Barley Genetics Newsletter

Volume 37

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U. Lundqvist
V. Carollo Blake

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Dr. Udda Lundqvist
Coordinator, Barley Genetics Newsletter
Nordic Genetic Resource Center
P.O. Box 41
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Phone: +46 40 536640
FAX: +46 40 536650
Cell phone: +46 70 624 1502
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Coordinator's Reports

Barley Genetics Newsletter 37:1-4 (2007)

Dominance and recessiveness of parameters of Aluminum-resistance of barley F_2 hybrids at different concentrations of stress factor

E. M. Lisitsyn and I. I. Lisitsyna
North-East Agricultural Research Institute, 166-a Lenin street, Kirov, 610007, Russia
e-mail: edaphic@mail.ru

Till now there is no uniform opinion in the scientific literature about number and type of action of genes coding barley aluminum resistance. For example, Rigin, Yakovleva (2001) considers, that it is controlled by two oligogenes, as a minimum, with possible action of genes with weaker effect. Other authors assume the control of the parameter by one dominant gene *Pht* [Stolen, Andersen, 1978], or gene *Alp* [Reid, 1971], both located on chromosome 4 [Minella, Sorrells, 1997].

Gourley et al [1990] concluded, that type of action of genes coding aluminum resistance in sorghum (additive, partially or completely dominant), depends not only on a researched genotype, but also on used Al concentration. Aniol [1995, 1996] has established, that when the concentration of aluminum in test solution is low (30-40 μM), cereal cultures (wheat, rye) use mechanisms that block accumulation of aluminum in roots (for example, chelation of aluminum at the expense of exudation of organic acids by root system), at higher concentration of aluminum in root growth environment (200-300 μM) the basic role is played by other physiological mechanisms of Al-resistance. Thus the author remarks [Aniol, 1997] that the aluminum resistance of wheat plants at a concentration of 296 μM is controlled by 2 genes and at a concentration of 592 μM aluminum resistance is controlled by three genes. He wrote, that genes located in D-genome of wheat, are expressed only at high Al concentration, and genes located on chromosome 5A are expressed at all studied concentrations.

The aim of our research was to determine the influence of Al concentration on a direction and character of dominance of parameters of roots growth of barley F_2 hybrid seedlings.

Material and Methods

The direct and reciprocal F_2 hybrids of four selection numbers of barley (№№ 565-98, 889-93, 999-93 and 1030-93), bred in North-East Agricultural Research Institute (Kirov, Russia) were taken for the analysis. By results of the preliminary laboratory analyses the parental forms of these hybrids differed significantly on a level of Al-resistance that corresponded to the research aim. A level of Al-resistance (relative root length - RRL) was estimated under conditions of rolled culture on five-day barley seedlings according to the technique described earlier [Lisitsyn, 2000] by division of value of root length of each individual seedling in test treatment variant (0.5 and 1.0 mM of aluminum as sulphate salt, pH 4.3) on value of average root length of control variant (without the stress factor, pH 6.0). Each sample volume consists of 99-105 seedlings in each treatment variant.

Character of dominance for parameters of root growth of F_2 hybrid plants was estimated by equation [Petr, Frey, 1966]:

$$d = \frac{F_2 - MP}{HP - MP}$$

where d = degree of dominance; F_2, HP, MP = means of F_2 hybrids, resistant parent value, and mid parent value, respectively.

Results and Discussion

Expression of Al-resistance genes appreciably depend on a concentration of aluminum in test solution and with its increase the resistance of all hybrids was reduced without exception (table 1).

Table 1. Parameters of root growth of barley F_2 hybrids under laboratory condition

Hybrid	Root length, mm			RRL, %	
	0 mM Al	0.5 mM Al	1.0 mM Al	0.5 mM	1.0 mM
565-98 x 889-93	109.2±1.5	71.2±1.2	56.3±1.0	65.2±0.6	51.6±0.5
889-93 x 565-93	103.0±1.1	84.7±1.3	71.3±1.2	82.3±0.7	69.2±0.7
565-98 x 999-93	113.6±1.6	71.8±1.8	48.3±1.2	63.2±0.9	42.6±0.6
999-93 x 565-98	103.3±2.2	65.8±0.9	55.3±1.2	63.7±0.5	53.5±0.7
565-98 x 1030-93	112.7±1.1	74.2±1.1	57.0±1.3	65.8±0.6	50.6±0.7
1030-93 x 565-98	110.8±1.4	79.3±1.3	65.2±1.0	71.6±0.7	58.8±0.5
889-93 x 999-93	107.7±2.2	76.0±1.7	61.0±1.5	70.5±0.7	56.6±0.8
999-93 x 889-93	106.9±1.1	70.7±1.5	58.2±0.8	66.1±0.8	54.5±0.4
889-93 x 1030-93	107.6±1.4	75.0±2.0	64.5±1.5	69.7±1.1	59.9±0.8
1030-93 x 889-93	102.1±1.6	79.0±1.0	62.9±0.8	77.4±0.6	61.6±0.5
999-93 x 1030-93	104.9±1.6	75.6±1.6	52.2±1.7	72.0±0.9	49.8±0.9
1030-93 x 999-93	111.2±1.2	77.4±1.0	59.6±1.2	69.5±0.5	53.6±0.6

As it is visible from data, submitted in table 2, depending on the cross and aluminum concentration used, for some hybrids the large value of root length was dominated, for others hybrids – the smaller value, but for the third part of hybrids dominance of root length was absent practically. It is possible to note the same character of dominance for RRL parameter. The similar phenomenon was earlier marked in the literature for other cereals. So, [Camargo, 1981, 1984] pointed out, that Al-resistance of wheat F_2 population was coded by dominant genes at concentration of aluminum 3 mg/l, but became recessive at increase of concentration of the stressful factor up to 10 mg/l. Similar results were described in the researches with wheat [Bona et al., 1994].

Table 2. Influence of direction of crossing on character of dominance of parameters of root growth of barley F_2 hybrids

Hybrid	Degree of dominance of a parameter				
	Root length			RRL	
	0 mM Al	0.5 mM Al	1.0 mM Al	0.5 mM	1.0 mM
565-98 x 889-93	0.33	-0.78	-1.94	-1.21	-5.35
889-93 x 565-93	-0.94	0.34	1.26	0.99	5.00
565-98 x 999-93	1.19	-1.42	-1.51	-4.65	-3.13
999-93 x 565-98	-0.44	-2.12	-0.70	-4.50	-0.85
565-98 x 1030-93	-0.81	-0.45	-0.51	-0.37	-0.40
1030-93 x 565-98	-2.00	-0.05	0.44	0.11	0.13
889-93 x 999-93	4.33	1.18	1.10	-0.16	0.23
999-93 x 889-93	3.80	-0.38	0.40	-1.16	-0.47
889-93 x 1030-93	-0.25	10.14	1.98	1.67	1.15
1030-93 x 889-93	-1.11	15.96	1.58	3.47	1.40
999-93 x 1030-93	-0.35	1.05	-4.00	0.59	0.17
1030-93 x 999-93	0.44	1.49	7.00	0.30	1.22

As it is follows from data, submitted in table 2, depending on a concrete combination of crossing domination of root length under control conditions, under both Al treatments and of RRL parameter can have positive or negative meanings, changing from negative super-domination till positive super-domination. Character and direction of domination can coincide for parameters of roots length under control conditions and under aluminum treatment, but sometimes can have an opposite direction.

Directions of crossing caused opposite character of dominance of researched parameters of Al-resistance for hybrids 565-98 x 889-93 and 889-93 x 565-98. This tendency is some less expressed at hybrids received from crossing of breeding numbers 565-98 and 1030-93. At the same time direct and reciprocal hybrids between breeding number 565-98 and breeding number 999-93 for main part of researched parameters have shown only different degree of dominance, but not its different direction.

Direct and reciprocal hybrids between selection numbers 889-93 and 1030-93 had least differences on a direction and character of dominance.

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Frequency distributions and composite interval mapping for QTL analysis in 'Steptoe' x 'Morex' barley mapping population

H. S. Rao[1, 2†], O. P. Basha[1], N. K. Singh[1], K. Sato[3], H. S. Dhaliwal[1]*
Indian Institute of Technology Roorkee, UA, India

[1]Department of Biotechnology, Indian Institute of Technology Roorkee, Roorkee 247667, Uttaranchal, INDIA
[2]Present address: 101, Maize Genetics Unit, Division of Genetics, LBS Building, Indian Agricultural Research Institute, New Delhi 110012, INDIA
[3]Barley Germplasm Center, Okayama University, Kurashiki 710-1146, JAPAN

*corresponding author Email: hsdhafbs@iitr.ernet.in
FAX: 91-1332-273560 Tel.: 01332-285259
[†]Additional author Email: hsr_f12@rediffmail.com

ABSTRACT

With the advancement of QTL mapping strategies, the traditional approaches for the identification of genes and their effects responsible for trait expression are gradually losing significance. The phenotypic data for heading days, plant height, peduncle length, number of tillers and stripe rust was recorded on 150 recombinant inbred line (RIL) population developed from a barley cross of 'Steptoe' and 'Morex'. Preliminary examinations of frequency distribution plots were fairly useful in the prediction of number of genes governing traits expression in barley (*Hordeum vulgare* L.). The predictions were then systematically confirmed through QTL mapping. Molecular marker data for the population available at the public domain (GrainGenes website) was used for the construction of linkage map and QTL analysis. Clear colinearity was observed between the number of QTLs identified and the number of genes predicted based upon frequency distribution study alone. A total of 17 QTLs were detected for the five traits evaluated. Several major QTLs were detected on chromosome 2H, which could serve as candidate for map-based studies of phenomena such as pleiotropism, recombination hot spots, gene-rich regions and QTL clustering.

Keywords. Barley, frequency distribution, quantitative trait loci, recombinant inbred line, peduncle length, stripe rust, gene rich region.

INTRODUCTION

Cultivated barley (*Hordeum vulgare* L.) is a diploid (2n=14) which ranks fourth among the most important cereal crops in the world after rice, wheat and maize. Barley belongs to the same tribe Triticeae as that of wheat and rye and it resembles wheat in many respects. Barley is however, more tolerant to soil salinity and drought than wheat. Many important traits of economic and agronomic importance in barley are quantitative in nature displaying continuous

variation. The efficiency of breeding programs depends on our knowledge of the genetic control and genomic location of QTLs governing the trait(s) of interest. With the advent of molecular markers (Botstein et al. 1980) and the user-friendly statistical software it has become possible to resolve and map the QTLs for complex traits on chromosomes.

QTL analysis in barley is significant not only for the crop itself but also for comparative mapping with other cereal crops. The identification of diverse taxa sharing segments of similar gene orders throughout their genomes has been the major outcome of comparative mapping where chromosome alignment has hastened identification of new genes for their ultimate introgression into suitable cultivars. The genetic maps of diploid wheat, *Triticum monococcum* and barley, *Hordeum vulgare* L. are remarkably conserved except for few regions where translocation and inversion of chromosome segments have taken place (Dubcovsky et al. 1996). There is also a high level of genomic conservation at specific regions with rice, maize and oat (Deynze et al. 1995, Han et al. 1998).

The results of several QTL mapping studies have indicated that there are only few major genes, which interact with numerous minor genes and environment to give continuous trait phenotype characteristic of quantitative traits. Thus examination of frequency distribution plots at single location is useful in assessing the probable number of major genes controlling a trait. This is particularly useful when resources are limiting and a decision has to be taken on priority basis before starting a breeding program for which trait QTL mapping experiment should be undertaken. The present article deals with the mapping of QTLs for a number of traits in a barley 'Steptoe' x 'Morex' RIL mapping population and its relationship with the predictive value of frequency distribution for the traits.

MATERIALS AND METHODS

Plant Material

150 recombinant inbred lines (RILs) derived from a cross between two barley (*Hordeum vulgare* L.) genotypes 'Steptoe' and 'Morex', obtained from Dr. Kazuhiro Sato, Okayama University, Japan was used as a mapping population and it was phenotyped for five traits. Each of the RILs and the parents were sown as a single one meter row with row to row spacing of 30cm in the experimental field at the Indian Institute of Technology Roorkee, India in the winter season of 2005. Normal fertilizers, irrigation and other agronomic practices were followed for growing the population. Both 'Steptoe' and 'Morex' are hulled, six-rowed spring barley varieties. 'Steptoe' is a late flowering and dwarf line with reduced peduncle, few tillers per plant and moderate resistance to stripe rust. On the other hand, 'Morex' is early flowering and tall genotype with long peduncle, more tillers per plant and high susceptibility to stripe rust.

Phenotypic Data

The data on five quantitative traits were recorded as the average of five competitive plants per RIL. The number of days to heading was recorded as the number of days from sowing till half of the tillers in a RIL had flowered. Plant height (cm) was recorded as the length of plant from the base at the soil surface to the tip of spike of the tallest tiller excluding awns. Peduncle

length was measured as the length of peduncle from the base of flag leaf to the base of basal spikelet of a spike. The number of effective tillers bearing spikes was taken as the number of tillers per plant. The data on natural incidence of stripe rust at the adult plant stage under field conditions was recorded as percent severity of the leaf area covered by stripes of uredia and the type of pustules, where the symbol S for susceptible was used for large pustules without any necrotic area; MS, MR for moderately susceptible/resistance for small pustules with or without necrotic areas around them and R for hypersensitive immune reaction without any pustule.

Data Analysis

The basic statistical analysis was performed for all the traits recorded. Mean, range and standard deviations were estimated. Correlation coefficient among various traits was calculated to infer probable inter-relationships between the traits studied. Frequency distribution plots for traits were presented as about ten phenotypic classes in the RIL population.

Genotypic data and Linkage mapping

Genotypic data for 343 molecular markers available at the public domain (GrainGenes website: http://www.gene.pbi.nrc.ca) for 150 RILs of 'Steptoe' x 'Morex' mapping population was utilized for the construction of linkage map. Standard χ^2 test was used to test the segregation pattern of each marker. Linkage map was constructed by using the software package MAPMAKER/EXP version 3.0 (Lincoln et al. 1992). A LOD score of 3.0 and a maximum recombination frequency of 0.40 were used to declare linkage between two markers.

QTL mapping

QTL analysis was performed using the method of Composite Interval Mapping (CIM) (Zeng 1994) as in QTL Cartographer version 2.5 (Wang et al. 2005). Composite interval mapping combines the approaches of interval mapping (IM) and Single Marker Analysis in a multiple regression framework. Initially it builds cofactors by selecting most significant markers through Single Marker Analysis methodology. Once the model containing cofactors is built, the entire genome is rescanned using interval mapping. We used model 6 with window size 10 cM where forward and backward regression method was utilized. Walk speed was set at 2 cM to scan the entire genome. We performed 1000 permutations at 0.05 significance level to balance type 1 and type 2 errors and declare appropriate threshold levels for QTL (Churchill and Doerge 1994). The best estimate of QTL location was assumed to correspond to the position having the peak significance level and the confidence interval was drawn according to 1-LOD support interval (Lander and Botstein 1989).

RESULTS

Frequency distribution for various traits

The frequency distributions for the five traits evaluated are given in Figure 1. Only plant height showed normal distribution while all other traits displayed various levels of skewedness. The days to heading trait was roughly partitioned into two phenotypic classes, one with early

heading habit while the other showing late heading trait. Peduncle length also showed two phenotypic classes but the distribution tended to be strongly influenced by embedded peduncle genotype rather than emerged peduncle. Tiller numbers showed broad range with transgressive segregation towards both ends. The histogram for stripe rust showed continuous disease distribution pattern and the phenotypic classes were clearly partitioned into five clusters.

Phenotypic data Analysis

Except for the heading days all traits showed transgressive segregation and their phenotypic values exceeded beyond both of the mean parental values (Table 1). The correlation coefficients between most of the trait combinations were found to be significant (Table 2). As expected peduncle length had extraordinarily high correlation with heading days and plant height. Peduncle length and heading habit were negatively correlated, i.e. the emerged peduncle inbred lines had more probability of early heading habit whereas the embedded peduncle lines had late heading. The significant positive correlation between plant height and peduncle extrusion could explain the fact that in taller plants, peduncle grew faster to emerge out of the boot leaf before anthesis.

TABLE 1. Trait means in parent and trait means, standard deviations (SD) and range in RILs of *Steptoe* x *Morex* population

	Parents		RIL population	
Trait	*Steptoe*	*Morex*	Range	Mean ± SD
Heading days	126.0	100.0	101.0 – 126.0	112.05 ± 7.35
Plant height (cm)	66.4	100.1	61.0 – 126.6	95.57 ± 13.27
Peduncle length (cm)	5.7	24.2	0 – 28.6	10.21 ± 6.61
Tiller number	2.6	3.1	1.2 – 6.4	3.49 ± 1.08
Stripe rust (%)	12.5	75	0 – 100	43.11 ± 22.83

TABLE 2. Correlation coefficient (r) among various traits in RIL population

	Plant height	Peduncle length	Tiller number	Stripe rust
Heading days	-0.5491*	-0.7392*	-0.4987*	-0.2056
Plant height		0.6360*	0.5112*	0.1595
Panicle exertion			0.3880*	0.1334
Tiller number				0.2111

* $P < 0.0001$

Linkage map

Out of the 434 polymorphic molecular markers data available at GrainGenes website, we selected 343 by rejecting markers with more than 40% missing genotypes and those showing segregation distortion at 0.05 significance level (χ^2 =3.841). Except for the two regions in chromosomes 5 (1H) and 6 (6H), the whole genome was adequately covered with markers and the centromeres were placed on consensus positions based on marker orders along the chromosomes. The order of markers and centromere positions did not vary much from their

established map positions. The combined length of the linkage map was 824.1 cM with average spacing of 2.40 cM between adjacent markers.

Genomic distribution of QTLs

QTLs detected by CIM analysis as implemented in QTL Cartographer version 2.5 are presented in Table 3. The parent contributing respective alleles for increasing trait value for heading days (HD), plant height (PH), peduncle length (PL), number of tillers (TN) and the allele conferring resistance to stripe rust (SR) were indicated in the table. In the present study, five QTLs were identified for heading days exceeding the threshold LOD score. 'Morex' parent contributed early heading alleles for all the QTLs identified. Most of the phenotypic variance was explained by the QTLs on 2H and 1H while those on 7H and 3H had only a minor effect. Identification of several plant height QTLs spread throughout genome (7H, 2H, 2H, 3H, 6H, 6H and 5H) supported the results of frequency distribution. The two QTLs on 2H and 3H together explained about 40% of the phenotypic variance. The alleles responsible for increase or decrease in height had come from both of the parents and thus supporting transgressive segregation observed for some of the RILs. Two major QTLs, one each on chromosomes 2H and 3H were identified for peduncle length while a third putative QTL detected on 1H had only a minor effect. Only one QTL was identified for tillering ability on chromosome 2H. For stripe rust, although four resistance QTLs spread across chromosomes 2H, 3H, 4H and 5H were identified, none of them explained significant phenotypic variance.

