *mat-d.14* is associated with SNP markers 2_1130 to 1_1019 (positions 175.48 to 183.54 cM) in 4H bins 12 to 13 and with SNP markers 1_0734 to 2_0379 (positions 159.32 to 163.56 cM) in 6H bins 12 to 13 of the Bowman backcrossed-derived line BW509 (2).

Description:
Early heading mutants at the *mat-d* locus (6) have a moderate increase in earliness (heading 3 days earlier than the parents) under field cultivation in Sweden (7, 8). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and are classified as a pronounced long-day type (4). Early heading is also associated with increased culm length and grain yield. The length of the peduncle is increased and mutants have longer spikes. Compared with the drastic maturity mutants at *eam8* (*mat-a*), *mat-b*, and *mat-c* loci, mutants at the *mat-d* locus have a normal number of the culm internodes (1, 5). Retention of the *mat-d.14* mutant in the Bowman backcross-derived line, BW509, needs to be confirmed because only plants with narrower leaf blades were recovered in progenies from crosses to Bowman. An error could have been made during backcrossing because BW509 retained SNP molecular markers in chromosome 4HL that are identical to those retain in BW513, the Bowman backcross-derived line for *mat-h.36* (see BGS 584) (2). Phenotypically BW509 and BW513 were very similar (3). BW509 and Bowman plants were phenotypically similar except for reduce leaf blade width and slightly lower grain yield (3).

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

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

Mutant used for description and seed stocks:
mat-d.14 (NGB 110014, GSHO 1790) in Bonus; *mat-d.14* in Bowman (PI 483237)*6 (BW509, NGB 20737).

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Prepared:

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

Revised:

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

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

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

Previous nomenclature and gene symbolization:
Praematurum-23 = *mat-23* (7).

Inheritance:
Monofactorial recessive (4).
Likely located in chromosome 1H (1); *mat-f.23* is associated with SNP markers 1_0764 to 1_1326 (positions 61.55 to 82.35 cM in 1H) in 1H bins 06 to 08 and with markers 1_0310 to 2_0152 (positions 285.74 to 298.99) in 5HL bin 15 of the Bowman backcross-derived line BW511 (1).

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

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

Mutational events
mat-f.23 (NGB 110023, GSHO 1792), *-f.780* (NGB 110780), *-f.875* (NGB 110875), *-f.891* (NGB 116846), *-f.908* (NGB 117439), *-f.932* (NGB 117463) in Bonus (PI 189763, NGB 14657); *-f.983* (NGB 117514) in Sv 79353.(5, 6, 7).

Mutant used for description and seed stocks:
mat-f.23 in Bonus (GSHO 1792, NGB 110023); *mat-f.23* in Bowman (PI 483237)*2 (GSHO 2284); *mat-f.23* in Bowman*5 (BW511, NGB 20739).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26: 509.

Revised:

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

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

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

Previous nomenclature and gene symbolization:
Praematurum-36 = *mat-36* (3).

Inheritance:
Monofactorial recessive (3).
Located in chromosome 4HL (1); *mat-h.36* is associated with SNP markers 2_1130 to 1_1019 (positions 175.48 to 183.54 cM) in 4H bins 12 to 13 of the Bowman backcross-derived line BW513 (1).

Description:
Early heading mutants at the *mat-h* locus show a drastic increase in earliness (heading 6 days earlier than the parents) under field cultivation in Sweden (3, 5). When grown under controlled environmental conditions, mutants are photo- and thermoperiod sensitive and have a pronounced long-day response (3). The Bowman backcross-derived line, BW513, line with the *mat-h.36* mutant is similar to BW509 line with the *mat-d.14* mutant in terms of both chromosomal SNP markers retained and phenotype attributes (1, 2). Plants with narrow leaves were found in progeny from the cross of the *mat-h.36* stock to Bowman. An error may have been made during backcrossing because the SNP molecular markers retained in chromosome 4HL of BW513 are identical to those retain in BW509 (see BGS 580) (1). BW513 and Bowman plants were phenotypically similar except for reduce leaf blade width and slightly lower grain yields (2).

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

Mutational events
mat-h.36 (NGB 110036, GSHO 1794)*, -h.935* (NGB 117466) in Bonus (PI 189763, NGB 14657) (3, 4).

Mutant used for description and seed stocks:
mat-h.36 (NGB 110036, GSHO 1794) in Bonus; *mat-h.36* in Bowman (PI 483237)*2 (GSHO 2286); *mat-h.36* in Bowman*7 (BW513, NGB 20741).

References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:511.

Revised:

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

BGS 585, Praematurum-i, *mat-i*

Stock number: BGS 585
Locus name: Praematurum-i
Locus symbol: *mat-i*

Previous nomenclature and gene symbolization:
Praematurum-37 = *mat-37* (7).

Inheritance:
Monofactorial recessive (4).
Located in chromosome 7HL (1); *mat-i.37* is associated with SNP markers 1_0885 to 3_0593 (positions 192.14 to 198.70 cM) in 7H bins 11 to 12 of the Bowman backcross-derived line BW514 (1).

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

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

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

Mutant used for description and seed stocks:
mat-i.37 (NGB 110037, GSHO 1795) in Bonus; *mat-i.37* in Bowman (PI 483237)*3 (GSHO 2287); *mat-i.37* in Bowman*7 (BW514, NGB 20742).

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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7. Lundqvist, U. (Unpublished).

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

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

BGS 592, Yellow head 2, *yhd2*

Stock number: BGS 592
Locus name: Yellow head 2
Locus symbol: *yhd2*

Previous nomenclature and gene symbolization:
Yellow head 2 = *yh2* (2).
Inheritance:
Monofactorial recessive (2).
Location is unknown; compared to Bowman no polymorphisms were observed in the Bowman backcross-derived line for *yhd2.b*, BW921 (1).

Description:
The *yhd2.b* seedlings are slightly yellow-green compared to normal sibs. The lighter green color persists until after heading. The phenotype is similar to that expressed by some chlorina mutants (3). Plants of the Bowman backcross-derived line for *yhd2.b*, BW921, headed 3 to 5 days later than Bowman and were 5 to 10% shorter. Other morphological traits of BW921 including yield were not different from the range of values recorded for Bowman (3).
Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (2).
Mutational events:
yhd2.b (Golden Compana, GSHO 757) in Compana (PI 539111) (2, 3).
Mutant used for description and seed stocks:
yhd2.b (GSHO 757 compared to Bowman no polymorphisms were observed in the Bowman backcross-derived line for *yhd2.b*, BW921 (1).) in Compana; *yhd2.b* in Bowman (PI 483237)*6 (GSHO 2037): *yhd2.b* in Bowman*8 (BW921, NGB 22350).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
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Prepared:
J.D. Franckowiak. 1998. Barley Genet. Newsl. 28:33.
Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:215.

BGS 595, Anthocyanin-deficient 4, *ant4*

Stock number: BGS 595
Locus name: Anthocyanin-deficient 4
Locus symbol: *ant4*

Previous nomenclature and symbolization:
Exrubrum = rub (4).

Inheritance:
Monofactorial recessive (6, 7).
Located in chromosome 4H (1); *ant4.16* is associated with SNP markers 2_1122 to 1_1500 (positions 47.7 to 115.92 cM) in 4H bins 05 to 08 of the Bowman backcross-derived line BW024 and with SNP markers 2_0972 to 1_0139 (positions 156.09 to 160.38 cM) in 6H bin 09 of BW024 (1).