TABLE 3. Chromosome mapping of various QTLs with nearest linked molecular marker for different traits

Trait	Chromosome	Marker interval	Position (cM)	LOD	Additive	R^2 x 100	Allele
Heading date	1 (7H)	ABC156d - ABG022A	41.61	4.35	1.8964	6.60	*S*
	2 (2H)	ABG005 - Pox	33.41	18.78	4.1443	31.42	*S*
	2 (2H)	Adh8 – CDO537	47.00	6.39	2.47	8.00	*S*
	3 (3H)	ABG471 - ABG399	38.11	3.22	1.6616	4.96	*S*
	5 (1H)	ABC307A-cMWG706A	31.31	11.69	3.2381	19.35	*S*
Plant height	1 (7H)	Pgk2B - PSR129	67.91	2.49	2.8861	4.72	*S*
	2 (2H)	ABG005 - Pox	33.41	8.83	-5.7128	18.43	*M*
	2 (2H)	Adh8 - CDO537	43.31	8.41	-6.1379	20.57	*M*
	3 (3H)	ABC156c - AtpbB	46.81	12.37	-5.7998	18.77	*M*
	6 (6H)	CDO497 - ABR335	40.91	3.07	3.2705	6.00	*S*
	6 (6H)	BCD340E - ksuD17	45.91	3.74	3.5796	7.24	*S*
	7 (5H)	ABG708 - Dor5	30.31	4.93	-4.2142	9.72	*M*
Peduncle length	2 (2H)	ABG358 - ABG459	28.71	19.30	-3.9943	36.24	*M*
	3 (3H)	ABG471 - ABG399	38.11	4.63	-2.6111	15.38	*M*
	5 (1H)	ABC307A	92.31	2.61	-1.7200	6.76	*M*
Tiller #	2 (2H)	MWG858 - ABG358	28.61	4.89	-0.3615	11.02	*M*
Stripe rust resistance	2 (2H)	MWG858 - ABG358	26.61	2.95	-4.9528	6.22	*S*
	3 (3H)	ABG377 - MWG555b	61.31	5.10	7.0202	11.30	*M*
	4 (4H)	ABC321 - ABR315	30.21	3.24	-5.1908	6.88	*S*
	7 (5H)	ABG391	124.81	2.64	-4.6547	5.56	*S*

DISCUSSIONS

Frequency distribution of various traits

RILs are inbred lines derived from a cross of two diverse parents in which the individual genes are resolved into homozygous progenies. If we construct a histogram on such a population, the number and size of phenotypic classes obtained is directly related to the number of genes influencing the trait. For example, if a single gene controls the trait, there will be two phenotypic classes of equal sizes and if two genes control the trait there will be three phenotypic classes in 1:2:1 size proportion. If we assume the genes are additive and explaining equal variance, their should be n + 1 number of phenotypic classes observed for n number of genes in the population for as many number of additive gene combinations. On the other hand if epistatic interactions were significant and the individual genes were contributing unequally towards the overall phenotype, the distribution of phenotypic classes becomes skewed. From the preliminary observation of histograms (Figure 1) the approximate number of genes responsible for each trait could be predicted. For example, there should be one gene explaining most of the phenotypic variance for heading days as we observed two broad phenotypic classes in the histogram. There should also be one more gene with lesser but significant effect, which is responsible for minor third phenotypic class in between the two major classes. Height is the perfect example of quantitative inheritance where we expect large number of alleles acting additively to give normal distribution. The presence of two phenotypic classes is the indicative of single gene inheritance for peduncle length, but their unequal proportion could be explained by presence of one more parallel allele contributing towards short peduncle length phenotype. Tillering trait showed normal distribution and large transgressive segregation beyond both parental types. Thus, in barley we do not expect tiller number to be governed by single gene. Although we observed only one QTL exceeding the threshold LOD score, there is an indication of two more putative QTLs on chromosomes 7H and 1H (Figure 3). Also, some of the QTLs on chromosomes 3H and 6H identified by Franckowiak and Lundqvist, 2002, Buck-Sorlin, 2002 and Babb and Muehlbauer, 2003, remained undetected in the present study. The most probable explanation could be that ‘Steptoe’ and ‘M’ are not diverse enough with respect to tillering ability and it actually limited the QTL mapping approach to detect all genes of the trait. Frequency distribution of stripe rust has shown overall normal disease distribution pattern clustered in three major segregative and two minor transgressive groups. Both parents were susceptible to stripe rust but the rust progressed slowly in ‘Steptoe’ with very low terminal severity, usually called slow rusting. The five classes for rust severity could be explained by the presence of four genes, each of which was contributing additively towards resistance to stripe rust. When the resistance alleles for all four genes were present in a single genotype (4R), maximum resistance is expected which was observed with zero percent rust severity in the first transgressive group. Similarly, genotypes with 3R+1S, 2R+2S, 1R+3S and 4S allele combinations explained second, third, fourth and fifth groups, respectively in the frequency distribution plot.

QTL Analysis

Heading Days: Days to Flower or heading days is considered to be an important trait for planning of a breeding program. Early-heading genotypes are preferred when the objective is to

grow a cultivar late or early in the growing season. Heading time in barley and wheat is governed by three major genetic systems: vernalization requirement (response to low temperature at the initial stages of plant development), photoperiod sensitivity (day length) and narrow-sense earliness (response to sum of temperature over a long period). Vernalization is the requirement of low temperature period to plants for transition from a vegetative to a reproductive phase. Among the *vrn* loci, *Vrn1* on the group 5 chromosomes of Triticeae (A, B, D and H genomes) are the most extensively characterized in terms of its effects and inheritance (Law et al. 1976, Galiba et al. 1993, Kato et al. 1999). The vernalization responsive phenotype is often found in conjunction with photoperiod sensitivity, a delay in flowering when plants are grown under short-day conditions (Karsai et al. 2001). Low vernalization requirement of barley was probably met with partially but longer photoperiod could be available only in the last week of March and hence delayed flowering in RILs with *Ppd*. The *Ppd* – H1 photosensitivity locus was first described by Laurie et al. (1994) on the short arm of chromosome 2H. In barley, *eps* 2S, located near the centromere region of the 2H chromosome has been reported to be a QTL for the environment independent narrow-sense earliness (Laurie et al. 1995). The RILs in the present investigation were sown without vernalization treatment. The QTL analysis carried out without partitioning of heading trait into three categories identified two significant QTL on 2H which probably represent *Ppd* and *eps* loci. Thus major effect on heading days under field conditions was due to the photoperiod and environment independent narrow sense earliness genes. Major role of 2H in determining heading days in barley is also inferred from the investigations carried out by Marquez-Cedillo et al. (2001), Kicherer et al. (2000), Karsai et al. (2005) and Qi et al. (1998) who detected heading days QTL on chromosomes 2H; 2H; 2H, 4H, 5H; and 2H, 7H, respectively.

Plant Height: Before the green revolution, one of the major causes of yield loss was lodging of tall cultivars during rain and strong winds. Plant height and culm stiffness are reported to be the two most important traits determining lodging resistance in cereal plants (Keller et al. 1999). Murthy and Rao (1980) and Stanca et al. (1979) have worked out significant correlation between lodging resistance and dwarfness in barley. Recently Chloupek et al. (2006) demonstrated the significance of different sets of semi-dwarf genes in the determination of different root system size that was further implicated with biotic and abiotic stresses. With the development of semi-dwarf varieties, yield loss was largely overcome and the plant utilized its resources in increasing harvest index rather than its biomass. If the objective of the breeding program is to enhance the grain production as in most instances, the breeder prefers dwarf variety but if the objective is to utilize the plant for dual purpose for fodder as well, then the breeder obviously goes with taller varieties. Several studies in the recent past had identified QTL for plant height in barley distributed throughout genome but the major QTLs identified in the present study on chromosome 2H and 3H were found to occur more often than others. For example, Thomas et al. (1995) detected plant height QTLs on 1H, 3H and 7H; Marquez-Cedillo et al. (2001) on 2H, 3H, 4H and 5H; Kicherer et al. (2000) identified on 2H and 3H; Qi et al. (1998) on 2H, 3H and 7H; Teulat et al. (2001) on 2H, 3H, 4H, 5H, 6H and 7H; Zhu et al. (1999) on 1H, 3H, 4H and 6H; and Chloupek et al. (2006) on 3H, 4H, 5H and 7H.

Peduncle length: Peduncle length is an important character in barley as the inability of spikes to emerge out of boot leaf not only eliminates outcrossing but also adversely affects the use of its photosynthetic contribution to seed-setting and seed development. From the preliminary

observation on correlation coefficient, we can predict that heading date and plant height jointly influences the ability of peduncle to emerge out since early heading and tall plants had emerged peduncle. We can infer that photoperiod (2H) had major effect on peduncle length while narrow sense earliness (2H and 1H) had relatively minor effect on peduncle length. Chromosome 3H also had significant influence on the trait which might be coming from major plant height QTL on the same chromosome. Hence, we can conclude that peduncle length is a composite trait whose component traits include heading days and plant height.

Number of Tillers: Tiller number is regarded as an important yield component in wheat, barley and rice as the number of effective tillers is equal to the number of spikes. The plants with lesser tiller number generally have long spikes with increased grain weight and overall sturdy plant architecture (Vasu at al. 2006). But the advantage of high tiller numbered plant is that the overall harvest index from single plant is much higher and it saves the unit area of land required to grow plants for similar yields. In the present study, the tillering ability of plants behaved as a single gene inherited trait and only one QTL on chromosome 2H could be detected. Although earlier studies have also indicated single gene inheritance pattern for the trait, chromosomal locations of QTLs were not consistent with the present study. Franckowiak and Lundqvist, 2002, Buck-Sorlin 2002 and Babb and Muehlbauer 2003 have identified major QTL *lnt1* on chromosome 3HL and a second QTL *cul2* on 6HL.

Stripe Rust: Stripe rust is a major disease in Triticeae and its causal organism in barley is a biotrophic fungus, *Puccinia striiformis* f. sp. *hordei*. The characteristic feature of the disease is the appearance of pale stripes on leaves followed by emergence of orange brown uredosori that contain fungal spores. Yield loss of upto 30 % may occur, as photosynthetic and metabolic capabilities of the plant are severely impaired. Rust resistance in Triticeae is mainly of two types viz., vertical and horizontal. Vertical resistance is race-specific conditioned by gene-for-gene interaction between host and pathogen (Flor 1946). Horizontal resistance, on the other hand is race-non-specific governed by multiple genes with small effects. The results of the present analysis show that the resistance QTLs identified were acting in a race non-specific manner where they prevent pathogen(s) to form a basic compatibility reaction. The 'Steptoe' is a slow stripe rusting genotype. The rust infection is of susceptible type but the disease progresses very slowly without causing an appreciable loss. Some of the QTLs for resistance mapped in the present study were colinear with the previously mapped QTL using different barley populations on chromosomes 4H, 5H (Chen et al. 1994); 2H, 3H, 1H, 6H (Toojinda et al. 2000); 1H, 2H, 4H, 6H, 7H (Berloo et al. 2001); 2H, 4H (Kicherer et al. 2000); and on 3H, 4H, 7H (Toojinda et al. 1998) using local rust pathotypes further confirming their race-non-specific resistance. The QTLs with their low individual phenotypic variances when pyramided in a single genotype could confer high overall resistance. The approach for pyramiding of resistance QTLs was well demonstrated for 1H, 4H and 7H conferring resistance to stripe rust at seedling stage in barley by Castro et al., (2003).

QTL clusters

Although the large genome size (4.9×10^9 bp) of barley makes the genetic manipulations difficult, some of the recent advances in comparative genomics have suggested the presence of recombination hot spots and gene-rich regions in Triticeae where targeted approaches could be utilized for genome analysis (Gill et al. 1996). Identification of multiple QTLs on chromosomes

2H and 3H were also indicative of gene-rich regions in barley. 2H is especially important because it contained QTLs for all of the traits analyzed in the present study. Aissani and Bernardi (1991) suggested the distribution of less conserved genes in euchromatic regions while the distribution of conserved genes in the heterochromatin region. This could be of evolutionary significance as the genes in euchromatin region exposed to manipulations were providing diversity for the plants to adjust to different environmental conditions while the genes of heterochromatin region might be regulatory in function, which must be conserved for their essential role in the very existence of the organism.

Although the QTL analysis is of tremendous use in the identification of genomic regions pertaining to the traits of economic importance, it fails to identify the complete set of genes of a biochemical pathway leading to the expression of trait. Many of the conserved genes for which there are no allelic variants cannot be detected by this approach. Such genes have been conserved through evolutionary forces and any attempt to change them could have deleterious effect on the survival ability of the organism.

CONCLUSION

It has been shown here that QTL mapping is an accurate approach for the identification of genes underlying a trait but it is also cost intensive to carry out such exercise for all traits. On the other hand, construction of frequency distribution plots in routinely developed mapping populations could be used as diagnostic assessment for the prediction of number and effects of genes before planning QTL mapping experiment. Although such an approach is very crude, it would be useful in making appropriate allocation of resources.

In the present study, it has been found that proximal region of chromosome 2H is of special interest as it contains QTLs for all of the traits studied explaining large phenotypic variances and thus the region could serve as candidates for further investigation. Significant correlation among various traits was because of QTL linked in coupling phase and in some of the instances pleiotropism cannot be ruled out. The other genomic regions of interest include chromosome 3(3H) and chromosome 5(1H), which harbors QTL for heading, peduncle length and plant height. Further study needs to be carried out to fine map and ultimately dissect out the individual genes in the region. Map-based cloning is gradually becoming a feasible approach for dissection of the QTL genes in Triticeae (Li et al. 2003). The individual QTL effects could be studied efficiently by generating near isogenic lines (NILs) in an organized backcross program, which specifically nullifies the background noise. In the recent past bioinformatics tools have gained significant importance to aid *in silico* comparative genomic studies in species with large unmanipulable genomes like barley and wheat with the help of well studied genomes such as *Arabidopsis thaliana*, rice and maize.

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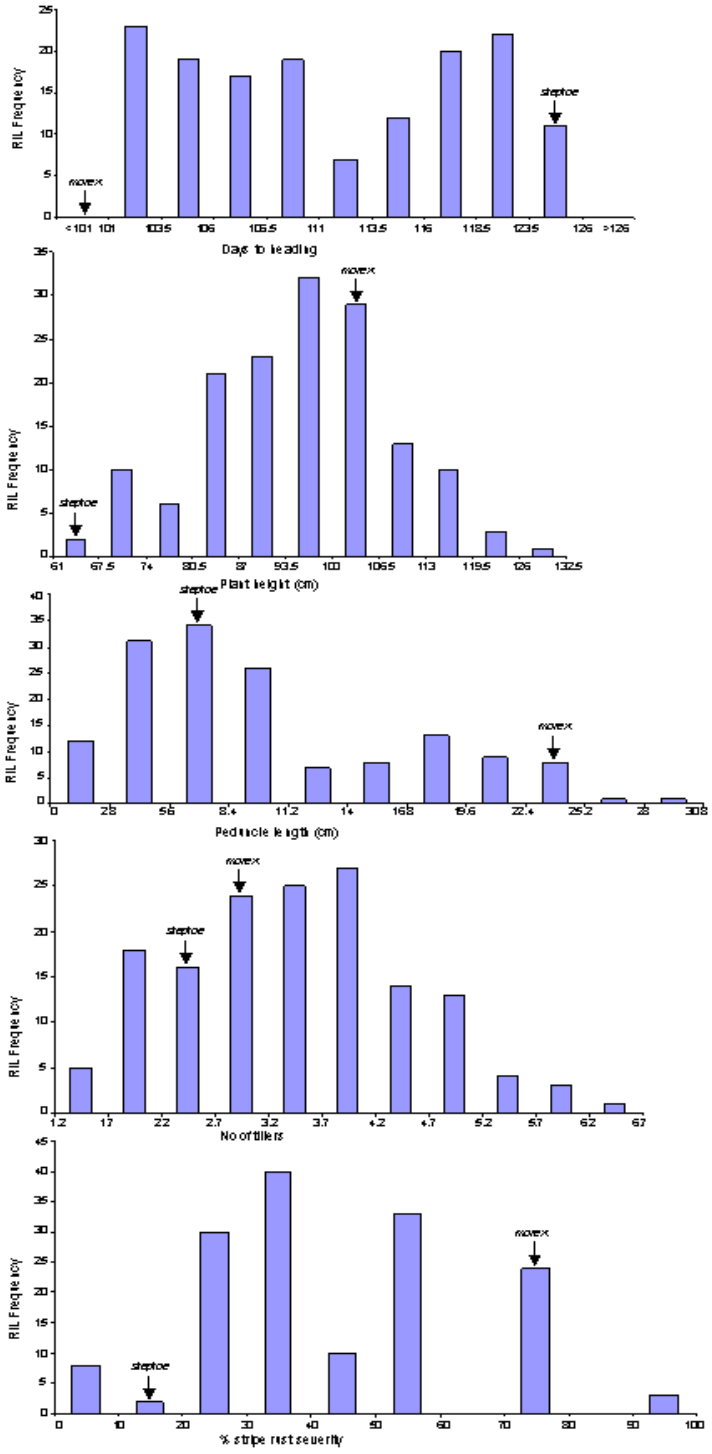

Figure 1. Frequency distribution plots for heading days (HD), plant height (PH), peduncle length (PL), tiller number (TN), and stripe rust (SR) in RILs of *Steptoe* x *M* population.