Description:
Depending on the growing conditions, a slight pigmentation can be observed in the auricles, awns and lemmas of *ant4* mutant plants. The amount of anthocyanin pigmentation was clearly decreased compared to the mother cultivars (5, 8). The original mutant alleles, *ant4.16* and *ant4.17*, were taller and later maturing than their mother cultivar Foma (5, 7). The Bowman backcrossed derived line for *ant4.16*, BW024, was 10 to 20% taller than Bowman in both field and greenhouse tests, partially because its peduncles were longer (2). Earlier heading of BW024 was observed under glasshouse and short-day conditions, but not under long-day conditions (2). BW024 plants lodged more than Bowman in field tests. The spikes of BW024 had one to three fewer kernels and rachis internodes were slightly shorter. Kernels of BW024 were 10 to15% lighter and grain yields were slightly lower than those of Bowman (2).

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

Mutational events:
ant4.11 (NGB 114560), *4.16* (NGB 114565, GSHO 1642), *4.17* (NGB 114566), *4.28* (NGB 114583), *4.31* (NGB 114586) in Foma (CIho 11333, NGB 14659) (7); *ant4.32* (NGB 114587) in Foma (5); *ant4.37* (NGB 114592) in Foma (7); *ant4.40* (NGB 114595) in Bonus (PI 189763, NGB 14657) (7); *ant4.44* (NGB 119349) in Bonus (6); *ant4.53* (NGB 111870) in Bonus (5); *ant4.124* in Nordal (NGB 13680) (5).

Mutant used for description and seed stock:
ant4.11 (NGB 114560) in Foma; *ant 4.16* (NGB 114565, GSHO 1642) in Foma; *ant4.16* in Bowman (PI 483237)*3 (GSHO 2267); *ant4.16* in Bowman*7 (BW024, NGB 20432).

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

Revised:

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

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

BGS 599, Proanthocyanidin-free 17, *ant17*

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

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

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

Description:

Under normal growing conditions no anthocyanin pigmentation is observed in the *ant17* mutant plants. The testa layers of the grain of the *ant17* mutants lack proanthocyanidins and catechins, but accumulate homoeriodictyol and chrysoeriol (8, 11). A full length cDNA clone from barley, coding for a protein consisting of 377 amino acids (42 kDa), has been isolated. It shows a homology of 71% to the flavanone-3-hydroxylase enzyme protein from *Antirrhinum majus* (13). It is likely that the *ant17* gene codes for one subunit and the *ant22* gene for the other subunit of the dimeric flavanone 3-hydroxylase enzyme, which catalyzes the conversion of flavanones into dihydroflavanols (8, 13). The mutant line *ant17.148* was released as cultivar Galant (12). Alleles at the *seg3* locus in the Bowman backcross-derived lines BW016 (*ant17.148*) and BW836 (*seg3.c*) showed variable reductions in kernel weight: Kernels of BW016 and BW836 were 1/3 to 1/2 normal weight while those of BW017, the backcross-derived line for *ant17.567*, were about 3/4 normal (3). Grain yields of BW017 were about 3/4 those of Bowman (3).

Origin of mutant:

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

Mutational events:

ant17.103, *17.104*, *17.105*, *17.139* (NGB 13697), *17.140*, *17.142*, *17.143*, *17.145* in Nordal (NGB 13680) (5); *ant17.107* in Alf (NGB13682) (4); *ant17.147*, *17.148* (Galant) (NGB 13698), *17.150*, *17.151*, *17.153*, *17.154*, *17.180*, *17.185* in Triumph (PI 268180, NGB 13678) (5); *ant17.352* in Triumph (6); *ant17.160* in Gula Abed (NGB 13681) (5); *ant17.165*, *17.167*, *17.169*, *17.171*, *17.174*, *17.182* in Ark Royal (PI 447006) (5); *ant17.192*, *17.193* in Georgie (PI 447012, NGB 13683) (5); *ant17.199* in Secobra 4681 (4); *ant17.200* in Secobra 4681 (6); *ant17.208* in Hege 876 (4); *ant17.210*, *17.211*, *17.217* in Hege 802 (5); *ant 17.216* in Hege 802 (6); *ant17.220*, *17.221*, *17.224*, in Secobra 4743 (NGB 13679) (5); *ant17.227* in Ca 59995 (6); *ant17.231* in Tron (5); *ant17.237*, *17.239*, *17.241*, *17.242*, *17.247*, *17.249* in Gunhild (PI 464655, NGB 13690) (5); *ant17.243*, *17.246* in Gunhild (6); *ant17.250*, *17.251*, *17.252*, *17.253*, *17.255* in Tokak (PI 264251) (5); *ant17.267*, *17.268*, *17.269* in Secobra 18193 (NGB 13684) (5); *ant17.270* in Secobra 18193 (6); *ant17.280* in Hege 550/75 (NGB 13692) (10); *ant17.288*, *17.289*, *17.290* in Hege 550/75 (5); *ant17.293*, *17.294, 17.295*, *17.296* in Bonus (NGB 14597, PI 189763) (5); *ant17.297*, *17.298*, 17.300, *17.301*, *17.307* in Ca 41507 (5); *ant17.306*, *17.340* in Ca 41507 (6); *ant17.316* in Ca 33787 (NGB 13693) (6); *ant17.318*, *17.321*, *17.326* in Harry (PI 491575) (6); *ant17.331* in Hege A2/A4 (6);

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

Mutant used for description and seed stock:

ant17.139 (NGB 13697) in Nordal; *ant17.148* (Galant, NGB 13698, GSHO 1628) in Triumph; *ant17.148* in Bowman (PI 483237)*4 (GSHO 1973, BW016, NGB 20424); *ant17.567* (GSHO 1629) in Manker; *ant17.567* in Bowman*5 (GSHO 1974); *ant17.567* in Bowman*7 (BW017, NGB 20425); *seg3.c* from Compana in Bowman (PI 483237)*7 (GSHO 1957, BW836, NGB 22273)

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Revised:

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U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:218-220.

BGS 600, Proanthocyanidin-free 18, *ant18*

Stock number: BGS 600
Locus name: Proanthocyanidin-free18
Locus symbol: *ant18*

Previous nomenclature and symbolization:

None.

Inheritance:

Monofactorial recessive (5, 6).

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

Description:

No anthocyanin pigmentation is observed in the *ant18* mutant plants. The ripe grains of the *ant18* mutants have a shrunken appearance (6). The testa layers of the grains of the *ant18* mutants lack proanthocyanidins and catechins but accumulate small amounts of dihydroquercetin (10, 11). The *ant18* gene has been isolated and sequenced. It codes for a protein with a deduced amino acid sequence of 354 residues and a molecular weight of 38.4 kDa (12). The *ant18* gene is the structural gene coding for the dihydroflavonol reductase enzyme, which catalyzes the conversion of dihydroflavonols into leucoanthocyanidins (10, 12, 15). The nucleotide sequences of the *ant18* genes from four *ant18* mutants have been analyzed in detail and the nature of the sodium azide induced mutations in the four mutants has been revealed (13). Plants of the Bowman backcross-derived line for *ant18.102*, BW018, were similar to Bowman, but kernels were thinner and lighter, 4.6 vs.5.7 mg. Grain yields of BW018 were 1/2 to 3/4 those of Bowman (3).

Origin of mutant:

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

Mutational events:

ant18.102 (GSHO 1630), *18.141*, *18.144* in Nordal (NGB 13680) (5); *ant18.106*, *18.111* in Alf (NGB 13682) (5); *ant18.146*, *18.186* in Triumph (PI 268180, NGB 13678) (5); *ant18.159* (NGB 13699),*18.161* (NGB 13700), *18.162* (NGB 13701), *18.164* (NGB 13702), *18.183* in Gula Abed (NGB 13681) (5); *ant18.166*, *18.170*, *18.175*, *18.176*, *18.177*, *18.178*, *18.179* in Ark Royal (PI 447006) (5); *ant18.168* in Triumph (6); *ant18.195*, *18.196*, *18.197* in Georgie (PI 447012, NGB 13683) (5); *ant18.198*, *18.204* in Secobra 4681 (5); *ant18.206* in Hege 876 (5); *ant18.209* in Hege 802 (5); *ant18.215*, *18.226* in Hege 802 (6); *ant18.234*, *18.235* in Tron (5); *ant18.236*, *18.240*, *18.244*, *18.248* in Gunhild (PI 464655, NGB 13690) (5); *ant18.254* in Tokak (PI 264251) (6); *ant18.256*, *18.257*, *18.258*, *18.259*, *18.260*, *18.261*, *18.262*, *18.263* in Tokak (5); *ant18.275*, *18.276*, *18.279* in VP116 (NGB 13691) (5); *ant18.281*, *18.286*, *18.291* in Hege 550/75 (NGB 13692) (5); *ant18.292* in Bonus (NGB 14657, PI 189763) (5); *ant18.299*, *18.302*, *18.303*, *18.304*, *18.309*, *18.339*, *18.341* in Ca 41507 (5); *ant18.319*, *18.323*, *18.324*, *18.325* in Harry (PI 491575) (6); *ant18.332* in Ca 603801 (6); *ant18.337* in Ackermann 724/5/7 (6); *ant18.342* in Secobra 18193 (*NGB* 13684) (5); *ant18.344* in NZ 716.01 (6); *ant18.356*, *18.357* in Hege 841/80 (6); ant18.365, *18.366* in Ca 36167 (6); *ant18.367* in Gimpel (PI 564720) (6); *ant18.374*, *18.376*, *18.377* in Fanette (6); *ant18.378* in Ca 33787 (NGB 13693) (6); *ant18.380*, *18.392*, *18.463* in Irene (6); *ant18.402* in Odin (6); *ant18.415* in Kaya (6); *ant18.425* in NZ 3789 (6); *ant18.427* in NZ 3789 (7); *ant18.428*, *18.429*, *18.431*, *18.433*, *18.435*, *18.436* in NZ 1836-3 (6); *ant18.442* in Ca 710516 (6); *ant18.448* in Catrin (6); *ant18.451* in Ca 601427 (6); *ant18.454*,

18.456, 18.459 in Ackermann 1734/5 (6); *ant18.460* in Pamela (6); *ant18.467* (NGB 23020), *18.468* (NGB 23021), *18.471* (NGB 23022) in Grit (PI 548764, NGB 13685) (6); *ant18.473*, *18.474* in Almudena (7); *ant18.478* in Zenit (PI 574447, NGB 13686) (6); *ant18.481* in Secobra 9709 (6); *ant18.505* in WA 8953-75 (5); *ant18.512* in 72AB3484 (5); *ant18.519* in WA9044-75 (5); *ant18.532*, *18.533*, *18.591*, 18.592, *18.617*, *18.618*, *18.621* in Advance (CIho 15804) (6); *ant18.610*, *18.611*, *18.613* in Andre, (PI 469107) (6); *ant18.623* in Klages (CIho 15478) (6); *ant18.638* in 8892-78 (14); *ant18.659*, *18.660* in Cougbar (PI 496400) (14); *ant18.1503*, *18.1506*, *18.1517*, *18.1518* in Amagi-Nijo (5); *ant18.1509* in Haruna-Nijo (5); *18.1531*, *18.1532* in Nirasaki-Nijo 14 (6); *ant18.1536* in Nirakei 62 (6); *ant18.1539* in Nirakei 63 (6); *ant18.5001*, *18.5002*, *18.5003*, *18.5004*, *18.5005*, *18.5008*, *18.5009*, *18.5010* in Igri (PI 428488) (8); *ant18.5018*, *18.5022*, *18.5023*, *18.5030*, *18.5041* in Sonja (PI 392047) (9); *ant18.5027* in Video (9); *ant18.5043* in Ackermann 27/4/98 (9); *ant18.5046*, 1*8.5048* in Lucia (9); *ant18.5049* in Marinka (9).

Mutant used for description and seed stock:

ant18.102 (GSHO 1630) in Nordal; *ant18.161* (NGB 13700) in Gula Abed; *ant18.162* (NGB 13701) in Gula Abed; *ant18.102* from Nordal in Bowman (PI 483237)*3 (GSHO 1856); *ant18.102* in Bowman*7 (BW018, NGB 20426).

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Revised:

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

BGS 613, Branched 1, *brc1*

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

Revised locus symbol:

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

Previous nomenclature and gene symbolization:

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

Inheritance:

Monofactorial recessive (2).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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Revised:

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

BGS 624, Opposite spikelets 1, *ops1*

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

Previous nomenclature and gene symbolization:
Opposite spikelets-3 = *op-3* (4, 5).

Inheritance:
Monofactorial recessive (4).
Location in chromosome 7HS (1); *ops1.3* is associated with SNP markers 2_1419 to 1_0965 (positions 0.00 to 38.08 cM) in 7H bins 01 to 03 of the Bowman backcross-derived line BW641 (1).

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

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

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

Mutant used for description and seed stocks:
ops1.3 (GSHO 2427, NGB 115379) in Bonus; *ops1.3* in Bowman (PI 483237)*6 (GSHO 2318); *ops1.3* in Bowman*7 (BW641, NGB 22206).

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

Revised:
U. Lundqvist and J.D. Franckowiak. 2013. Barley Genet. Newsl. 43:165.
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:226.

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

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

Previous nomenclature and gene symbolization:
Viviparoides-5 = *viv-5* (4, 5).

Inheritance:
Monofactorial recessive (3, 5).
Located in chromosome 2H (2); *viv-a.5* is associated with SNP markers 2_0177 to 2_0528 (positions 63.96 to 116.78 cM) in 2H bins 05 to 08 of the Bowman backcross-derived line BW896 (2).

Description:
Tillers of *viv-a* plants may remain vegetative and fail to produce reproductive structures. The apex of the tillers remains vegetative as the culm elongates. Occasionally a short, malformed spike is formed in a lateral position (1, 5). For the Bowman backcross-derived line for *viv-a.5*, BW896, only a few tiller exhibited the typical viviparoides phenotype in most environments. BW896 plants were 5 to 20 cM shorter than Bowman and they lodged easily. Peduncle and awn lengths were slightly reduced and heading was delayed about six days. Kernels of BW896 were thinner, 3.5 vs. 4.0 mm, and weighed less, 4.2 vs. 5.6 mg. Grain production varied almost none to nearly 50% of that for Bowman (3).

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

Mutational events:
viv-a.5 (NGB 115364, GSHO 2498) in Foma (CIho 11333, NGB 14659) (5).

Mutant used for description and seed stocks:
viv-a.5 (GSHO 2498, NGB 115364) in Foma; *viv-a.5* in Bowman (PI 483237)*3 (GSHO 2364); *viv-a.5* in Bowman*4 (BW896, NGB 22329).

References:
1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
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Prepared:
U. Lundqvist and J. D. Franckowiak. 2002. Barley Genet. Newsl. 32:128.

Revised:
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:227.

BGS 629, Mottled leaf 6, *mtt6*

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (2).
Located in chromosome 7HS (1); *mtt6.g* is associated with SNP markers 1_0851 to 2_1437 (positions 17.32 to 20.56 cM) in 7H bin 02 of the Bowman backcross-derived line BW604 (1).
Description:
When grown in the greenhouses, the *mtt6.g* seedlings are slightly pale green in color and develop a white necrotic region partially across the blade of the first leaf. Occasionally white necrotic blotches or region develop in subsequent leaf blades. Plants are taller than normal sibs and remain a slightly pale shade of green until maturity. Plant vigor appears normal (2). Plants of the Bowman backcross-derived line for *mtt6.g*, BW604, headed 1 to 4 days later than Bowman plants. BW604 plants varied from slightly taller to shorter, had slightly longer peduncles and larger leaf blades, and had 2 to 4 more kernels per spike. Compared to Bowman, kernels of BW604 were 5 to 10% lighter and grain yields varied from 30 to 95% of those for Bowman (2).
Origin of mutant:
A spontaneous mutant in selection ND6809 from a ND2654-31/Karl cross (2).
Mutational events:
mtt6.g (GSHO 2411) in ND6809-1 (2).
Mutant used for description and seed stocks:
mtt6.g (GSHO 2411) in ND6809; *mtt6.g* in Bowman (PI 483237)*8 (GSHO 2311, BW604, NGB 22170).
References:
1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
2. Franckowiak, J.D. (Unpublished).
Prepared:
J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:130.
Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:228.