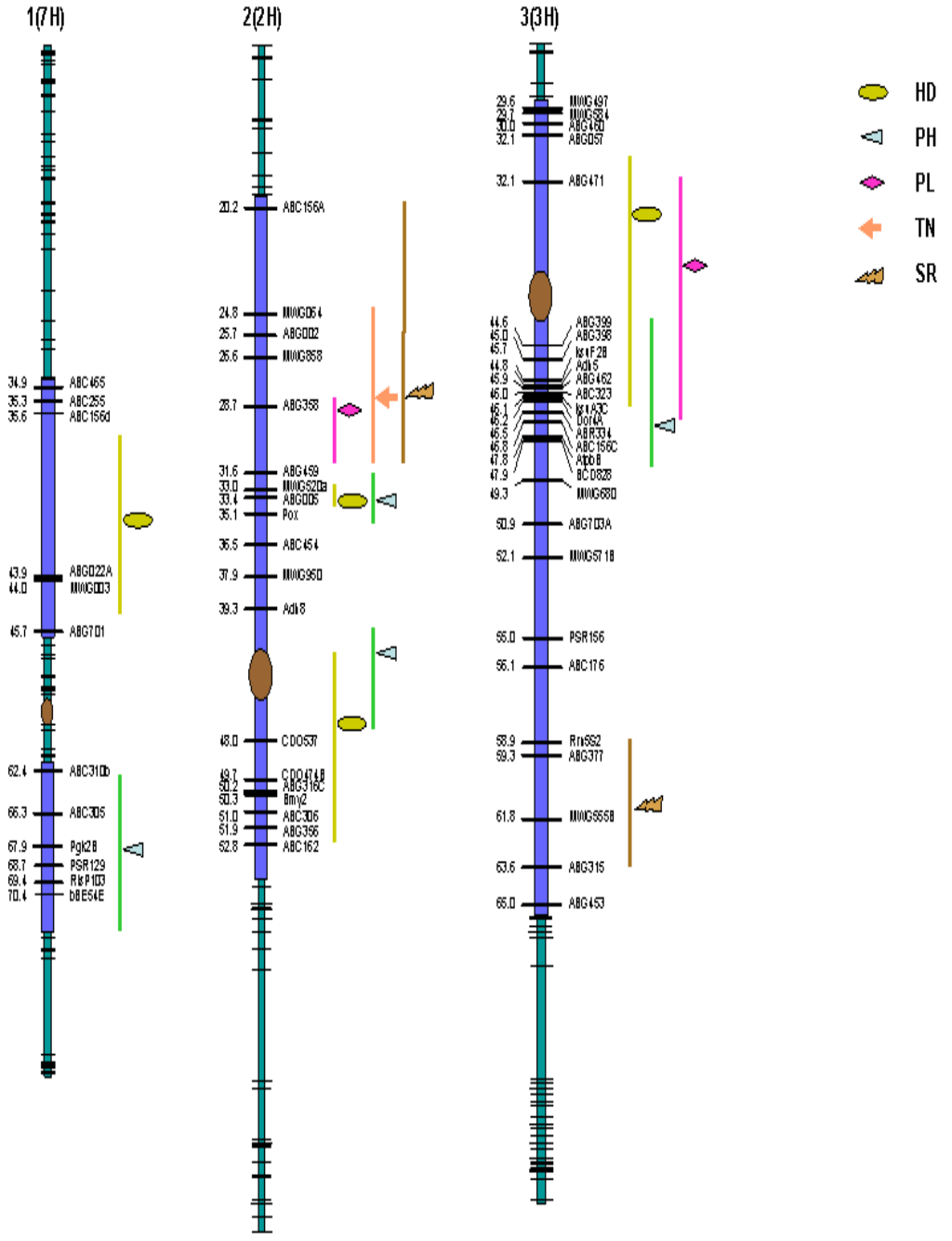

Figure 2. Genetic map of SM barley RIL population with 343 molecular markers indicating QTLs for heading days (HD), plant height (PH), peduncle length (PL), number of tillers (TN) and stripe rust (SR). Vertical bar and the symbols represent confidence interval and peak LOD scores respectively for various QTLs

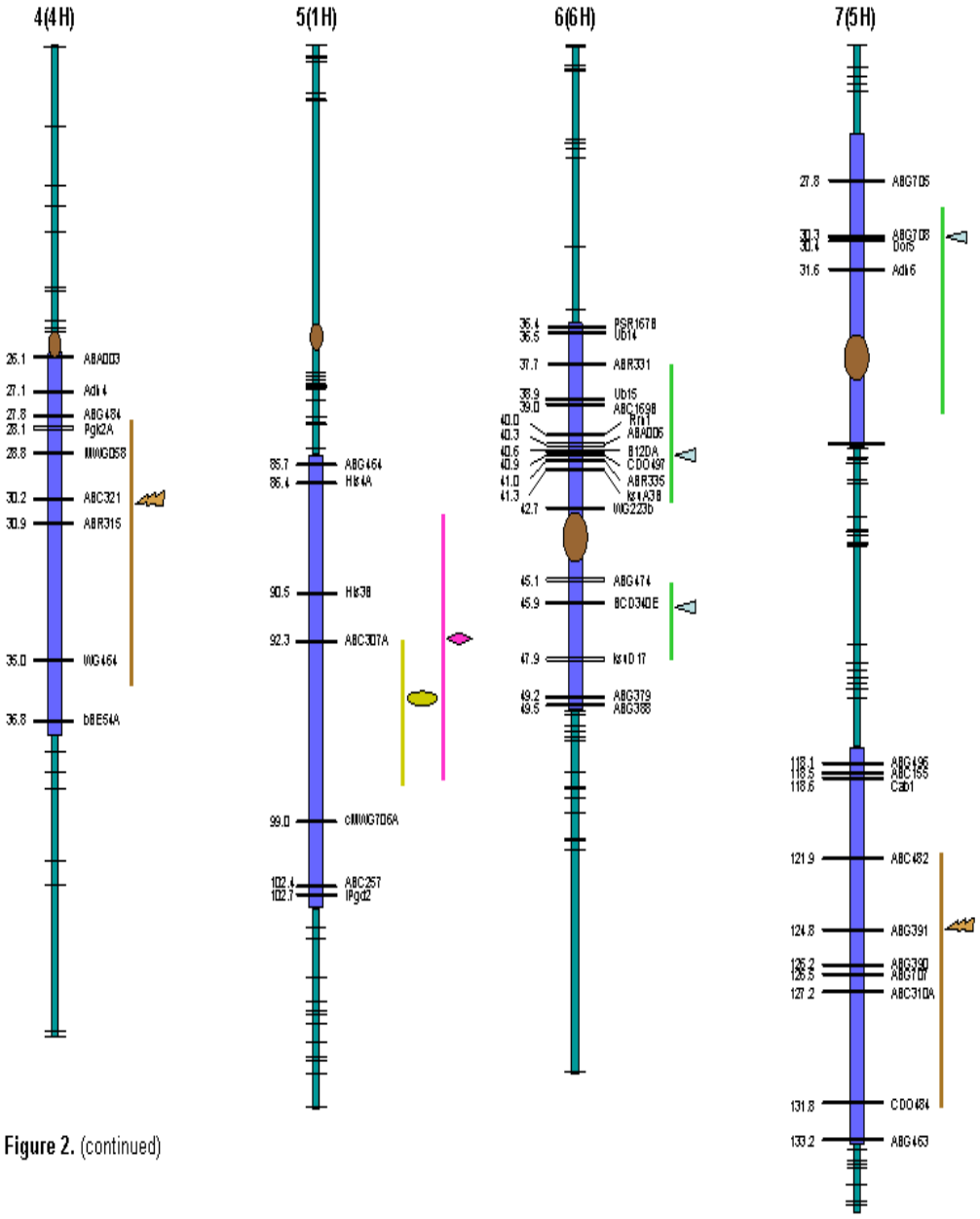

Figure 2. (continued)

Figure 2. (continued) Genetic map of SM barley RIL population with 343 molecular markers indicating QTLs for heading days (HD), plant height (PH), peduncle length (PL), number of tillers (TN) and stripe rust (SR). Vertical bar and the symbols represent confidence interval and peak LOD scores respectively for various QTLs.

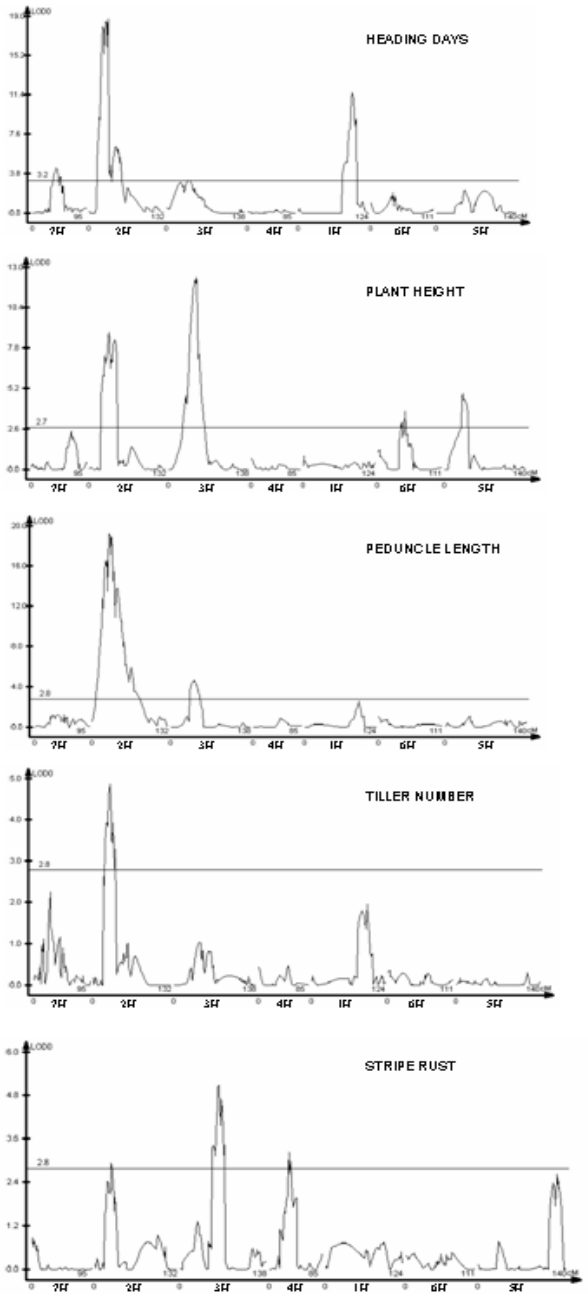

Figure 3. QTL likelihood maps for various traits obtained from composite interval mapping (CIM) analysis indicating LOD score along the ordinate while genetic map (all chromosomes together) along the abscissa. The respective threshold LOD estimated by 1000 permutations at 0.05 significance, are represented as horizontal line.

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PCR-based markers targeting barley putative grain yield and quality QTLs regions

Isabel A. del Blanco*, Deric A. Schmierer, Andris Kleinhofs and Steven E. Ullrich
Department of Crop and Soil Sciences, Washington State University, Pullman, WA, 99164-6420
*e-mail: mailto:blanco@wsu.edu

Abstract
Eight restriction fragment length polymorphism (RFLP) and two genes delimiting, or included in, chromosome fragments containing putative QTLs for grain yield and quality were sequenced and converted to PCR-markers. Eight markers were co-dominant between two-rowed barley cultivars Harrington and Baronesse after digestion with restriction enzymes. Three were dominant-recessive after designing specific primers exploiting single nucleotides polymorphisms (SNPs) between those two cultivars.

Introduction

Two chromosomal regions from Baronesse have been reported as containing putative grain yield QTLs, one on chromosome 2(2HL) (between markers ABG461C and MWG699) and the other on chromosome 3(3HL) (between markers MWG571A and MWG961) (Schmierer et al., 2004). Subsequent analysis of Harrington/Baronesse derived inbred lines suggested other additional regions as candidates for grain yield QTLs. These regions are on chromosome 7(5HL) (between markers ABC717 and ABC718) and on the telomeric region of the short arm of chromosome 2(2HS) (ABG058).

Since RFLP methodology needs large amounts of DNA and entails a complex procedure with radioactively labeled probes and Southern blotting, which requires several days to produce results, we converted RFLP targeting those putative QTL regions to PCR-markers: cleaved amplified polymorphic sites (CAPS) and SNPs. The conversion of RFLP clones to PCR-based markers rendered a much simpler technique that facilitated the screening of large numbers of genotypes at the seedling stage, since it requires a small amount of DNA.

Materials and Methods

Genomic DNA extraction was modified from Edwards et al. (1991); the modification added an extra-step of chloroform-isoamyl alcohol (24:1) extraction. CAPS were developed from RFLP clones. Primers were designed from the cloned sequences and used to amplify genomic DNA from the parental cultivars Harrington and Baronesse. If no fragment length polymorphism was observed, the fragments from both parents were sequenced to discover SNPs. These SNPs were analyzed to identify restriction enzymes that could be used to develop CAPS, or to design cultivar-specific primers. CAPS markers were also developed for gene *Dhn1* (Choi et al., 2000) and a candidate gene for seed dormancy and/or pre-harvest sprouting, *GA20-oxidase* (Li et al., 2004). Reactions for SNPs were set under stringent conditions (annealing temperatures ~ Tm) and short cycles (annealing ≤ 15 s). Extensions were 1min or 2min depending on product size.

Primer3 software (Rozen and Skaletsky, 2000) assisted the process of primer design. PCR products were visualized on 1% or 2%, depending on the fragment size, agarose gel under UV light. PCR products were purified with Exonuclease I (Exo-SAP-IT, UBS, Cleveland, OH). Sequencing reactions were performed on an Applied Biosystems 3100 Genetic Analyzer (Perkin Elmer Applied Biosystem Division, Foster City, CA) with the ABI PRISM Big Dye Terminator v3.1 cycle sequencing kit. Products were confirmed by sequencing in both directions. Analysis of sequences to find restriction sites and/or SNPs was done with the tools provided by the San Diego Super Computer Center (SDSC, http://workbench.sdsc.edu).

Results and Discussion

Details of developed PCR markers are listed in Tables 1 (CAPS) and 2 (SNPs). CAPS marker MWG699 yielded small fragments difficult to visualize after digestion with enzyme *Taq1,* even when 3% UltraPure Agarose-1000 was used to run PCR products. To avoid this problem, cultivar-specific markers were developed taking advantage of SNPs between the parental genotypes. The two SNP sites are different than the *TaqI* restriction site, for this reason they are considered two different markers for locus MWG699.

Table 1. Summary of developed CAPS markers, their location, primers and restriction enzymes

Chr.	Locus	Bin	Forward primer Reverse primer	Enzyme
3(3H)	MWG571A	009	5'-GTATCGTCAACACGGCAGCGT-3' 5'-TACCTGTCAGAAGTGCAGTACC-3'	*Bam*HI
3(3H)	MWG961	012	5'-TCAACTCCAGCCTTCACACACAAC-3' 5'-AAGACGAAGGAGACGTTGTTCATG-3'	*Bsg*I
2(2H)	MWG699	010	5'-ACCCACTGGGTTTGATACTACAAAG-3' 5'-GTGATGTTATTGGTGACTTGAACTC-3'	*Taq*I*
1(7H)	MWG851A	001	5'-CAAGAACTCCATTCCAATGTACCTG-3' 5'-TACTTCCAGATCCATGACAAGCTAC-3'	*Hae*III, *Msp*I
7(5H)	*Dhn1***	011	5'-TCACTGTTCGTACTTCGTAGCACC-3' 5'-TCCGCAGTTGCTCCTCCAAT-3'	*Taq*I, *Hpy*CH4 IV
7(5H)	ABC309	015	5'-CAGAGATACCACTGGGATTCTAAAC-3' 5'-CGAAAACCCTAGGAGAGCTAATC-3'	*Hinf*I
7(5H)	MWG2249	015	5'-AGCCATGCCGGTCTTGTCAAGAAAG-3' 5'-ATGCATCTGATCCCTGGAGAAGAAC-3'	*Alu*I
7(5H)	*GA20-oxidase*	015	5'-GTCCATCATGCGCCTCAACTACTAC-3' 5'-TAGCAAATCTTGCCATCCATCCATG-3'	*Ava*I

* Restriction enzyme (TaqI) previously reported by Tanno et al. (2002) in a different population

** Primers from Choi et al. (TAG 101:350-354)

Table 2. Cultivar-specific PCR primers developed exploiting nucleotide polymorphisms between Harrington (H) and Baronesse (B) cultivars

Chr.	Locus	Bin	Forward primer Reverse primer
2(2H)	MWG699-H*	010	5'-ATGGCTATCGCTTGACCAA-3' 5'-GTGATGTTATTGGTGACTTGAACTC-3'
2(2H)	MWG699-B*	010	5'-ATGGCTATCGTTTGACCAG-3' 5'-GTGATGTTATTGGTGACTTGAACTC-3'
2(2H)	ABG058-H	001	5'-TCTAGGCTTGCATTTGTCTACAAAG-3' 5'-ATGCTGCTTCGCTGTCTACAATAAC-3'
2(2H)	ABG058-B	001	5'-CAATAATCTCTCTTGCCATCATGCC-3' 5'-ATGCTGCTTCGCTGTCTACAATAAC-3'
7(5H)	ABC717-H*	009	5'-AACCAAGGCTACCAAGGTAATCCTG-3' 5'-CTCGTACTAACTTCCTACATGGCAA-3'
7(5H)	ABC717-B*	009	5'-AACCAAGGCTACCAAGGTAATCCTG-3' 5'-CTCGTACTAACTTCCTACATGGCAC-3'

*Note: These primers require stringent conditions when running PCR

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Genetic Architecture for Yield and Quality Component Traits Over Two Environments in Barley (*Hordeum vulgare* L.)

Ambresh Kumar Verma, S.R. Vishwakarma and P.K. Singh

Department of Genetics and Plant Breeding
Narendra Deva University of Agriculture and Technology,
Kumarganj, Faizabad, (UP) 224 229, INDIA.
e-mail: ambreshv@gmail.com

Abstract

Triple test-cross analysis involving three testers K-560, Narendra Jau-3 and their hybrid K-560 x Narendra Jau-3, were cross to 15 strains/varieties of barley to estimate the epistatic, additive and dominance components of genetic variance. Modified triple test-cross was done for eleven metric traits in two [normal fertile soil (E_1) and saline sodic soil (E_2)] environments. Epistasis was evident for all the characters under study in both environments except plant height in E_2, protein content in E_1 and lysine content in both conditions. The i type epistasis was significant for seed yield per plant in E_1 only, while j and l type epistasis were significant for most of the traits. Additive (D) component was important in all cases in both conditions except number of effective tillers per plant in E_1 and lysine content in E_1 & E_2 where as non fixable dominance (H) component were significant for all the characters in both conditions except number of effective tillers per plant in E_1, length of main spike in E_2 and lysine content in both environments. The most of the traits showed partial dominance and directional element, F was non- significant for all the traits, suggesting ambidirectional nature of dominance.