BGS 631, Brachytic 3, *brh3*

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

Revised locus symbol:

The *brh3* mutants are alleles at the *ert-t* (Erectoides-t) or *BRASSINOSTEROID-6-OXIDASE* (*HvBRD*) locus, which encodes a barley brassinosteroid-6-oxidase (2). See BGS 566 for more information on the alleles at the *ert-t* or *HvBRD* locus.

Previous nomenclature and gene symbolization:

Brachytic-g = *brh.g* (4).
Brachytic-h = *brh.h* (1, 4).
Brachytic-i = *brh.i* (1, 4).
Brachytic-y = *brh.y* (1, 4).
Erectoides-t.55 = *ert-t.55* (1, 8, 10).
Brachytic 4 = *br4* (11).

Inheritance:

Monofactorial recessive (4, 6).
Located in chromosome 2HS (1, 3); *brh3.g* is approximately 11.4 cM distal from SSR marker Bmac0134 (1), near the boundary between 2H bins 01 and 02 (1); *brh3.g* is associated with markers 2_0609 to 1_1059 (positions unmapped to 17.96) in 2H bin 02 of the Bowman backcross-derived line BW091 (3); *brh3.y* is associated with markers 1_0326 to 1_0180 (positions 16.91 to 40.06) in 2H bins 02 to 04 of the Bowman backcross-derived line BW094 (3); no SNP markers different from those of Bowman were retained in 2HS Bowman backcross-derived line for *brh3.i*, BW093 (3); the *brh3* mutants are in the *HvBRD* locus, which encodes for a brassinosteroid-6-oxidase, and is located in the telomeric region of 2HS (2); in 2H bin 02.

Description:

The seedling leaf of *brh3* plants is shorter than that of normal sibs. Plants are 2/3 to 3/4 of normal height and the number of tillers per plant is reduced. Awns are fine with slightly curly tips and are about 1/2 normal length. Spikes of *brh3* plants have a slightly elongated first rachis internode. Seed set may be reduced when plants are grown under greenhouse conditions (5). Spikes are semi-compact, rachis internode length is about 2.7 mm in the original mutant, and culm length is about 2/3 of normal. These phenotypic traits, included the dense spike and short awn, are inherited together (1, 5). Based on general appearance of the plants, the *ert-t.55* mutant can be placed in the brachytic class of semidwarf mutants (1, 11). The *brh3* mutants exhibited the brassinosteroid-deficient phenotype: shorter rachis internode length, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (2). The Bowman backcross-derived lines for *brh3.g* and *brh3.y*, BW091 and BW094, had kernels that were shorter, 8.7 vs 9.7 mm, and lighter, 4.6 vs 5.6 mg, than those of Bowman. Grain yields of BW091 and BW094 varied from 1/3 to 2/3 those of Bowman (5).

Origin of mutant:

Probably sodium azide induced mutants in Birgitta (NSGC 1870, NGB 1494 and 14667) (9).

Mutational events:

brh3.g (GSHO 1672, 17:10:1, DWS1002) in Birgitta (NSGC 1870, NGB 1494 and 14667) (1, 4, 6); *brh3.h* (GSHO 1673, 17:11:3, DWS1003) in Birgitta; *brh3.i* (GSHO 1674, 17:12:1, DWS1004) in Birgitta (4, 6, 9); *brh3.y* (GSHO 1688, 10001, DWS1230) in Bido

(PI 399485) (1, 4, 7). The *brh3.g* and *brh3.h* lines may be the same mutational event as a seed mixture was observed in the original seed lots (5) and both stocks have the same nonsense mutation in the *ert-t* (*HvBRD*) coding region (2).

Mutant used for description and seed stocks:

brh3.g (GSHO 1672) in Birgitta; *brh3.g* in Bowman (PI 483237)*7 (GSHO 2167, BW 091, NGB 20497); *brh3.h* in Bowman*2 (GSHO 2168, BW092, NGB 20498); *brh3.i* in Bowman*6 (GSHO 2169); *brh3.i* in Bowman *7 (BW093, NGB 20499); *brh3.y* from Bido in Bowman*5 (GSHO 2178); *brh3.y* in Bowman*6 (BW094, NGB 20500). See BGS 566 for information about additional mutants at this locus.

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.
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10. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. Hereditas 61:115-178.
11. Tsuchiya, T. 1976. Allelism testing of genes between brachytic and erectoides mutants. Barley Genet. Newsl. 6:79-81.

Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 2015. Barley Genet. Newsl. 45:229-230.

BGS 653, Brachytic 10, *brh10*

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

Previous nomenclature and gene symbolization:
Brachytic-l = *brh.l* (4).

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 2HS (1); *brh10.l* is approximately 12.9 cM distal from SSR marker Bmac0850 in 2H bin 08 (1); *brh101.l* is associated with SNP markers 1_1054 to 2_0960 (positions 83.83 to 120.83 cM) in 2H bins 06 to 09 of the Bowman backcross-derived line BW081 (2).

Description:
Plants of the *brh10.l* mutant are about 3/4 normal height and peduncles are over 3/4 normal length. Awns are about 3/4 of normal length. Rachis internodes are slightly shorter than those of normal sibs, but the number of fertile rachis nodes is increased by over 2. Seedling leaves of *brh10.l* plants are relatively short (1, 3). Kernels of the Bowman backcross-derived line for *brh10.l*, BW081, were shorter (7.9 vs. 9.6 mm) and 10 to 20% lighter than those of Bowman. BW081 plants showed an erect growth habit and grain yields averaged 20% less than those of Bowman (1, 3). Awns of BW081 were slightly shorter, 8 vs. 11 cm beyond terminal kernel, and rachis internodes were shorter, 3.7 vs.4.5 mm. BW081 plants headed 2 to 4 days later than Bowman and had 2 to 3 more kernels per spike (3).

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

Mutational events:
brh10.l (17:15:2, DWS1007, GSHO 1677) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5, 6).

Mutant used for description and seed stocks:
brh10.l (GSHO 1677) in Birgitta; *brh10.l* in Bowman (PI 483237)*7 (GSHO 2171); *brh10.l* in Bowman*8 (BW081, NGB 20488).

References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
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6. Lehmann, L.C. 1985. (Personal communications).

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

Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:231.

BGS 654, Brachytic 11, *brh11*

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

Previous nomenclature and gene symbolization:
Brachytic-n = *brh.n* (4).
Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 5HS (1); *brh11.n* is about 6.7 cM proximal from SSR marker Bmac0113 in 5H bin 04 (1); *brh11.n* is associated with SNP markers 1_0688 to 2_1121 (positions 52.12 to 105.90 cM) in 5H bins 03 to 06 and with SNP markers 2_0062 to 2_1151 (positions 51.44 to 78.94 cM) in 4H bins 06 to 08 of the Bowman backcross-derived line BW082 (2).
Description:
Plants of the *brh11.n* mutant are 2/3 to 3/4 normal height and peduncles are 3/4 to 5/6 normal length. The length of the rachis internodes is about 3/4 as long as those of normal sibs. Seedling leaves of *brh11.n* plants are relatively short (1, 3). Kernels of the Bowman backcross-derived line for *brh11.n*, BW082, were shorter (7.2 vs. 9.6 mm) and about 25% lighter (4.6 vs. 5.7 mg) than those of Bowman. BW082 plants had an erect growth habit and grain yields averaged less than 1/2 of those for Bowman (1, 3). Rachis internodes of BW082 were shorter, 3.4 vs. 4.5 mm. Also, peduncles were shorter. 22 vs. 30 cm, and awns were slightly shorter. BW082 plants headed 2 to 4 days later than Bowman (3).
Origin of mutant:
A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (6).
Mutational events:
brh11.n (17:19:2, DWS1011, GSHO 1679) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (4, 5).
Mutant used for description and seed stocks:
brh11.n (GSHO 1679) in Birgitta; *brh11.n* in Bowman (PI 483237)*6 (GSHO 2172, BW082, NGB 20489).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
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6. Lehmann, L.C. 1985. (Personal communications).
Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:294.
Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:232.