Key words: barley, modified triple test-cross, genetic variation, protein content, seed yield

Introduction

To enable present barley varieties acceptable in the international market, there is need to develop better quality genotypes suitable for making product with consumer acceptability. Thus there is an urgent need to improve grain quality as well as develop better quality genotypes for suitable processing industry. The consumer acceptability of genotype is affected by chemical constituent of the grains. It is therefore, desirable to access basic physiochemical characteristics of the grains so that these can be combined with high yield. The information about nature and magnitude of genetic components of variance for yield and quality characters is essential for planning an efficient breeding programme in any crop. The modified triple test-cross analysis of (Ketata *et al*., 1976) provide efficient detection and estimation of epistatic variance along with unbiased estimates of additive and dominance component of genetic variance in determining the inheritance of eleven traits in barley using modified triple test-cross (TTC) analysis.

Materials and Methods

Two barley pure lines, viz. testers K-560, Narendra Jau-3 and their hybrid (K-560 x Narendra Jau-3) were cross to 15 lines (Kedar, RD-2552, Narendra Jau-1, Narendra Jau-2, Narendra Jau-4, RD-2035, BL-2, BH-512, Ratna, Jagrati, DL-88, Azad, K-603, NDB-1173 and RD-2624) of barley to develop a set of 45 crosses. The experimental materials consisting of 3 testers, 15 lines,

30 single crosses and 15 three-way crosses were evaluated in randomized block design with three replications during *rabi* 2004-05 in two viz. normal fertile soil (E_1) and saline sodic (E_2) condition at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture & Technology, Kumarganj , Faizabad, U.P. India. Each entry was shown in a 3 m long single row plant with 10 cm spacing within and 25 cm between rows. Observations were recorded on five randomly selected competitive plants for eleven quantitative traits (Table 1). The pelshenke vale, protein content and lysine content were estimated by the method of (Pelshenke, 1933; Lowery's, 1951; and Felker *et al*.; 1978) respectively. Character means were used for modified triple test- cross analysis (Ketata *et al*., 1976).

Results and Discussion

The triple test-cross (TTC) analysis revealed that significant epistasis was present for all the characters in both environments except plant height in E_2 , protein content in E_1 and lysine content in both conditions (Table 1). The partitioning of epistasis in to i and j and l types showed that additive x additive (i) interaction was significant for seed yield per plant in normal fertile soil condition only. The j and l type epistasis was significant for all the characters in both the environments except days to maturity and protein content in E_1 while lysine content in both environments. Existence of significant epistasis in inheritance of seed yield and some other yield components in barley was reported by others also (Gorshkova and Gorodov, 1981). Greater importance of j and l type epistasis than i component was reported earlier by (Singh, *et al*., 1984; Tripati and Singh, 1983; Verma and Yunus, 1986.). On the contrary, (Nanda, *et al*., 1982) reported i type epistasis to be more important than j and l type epistasis, and (Singh, 1980) reported equal importance of these two sub components. The estimates of the components of genetic variance, additive (D), dominance (H) and F components and the degree of dominance ($H/D^{0.5}$) are given in Table 2. The additive (D) component was important in all cases in both conditions except number of effective tillers per plant in E_1 and lysine content in E_1 & E_2 where as non fixable dominance (H) component was significant for all the characters in both condition except number of effective tillers per plant in E_1, length of main spike in E_2 and lysine content in both environments. The estimates of D were higher than H for most of the traits, which suggested partial dominance. The directional element of dominance, F was non-significant for all the characters in both environments indicated presence of ambidirectional dominance, and alleles with increasing and decreasing effects appear to be dominant and recessive to the same extent. The significant of additive component for seed yield and quality component traits, except number of effective tillers per plant and lysine content indicates that substantial improvement in yield status can still be achieved by following conventional breeding procedure in barley. The significant contribution of additive x additive type epistasis for seed yield suggested that this component should not be ignored while predicting the recombinants extractable from segregating generations. Further results provided evidence of j and l type epistasis for most of the traits studied. However, in autogamus crops like barley, where commercial exploitation of hybrid has started, this type of epistasis is of more use.

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Table 1. ANOVA (mean square) of triple test-cross to test epistasis for eleven characters in barley under normal fertile soil (E_1) and saline sodic soil condition (E_2)

Sources of variation	Environ-ments	d.f.	Days to maturity	Plant height (cm)	No. of effective tillers /plant	Length of main spike (cm)	Grains per spike	Seed yield/ plant (g)	1000 seed weight (g)	Pelshenke value (minutes)	Protein content (%)	Lysine content (%)	Husk content (%)
'i' Type epistasis	E_1	1	7.20	3.99	0.17	10.86	428.76	22.36*	9.16	2121.80	0.61	0.75	5.83
	E_2		369.80	220.81	8.28	3.64	366.35	300.13	0.793	1355.77	2.11	1.49	1.12
'j+I' type pistasis	E_1	14	37.53	34.78**	8.13**	1.64**	206.09**	81.08**	25.28**	315.23**	4.40	0.56	205.13**
	E_2		74.66**	43.17**	11.57**	1.21**	307.31**	169.98**	23.90*	330.28**	7.46**	0.97	131.66**
Total epistasis	E_1	15	35.51*	32.73**	7.60**	2.25**	220.93**	77.16**	24.20**	435.66**	4.15	0.57	191.84**
	E_2		94.33**	55.01	11.35**	1.37**	311.24**	178.65**	22.36*	398.64**	7.10**	0.90	122.96**
'i' type epistasis x blocks	E_1	2	1.80	1.00	4.34**	2.71**	107.19**	5.59	2.29**	530.45**	0.15	0.19	1.46
	E_2		92.45**	55.20*	2.07**	0.91**	91.59*	75.03**	0.198	338.94**	0.527	3.73	0.28
'j+I' type epistasis x blocks	E_1	28	15.64	7.92	0.14	0.43	24.12	3.34	0.18	32.68	9.62	1.28	2.03
	E_2		2.53	14.17	0.32	0.15	23.78	0.723	12.15	11.18	0.71	1.80	0.31
Total epistasis x blocks	E_1	30	14.72	7.46	0.14	0.55	29.66	3.49	0.32	36.86	10.00	2.42	1.99
	E_2		8.53	16.91	0.43	0.20	28.30	5.68	11.36	33.03	0.69	2.68	0.49

*, ** Significant at 5% and 1% probability levels, respectively.

Table 2. Estimates of additive (D) and dominance (H) components of variance, parameter F, and degree of dominance $(H/D)^{0.5}$ in barley under normal fertile soil (E_1) and saline sodic soil (E_2) condition

Sources of variation	Environ-ments	Days to maturity	Plant height (cm)	Number o f effective tillers / plant	Length of main spike (cm)	Grains per spike	Seed yield/ plant (g)	1000 seed weight (g)	Pelshenke value (minutes)	Protein content (%)	Lysine content (%)	Husk content (%)
D	E_1	25.51**	429.12**	4.67	4.70**	520.15**	67.72**	17.21**	250.46**	16.77**	1.63	125.83**
	E_2	40.72**	150.58**	2.64**	2.60**	239.90**	50.43**	22.74**	190.35**	14.75**	1.90	78.26**
H	E_1	20.09**	20.06**	3.11	1.46**	167.30**	33.78**	12.57**	374.09**	4.89**	0.86	77.24**
	E_2	37.45**	45.28**	4.41**	0.76	224.90**	69.57**	10.56**	237.02**	8.30**	0.65	57.05**
$(H/D)^{0.5}$	E_1	0.60	0.22	0.82	0.56	0.57	0.71	0.85	1.22	0.54	0.74	0.83
	E_2	0.96	0.55	1.29	0.54	0.81	1.17	0.68	1.12	0.75	0.58	0.85
F	E_1	0.28	0.18	0.31	0.03	0.02	0.04	0.26	-0.08	-0.06	-0.25	0.20
	E_2	0.10	-0.02	0.15	0.12	0.11	-0.10	0.20	-0.27	0.01	-0.05	0.19

*, ** Significant at 5% and 1% probability levels, respectively.

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Line x Tester Analysis in Barley (*Hordeum vulgare* L.) Across Environments

Ambresh Kumar Verma, S.R. Vishwakarma and P.K. Singh

Department of Genetics and Plant Breeding
Narendra Deva University of Agriculture and Technology,
Kumarganj, Faizabad, (UP) 224 229 India.
e-mail: ambreshv@gmail.com

Abstract

A combining ability effects study was conducted through line x tester analysis under normal fertile and saline sodic soil environments. The results indicated the predominance of non-additive gene action for all the traits. The line Kedar and tester K-560 in normal fertile soil and tester Lakhan in saline sodic soil while RD-2552, Narendra Jau-4 and NDB-1173 under both environments proved good general combiners for seed yield and quality components characters. The crosses Kedar x K-560, K-603 x K-560, DL-88 x Lakhan and RD-2035 x K-560 in normal and RD-2552 x Narendra Jau-3, Narendra Jau-1 x K-560, Narendra Jau-4 x Lakhan, NDB-1173 x K-560, and RD-2624 x K-560, in saline sodic soil while RD-2552 x Lakhan, RD-2035 x Narendra Jau-3, BL-2 x Lakhan and Jagrati x K-560 in both environment exhibited highest sca effects for seed yield and other quality traits, showing their desirability to offer transgressive segregants in succeeding generations.

Key words: barley, combining ability, gene action, protein content, lysine content.

Introduction

Research on barley (*Hordeum vulgare* L.) bears special significance due to its great elasticity of adaptation under various stresses and lot of potential both for domestic and industrial uses. Barley also has been very important winter cereal crop in India , because of its versatile nature, lower cost of cultivation, superior nutritional qualities and many other uses. The major uses of barley grains, however are in the production of malt, which is used to make beer, beverage industrial alcohol, whisky, malt syrups, malted milk and vinegar. The spent malt after brewing is used as feed. Combining ability analysis helps in identification of desirable parents and crosses for their further exploitation in breeding programme. Therefore, the present study was undertaken to estimate combining ability effects for yield and quality components characters and also to identify suitable parents and crosses in barley under normal fertile and saline soil environments.

Materials and Methods

The material consisted of 15 lines, namely RD-2552, Narendra Jau-1, Narendra Jau-2, Narendra Jau-4, RD-2035, BL-2, BH-512, Ratna, Kedar, Jagrati, DL-88, Azad, K-603, NDB-1173 and RD-2624 with 3 testers viz., Narendra Jau-3, K-560 and Lakhan crosses were attempted in line x tester fashion. The resulting 45 F_{1s} along with lines and testers were planted in a randomized block design with three replicates during *rabi* 2004-2005 under normal fertile soil and saline sodic environments at Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad. Each treatment (genotype) was shown in 3 m length having row to row and plant to plant distance of 25 cm and 10 cm, respectively. The observations were recorded on days to maturity, plant height (cm), number of effective tillers/plant, length of main

spike (cm), grains per spike, seed yield/plant (g), 1000 seed weight (g), pelshenke value (minutes), protein content (%), lysine content (%) and husk content (%) on five randomly selected plants from each replication and environments. The combining ability analysis was carried out following the method proposed by (Kempthorne,1957).

Results and Discussion

The analysis of variance for combining ability for eleven characters showed that variances due to gca and sca were significant for the characters like days to maturity, plant height, length of main spike, grains per spike, seed yield per plant, 1000 seed weight, pelshenke value, protein content and husk content under both normal fertile and saline sodic soil conditions, suggesting thereby importance of both additive and non additive gene actions for the inheritance of these characters. The role of both additive and non-additive effects to grain yield and its component characters in barley have been reported previously (Choo *et al.*,1988; Bhatnagar and Sharma1995;1998). However, the component of variation due to sca was higher than gca for all the characters in all the environments indicating the predominance of non-additive gene action. Such results infers that the chosen material had high selection history. Similar results of predominance of sca variance over gca variance have also been reported by (Guo and Xu,1994; Phogat *et al.*1995; Madic,1996; El-Seidy,1997a & 1997b; Bouzerzour and Djakoune,1998).

A perusal of the gca estimates (Table1) showed that the parents RD-2552, Narendra Jau-4, NDB-1173 in both environments while, Kedar & K-560 in E_1, and Lakhan in E_2 were the best combiners for seed yield and good/ medium combiner for most of the important yield and quality component characters. Further the parents Ratna, Narendra Jau-1, RD-2552, Narendra Jau-3, Narendra Jau-1 for early maturity, Lakhan, Narendra Jau-1 for dwarf plant height, Azad, RD-2624, NDB-1173 and Ratna for high protein content and Narendra Jau-1, Narendra Jau-2 and Lakhan for high lysine content were found to be good general combiners in both the environments.

Significant gca values indicated the importance of additive or additive x additive gene effect as earlier reported by (Griffing,1956). In view of this, these parents offered the best possibilities for the development of improved lines of barley through hybridization programme. It is, therefore, recommended that to improve yield one should breed for superior combining ability for the component traits with an ultimate objective to improve the pace of its genetic improvement.

The estimates of specific combining ability effects of top five ranking crosses for all the characters are present in Table 2. The perusal of sca effects revealed that crosses Kedar x K-560, K-603 x K-560, DL-88 x Lakhan RD-2552 x K-560 in normal and RD-2552 x Narendra Jau-3, Narendra Jau-1 x K-560, Narendra Jau-4 x Lakhan, NDB-1173 x K-560 & RD-2624 x K-560 in saline sodic and RD-2552 x Lakhan, RD-2035 x Narendra Jau-3, BL-2 x Lakhan and Jagrati x K-560 under both environments were for seed yield per plant and with other characters. The crosses RD-2035 x Narendra Jau-3 and BL-2 x Lakhan are excellent crosses for seed yield in both environments. Therefore, these crosses should be particularly exploited vigorously in future breeding programmes to obtain good segregants which would lead to buildup a population with high genetic yield potential with develop salt tolerant genotypes.

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Table 1. Estimates of general combining ability (gca) effects of parents (lines & testers) for 11 characters in barley under normal fertile soil condition (E_1) & saline sodic soil condition (E_2)

Parents	Environ-ments	Days to maturity	Plant height (cm)	No. of effective tillers /plant	Length of main spike (cm)	Grains /spike	Seed yield/ plant (g)	1000 seed weight (g)	Pelshenke value (minute)	Protein content (%)	Lysine content (%)	Husk content (%)
Kedar	E_1	0.63**	3.45**	0.40*	-0.18*	-0.71	1.02*	1.10*	6.58**	0.39**	-0.12**	2.30**
	E_2	1.23**	5.76**	0.26	-0.13	-0.72	0.73	0.99**	5.25**	0.27**	-0.26**	1.35**
K-603	E_1	-0.12	-0.62	0.20	-0.26**	-3.08**	-0.45	-1.04*	-1.92*	0.26**	-0.18**	0.13
	E_2	-1.27**	3.62**	-0.27	-0.60**	-5.51**	-1.58**	-1.67**	-1.67	0.26**	-0.13**	0.44*
DL-88	E_1	0.63**	3.85**	-1.02**	-0.63**	-4.14**	-3.04**	-0.74	0.33	-0.21**	0.02	-1.67**
	E_2	-0.19	3.40**	-0.34	-0.46**	-1.82*	-0.77	-0.86**	0.58	-0.32**	0.07**	-1.23**
RD-2552	E_1	-0.62**	-4.96**	0.14	0.04	6.76**	1.19*	-1.11*	-9.92**	-0.68**	0.25**	-1.88**
	E_2	-0.69**	-2.65**	0.37*	0.11	4.37**	1.83**	-0.83**	-7.58**	-0.52**	0.33**	-1.15**
Azad	E_1	2.21**	-6.84**	-0.11	0.17*	4.86**	0.53	0.11	7.16**	2.06**	-0.59**	1.24**
	E_2	2.56**	0.42	0.08	0.18	5.20**	0.57	0.08	6.17**	1.94**	-0.53**	0.93**
Narendra Jau -1	E_1	-0.62**	-2.76**	0.34*	0.32**	-0.54	0.54	0.55	-0.34	-1.38**	0.56**	-0.23
	E_2	-0.52*	-4.57**	0.29	0.19	1.50	0.71	0.67**	0.42	-0.49**	0.59**	-0.60**
Narendra Jau -2	E_1	-1.54**	3.59**	0.08	0.80**	1.23	0.48	0.28	-3.42**	-1.68**	0.51**	1.50**
	E_2	0.06	-4.55**	0.33	0.49**	0.34	0.46	0.14	-3.25**	-1.77**	0.52**	1.44**
Narendra Jau -4	E_1	0.29	-2.66**	1.31**	0.65**	4.73**	3.54**	-0.32	-6.76**	-1.01**	0.34**	0.35
	E_2	1.14**	2.68**	0.50**	0.50**	1.78	0.90*	-0.29	-6.83**	-1.05**	0.10**	0.69**
NDB-1173	E_1	-2.71**	-1.98**	-0.11	0.71**	6.99**	2.14**	1.75**	-1.76*	0.93**	-0.28**	-1.99**
	E_2	-2.11**	-4.08**	0.00	0.52**	6.08**	1.24**	2.09**	-1.67	0.99**	-0.32**	-1.98**
RD-2035	E_1	0.13	0.22	-0.21	-0.23*	4.15**	0.66	-0.99*	-2.34**	-0.35**	0.11**	1.05**
	E_2	-0.36	-1.69**	0.09	-0.15	3.43**	0.02	-0.94**	-2.08*	-0.46**	0.12**	0.98**
RD-2624	E_1	0.71**	-3.44**	-0.45**	-0.38**	-9.32**	-3.52**	-1.60**	0.08	1.63**	-0.40**	-0.63**
	E_2	-0.19	-0.77	-0.60**	-0.05	-3.70**	-2.36**	-1.47**	0.33	1.54**	-0.35**	-0.40
BL-2	E_1	1.54**	1.89**	0.43*	-0.13	-2.49*	0.63	0.29	3.24**	-0.09*	-0.03	-1.33**
	E_2	0.23	-2.29**	0.36*	-0.08	-3.35**	0.66	0.03	3.33**	-0.18**	-0.04**	-1.35**
Jagrati	E_1	1.13**	4.50**	-0.26	-0.32**	-4.47**	-1.22**	1.20**	1.24	-0.30**	0.15**	0.93**
	E_2	1.39**	-2.44**	-0.45*	-0.21	-3.45**	-0.98*	1.12**	1.58	-0.47**	0.18**	0.69**
BH-512	E_1	-0.12	7.09**	-0.31	-0.36**	1.19	-0.74	0.03	0.99	0.02	-0.05	2.49**
	E_2	0.31	4.29**	-0.18	-0.35*	0.12	-0.41	0.12	-0.33	-0.07**	-0.03*	2.14**
Ratna	E_1	-1.54**	-1.34*	-0.44**	-0.21*	-5.17**	-1.75**	0.49	6.83**	0.41**	-0.29**	-2.26**
	E_2	-1.61**	2.87**	-0.45*	0.04	-4.27**	-1.04*	0.83**	5.75**	0.33**	-0.25**	-1.94**
SE (gi) lines	E_1	0.22	0.64	0.17	0.09	0.97	0.45	0.45	0.75	0.04	0.03	0.21
	E_2	0.22	0.52	0.17	0.13	0.93	0.45	0.21	0.88	0.03	0.01	0.20
SE(gi-gj) lines	E_1	0.31	0.90	0.23	0.13	1.37	0.64	0.64	1.05	0.06	0.04	0.30
	E_2	0.31	0.74	0.25	0.19	1.31	0.64	0.30	1.24	0.04	0.02	0.29
K-560	E_1	0.88**	1.83**	0.27**	0.18**	0.68	0.76**	0.19	-5.77**	0.18**	-0.04**	-1.20**
	E_2	1.31**	-0.87**	0.07	0.05	0.41	0.41	-0.22*	-5.17**	0.14**	-0.06**	-0.87**
Narendra Jau-3	E_1	-0.81**	2.69**	0.31**	0.09	-0.18	0.21	0.24	1.94**	0.07**	-0.06**	0.17
	E_2	-0.36**	0.59*	-0.04	0.08	0.48	-0.02	0.17	1.97**	0.34**	-0.11**	-0.12
Lakhan	E_1	0.10	-6.63**	-0.90**	-0.16**	0.79	-1.11**	-0.42	2.30**	-0.44**	0.22**	1.37**
	E_2	0.02	-0.70*	0.17	-0.05	0.09	0.78**	0.15	2.06**	-0.60**	0.26**	1.40**
SE (gi) testers	E_1	0.11	0.33	0.09	0.05	0.5	0.23	0.23	0.39	0.02	0.02	0.11
	E_2	0.11	0.27	0.09	0.07	0.48	0.23	0.11	0.45	0.01	0.01	0.10
SE(gi-gj) testers	E_1	0.16	0.46	0.12	0.06	0.71	0.33	0.33	0.54	0.03	0.02	0.15
	E_2	0.16	0.38	0.13	0.10	0.68	0.33	0.15	0.64	0.02	0.01	0.15

* Significant at 5% probability level, ** Significant at 1% probability level

Table 2. Promising crosses for seed yield and quality component in barley under normal fertile soil and saline sodic soil condition.