BGS 655, Brachytic 12, *brh12*

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

Previous nomenclature and gene symbolization:
Brachytic-o = *brh.o* (4).
Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 5HS (1); *brh12.o* is approximately 13.5 cM distal from SSR marker Bmag0387 in 5H bin 03 (1); *brh12.o* is associated with SNP markers 1_1198 to 2_1244 (positions 73.70 to 91.0 cM) in 5H bins 04 to 05 of the Bowman backcross-derived line BW083 (2).
Description:
Plants of the *brh12.o* mutant are 2/3 to 3/4 of normal height. Awns and peduncles are about 3/4 normal length. The length of the rachis internodes is about 3/4 of normal sibs. Seedling leaves of *brh12.o* plants are relatively short (1, 3). Kernels of the Bowman backcross-derived line for *brh12.o*, BW083, were shorter (7.3 vs. 9.2 mm) and about 20% lighter than those of Bowman. Grain yields of BW083 averaged slightly more than 1/2 of those for Bowman (1, 3).
Origin of mutant:
A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (6).
Mutational events:
brh12.o (17:20:2, DWS1012, GSHO 1680) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5, 6).
Mutant used for description and seed stocks:
brh12.o (GSHO 1680) in Birgitta; *brh12.o* in Bowman (PI 483237)*7 (GSHO 2173, BW083, NGB 20490).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
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Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:295.
Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:233.

BGS 656, Brachytic 13, *brh13*

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

Previous nomenclature and gene symbolization:

Brachytic-p = *brh.p* (5).
Brachytic-ac = *brh.ac* (2, 5).
Hordeum vulgare Constitutive Photomorphic Dwarf = *HvCPD* (2).

Inheritance:

Monofactorial recessive (5, 7).
Located in chromosome 5HS (1, 2, 3); *brh13.p* is approximately 8.7 cM distal from SSR marker Bmag0387 in 5H bin 03 (1); *brh13.p* is associated with SNP markers 2_1324 to 2_1121 (positions 47.40 to 105.91 cM) in 5H bins 02 to 06 of the Bowman backcross-derived line BW084 (3); the Bowman backcross-derived line for *brh13.ac* (*brh18.ac*), BW089, was not evaluated by Druka et al. (3); the *brh13* (*HvCPD*) locus is positioned at 44.24 cM (2) on the barley genome map (9, 10).

Description:

Plants of the *brh13.p* mutant are about 2/3 normal height, and their awns are about 1/2 normal length. Peduncles and leaf blades are about 2/3 and 3/4 normal length, respectively (1, 6). The length of the rachis internodes is about 5/6 that of Bowman, 3.8 vs 4.3 mm. The spikelets at the tip of the spike are close together giving a fascinated appearance. Seedling leaves of *brh13.p* plants are relatively short. Plants lodge relatively easily (1, 6). Kernels of the Bowman backcross-derived line for *brh13.p*, BW084, were about the same size as those of Bowman, but kernel weights averaged about 20% less and test weight was lower. BW084 plants had erect growth habit and their grain yields averaged about 1/2 those of Bowman (6). The *brh13.p* mutant shows a brassinosteroid deficient phenotype including reduced culm length due to short upper internodes, irregular rachis internode length, short awns, acute leaf angles, and strongly undulating leaf margins (2). The *brh13.p* mutant is at the *brh13* (Brachytic 13) or *CONSTITUTIVE PHOTOMORPHOGENIC DWARF* (*HvCPD*) locus, which encodes the barley C-23α-hydroxylase cytochrome P450 90A1 (CYP90A1) (2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (8).

Mutational events:

brh13.p (18:02:4, DWS1013, GSHO 1681) in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (6, 7); *brh13.ac* (*brh18.ac*) (402B, DWS1277, GSHO 1670) in Mo6/4*Triumph (CIho 11612, GSHO 2465) (2, 4, 5, 7); based on allelism tests conducted by Dockter et al. (2) *brh18.ac* (BGS659) is renamed *brh13.ac*.

Mutant used for description and seed stocks:

brh13.p (GSHO 1681) in Birgitta; *brh13.p* in Bowman (PI 483237)*6 (GSHO 2174, BW084, NGB 20491); *brh13.ac* (GSHO 1670) in Mo6/4*Triumph; *brh13.ac* in Bowman*6 (GSHO 2182, BW089, NGB 22474).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson.

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6. Franckowiak, J.D. (Unpublished).
7. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
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10. The International Barley Genome Sequencing Consortium. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature 491:711-716.

Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:296.
Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:234-235.

BGS 658, Brachytic 17, *brh17*

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

Previous nomenclature and gene symbolization:
Semidwarf mutant = Mo4 (6).
Brachytic-ab = *brh.ab* (4).

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 5HS (1); *brh17.ab* is approximately 11.6 cM proximal from SSR marker Bmag0387 in 5H bin 03 (1); *brh17.ab* is associated with SNP markers 1_0688 to 2_1344 (positions 52.12 to 98.42 cM) in 5H bins 03 to 06 of the Bowman backcross-derived line BW088 (2).

Description:
Plants of the *brh17.ab* mutant are about 3/4 normal height and awns are 5/6 of normal length. Peduncles are slightly shortened. Rachis internodes are about 20% shorter than those of normal sibs. Seedling leaves of *brh17.ab* plants are relatively short (1, 3). Compared to Bowman, kernels of the Bowman backcross-derived line for *brh17.ab*, BW088, were shorter (7.7 vs. 9.7 mm) and nearly 20% lighter, 5.0 vs. 5.9 mg. Lodging was reduced in BW088 and grain yields averaged 2/3 those of Bowman (1, 3). BW088 plants headed 1 to 2 days later than Bowman plants, were 10 to 15 cm shorter and had slightly shorter awns and peduncles (3).

Origin of mutant:
A sodium azide induced mutant in Morex (CIho 15773) (7).

Mutational events:
brh17.ab (Wa14355-83, Mo4, DWS1260, GSHO 1669) in Morex (CIho 15773) (5, 6).

Mutant used for description and seed stocks:
brh17.ab (GSHO 1669) in Morex; *brh17.ab* in Bowman (PI 483237)*6 (GSHO 2181, BW088, NGB 20495).

References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
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7. Ullrich, S.E., and Aydin, A. 1988. Mutation breeding for semi-dwarfism in barley. p. 135-144. *In* Semi-dwarf Cereal Mutants and Their Use in Cross-breeding III. IAEA-TECDOC-455. IAEA, Vienna.

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

Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:236.

BGS 659, Brachytic 18, *brh18*

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

Revised locus symbol:

The *brh18.ac* mutant is an allele at the *brh13* (Brachytic 13) or *CONSTITUTIVE PHOTOMORPHOGENIC DWARF* (*HvCPD*) locus, which encodes the barley C-23α-hydroxylase cytochrome P450 90A1 (CYP90A1) (2). See BGS 656 for more information on the alleles at the *brh13* or *HvCPD* locus.

Previous nomenclature and gene symbolization:

Brachytic-ac = *brh.ac* (5).
Brachytic 18.ac = *brh18.ac*.

Inheritance:

Monofactorial recessive (5, 7).
Located in chromosome 5HS (1); *brh13.ac* (*brh18.ac*) is approximately 9.2 cM distal from SSR marker Bmac0163 in 5H bin 01 (1); *brh13.ac* was not evaluated by Druka et al. (3); the *brh13.ac* mutant is in the *HvCPD* gene and is positioned at 44.24 cM (2) on the barley genome map (8, 9).

Description:

Plants of the *brh13.ac* mutant are about 2/3 normal height and awns are less than 2/3 of normal length. Seedling leaves of *brh13.ac* plants are relatively short (1, 4). Peduncles are slightly coiled and about 3/4 as long as those of normal sibs (1, 2, 5). Rachis internodes of the Bowman backcross-derived line for *brh13.ac* mutant, BW089, were about 20% shorter than those of Bowman. BW089 plants were about 2/3 the height of Bowman plants and the extension of awns beyond the tip of the spike was about half as far. Kernels of BW089 plants were slightly lighter than those of Bowman, but about 10% shorter. Lodging was reduced, but grain yields averaged about 1/2 that for Bowman (6). The *brh13.ac* mutant shows a brassinosteroid deficient phenotype including reduced culm length due to short upper internodes, irregular rachis internode length, short awns, acute leaf angles, and undulating leaf margins (2).

Origin of mutant:

An induced mutant backcrossed into Triumph (CIho 11612, GSHO 2465) (4).

Mutational events:

brh13.ac (402B, DWS1277, GSHO 1670) in Mo6/4*Triumph (CIho 11612, GSHO 2465) (4, 5, 7); *brh13.p* mutant (18:2:4, DWS 1013, GSHO 1681) in Birgitta (NSCG 1870, NGB 1494, NGB 14667) (2).

Mutant used for description and seed stocks:

brh13.ac (GSHO 1670) in Mo6/4*Triumph; *brh13.ac* in Bowman (PI 483237)*6 (GSHO 2182, BW089, NGB 22474).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.

3. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendrarnin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. Plant Physiol. 155:617-627.
4. Falk, D. 1985. (Personal communications).
5. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
6. Franckowiak, J.D. (Unpublished).
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9. The International Barley Genome Sequencing Consortium. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature 491:711-716.

Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:299.
Revised:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:237-238.

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

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

Revised locus symbol:

The *ari-u.245* mutant is an allele at the *ert-t* (Erectoides-t) or *BRASSINOSTEROID-6-OXIDASE* (*HvBRD*) locus, which encodes a barley brassinosteroid-6-oxidase (1). See BGS 566 for more information on the alleles at the *ert-t* or *HvBRD* locus.

Previous nomenclature and gene symbolization:

Breviaristatum-245 = *ari.245* (4).

Inheritance:

Monofactorial recessive (4).

Located in chromosome 2HS (1, 2); *ari-u.245* is associated with SNP markers 2_0609 to 2_1377 (positions about 13.0 to 20.11 cM) in 2H bin 02 of the Bowman backcrossed-derived line BW031 (2); the *ari-u.245* mutant is an allele at the *ert-t* or *HvBRD* locus, which encodes for a brassinosteroid-6-oxidase, and is located in the telomeric region of 2HS (1); in 2H bin 02.

Description:

Plants of the *ari-u.245* mutant have reduced awn length, about 2/3 of normal with an undulated awn tip and an erect or brachytic growth habit (4). In the Bowman backcross-derived line for *ari-u.245*, BW031, a brachytic-like growth habit was observed, but expression of morphological traits was variable among nurseries with plant growth more reduced in moisture stressed nurseries. BW031 plants were 10 to 40% shorter and peduncles were 20 to 40% shorter compared to Bowman plants. Awn lengths of BW031 plants were 2/3 to 3/4 those for Bowman and rachis internode length varied from 2.9 to 4.3 mm compared to about 4.5 mm for Bowman. Kernels of BW031 were slightly smaller and 20% lighter. Grain yields varied from less than 1/3 to 3/4 of the Bowman yields (3). The variability in trait expression over environments observed in BW031 could be described as phenotypic plasticity, see Lacaze et al. (5). The *ari-u.245* mutant in BW031 plants exhibited the brassinosteroid-deficient phenotype: shorter rachis internode length, short awns, acute leaf angles, slightly undulating basal leaf blade margins, and a slightly elongated basal rachis internode (1).

Origin of mutant:

An N-methyl-N-nitrosourea induced mutant in Foma (CIho 11333, NGB 14659) (4, 6).

Mutational events:

ari-u.245 (NGB 116055) in Foma (CIho 11333, NGB 14659) (4, 6); *ari-u.304* (previously named *ari-o.304*) (NGB 116129) in Kristina (NGB 1500, NGB 14661) (1. 6).

Mutant used for description and seed stocks:

ari-u.245 (NGB 116055) in Foma; *ari-u.245* via ND14701 in Bowman (PI 483237)*5 (BW031, NGB 20439).

References:

1. Dockter, C., D. Gruszka, I, Braumann, A. Druka, I. Druka, J. Franckowiak, S.P. Gough, A. Janeczko, M. Kurowska, J. Lundqvist, U. Lundqvist, M. Marzec, I. Matyszczak, A.H. Müller, J. Oklestkova, B. Schulz, S, Zakhrabekova, and M. Hanson. 2014. Induced variations in brassinosteroid genes define barley height and sturdiness, and expand the green revolution genetic toolkit. Plant Physiol. 166:1912-1927.

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

Prepared:
J.D. Franckowiak and U. Lundqvist. 2011. Barley Genet. Newsl. 41:200.
Revised:
U. Lundqvist and J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:239-240.

BGS 716, Intense blue aleurone 1, *ibl1*

Stock number: BGS 716
Locus name: Intense blue aleurone 1
Locus symbol: *ibl1*

Previous nomenclature and gene symbolization:
Intense blue aleurone = *ibl* (1, 2).

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

Description:
The *ibl1.a* variant was identified based on mature aleurone color. Two new colors, brick red and intense blue, were found in the Abyssinian lines, Ethiopian 637 and Ab 2231, respectively. Aleurone color expression is influenced by the environment in much the same way as that of normal blue, but they are reasonably distinct from normal blue and white aleurones in well grown material (1). The *ibl1.a* gene intensifies the red anthocyanin pigmentation of base of seedlings and on the culms of maturing plants (3).

Origin of mutant:
Natural occurrence in Ethiopian 637 (GSHO 2508) (1).

Mutational events:
ibl1.a in Ethiopian accessions Ethiopian 637 (GSHO 2508) and in Ab 2231 (1, 2).

Mutant used for description and seed stocks:
ibl1.a in Ethiopian 637; *ibl1.a* with *blx4.d* (blue aleurone 4) and *nud1.a* (naked caryopsis 1) in Bowman*4/ICARDA Green//Ethiopian 637 (BW417, NGB 20650) produces red aleurone color; *ibl1.a* with *Blx1.a* (Blue aleurone 1) and *nud1.a* (naked caryopsis 1) in Bowman*4/ICARDA Green//Ethiopian 637 (BW418, NGB 20651) produces deep blue aleurone color.

References:
1. Finch, R.A., and G.E. Porter. 1976. A single gene determining two new aleurone colours in barley. Barley Genet. Newsl. 6:26-27.
2. Finch, R. A., and E. Simpson. 1978. New colours and complementary colour genes in barley. Z. Pflanzenzücht. 81:40-53.
3. Franckowiak, J.D. (Unpublished).

Prepared:
J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:241.

BGS 730, Labile 1, *lab1*

Stock number: BGS 730
Locus name: Labile 1
Locus symbol: *lab1*

Previous nomenclature and gene symbolization:

Hordeum irregulare (2, 5).