Characters	Normal fertile soil environment	Saline sodic soil environment
Days to maturity	Kedar x Lakhan, RD-2552 x K-560, RD-2552 x Narendra Jau-3, Narendra Jau-1 x K-560, RD-2624 x Lakhan	K-603 x K-560, RD-2624 x Lakhan, Narendra Jau-1 x K-560, Kedar x Lakhan, Jagrati x Narendra Jau-3
Plant height (cm)	Jagrati x Lakhan, BL-2 x Lakhan, Narendra Jau-2 x Lakhan, RD-2035 x Lakhan, Kedar x Narendra Jau-3	Ratna x Narendra Jau-4, BL-2 x Lakhan, DL-88 x K-560, RD-2035 x Lakhan, RD-2624 x Lakhan
Number of effective tillers/plant	RD-2035 x K-560, BL-2 x Narendra Jau-3, Jagrati x K-560, BL-2 x Lakhan	Narendra Jau-1 x K-560, Narendra Jau-4 x Lakhan, NDB-1173 x K-560, RD-2035 x Narendra Jau-3
Length of main spike (cm)	K-603 x K560, K-603 x Narendra Jau-3, DL-88 x Lakhan, RD-2035 x K-560,Jagrati x K-560	DL-88 x Lakhan, NDB-1173 x Lakhan, RD-2035 x Lakhan
Grains/spike	BL-2 x Lakhan, Kedar x K-560, K-603 x K-560, DL-88 x Lakhan, RD-2035 x Lakhan	BL-2 x Lakhan, RD-2624 x K-560, DL-88 x Lakhan, Narendra Jau-4 x Narendra Jau-3, RD-2035 x Narendra Jau-3
Seed yield per plant (g)	BL-2 x Lakhan, RD-2035 x Narendra Jau-3, Jagrati x K-560, RD-2552 x Lakhan, Kedar x K-560	Narendra Jau-1 x K-560, Narendra Jau-4 x Lakhan, NDB-1173 x K560, RD-2053 x Narendra Jau-3, BL-2 x Lakhan
1000-seed weight (g)	BL-2 x Lakhan, Jagrati x K-560, RD-2035 x Narendra Jau-3, Narendra Jau-4 x Lakhan,	BL-2 x Lakhan, Narendra Jau-4 x Lakhan RD-2552 x Narendra Jau-3, RD-2035 x Narendra Jau-3, Jagrati x Narendra Jau-3
Pelshenke value (minute)	Narendra Jau- 1 x K-560, RD-2552 x K-560, RD-2624 x Lakhan, Narendra Jau- 4 x K-560, BL-2 x Narendra Jau-3	RD-2552 x K-560, Narendra Jau- 4 x Lakhan, RD-2552 x Narendra Jau-3, RD-2035 x Narendra Jau-3, Jagrati x Narendra Jau-3
Protein content (%)	RD-2552 x K-560, Narendra Jau-4 x K-560, Kedar x Narendra Jau-3, BH-512 x Lakhan, Ratna x K-560	Narendra Jau-4 x K-560, RD-2552 x K-560, K-603 x Narendra Jau-3, NDB-1173 x K-560, Kedar x Narendra Jau-3
Lysine content (%)	DL-88 x K-560, Kedar x K-560, K-603 x K-560, RD-2035 x Narendra Jau-3, RD-2552 x Lakhan	K-603 x K-560, DL-88 x K-560, Narendra Jau-4 x Lakhan, Kedar x Lakhan, Narendra Jau-4 x Narendra Jau-3
Husk content (%)	Narendra Jau-2 x Narendra Jau-3, Kedar x Narendra Jau-3, K-603 x K-560, Azad x K-560, DL-88 x K-560	Narendra Jau-2 x Narendra Jau-3, Kedar x Narendra Jau-3, Narendra Jau-4 x Narendra Jau-3, K-603 x K-560, DL-88 x K-560

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Four new barley mutants

Sandra AI Wright[1], Manochehr Azarang[2], Anders B Falk[3]
[1]Dipartimento di Scienze Animali, Vegetali e dell'Ambiente, Facoltà di Agraria, Università del Molise, Campobasso, Italy
[2]Maselaboratorierna, Uppsala, Sweden [3]Department of Plant Biology and Forest Genetics, University of Agricultural Sciences, Uppsala, Sweden

Introduction

We screened a fast-neutron mutated barley population to isolate and characterize barley lesion mimic mutants. The albino mutant frequency in this population was found to be around 2%, suggesting that a sufficiently high level of mutants could potentially be found. From a screen of about 5000 M2 spikes, we found four mutants that were characterized by the presence of necrotic or chlorotic leaf areas in the form of spots or stripes. The four mutants were designated 1661, 2721, 3091 and 3550. The mutants were characterized with respect to their visual appearance. In order to relate these mutants properly to previously described barley lesion mimic mutants, we cultivated all previously described barley mutants with aberrant leaf phenotypes (Davis *et al.*. 1997) and compared the phenotypes to those of the newly obtained mutants.

Materials and Methods

The near-isogenic barley line Bowman(*Rph3*) was obtained from Dr Jerry D. Franckowiak, North Dakota, USA. It was constructed by introgression of the *Rph3* resistance gene from the cultivar Estate into the cultivar Bowman, and represents the 7th backcross. Mutation was performed with fast neutrons at the International Atomic Energy Agency (IAEA), Vienna, Austria, with a dose of 5 Gy. Five thousand M2 spikes were sown and the mutant plants were screened for aberrant leaf phenotype. Selected mutants were backcrossed twice to wildtype Bowman (*Rph3*), and their phenotypes were analyzed using the backcrossed material. Plants were grown either in a greenhouse or in caged outdoor compartments during the summer. Experiments were done in controlled growth chambers at 22°C with 16/8 hours of light/darkness (long day conditions), or 8/16 hours of light/darkness (short day conditions). Allelism tests were done as inspections of leaf phenotypes of F1 plants resulting from crosses between relevant mutants. An AFLP-based procedure was used to screen for molecular markers linked to the mutants (Castiglioni *et al*. 1998).

Results and Discussion

Mutant 1661 displays chlorotic stripes (Figure 1). These stripes are most pronounced on the first leaf. Under long day conditions, the stripes do not appear on the later emerging leaves and the plants eventually seem to recover from the phenotype conferred by the mutation. Under short day conditions the mutation is semi-lethal since all leaves develop the characteristic chlorotic stripes and the plants fail to reach maturity and produce seeds. However, the phenotype initially proves to be more severe under long day conditions. Mutant 1661 is phenotypically similar to the previously described mutants mottled leaf 1 and mottled leaf 5, which have clearly marked white

bands across the leaves (Davis *et al*. 1997). Allelism tests indicated that 1661 is not allelic to these. None of the pre-mapped Proctor-Nudinka AFLP markers were linked to mutant 1661.

Mutant 2721 is characterized by chlorotic leaf spots and streaks that coalesce and eventually form large white patches on the leaves (Figure 1). The phenotype is displayed on all leaves and as the leaves mature, the white regions gradually become darker, seeming to undergo necrosis and death. Often the necrosis affects the leaf edges, resulting in wrinkled leaf edges. Under short day conditions, the leaf phenotype is delayed by several days and is reduced in severity. Eventually all leaves display the phenotype even under short day conditions. The mutant initially appears to be similar to the mottled leaf 2 (Davis *et al*. 1997) and mottled leaf 6 (Franckowiak 2002) mutants, which display yellow bands on the leaves. However, these mutants do not display the necrosis of 2721. Allelism tests suggest that 2721 is not allelic to the mottled leaf mutants. None of the pre-mapped Proctor-Nudinka AFLP markers were linked to mutant 2721.

Mutant 3091 has brown spots towards the leaf tips and leaf edges, particularly on the first leaf (Figure 1). Short days do not significantly alter the phenotype. The leaf phenotype resembles those of mutants *nec4* and *nec5* (Davis *et al.*. 1997). However, allelism tests indicate that mutant 3091 is not allelic to either of these two. For the mutation in 3091, linkage was detected to the AFLP marker E37M33-6 on barley chromosome 3 (3H).

Mutant 3550 has conspicuous black or brown spots on the leaves (Figure 1). The spots usually do not coalesce. They appear on all above-ground parts of the plant including the bristles. Mutant 3550 is delayed in maturation and ripening, with seeds being ready for harvest about four weeks later than in the wildtype. Short day conditions lead to a slightly less pronounced phenotype. Mutant 3550 is similar to the *nec1* mutant (Davis *et al*. 1997), but allelism could be ruled out due to different mapping positions. The mutation in 3550 was localized on chromosome 7 (5H). Linkage was detected to the AFLP markers E40M38-7, E36M36-5, E42M36-14, E42M40-2 and E41M32-5.

References:

Castiglioni, P., Pozzi, C., Heun, M., Terzi, V., Müller, K.J., Rodhe, W. and Salamini, F. 1998. An AFLP-based procedure for the efficient mapping of mutations and DNA probes in barley. Genetics 149:2039–2056.

Davis, M.P., J.D. Franckowiak, T. Konishi, and U. Lundqvist, 1997. New and revised descriptions of barley genes. Barley Genetics Newsletter 26: 22-516.

Franckowiak, J.D. 2002., BGS 629 Mottled leaf 6. Barley Genetics Newsletter 32:170.

Figure 1. Leaf phenotypes of the parent cultivar Bowman(*Rph3*) and four lesion mimic mutants; 1661, 2721, 3091, 3550.

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The Scandinavian Barley Chlorophyll Mutation Collection

Mats Hansson
Department of Biochemistry, Lund University
P.O. Box 124, SE-221 00 Sweden

Barley (*Hordeum vulgare* L.) *albina*, *striata*, *chlorina*, *tigrina*, *viridis* and *xantha* mutants, which can be obtained from the Department of Biochemistry, Lund University, Sweden.

The collection was previously held at the Carlsberg Laboratory, Copenhagen, Denmark, by Professor Diter von Wettstein.

Please contact the cordinator for Nuclear genes affecting the chloroplast:

Mats Hansson
Department of Biochemistry
Lund University
Box 124
SE-22100 Lund, Sweden
Tel. +46 46 2220105
Fax +46 46 2224116
Email mats.hansson@biochemistry.lu.se

Available mutants are marked by "×". If missing, the mutant might be present in the collection of the Nordic Gene Bank (www.nordgen.org).

Albina mutants

alb 7	×
alb 10	
alb 11	×
alb 12	
alb 13	×
alb 14	
alb 15	
alb 16	×
alb 17	×
alb 18	×
alb 19	×
alb 20	
alb 21	

alb 22	×
alb 24	×
alb 25	×
alb 26	×
alb 27	×
alb 28	×
alb 29	
alb 30	
alb 32	×
alb 33	
alb 34	
alb 35	
alb 36	

alb 37	
alb 38	
alb 40	
alb 41	
alb 42	×
alb 43	
alb 44	
alb 45	×
alb 46	×
alb 47	
alb 48	
alb 49	
alb 50	×
alb 51	
alb 52	×
alb 53	
alb 54	
alb 55	×
alb 56	
alb 57	
alb 58	
alb 59	×
alb 60	×
alb 61	
alb 62	
alb 63	
alb 64	
alb 65	
alb 66	×
alb 67	
alb 68	
alb 69	
alb 70	
alb 71	
alb 72	
alb 73	
alb 74	
alb 75	
alb 76	×
alb 77	
alb 78	×
alb 80	
alb 81	×
alb 82	

alb 83	
alb 84	
alb 85	
alb 86	
alb 87	
alb 88	
alb 89	×
alb 90	×
alb 91	
alb 92	
alb 94	
alb 95	×
alb 96	
alb 97	
alb 98	
alb 99	
alb 100	
alb 101	
alb 102	
alb 103	
alb 104	
alb 105	
alb 106	
alb 107	
alb 108	
alb 109	
alb 110	
alb 111	×
alb 112	
alb 113	×
alb 114	
alb 115	
alb 116	
alb 117	
alb 118	
alb 119	
alb 120	
alb 122	×
alb 123	
alb 124	
alb 125	
alb 126	
alb 127	
alb 128	

alb 129	
alb 130	
alb 131	
alb 132	
alb 133	×

alb 134	×
alb 135	

Striata mutants

Arnason	×
Arnason grøn	
striata 4	×
striata 6	×
striata 7	×
striata 8	
striata 11	
striata 12	
striata 13	
striata 15	
striata 16	
striata 17	
striata 19	
striata 21	
striata 22	×
striata 23	
striata 26	
striata 33	×
striata 34	×
striata 35	×
striata 36	×
striata 37	
striata 38	
striata 39	
striata 104	×
striata 105	×

Chlorina mutants

clo 101	×
clo 102	×
clo 103	×
clo 104	×
clo 105	×
clo 106 L	×
clo 106 L (A+B)	×
clo 106 line LA	
clo 106 line LB	
clo 106 line M	×
clo 106 line ML	×
clo 107	×
clo 108	×
clo 109	×
clo 110	×
clo 111	×
clo 112	×
clo 113	×
clo 114	×
clo 115	×
clo 116	×
clo 117	×
clo 118a	×
clo 118b	×
clo 119	×
clo 121	×
clo 122	×
clo 123	×
clo 124	×
clo 125 = Xan-h.Clo125	×
clo 126	×
clo 127	×
clo 130	×
clo 131a	
clo 131b	
clo133a	×
clo133b	×
clo 134	×
clo135	×

clo 136	×
clo 137	×
clo 138	×
clo 140	×
clo 141	×
clo 142	×
clo 143	×
clo 144	×
clo 145	×
clo 146	×
clo 147	×
clo 148	×
clo149	×
clo 150	×
clo 151	×
clo 152	×
clo 153	×
clo 154	×
clo 155	×
clo 157 = Xan-h.Clo157	×
clo 158	×
clo 159	×
clo 160	×
clo 161 = Xan-h.Clo161	×
clo 164	×
clo 165	×
clo 166	×
clo 167 het	
clo170	×
clo 171	×
clo 173	×
clo 174	×
clo 175	×
clo 176	×
clo 177	
clo 179	×
clo 180	×

Tigrina mutants

tig 1	×
tig 3	
tig 6	×
tig 7	×
tig 11	×
tig 12	×
tig 13	
tig 14	
tig 15	×
tig 17	
tig 18	
tig 19	×
tig 20	×
tig 21	×
tig 22	

tig 23	×
tig 24	×
tig 24 hom	
tig 25	×
tig 26	×
tig 27	×
tig 28	×
tig 29 hom	×
tig 30	×
tig 31	×
tig 32	×
tig 33	×
tig 34	×

Viridis mutants

vir 10	×
vir 11	×
vir 12	×
vir 13	×
vir 14	×
vir 15	×
vir 17	×
vir 18	×
vir 19	×
vir 21	×
vir 23	×
vir 24	×
vir 25	×
vir 27	×
vir 29	×
xan 75 = vir 30	×
vir 33	×
vir 34	×
vir 35	×
vir 38	×
vir 39	×

vir 41	×
vir 42	×
vir 43	×
vir 44	×
vir 45	×
vir 46	×
vir 47	×
vir 49	×
vir 50	×
vir 51	
vir 52	×
vir 55	×
xan 76 = vir 56	×
vir 59	
vir 60	×
vir 61	×
vir 63	×
vir 64	×
vir 65	×
vir 68	×
vir 69	×

vir 101	×
vir 102	×
vir 103	
vir 104	×
vir 105	
vir 106	
vir 107	
vir 108	
vir 109	
vir 109	
vir 110	
vir 111	
vir 112	
vir 113 light	
vir 113 dark	
vir 114	
vir 115	×
vir 119	
vir 120	×
vir 121	×
vir 122	×
vir 123	×
vir 129	
vir 130	×
vir 131	
vir 132	×
vir 133	×
vir 134	

vir 135	
vir 137	×
vir 138	
vir 139	
vir 141	
vir 142 hom	
vir 142	
vir 143	×
vir 144	
vir 145 hom	
vir 145	
vir 149	
vir 152	×
vir 156	×
vir 157	×
vir 158	
vir 159	×
vir 160	×
vir 165	
vir 166	×
vir 167	
vir 168	×
vir 169	
vir 170 = xan 83	×
vir 519	×

Xantha mutants

xan 3	×
xan 10	×
xan 11	×
xan 12	×
xan 13	×
xan 14	
xan 15	×
xan 16	×
xan 17	×
xan 18	×
xan 19	×

xan 20	×
xan 21	×
xan 22	
xan 23	×
xan 24	
xan 25	×
xan 26	×
xan 27	×
xan 28	×
xan 29	
xan 30	×

xan 31	×
xan 32	
xan 33	
xan 35	×
xan 37	×
xan 38	×
xan 39	×
xan 40	×
xan 41	×
xan 42	×
xan 43	
xan 44	×
xan 45	×
xan 46	×
xan 47	×
xan 48	×
xan 49	×
xan 50	×
xan 51	×
xan 52	×
xan 53	×
xan 54	
xan 55	×
xan 56	×
xan 57	×
xan 58	×
xan 59	×
xan 60	×
xan 62	×
xan 63	×
xan 64	×
xan 65	
xan 66	
xan 68	×
xan 69	
xan 70	
xan 71	×
xan 72	×
xan 73	×
xan 74	×
xan-q.75 = vir30	
xan-q.76 = vir56	
xan-q.77 = vir-xa1	

xan-q.78 = vir-alb1	
xan-q.79 = xa-alb3	
xan-q.80 = alb-l.26	
xan 81 = Proto 1	×
xan 82 = Proto 2	×
xan 83 = vir 170 (Proto 3)	×
xan 84 = Proto 4	×
xan 101	
xan 102	
xan 103	
xan 104	
xan 105	
xan 106	
xan 107	

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CAPS markers targeting barley *Rpr1* region

Ling Zhang* and Andris Kleinhofs
Department of Crop and Soil Sciences
Washington State University, Pullman, WA, 99164-6420
*E-mail: lzhang1@wsu.edu

Abstract
Eight cleaved amplified polymorphic sequences (CAPS) markers were developed around *Rpr1* genetic region. Eight markers were co-dominant between barley cultivars Morex and Steptoe after digestion with restriction enzymes.