Hordeum vulgare L. convar. *labile* (Schiem.) Mansf.) (6, 7).

Inheritance:

Located in chromosome 5HL (6); *lab1.a* is at approximately 80 cM of 5HL in an interval of 5.7 cM between closely linked markers BAR and ge00066s01 (6), likely in 5H bins 08 or 09.

Description:

The *lab1.a* variant causes variable spikelet development at rachis nodes and is characterized by missing kernels or a variable number of fertile spikelets at each rachis node in six-rowed spikes (2, 5). The genetic background for *labile* phenotype is based on a six-rowed genotype with the recessive allele *vrs1.a* at the six-rowed spike 1 locus and dominant *Int-c.a* allele present at the intermedium spike-c loci (7). Suppression of lateral spikelet development starts in late stamen primordium (6).

Origin of mutant:

Natural occurrence in barley accessions from Ethiopia (1, 2, 3, 4, 5).

Mutational events:

lab1.a in PI 95306 and PI 25672 from Ethiopia.

Mutant used for description and seed stocks:

lab1.a in HOR2573 and HOR5465 from Ethiopia (6).

References:

1. Abay, F., and A. Bjørnstad. 2009. Specific adaptation of barley varieties in different locations in Ethiopia. Euphytica 167:181-195.

2. Åberg, E., and G.A. Wiebe. 1945. Irregular barley, *Hordeum irregulare*, sp. nov. J. Wash. Acad. Sci. 35:161-164.

3. Bjørnstad, A., and F. Abay. 2010. Multivariate patterns of diversity in Ethiopian barleys. Crop Sci. 50:1579-1586.

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5. Harlan, H.V. 1914. Some distinctions in cultivated barleys with reference to their use in plant breeding. Vol 137 Gov. Print. Off., U.S. Dept. Agr. Bull., illus. p. 38. Washington.

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Prepared:

J.D. Franckowiak. 2015. Barley Genet. Newsl. 45:242.

BGS 731, Required for *Puccinia graminis* resistance 2, *rpr2*

Stock number: BGS 731
Locus name: Required for *Puccinia graminis* resistance 2
Locus symbol: *rpr2*

Previous nomenclature and gene symbolization:
ɣ08-118; R43-22#1 (3).

Inheritance:
Monofactorial recessive (2, 3)
Location in chromosome 6H (2); mapped to a 0.6 cM interval in 6H between markers Locus_6H_331 and GMS006 (2).

Description:
The *rpr2.b* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in the cultivar, Morex, which has the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr2.b* mutant has been partially characterized (2) with infection type (IT) range of 2.1; to 3; with a mode 3.2 (rated by 1), or IT of 3-2 to 3 (rated by 2), or IT of 2-3- (rated by 5). The *rpr2.b* mutant is not allelic to *rpr1.a*, *rpr3.c*, *rpr4.d; rpr5.e*, or *rpr6.f* (2, 3). Barley often exhibits mesothetic reactions with two or more ITs on a single leaf; therefore, ITs observed are recorded in order of their prevalence (4). Overall the *rpr2.b* mutant stock is moderately susceptible as opposed to the parent line Morex, which is typically rated as moderately resistant. (3, 4). The RPG1 protein is present in the *rpr2.b* line and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3). [Infection type (IT) for wheat stem rust (*Puccinia graminis* f. sp. *tritici*) seedling reaction is based on a 0-4 scale, defined by Stackman et al. (4), where 0 is highly resistant and 4 is highly susceptible with the in between numbers representing intermediate reactions which are further modified by + or – and a fleck which indicates a small necrotic area. IT1 indicates minute uredinia; IT2 small uredinia with chlorosis; IT3 medium uredinia often with chlorosis; and IT4 indicates large uredinia with chlorosis (4).]

Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:
rpr2.b (ɣ08-118; R43-22#1, GSHO 3693) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:
rpr2.b (ɣ08-118; R43-22#1, GSHO 3693) in Morex; *rpr2.b* in F_2 seed lots GSHO 3694 and GSHO 3695 (3).

References:
1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:243.

BGS 732, Required for *Puccinia graminis* resistance 3, *rpr3*

Stock number: BGS 732
Locus name: Required for *Puccinia graminis* resistance 3
Locus symbol: *rpr3*

Previous nomenclature and gene symbolization:
ɣ08-112; R12-31#3 (3).
Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.
Description:
The *rpr3.c* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr3.c* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): range of 3- to 3+ (rated by 2); or MR with an IT range of 1.2 to 2 (rated by 1); or an It of 2.3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpg3.c* mutant is not allelic to *rpr1.a, rpr2.b, rpr4.d, rpr5.e, or rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).
Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).
Mutational events:
rpr3.c (ɣ08-112; R12-31#3, GSHO 3696) in Morex (CIho 15773) (2, 3).
Mutant used for description and seed stocks:
rpr3.c (ɣ08-112; R12-31#3, GSHO 3696) in Morex.
References:
1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).
Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:244.

BGS 733, Required for *Puccinia graminis* resistance 4, *rpr4*

Stock number: BGS 733
Locus name: Required for *Puccinia graminis* resistance 4
Locus symbol: *rpr4*

Previous nomenclature and gene symbolization:
γ08-114; R36-37#1 (3).

Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.

Description:
The *rpr4.d* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr4.d* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 2.1 to 3.2 with a mode 3.2 (rated by 1); IT range of 3- to 3+ (rated by 2), or IT range of 3.3+ to 3.3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr4.d* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr5.e*, or *rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).

Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:
rpr4.d (γ08-114; R36-37#1, GSHO 3697) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:
rpr4.d (γ08-114; R36-37#1, GSHO 3697) in Morex.

References:
1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:245.

BGS 734, Required for *Puccinia graminis* resistance 5, *rpr5*

Stock number: BGS 734
Locus name: Required for *Puccinia graminis* resistance 5
Locus symbol: *rpr5*

Previous nomenclature and gene symbolizartion:
γ08-117; R42-33#5 (same as γ08-116) (3).

Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.

Description:
The *rpr5.e* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr5.e* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 2 to 3.2 with a mode 2.3,3.2 (rated by 1); IT range of 3- to 3 (rated by 2), or 3.3-.2 (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr5.e* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, or *rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).

Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).

Mutational events:
rpr5.e (γ08-117; R42-33#5, GSHO 3699) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:
rpr5.e (γ08-117; R42-33#5, GSHO 3699) in Morex; *rpr5.e* (γ08-116; R42-33#1, GSHO 3699) in Morex (3). (These are selections from the same original seed lots, but they were both submitted and assigned different GSHO numbers).

References:
1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).

Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:246.

BGS 735, Required for *Puccinia graminis* resistance 6, *rpr6*

Stock number: BGS 735
Locus name: Required for *Puccinia graminis* resistance 6
Locus symbol: *rpr6*

Previous nomenclature and gene symbolization:
γ08-119; R47-23#1 (1).
Inheritance:
Monofactorial recessive (1, 2).
Location is unknown.
Description:
The *rpr6.f* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr6.f* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 2.3- to 3+ (rated by 1) or IT range of 2.3- to 3.3- (rated by 4) based on a 0-4 scale, defined by Stakman et al. (3). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr6.f* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, or *rpr5.e* (1, 2) The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (1, 2).
Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (2).
Mutational events:
rpr6.f (γ08-119; R47-23#1, GSHO 3700) in Morex (CIho 15773) (1, 2).
Mutant used for description and seed stocks:
rpr6.f (γ08-119; R47-23#1, GSHO 3700) in Morex.
References:
1. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
2. Kleinhofs, A. (Unpublished).
3. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
4. Steffenson, B.J. (Unpublished).
Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:247.