Introduction

In barley, resistance to *Puccinia graminis* f. sp. *tritici* pathotype MCC requires the presence of at least of two host genes, *Rpg1* (Brueggeman et al., 2002) and *Rpr1* (Zhang et al., 2006). Mutational analysis and transcript-based cloning were used to isolate 3 candidate *Rpr1* genes. These 3 candidate *Rpr1* genes, HU03D17U_s_at, Contig4901_s_at and Contig7061_s_at were mapped to chromosome 4 bin 5. Screening recombinants between the three candidate genes will identify the real *Rpr1* gene. Therefore, molecular markers in this region are needed.
Cleaved amplified polymorphic sequences (CAPS) markers are PCR-based markers, requires a small amount of genomic DNA, which will facilitate the screening of large numbers of genotypes at the seedling stage. 141 probesets representing a major *Rpr1* eQTL served as a starting point to develop CAPS markers. Here we report the development and mapping of CAPS markers in the *Rpr1* region.

Materials and Methods

CAPS markers development

Plant genomic DNA extraction was modified from Edwards et al. (1991); the modification added an extra-step of chloroform-isoamyl alcohol (24:1) extraction. Barley EST unigene sequences (HarvEST assembly#21; http://harvest.ucr.edu/) were used as templates for primer design. RFLP clone MWG058 was sequenced using primers T3 and T7 with the BigDye terminator system on ABI Prizm 377 DNA sequencer (Applied Biosystems) at the Bioanalytical Center, Washington State University, Pullman. A pair of primers was designed from the MWG058 sequence. All the primer pairs listed in Table 1 were used to amplify genomic DNA from the parent cultivars Morex and Steptoe. All PCRs of 20µl contained 20-50ng of genomic DNA, 0.1mMdNTP mix, 12.5 pmol of each primer, 1µl of RedTaq DNA polymerase (Sigma), and 2 µl of 10xRedTaq reaction buffer. Amplification was performed in a PTC-100 programmable thermal controller (MJ Research, Cambridge, MA) at 95°C for 4 min, followed by 35 cycles of 95°C for 1 min, 60°C for 1 min, and 72°C for 1 min; this was followed by 7 min at 72°C. PCR products were purified using the Gel Extraction Kit (Qiagen, Valencia, CA) and sequenced. Steptoe sequence was compared to the Morex sequence in order to identify single nucleotide polymorphisms (SNPs) that could be utilized for CAPS marker development. Sequence analysis was done by VectorNTI software (Invitrogen). SNPs were identified and restriction enzymes (New England

BioLabs) were selected (Table 1). All the PCR products were digested directly using restriction enzymes correspondingly. Cleaved PCR products were then separated on 1% agarose gel.

Genetic mapping

The Steptoe x Morex "minimapper" population consisting of 35 selected doubled-haploid lines (DHL), was used to map the molecular markers to the barley Bin map (Kleinhofs and Graner 2002). CAPS marker genetic order and the distance between snp_3139 and LZ2502 was estimated based on segregation data from Steptoe x *Rpr1* F2 population.

Results and Discussion

Details of developed CAPS markers are listed in Tables 1 and Fig. 1. Molecular mapping in Steptoe x Morex population with CAPS markers showed that LZ6641, LZ13393 and LZ10152 co-segregated with LZMWG058, ABG484 and BCD453B, respectively. Markers snp_3139 (Druka, personal communication) and LZ2502 are the closest to *Rpr1* delimiting the 3 markers LZ17u, LZ4901 and LZ7061 that co-segregate with *Rpr1*. LZ2502 and sn3139 are about 1cM apart and can be used to screen recombinants in Steptoe x *rpr1* F2 population.

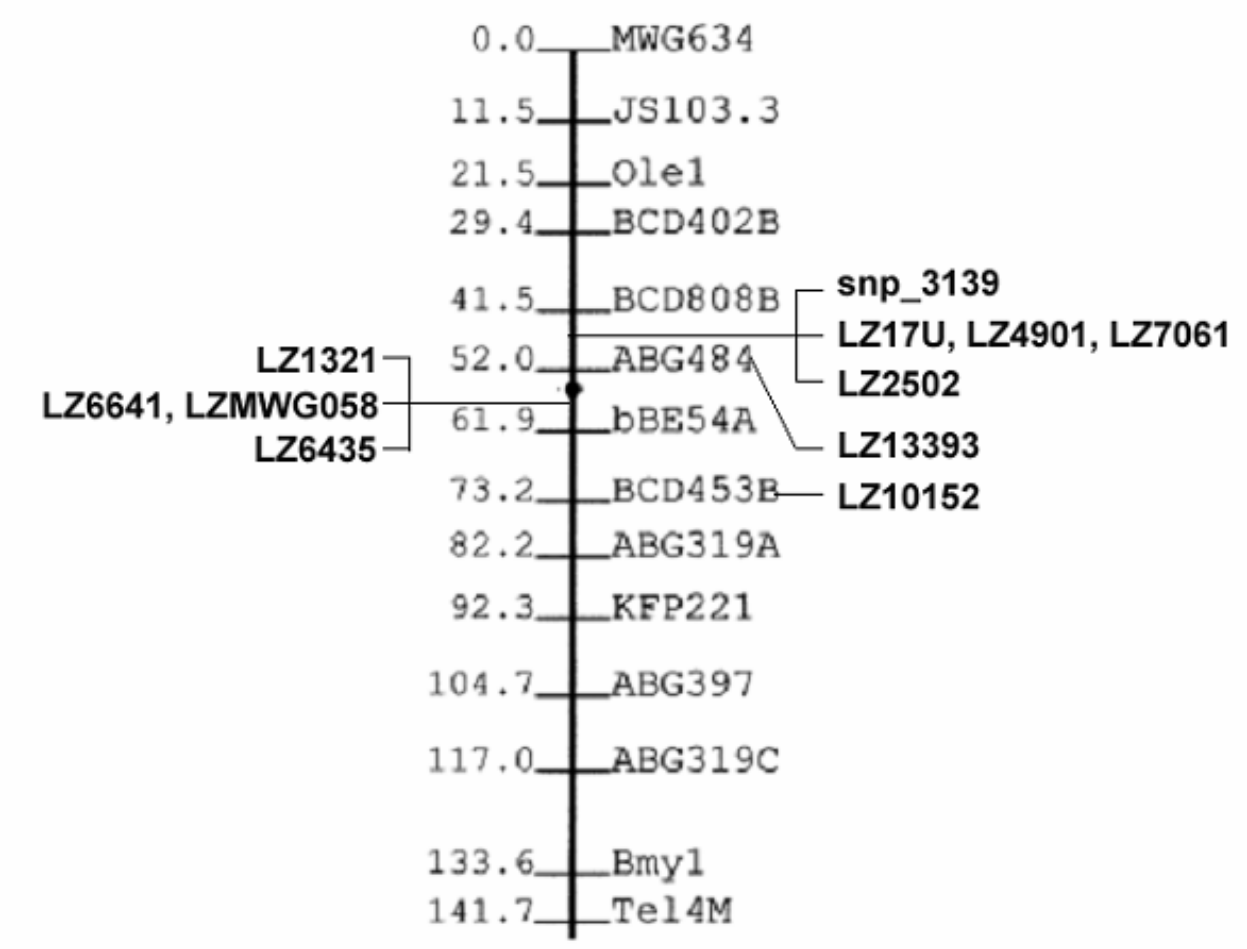

Figure 1. Chromosome locations of eight CAPS marker in barley chr. 4 (4H).

Table 1. Summary of developed CAPS markers, primers, restriction enzymes and annotation. All the CAPS markers were mapped to Chr 4 (4H), except LZ15227 was mapped to Chr 7 (5H).

Markers	Affymetrix Probesets	Forward Primer Reverse Primer	Enzyme	Annotation
LZ2502	Contig 2502_at	2502F: AGCTTCAGCTTCAGGTCGAT 2502R: GAAACTTAGAACCTGAACC	HpyCH4V	putative IAA1 protein
LZ6641	Contig 6641_at	6641F: TGATTGATCCTTTGCTGTCT 6641R: CTGGAAAGCGTTCAAATGCT	AvaII	putative expressed SLT1 protein
LZ6435	Contig 6435_at	6435F:ACACCAGGAAGATCATCGAC 6435R:ACAATGGAGAACACATGGTT	DdeI	phosphoenolpyruvate carboxy-kinase (ATP) -like protein
LZ13393	Contig 13393_at	13393F:AAGTGGACCGCGAAGCACGT 13393R:GCAGCATGTCAGGTTATACA	AvaII	hypothetical protein
LZ15227	Contig 15227_s_at	15227F:ATGGACTAATGACCCCAACA 15227R:TGCAACACACAAAGCCAGTC	AseI	microtubule associated protein
LZ1321	Contig 1321_at	1321F: CACTATCGACTTCCCGGAAT 1321R: ACTGCAATCAGGGTTCATCA	Sau3A or MboI	calmodulin
LZ10152	Contig 10152_at	10152F: AGATCTCCGGCTACGTGCTG 10152R: CGTACATCAGCTCGAAGAAA	Sau3A or MboI	putative membrane protein
LZMWG058[a]		MWG058F: ATTCATGCATCTACCCATCTCA MWG058R: TTGGATTGGCTAGAATCCTGGA	BtsI	unknown
snp_3139[b]		3139F: AACCACGCAGCAAGCCTAT 3139R: CTCGCTTCCTCCGTCATCAT	DdeI	unknown

[a]LZMWG058 was developed from RFLP clone MWG058.
[b]snp_3139 sequence provided by Druka A, Scottish Crop Research Institute (SCRI), Invergowrie, Dundee DD2 5DA, UK

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Tolerance to high copper ions concentration in the nutrient medium of some Bulgarian barley cultivars

J. Stoinova[1], S. Phileva[1], M. Merakchyiska[2] and S. Paunova[2]
[1] D. Kostov Institute of Genetics, Bulgarian Academy of Sciences, 1113 Bulgaria
[2] M. Popov Institute of Plant Physiology, Bulgarian Academy of Sciences, 1113 Bulgaria

Abstract. The winter two-rowed barley cultivars Obzor, Krasii 2, Vihren and Karan were examined for tolerance to environmental copper ions pollution. The plants were treated with 10^{-6} M and 10^{-5} M $CuSO_4.5H_2O$ for 7 days. It was found that under 10^{-6} M the roots of cultivars Krassi 2 and Vihren were longer by 9% and 16% respectively, while plant green part was identical to that of the control. The root of cultivar Karan was severely inhibited its length reaching 77% that of the control. The green part was less affected. The data suggest that cultivars Krasii 2 and Vihren are tolerant while cultivar Karan is susceptible to increased copper ions concentration in the environment.

Key words: barley, tolerance, copper ions

Barley is an economically important crop being efficiently used in animal husbandry and brewing. Resistant to abiotic and biotic stress barley cultivars are a reliable tool to produce high quality stuff avoiding diverse chemical substances for pest control and other agricultural practices. Acevedo and Fereres (1993) concluded that breeding for abiotic stress resistance is becoming more promising with the recognition that selection showed be carried out in the target environment and that it is related to narrow adaption.

During the last decades barley resistance to certain heavy metals has been examined in different aspects. It was shown that increased boron concentration in the environment reduce plant growth rate, while relative susceptibility of the genotypes to boron toxicity was not affected (Nable et al.,1999). The effect of high boron concentration on barley was studied on cell level (Jenkin et al.,1993). Data from studies with leaf protoplasts revealed that lack of cell walls prevents manifestation of differences between tolerant and susceptible barley genotypes. Treatment of *H. vulgare* seeds with nickel sulphate resulted into morphological alterations and increased chlorophyll and protein percentage, as well as that of the aberrant cells (Mishra and Singh, 1999). Addition of copper (2-4 kg/ha) led to higher grain yield from wheat, rye and oats (Piening et al., 1989). Tang et al. (2000) studied the location of genes for tolerance to aluminium and found that the latter is disposed to the long arm of 4H chromosome, while according to Rigin and Yakovleva (2001) the tolerance is coded by two polygenes.

The purpose of this investigation was to examine the tolerance to increased copper ions concentration in the nutrient medium of four Bulgarian barley cultivars.

Materials and Methods

The winter two-rowed cultivars Obzor, Krassi 2, Vihren and Karan were studied. The seeds were germinated in moist filter paper rols in a semi-dark chamber at 18° C. After germination (2.5 – 3.5 cm root length) the shoots were transffered on a solution containing 10^{-6} M or 10^{-5} M $CuSO_4.5H_2O$ at a temperature of while the control plants were grown in distilled water. All

plants were grown at 12 h illumination/12 h dark and 20°- 24° C. After 7 days treatment biometric data were collected. To determine copper tolerance of the plants usually the tolerance index (Simon, 1978) was used, i.e. the plant growth in a heavy metal polluted medium was compared to that under control conditions:

$$IT = \frac{\text{growth in a polluted medium}}{\text{growth under control conditions}} 100$$

The data of copper influence on length of root and shoot have been processed by the variation statistical method.

Results and Discussion

A three-fold treatment with 10^{-6} M copper ions concentration of the root (cultivar Obzor) caused inhibition (93-94% as compared to the control) or stimulation up to 103%. In the case of the cultivar Karan the roots were strongly inhibited their length varying from 62% to 94% of the control. The plants of the cultivar Krassi 2 and cultivar Vihren responded to two of the treatments through stimulated root growth from 122% to 135% and from 116% to 129%, respectively. The shoot length was less affected, some inhibition varying from 1% to 6% or stimulation up to 2 – 4% being manifested by the cultivars Obzor, Krassi 2 and Vihren. More significant inhibition was manifested by cultivar Karan.

The higher (10^{-5} M) copper ions concentration severely inhibited both root and shoot of the plants from all cultivars after the three treatment accomplished.

The mean data (Table 1) show that 10^{-6} M ions stimulate (9-16%) root growth of the plants from cultivars Krassi 2 and Vihren while the roots of the plants from Karan reaced only 77% of the control. The green part of the plants was equal to that of the control ones. The variation coefficients revealed slight heterogenic variation, while the plant green part length variation was homogenic, exept that for cultivar Karan. Higher (10^{-5} M) copper ions concentration highly reduced root growth, root length reaching 32-41% that of the control. The aboveground part of the plants from cultivar Krassi 2 and cultivar Vihren was identical to that of the control while those of cultivar Karan and Obzor were 69-75% that of the control. The variation coefficients revealed slight heterogenic variation.

Under 10^{-6}M copper ions concentration root mass of cultivar Obzor and cultivar Karan reaching 90-91% that of the control, the negative effect being stronger than that exerted on cultivars Krassi 2 and Vihren. The green part mass increased (1-3%) in the case of cultivar Obzor, cultivar Krassi 2 and cultivar Vihren, while that of cultivar Karan was slightly inhibited.

10^{-5} M copper ions concentration redused plant green part and root mass to 75-79% and 52-61%, respectively.

To conclude, the cultivars Krassi 2 and Vihren manifested tolerance to increased copper ions concentration in the environment as under 10^{-6} M the root was 9-16% longer than that of the control combined with less reduction of the mass (94%) of the control. The grain yield was 672 kg/da and 677 kg/da, respectively. Therefore, they are suitable for cultivation in highly polluted regions.

Cultivar Karan proved to be susceptible to copper pollution its root being severely reduced.

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Table 1. Influence of copper ions on the length of root and shoot

Variant	Cultivar	Length root			Length shoot		
		%control	M ± m	Vc%	%control	M ± m	Vc%
Control	Obzor	100	12.0 ± 0.13	10.57	100	14.30 ± 0.13	8.93
10^{-6}M		97	11.7 ± 0.18	12.84	99	14.20 ±.0.13	7.88
10^{-5}M		38	4.6 ±.0.36	14.82	75	10.67 ±.0.13	11.91
Control	Krassi 2	100	12.8 ± 0.21	15.28	100	14.40 ±.0.13	9.62
10^{-6}M		116	14.8 ± 0.23	15.51	100	14.40 ± 0.12	8.49
10^{-5}M		41	5.3 ± 0.25	12.40	73	10.50 ± 0.11	11.11
Control	Vihren	100	13.7 ± 0.29	19.65	100	16.40 ± 0.15	8.40
10^{-6}M		109	15.0 ± 0.23	15.29	99	16.20 ±.0.16	9.47
10^{-5}M		40	5.5 ± 0.08	15.75	72	11.80 ± 0.16	12.85
Control	Karan	100	14.5 ± 0.23	14.65	100	15.40 ± 0.18	10.26
10^{-6}M		77	11.2 ± 0.22	16.50	98	15.10 ± 0.21	12.16
10^{-5}M		32	4.6 ± 0.08	16.49	69	10.60 ± 0.19	16.15

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Rules for Nomenclature and Gene Symbolization in Barley

Jerome D. Franckowiak[1] and Udda Lundqvist[2]
[1]HermitageResearch Station
Queensland Department of Primary Industries and Fisheries
Warwick, Queensland 4370, Australia
[2]Nordic Gene Bank
P.O. Box 41, SE-230 53 Alnarp, Sweden

In this volume of the Barley Genetics Newsletter the recommended rules for nomenclature and gene symbolization in barley as reported in BGN 2:11-14, BGN 11:1-16, BGN 21:11-14, BGN 26:4-8, and BGN 31:76-79 are again reprinted. Also, the current lists of new and revised BGS descriptions are presented by BGS number order (Table 1) and by locus symbol in alphabetic order (Table 2) in this issue.