BGS 736, Required for *Puccinia graminis* resistance 7, *rpr7*

Stock number: BGS 736
Locus name: Required for *Puccinia graminis* resistance 7
Locus symbol: *rpr7*

Previous nomenclature and gene symbolization:
γ08-115; R3-18#3 (2).
Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.
Description:
The *rpr7.g* mutant induced a moderate susceptible reaction to *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. E. Henn (*Pgt*) race MCCF in a cultivar, Morex, having the *Rpg1.a* gene (see BGS 511) for resistance to *P. graminis* (wheat stem rust). The *rpr7.g* mutant has been partially characterized (2) with infection type (IT) of moderately susceptible (MS): IT range of 1,2 to 3 with a mode 2.3-3.2 (rated by 1); IT of 3 (rated by 2), or IT range of 2.3 to 3.3- (rated by 5) based on a 0-4 scale, defined by Stakman et al. (4). The parent line Morex is rated as moderately resistant. For description of IT ratings, see the BGS description for *rpr2* (BGS 731). The *rpr7.g* mutant is not allelic to *rpr1.a, rpr2.b, rpr3.c, rpr4.d*, *rpr5.e*, or *rpr6.f* (2, 3). The RPG1 protein is present and apparently functional as indicated by the observations that the RPG1 protein was phosphorylated within 15 min of inoculation with *Pgt* race MCCF urediniospores and degraded within 24 hrs of infection as expected for a functional RPG1 protein (2, 3).
Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (3).
Mutational events:
rpr7.g (γ08-115; R3-18#3, GSHO 3701) in Morex (CIho 15773) (2, 3).
Mutant used for description and seed stocks:
rpr7.g (γ08-115; R3-18#3, GSHO 3701) in Morex.
References:
1. Brueggeman, R.S. (Unpublished).
2. Gill, U.S. 2012. Understanding and characterizing the genes associated with *Rpg1* mediated resistance pathway against stem rust. Ph.D. Thesis. Washington State University, Pullman.
3. Kleinhofs, A. (Unpublished).
4. Stakman, E.C., D.M. Steward, and W.Q. Loegering. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. U.S. Dep. Agric. ARS E-617.
5. Steffenson, B.J. (Unpublished).
Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:248.

BGS 737, Required for resistance to *Cochliobolus sativus* 1, *rcr1*

Stock number: BGS 737
Locus name: Required for resistance to *Cochliobolus sativus*
Locus symbol: *rcr1*

Previous nomenclature and gene symbolization:
γ08-122; (R4-29) (2).
Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.
Description:
Plants with the *rcr1.a* mutant at the *rcr1* locus exhibited a susceptible reaction following inoculation with *Cochliobolus sativus* (Ito & Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] isolate ND85F. When rated following inoculation at the seedling stage, 10 individual plants of the *rcr1.a* mutant stock ranged from 5.5 to 6.5 with a mean 6.1 compared to rating of 3.5 to 4.5 with a mean of 3.7 for its moderately resistant parent Morex (2, 3). The six-rowed spring barley cultivar Morex has been reported to have the *Rcs5.e* (Reaction to *Cochliobolus sativus* 5) gene and at least two other QTL that in combination confer resistance to *C. sativus* (1, 4, 5).
Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (2).
Mutational events:
rcr1.a (γ08-122; R4-29, GSHO 3702) in Morex (CIho 15773) (2, 3).
Mutant used for description and seed stocks:
rcr1.a (γ08-122; R4-29, GSHO 3702) in Morex.
References:
1. Bilgic, H., B.J. Steffenson, and P.M. Hayes. 2005. Comprehensive genetic analyses reveal differential expression of spot blotch resistance in four populations of barley. Theor. Appl. Genet. 111:1238-1250.
2. Kleinhofs, A. (Unpublished).
3. Steffenson, B.J. (Unpublished).
4. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.
5. Zhou, H., and B. Steffenson. 2013. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breeding 32:139-154.
Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:249.

BGS 738, Required for resistance to *Cochliobolus sativus* 2, *rcr2*

Stock number: BGS 738
Locus name: Required for resistance to *Cochliobolus sativus* 2
Locus symbol: *rcr2*

Previous nomenclature and gene symbolization:
γ08-123; (R14-40) (2).
Inheritance:
Monofactorial recessive (2, 3).
Location is unknown.
Description:
Plants with the *rcr2.b* mutant at the *rcr2* locus exhibit a susceptible reaction following inoculation with *Cochliobolus sativus* (Ito & Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] isolate ND85F. When rated following inoculation at the seedling stage, 10 individual plants of the *rcr2.b* mutant stock ranged from 3.5 to 4.5 with a mean 4.0 compared to rating of 3.5 to 4.5 with a mean of 3.7 for its moderately resistant parent Morex (2, 3). The six-rowed spring barley cultivar Morex has been reported to have the *Rcs5.e* (Reaction to *Cochliobolus sativus* 5) gene and at least two other QTL that in combination confer resistance to *C. sativus* (1, 4, 5).
Origin of mutant:
A gamma-ray induced mutant in Morex (CIho 15773) (2).
Mutational events:
A gamma-ray induced mutant in Morex (CIho 15773) (2).
Mutant used for description and seed stocks:
rcr2.b (γ08-123; R14-40, GSHO 3703) in Morex.
References:
1. Bilgic, H., B.J. Steffenson, and P.M. Hayes. 2005. Comprehensive genetic analyses reveal differential expression of spot blotch resistance in four populations of barley. Theor. Appl. Genet. 111:1238-1250.
2. Kleinhofs, A. (Unpublished).
3. Steffenson, B.J. (Unpublished).
4. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.
5. Zhou, H., and B. Steffenson. 2013. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breeding 32:139-154.
Prepared:
A. Kleinhofs. 2015. Barley Genet. Newsl. 45:250.

BGS 739, Required for resistance to *Cochliobolus sativus* 3, *rcr3*

Stock number: BGS 739
Locus name: Required for resistance to *Cochliobolus sativus* 3
Locus symbol: *rcr3*

Previous nomenclature and gen symbolization:

γ08-124 (2).

Inheritance:

Monofactorial recessive (2, 3).

Location is unknown.

Description:

Plants with the *rcr3.c* mutant at the *rcr3* locus exhibit a susceptible reaction following inoculation with *Cochliobolus sativus* (Ito & Kurib.) Drechs. ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.] isolate ND85F. When rated following inoculation at the seedling stage, 10 individual plants of the *rcr3.c* mutant stock ranged from 4.0 to 4.3 with a mean 4.1 compared to rating of 3.5 to 4.5 with a mean of 3.7 for its moderately resistant parent Morex (2, 3). The six-rowed spring barley cultivar Morex has been reported to have the *Rcs5.e* (Reaction to *Cochliobolus sativus* 5) gene and at least two other QTL that in combination confer resistance to *C. sativus* (1, 4, 5).

Origin of mutant:

A gamma-ray induced mutant in Morex (CIho 15773) (2).

Mutational events:

rcr3.c (γ08-124, GSHO 3704) in Morex (CIho 15773) (2, 3).

Mutant used for description and seed stocks:

rcr3.c (γ08-124, GSHO 3704) in Morex.

References:

1. Bilgic, H., B.J. Steffenson, and P.M. Hayes. 2005. Comprehensive genetic analyses reveal differential expression of spot blotch resistance in four populations of barley. Theor. Appl. Genet. 111:1238-1250.

2. Kleinhofs, A. (Unpublished).

3. Steffenson, B.J. (Unpublished).

4. Steffenson, B.J., P.M. Hayes, and A. Kleinhofs. 1996. Genetics of seedling and adult plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley. Theor. Appl. Genet. 92:552-558.

5. Zhou, H., and B. Steffenson. 2013. Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley breeding germplasm. Mol. Breeding 32:139-154.

Prepared:

A. Kleinhofs. 2015. Barley Genet. Newsl. 45:251.