1. In naming hereditary factors, the use of languages of higher internationality should be given preference.

2. Symbols of hereditary factors, derived from their original names, should be written in Roman letters of distinctive type, preferably in italics, and be as short as possible.

   AMENDMENT: The original name should be as descriptive as possible of the phenotype. All gene symbols should consist of three letters.

   COMMENTS: All new gene symbols should consist of three letters. Existing gene symbols of less than three letters should be converted to the three-letter system whenever symbols are revised. When appropriate, one or two letters should be added to existing symbols.

   For example, add the letters "*ap*" to "*K*" to produce the symbol "*Kap*" to replace "*K*" as the symbol for Kapuze (hooded). As another example, add the letters "*ud*" to "*n*" to produce the symbol "*nud*" to replace "*n*" as the symbol for naked seed. Similarly the letter "*g*" can be added to "*ms*" to produce the symbol "*msg*" for genetic male sterility and the letter "*e*" can be added to "*ds*" to produce the symbol "*des*" for desynapsis. When inappropriate or when conflicts arise, questions should be referred to the Committee on Genetic Marker Stocks, Nomenclature, and Symbolization of the International Barley Genetics Symposium for resolution.

3. Whenever unambiguous, the name and symbol of a dominant begin with a capital letter and those of a recessive with a small letter.

AMENDMENT: When ambiguous (co-dominance, incomplete dominance, etc.) all symbols should consist of a capital letter followed by two small letters that designate the character, a number that represents a particular locus, and a letter or letters that represents a particular allele or mutational event at that particular locus.

COMMENTS: As an example, the letters "*Mdh*" can be used to designate the character malate dehydrogenase, "*Mdh1*" would represent a particular locus for malate dehydrogenase and "*Mdh1a*", "*Mdh1b*", "*Mdh1c*", etc. would represent particular alleles or mutational events at the "*Mdh1*" locus. Row number can be used as an example of symbolizing factors showing incomplete dominance. At the present time, the symbol "*v*" is used to represent the row number in *Hordeum vulgare*, "*V*" is used to represent the row number in *Hordeum distichum*, and "V^t" is used to represent the row number in *Hordeum deficiens*. According to the amendment to Rule 3, if row number were to be designated by the letters "*Vul*", the designation of the locus on chromosome 2 would then become "*Vul1*" and the alleles "*v*", "*V*", and "V^t" would be designated "*Vul1a*", "*Vul1b*", and "*Vul1c*".

SUPPLEMENTARY AMENDMENT: A period should be placed before the allele symbol in the complete gene symbol.

COMMENTS: Since DNA sequences similar to those of the original locus may occur at several positions in the *Hordeum vulgare* genome, a three-letter symbol plus a number is inadequate to represent all potential loci. Also, both numbers and letters have been assigned to specific mutants and isozymes in *Hordeum vulgare*. The six-rowed spike locus is used as an example although the symbol *Vul1* for row number in *Hordeum vulgare* is not recommended because the botanical classification of *Hordeum* spp has changed. The locus symbol *vrs1* and the name six-rowed spike 1 are recommended for the *v* locus. Gene symbols recommended for common alleles at the *vrs1* locus are *vrs1.a*, *vrs1.b*, *vrs1.c*, and *vrs1.t* for the "*v*", "*V*", "v^{lr}", and "V^t" genes, respectively.

4. Literal or numeral superscripts are used to represent the different members of an allelic series.

AMENDMENT: All letters and numbers used in symbolization should be written on one line; no superscripts or subscripts should be used.

5. Standard or wild type alleles are designated by the gene symbols with a + as a superscript or by a + with the gene symbol as a superscript. In formulae, the + alone may be used.

AMENDMENT: This rule will not be used in barley symbolization.

6. Two or more genes having phenotypically similar effects are designated by a common basic symbol. Non-allelic loci (mimics, polymeric genes, etc.) are distinguished by an additional letter or Arabic numeral either on the same line after a hyphen or as a subscript. Alleles of independent mutational origin may be indicated by a superscript.

AMENDMENT: Barley gene symbols should consist of three letters that designate the character, a number that represents a particular locus, and a letter or letters that represents a particular allele or mutational event at that particular locus. All letters and numbers should be written on the same line without hyphens or spaces. Alleles or mutational events that have not been assigned to a locus should be symbolized by three letters that designate the character followed by two commas used to reserve space for the locus number when determined, followed by a letter or letters representing the particular allele or mutational event. After appropriate allele testing, the correct locus number will be substituted for the commas. Where appropriate (when assigning new symbols or when revising existing symbols) letters representing alleles or mutational events should be assigned consecutively without regard to locus number or priority in discovery or publication.

COMMENTS: The use of the proposed system of symbolization can be illustrated by the desynaptic mutants. Two loci are known: *lc* on chromosome 1 (7H) and *ds* on chromosome 3 (3H). These will be resymbolized as *des1a* and *des2b*. A large number of desynaptic mutants have been collected. They will be designated *des,,c*, *des,,d*, *des,,e*, etc. If allele tests show that *des,,c* is at a different locus than *des1* and *des2*, *des,,c* will become *des3c*. If allele tests show that *des,,d* is at the same locus as *des2*, *des,,d* will become *des2d*. In practical use, the symbol *des* will be used when speaking of desynapsis in general or if only one locus was known for the character. The symbol *des2* will be used when speaking of that particular locus, and the symbol *des2b* will be used only when speaking of that particular allele or mutational event. If additional designation is needed in particular symbolization, it can be obtained by adding numbers behind the allele letters, and, if still further designation is needed, letters can be added to the symbol behind the last number. Symbolization consisting of alternation of letters and numbers written on the same line without hyphens or spaces will allow for the expansion of the symbol as future needs arise. In any work with large numbers of polymeric gene mutants, every mutant has to be given a designation not shared by any other mutant of this polymeric group and this designation should become a part of the permanent symbol representing that particular allele or mutational event. This requirement can be met by assigning allele designations in consecutive order without regard to locus number.

SUPPLEMENTARY AMENDMENT: A period should be used instead of two commas in gene symbols for mutants within a polymeric group that can not be assigned to a specific locus.

COMMENTS: The *des* symbol should be used when referring to desynapsis in general; *des1* and *des2*, for specific loci; *des1.a* and *des2.b* for specific genes or alleles at their respective loci; and *des.c*, *des.d*, *des.e* etc., for desynaptic mutants not assigned to a specific locus.

SUPPLEMENTARY AMENDMENT:
Even if the locus in question is the only one known that affects a given phenotype, the three-letter basic symbol is followed by a serial number.

7. Inhibitors, suppressors, and enhancers are designated by the symbols *I, Su,* and *En*, or by *i, su,* and *en* if they are recessive, followed by a hyphen and the symbol of the allele affected.

AMENDMENT
This rule is no longer appicable and will not be used in barley symbolization.

8. Whenever convenient, lethals should be designated by the letter *l* or *L* and sterility and incompatibility genes by *s* or *S*.

AMENDMENT: This rule will not be used in barley symbolization.

COMMENTS: J.G. Moseman (BGN 2:145-147) proposed that the first of the three letters for designating genes for reaction to pests should be *R*. The second and third letters will be the genus and species names of the pest.

SUPPLEMENTARY COMMENT: A motion was passed during the workshop on "Linkage Groups and Genetic Stock Collections" at the Fifth International Barley Genetics Symposium in 1986 (Barley Genetics V:1056-1058, BGN 17:1-4), that the International Committee for Nomenclature and Symbolization of Barley Genes should "recommend use of *Ml* as the designation of genes for resistance to powdery mildew."

9. Linkage groups and corresponding chromosomes are preferably designated by Arabic numerals.

SUPPLEMENTARY AMENDMENT: The current wheat homoeologous group numbering scheme (the Triticeae system) is recommended for *Hordeum vulgare* chromosomes. Arabic numerals followed by an H will indicate specific barley chromosomes. The *H. vulgare* chromosomes should be 7H, 2H, 3H, 4H, 1H, 6H, and 5H instead of 1, 2, 3, 4, 5, 6, and 7, respectively.

10. The letter *X* and *Y* are recommended to designate sex chromosomes.

AMENDMENT: This rule will not be used in barley symbolization.

11. Genic formulae are written as fractions with the maternal alleles given first or above. Each fraction corresponds to a single linkage group. Different linkage groups written in numerical sequence are separated by semicolons. Symbols of unlocated genes are placed within parenthesis at the end of the formula. In euploids and aneuploids, the gene symbols are repeated as many times as there are homologous loci.

12. Chromosomal aberrations should be indicated by abbreviations: *Df* for deficiency, *Dp* for duplication, *In* for inversion, *T* for translocation, *Tp* for transposition.

13. The zygotic number of chromosomes is indicated by 2n, the gametic number by n, and basic number by x.

14. Symbols of extra-chromosomal factors should be enclosed within brackets and precede the genic formula.

The following recommendations made by the International Committee for Nomenclature and Symbolization of Barley Genes at the Fourth International Barley Genetics Symposium in 1981 (Barley Genetics IV:959-961) on gene and mutation designations were as follows.

AMENDMENT:

A. Present designations for genes and mutations. - Most of the present designations should be maintained. However, new designations may be given, when additional information indicates that new designations would aid in the identification of genes and mutations.

B. New designations for genes and mutations. - New genes or mutations will be designated by characteristic, locus, allele, and then the order of identification or mutational event. Three letters will be used to identify new characteristics. Consecutive numbers will be used to identify the order of identification or mutational event. Loci will be designated by numbers and alleles by letters when they are identified. For example, *des-6* indicates that this is the sixth gene or mutation identified for the characteristic *des* (desynaptic). *des 1-6* and *des 2-7* indicate that gene or mutational events 6 and 7 for the desynaptic characteristic have been shown to be at different loci and those loci are then designated 1 and 2, respectively. *des 1a6* and *des 1b8*, indicate that the gene or mutational events 6 and 8 for the characteristic desynaptic have been shown to be at different alleles at locus 1 and those alleles are then designated a and b.

SUPPLEMENTARY COMMENT:

A motion was passed during the workshop of the "Nomenclature and Gene Symbolization Committee" at the Fifth International Barley Genetics Symposium in 1986 (Barley Genetics V:1056-1058) that "the recommended systems for Nomenclature and Gene Symbolization of the International Committee be published annually in the Barley Genetics Newsletter."

SUPPLEMENTARY COMMENT 2:

At the workshop for ”Recommendations of Barley Nomenclature” held at Saskatoon, July 31, 1996 and adopted at the General Meeting of the Seventh International Barley Genetics Symposium, it was recommended that a period instead of a dash be used to designate the allele portion of the gene symbol. Consequently, the first gene symbol for the characteristic *des* (desynapsis) should be expressed as *des1.a*. The code *des1* identifies a specific locus. The period indicates that the symbol *a* identifies a specific allele or mutational event that produces a desynaptic phenotype. (The allele symbol *a* will be always associated with this specific desynaptic mutant even if the locus symbol is changed based on subsequent research results.)

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REPORTS OF THE COORDINATORS

Overall coordinator's report

Udda Lundqvist
Nordic Gene Bank
P.O. Box 41. SE-230 53 Alnarp

e-mail: udda@nordgen.org

Since the latest overall coordinator's report in Barley Genetics Newsletter Volume 36, some changes of the coordinators have taken place. I do hope that most of you are willing to continue with this work and provide us with new important information and literature search in the future. A replacement was found for Chromosome 4H, namely Arnis Druka, Genetics Programme at the Scottish Crop Research Institute, Invergowrie, Dundee, United Kingdom. Please observe some address changes have taken place since the last volume of BGN. Jerry Franckowiak, the Coordinator for chromosome 2H, the semi-dwarf collection and all his immense efforts creating isogenic lines in the Bowman genetic background of many different barley genetic stocks has moved from North Dakota State University to Warwick, Queensland, Australia. The Curator, An Hang, for the Barley Genetics Stock Center at the USDA-ARS station at Aberdeen, Idaho, USA, has retired during the year 2007. Dr. Harold Bockelman from the same station is nominated as successor. An Hang has been involved and engaged in Barley Genetics since many decades, first together with Tak Tsuchiya at Fort Collins, Colorado and since 1990 at Aberdeen, Idaho. He took care of the move of all genetic barley stocks from Fort Collins to Aberdeen, has been evaluating and increasing most of them. He has been a considerable collaborator and colleague to the barley community, handled with big carefulness all the different barley types and transferred a large knowledge to all of us. I take this opportunity to thank him for all his kindness, helpfulness, enthusiasm and inspiration during all these years. All the best wishes to him in the future and his retirement. But I want to thank those who have resigned for their good corporation and the reliability of sending informative reports during all the years.

In this connection I also want to call upon the barley community to pay attention on the AceDB database for 'Barley Genes and Barley Genetic Stocks'. It contains much information connected with images and is useful for barley research groups inducing barley mutants and looking for new characters. It gets updated continuously and some more images are added to the original version. The searchable address is: www.untamo.net/bgs

In some months the 10th International Barley Genetics Symposium will be organized in Alexandria, Egypt. I hope that many of you will be to participate in the meetings. It is of big importance to discuss the future of different items, especially the coordination system and the future of Barley Genetics Newsletter. I would like to encourage the coordinators and their colleagues already to-day to provide me with suggestions, ideas, items or topics to be brought up during the meetings.

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List of Barley Coordinators

Chromoosome 1H (5): Gunter Backes, The University of Copenhagen, Faculty of Life Science, Department of Agricultural Sciences, Thorvaldsensvej 40, DK-1871 Fredriksberg C, Denmark. FAX: +45 3528 3468; e-mail: <guba@life.ku.dk>

Chromosome 2H (2): Jerry. D. Franckowiak, Hermitage Research Station, Queensland Department of Primary Industries and Fisheries, Warwick, Queensland 4370, Australia, FAX: +61 7 4660 3600; e-mail: <Jerome.franckowiak@dpi.qld.gpv.au>

Chromosome 3H (3): Luke Ramsey, Genetics Programme, Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. FAX: +44 1382 562426. E-mail: <Luke.Ramsey@scri.sari.ac.uk>

Chromosome 4H (4): Arnis Druka, Genetics Programme, Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. FAX: +44 1382 562426. e-mail: <adruka@scri.sari.ac.uk>

Chromosome 5H (7): George Fedak, Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, ECORC, Ottawa, ON, Canada K1A 0C6, FAX: +1 613 759 6559; e-mail: <fedakga@agr.gc.ca>

Chromosome 6H (6): Duane Falk, Department of Crop Science, University of Guelph, Guelph, ON, Canada, N1G 2W1. FAX: +1 519 763 8933; e-mail: <dfalk@uoguelph.ca>

Chromosome 7H (1): Lynn Dahleen, USDA-ARS, State University Station, P.O. Box 5677, Fargo, ND 58105, USA. FAX: + 1 701 239 1369; e-mail: <DAHLEENL@fargo.ars.usda.gov>

Integration of molecular and morphological marker maps: Andy Kleinhofs, Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA. FAX: +1 509 335 8674; e-mail: <andyk@wsu.edu>

Barley Genetics Stock Center: An Hang, USDA-ARS, National Small Grains Germplasm Research Facility, 1691 S. 2700 W., Aberdeen, ID 83210, USA. FAX: +1 208 397 4165; e-mail: <anhang@uidaho.edu>
and
Harold Bockelmann, National Small Grains Collection, U.S. Department of Agriculture – Agricultural Research Service, 1691 S. 2700 W., Aberdeen, ID 83210, USA. FAX: +1 208 397 4165. e-mail: <nsgchb@ars-grin.gov>

Trisomic and aneuploid stocks: An Hang, USDA-ARS, National Small Grains Germplasm Research Facility, 1691 S. 2700 W., Aberdeen, ID 83210, USA. FAX: +1 208 397 4165; e-mail: <anhang@uidaho.edu>

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

List of Barley Coordinators (continued)

Desynaptic genes: Andreas Houben, Institute of Plant Genetics and Crop Plant Research, Corrensstrasse 3, DE-06466 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: Brian Steffenson, Department of Plant Pathology, University of Minnesota, 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108-6030, USA. FAX: +1 612 625 9728; e-mail: <bsteffen@umn.edu>

Eceriferum genes: Udda Lundqvist, Nordic Gene Bank, P.O. Box 41, SE-230 53 Alnarp, Sweden. FAX:.+46 40 536650; e-mail: < udda@nordgen.org>

Chloroplast genes: Mats Hansson, Department of Biochemistry, University of Lund, Box 124, SE-221 00 Lund, Sweden. FAX: +46 46 222 4534 e-mail: <mats.hansson@biochemistry.lu.se>

Genetic male sterile genes: Mario C. Therrien, Agriculture and Agri-Food Canada, P.O. Box 1000A, R.R. #3, Brandon, MB, Canada R7A 5Y3, FAX: +1 204 728 3858; e-mail: <MTherrien@agr.gc.ca>

Ear morphology genes: Udda Lundqvist, Nordic Gene Bank, P.O. Box 41, SE-230 53 Alnarp, Sweden. FAX: +46 40 536650; e-mail: < udda@nordgen.org>
or
Antonio Michele Stanca: Istituto Sperimentale per la Cerealicoltura, Sezione di Fiorenzuola d'Arda, Via Protaso 302, IT-29017 Fiorenzuola d'Arda (PC), Italy. FAX +39 0523 983750, e-mail: <michele@stanca.it>

Semi-dwarf genes: Jerry D. Franckowiak, Hermitage Research Station, Queensland Department of Primary Industries and Fisheries, Warwick, Queensland 4370, Australia, FAX: +61 7 4660 3600; e-mail: < Jerome.franckowiak@dpi.qld.gpv.au >

Early maturity genes: Udda Lundqvist, Nordic Gene Bank, P.O. Box 41 SE-230 53 Alnarp, Sweden. FAX: +46 40 536650; e-mail: <udda@nordgen.org>

Biochemical mutants - Including lysine, hordein and nitrate reductase: Andy Kleinhofs, Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA. FAX: +1 509 335 8674; e-mail: <andyk@wsu.edu>

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: <rislam@waite.adelaide.edu.au>

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Coordinator's Report: Barley Chromosome 1H (5)

Gunter Backes

The University of Copenhagen
Faculty of Life Sciences
Department of Agricultural Sciences
Thorvaldsensvej 40
DK-1871 Frederiksberg C, Denmark

guba@life.ku.dk

In Arabidopsis, *HLM1* encodes the cyclic nucleotide-gated ion channel 4. A mutant plant for this gene shows necrotic lesions and thereby similarities to the hypersensitive response (HR) to pathogens. Rostoks *et al*. (2006) isolated the homolog of this gene from the previously characterized barley mutant *nec1* and localized the gene in the 'Steptoe' x 'Morex' "minimapper population" to chromosome 1H, Bin9.

In an attempt to localize transcription factors (TFs) belonging to the gene family of C-repeat binding factors (CBF), their regulators and MYB-TFs, altogether known to regulate plant response to cold and drought stress, Tondelli *et al*. (2006) localized several homologs to the respective *Arabidopsis* genes in a joined map of the three populations 'Nure' × 'Tremois', 'Proctor' × 'Nudinka' and 'Steptoe' × 'Morex'. Further, they compared the loci of these putative TFs with the position of published QTLs. They localized 9 homologs and assigned two further homologs by wheat-barley addition lines to the respective chromosomes. On chromosome 1H they localized *HvMYB4* to Bin6, a homolog to *AtMyb2* from *Arabidopsis* and *OsMYB4* from rice, both known to be part of the regulation processes during abiotic stresses.

In a similar effort, Skinner *et al*. (2006) localized the barley homologs of 14 *Arabidopsis* CBF-TFs and 2 further TFs in the barley populations 'Steptoe' × 'Morex' and 88Ab536 × 'Strider'.The authors also tested the 'Steptoe' × 'Morex' population in climatic chambers for cold tolerance and localized QTLs based on these data. On chromosome 1H, they localized *HvZFP16-1*, a homolog to *AtZAT12*, to Bin4. A further homolog of the same Arabidopsis gene, *HvZFPR16-2* was assigned to 1H by wheat-barley addition lines. A QTL for cold tolerance was localized on 1H, Bin11, by a LOD score of 5.7. No co-localization between the QTLs and the TFs localized in this study was found. Nevertheless, comparison with literature indicated QTLs at the position of two candidate gene loci on 5H.

The same group (Szücs *et al*. 2006) published results describing the localization of photoreceptor genes and vernalization-related genes together with QTLs for photoperiod response. Mapping of both, the candidate genes and QTLs, was carried out in DH populations of the crosses 'Dicktoe' × 'Morex' and 'Dicktoe' × 'Kompolti korai'. While none of the candidate genes was localized on chromosome 1H, two QTL were detected with the 'Dicktoo' × 'Morex' population: a major QTL in Bin11 and a further QTL in Bin12.

In order to localize qualitative and quantitative resistance against rice blast in barley, Inukai *et al*. (2006) analyzed a segregating DH population from the cross 'Baroness' × BCD47 with two different rice blast isolates in a greenhouse experiment. For one of the isolates, a qualitative segregation was found and consequently a new resistance gene, *RMo1*, was localized on chromosome 1H, Bin2 at or near the position of the *Mla*-locus. For the other isolate, a

quantitative segregation was found and a major QTL was detected at the position of *RMo1*, while further 3 QTLs were localized on the chromosomes 3H, 4H and 7H.

Jafary *et al*. (2006) investigated the inheritance and specificity of plant factors that determine the degree of basal defence by host- and nonhost pathogens. For this purpose, they analyzed 152 RILs from the cross 'Vada' x 'SusPtrit' with 2 rust isolates from barley rusts and 8 isolates from rusts with no barley-specificity, isolated from cultivated and wild *Poaceae*. 'SusPtrit' is an experimental barley accession selected for susceptibility to the wheat leaf rust fungus *Puccinia triticina*. On chromosome 1H, an R-gene against the fungus *Puccinia hordei-secalini* was localized. *P. hordei-secalini* has no host-specificity for *H. vulgare*. Furthermore, three different QTLs were detected. One of them conferred resistance against *P. hordei-murini*, one against *P. graminis* f.sp. *lolii* and one against *P. graminis* f.sp. *tritici*. Only the latter has barley-specificity. As the linkage map for 1H in this analysis purely consisted of AFLP marker, it was not possible to assign the R-gene or QTLs to the Bin-map.

A new qualitative resistance gene against spot blotch, *Rcs6*, caused by *Cochliobolus sativus*, was localized on chromosome 1H either proximal on Bin1 or distal on Bin2 by Bilgic *et al*. (2006). They tested the DH population 'Calcuchima-sib' × 'Bowman-BC' with two different isolates both on seedlings in the greenhouse and on adult plants in the field. While one isolate identified the above mentioned resistance gene both in the seedlings and the adult plants, the other isolate detected different quantitative resistance loci for the greenhouse compared with the field, none of them on the position of *Rcs6*.

Rsp2 and *Rsp3*, originally designated Sep_2 and Sep_3, are barley resistance genes against speckled leaf blotch in barley, caused by *Septoria passerinii*. These genes were mapped by Zhong *et al*. (2006) in an $F_{2:3}$ population of the cross 'Foster' x 'Clho 4780' based on seedling tests with a specific isolate. These two genes are either closely linked or allelic and are localized on chromosome 1H and, as estimated by the flanking markers, more exactly in Bin3.

Sameri *et al*. (2006) localized QTLs for different agronomic traits in an RIL population derived from a cross between two Japanese barley varieties 'Azumamugi' and 'Kanto Nakate Gold'. 'Azumamugi' is an oriental type barley, while 'Kanto Nakate Gold' belongs to the occidental type of barley varieties in Japan. The agronomic traits were evaluated in a field experiment on one location over two years. On chromosome 1H, one QTL for days to heading was localized near the position of *Ppd-H2* (photoperiod sensitivity, Bin9/10) and one QTL for days to heading and days to maturity was detected near the position of *eam8* ('early maturity', Bin14).

In an $F_{2:4}$ population from a cross between two wild barleys (*H. v.* ssp. *spontaneum*) from Israel, Vanhala and Stam (2006) localized QTL for seed dormancy. One of the lines ('Mehola') originates from the Jordan valley with low humidity and shows high seed dormancy, while the other line ('Ashkelon') originates from the Mediterranean coast with relatively high humidity and shows low dormancy. The germination rate was tested after 0 days, 14 days, 28 days and 42 days of after-ripening at + 40° C. On chromosome 1H, the only QTL where the 'Ashkelon'-allele prolongated the dormancy was found, while for the four other QTLs, on chromosomes 2H, 5H, 6H and 7H, 'Mehola' contributed the allele with the higher dormancy. As the map of 1H was solely based on AFLPs, it was not possible to assign the position to a Bin.

QTLs for grain yield (Bin11/12), heading date (Bin7), plant height (Bin14), ear length (Bin9, Bin13), spikelets/spike (Bin8/9), grain/spike (Bin8/9), spikes/plant (Bin12) and 1000-grain mass (Bin9, Bin11/12) were detected on chromosome 1H in an advanced-backcross experiment (Li *et*

al. 2006). The wild barley parent was the line 'HS584', and the recurrent cultivated parent was the variety 'Brenda'. The field trials were carried out on 2 locations during four years. The map positions of the marker were based on the 'Igri' × 'Franka' and 'Steptoe' × 'Morex' SSR maps ((Li *et al*., 2003).

In another advanced-backcross with the wild barley line 'ISR42-8' and the recurrent cultivated parent 'Scarlett', von Korff *et al*. (2005) analyzed agronomic traits in a field experiments (four locations during two years). On 1H, QTLs were found for ears per m² (Bin14), heading date (Bin13), plant height (Bin13), harvest index (Bin13, Bin14) and yield (Bin6-8).

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Coordinator's report: Chromosome 2H (2)

J.D. Franckowiak

Hermitage Research Station
Queensland Department of Primary Industries and Fisheries
Warwick, Queensland 4370, Australia

e-mail: jerome.franckowiak@dpi.qld.gpv.au

Komatsuda *et al*. (2007) cloned the six-rowed spike 1 (*vrs1*) gene located on chromosome 2HL of barley. Expression of the *Vrs1* was strictly localized in the lateral-spikelet primordia of immature spikes and suggests that the VRS1 protein suppresses development of lateral spikelets. Phylogenetic analysis of the six-rowed cultivars and mutants demonstrated that six-rowed spike trait originated repeatedly from two-rowed barley, at least three different origins among domesticated accessions. Also, the DNA sequence defects in many of *vrs1* mutants held in the Nordic Gene Bank were identified.

When the DNA sequence of *vrs1* was determined, Pourkheirandish *et al*. (2007) found that the region around the *vrs1* locus was collinear with rice chromosome 4. However, the rice orthologue for the *vrs1* sequence was found on rice chromosome 7. The authors speculated that a transposition of the chromosomal segment *Vrs1* to chromosome 2H occurred during the evolution of barley. Pourkheirandish *et al*. (2007) also reported that the *vrs1* locus is a region of suppressed recombination based on the study of more than 13,000 gametes.

Řepková *et al*. (2006) reported on the mapping of four new sources of resistance to powdery mildew, caused by *Blumeria graminis* f. sp. *hordei*, that were identified in accessions of wild barley, *Hordeum vulgare* ssp. s*pontaneum*. Accession PI 466197 was found to have two dominant resistance genes. One is an allelic at the *mla* locus and the other was located on chromosome 2HS based on a highly significant linkage with molecular marker Bmac0134.

Dahleen and Franckowiak (2006) found that *cer-zt* locus is located on chromosome 2HS based on linkage to molecular marker Bmac0134 in bin 2H-1. The *cert-zt.389* mutant has very little surface wax on the spike (Lundqvist and Franckowiak, 1997), but little effect on other agronomic traits except a slightly increased number of kernels per spike (Dahleen and Franckowiak, 2006).

Based on the analysis of 134 recombinant chromosome substitution lines (RCLs) from the BC_3 generation of the backcross of wild barley line (OUH602) into 'Haurna Nijo', Hori *et al*. (2005) found that QTLs for short spike and lax spike are on chromosome 2HL near the closed flowering (cleistogamy, *cly1*/*Cly*2) locus of Haurna Nijo. In a previous paper, Hori *et al*. (2003) reported that these QTLs plus one for short culm were observed in a population of doubled-haploid lines from a Haurna Nijo/OUH602 cross.

Using recombinant inbred lines, Yun *et al*. (2005) found a QTL for resistance to Septoria speckled leaf blotch (SSLB, caused by *Septoria passerinii* Sacc.) from *H. vulgare* subsp. *spontaneum*, located in bins 7 to 11 of chromosome 2H. They examined a recombinant inbred line (RIL) population developed from a cross between wild barley accession OUH602 and the two-rowed malting cultivar 'Harrington' for reaction to SSLB. About 40% of the variation in

response to SSLB was explained by the QTL on 2H, named QTL Rsp-2H-7-ll. The mapped disease resistances were validated using an advanced backcross population ($BC_2F_{6:8}$) from the same donor parent, but having two more backcrosses to Harrington (Yun *et al*., 2006).

A QTL regulating synthesis of cell wall (1,3;1,4)-beta-D-glucans was located between the markers *Adh8* bin 6 and ABG019 bin 7 with the peak closer to ABG019 on 2H (Burton *et al*., 2006). The cellulose synthase-like (*CslF*) gene cluster in cereals was identified as candidates responsible for mediating cell wall (1,3;1,4)- ß -D-glucan synthesis using of rice synteny and by transforming Arabidopsis (Burton et al., 2006). The research was based on the map location of a major QTL for (1,3;1,4)-ß-D-glucan content of un-germinated barley grains on 2H. This report is believed the first example of a map-based cloning of a QTL in barley.

Korff *et al*. (2006) reported on a large number of QTLs for agronomic traits detected in doubled-haploid lines from the second backcross of 'Scarlett' backcrossed to *Hordeum vulgare* ssp. *spontaneum* accession ISR42-8. Using a population 301 BC_2DH in eight environments, they reported detection of 86 QTLs for nine agronomic traits. The QTLs having large effects that were associated with chromosome 2H included: ears/m2, days to head (*Eam1* or *Ppd-H1*), plant height (*sdw1* from Scarlett), and yield.

Yin *et al*. (2005) confirmed that a QTL having an important effect on preflowering duration in the 'Apex'/'Prisma' population of 94 recombinant inbred lines (RILs) was located on the long arm of chromosome 2H. The other QTL having a large effect was located on chromosome 3H at the same position as the *sdw1* gene from Prisma.

Dragan *et al*. (2007) located two members of the nicotianamine synthase (NAS) family of genes on the short arm of chromosome 2H (2HS). Nicotianamine is involved chelation of iron and other heavy metals and their transport in the plant.

The number of molecular markers located on chromosome 2H has been increased by several studies. Beaubien and Smith (2006) placed 7 of the 60 new mapped SSR markers on 2H at bin positions that previously had been identified as being poorly covered by SSR markers currently available. Stein *et al*. (2007) published an expressed sequence tag (EST)-based map for barley based 200 anchor markers from three previously published maps. The map contained 1,055 loci and a map size of 1,118.3 cM. The map for 2H contained 179 EST loci and a map length of 165.1 cM. Using barley-wheat addition lines and the Barley1 Affymetrix GeneChip probe array, Cho *et al*. (2006) associated 1,787 of 4,104 transcript accumulation patterns detected in Betzes, but not Chinese Spring, with specific barley chromosomes. Of these 271 were associated with the 2H addition line of Chinese Spring.

Takahashi *et al*. (2006) mapped in barley miniature inverted-repeat transposable elements (MITEs), which represent a large superfamily of transposons that is moderately to highly repetitive and frequently found near or within plant genes. To elucidate the organization of MITEs in the barley genome, MITEs were integrated into the genetic map of barley using 93 doubled haploid lines from a Haruna Nijo by *H. vulgare* ssp. *spontaneum* accession OUH602 cross. They described the use of MITEs in amplified fragment length polymorphism (AFLP) mapping and demonstrate their superiority over conventional AFLP mapping. A total of 214 loci covered a total map distance of 1,165 cM, and 39 were placed on 2H.

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Coordinator's Report: Barley Chromosome 3H

L. Ramsay

Genetics Programme
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK.

e-mail: Luke.Ramsay@scri.ac.uk

Over the last year there have been a number of publications reporting the mapping of genes and QTL on barley chromosome 3H. One of the highlights of this reporting period was the genetic mapping of over 1000 genes, including 179 on 3H, by Stein *et al.* (2007). This worked confirmed the syntenic relationship of 3H to rice chromosome 1 and importantly put the detailed EST information underlying this and previous reports in the public domain. This includes the details of which genes are represented by the EST derived microsatellites reported by Varshney *et al.* (2006) that included 35 that map to 3H. Another report of EST derived microsatellites with the associated EST information, including 11 on 3H, was that of Beaubien and Smith (2006).

Another important general mapping paper was the development of a consensus map derived from DArT marker loci (Wenzl *et al*, 2006) that opens up the possibility of using loci derived from this technology as proxies for more expensive genic markers. Also of importance is the detailed consensus map presented by Marcel *et al.* (2007) which brings together standard AFLP, microsatellite and RFLP loci and that will allow additional alignment of past work with the positions of genic loci.

A range of QTL on chromosome 3H were again reported this year. In a RIL population derived from a cross between Azumamugi and Kanto Nakate Gold studied by Sameri *et al.* (2006) QTL were found on 3H for a range of agronomic characters including plant height, spike length and awn length. The position of the QTL found indicates that they are due to the segregation of *uzu* in the population. Li *et al*. (2006) reported the positions of QTL for a range of agronomic traits using recombinant chromosome substation lines derived from a *Hordeum vulgare* subsp. *vulgare* (cltv. Brenda) by *Hordeum vulgare* subsp. *spontaneum* (accession HS584) cross to delineate association with genomic regions. The QTL found on 3H included those for yield and components such as spikelet no. per spike, grain no. per spike, thousand-grain mass as well as other traits such as heading date, plant height, ear length, leaf length and leaf area. A QTL for resistance on 3H was also found to leaf rust in two trials which may relate to the two QTL for leaf rust resistance found on chromosome 3H in a consensus map by Marcel *et al.* (2007) in a summary of work on six mapping populations. One of the populations used in the construction of this consensus map, L94 x Vada, was also tested for mildew and scald resistance and a novel powdery mildew resistance QTL designated Rbgq2 was detected on 3H which did not map to a region where a major gene for powdery mildew has previously been reported (Shtaya *et al.* 2006). Another of the populations included in the report of Marcel *et al.* 2007 was that derived from a cross between an experimental line SusPrit and Vada to study the inheritance of non-host immunity to rusts (Jafary *et al*. 2006). This work found three QTL on 3H associated with host and non-host resistance to *Puccinia* spp. Other disease QTL reported on 3H included the improved resolution of spot blotch resistance QTL on the Calicuchima-sib / Bowman BC population by Bilgic *et al.* (2006) and a scald resistance QTL on the long arm of 3H identified using a partial map of a doubled haploid population derived from a Mundah/Keel cross (Cheong *et al.*, 2006).

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Coordinator's Report: Chromosome 4H

Arnis Druka

Genetics Programme
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK.

e-mail: adruka@scri.sari.ac.uk

Several papers that relate to the genes on chromosome 4H have been published in 2006 - 2007. At least four of them combine mRNA abundance analyses with phenotypic trait genetic analyses clearly showing added value of such approach (Malatrasi *et al.*, 2006; Zhang *et al.*, 2006; Wang *et al*., 2007 and Walia *et al.*, 2007).

The *HvMATE* gene, encoding a multidrug and toxic compound extrusion protein has been identified as a candidate controlling aluminium (Al) tolerance in barley. The gene itself was found not to be polymorphic between Al-tolerant and sensitive cultivars, but it accumulates mRNA 30 times more in the Al tolerant cultivar. *HvMATE* mRNA accumulation was measured in the F(2:3) families and was found significantly correlated with the Al tolerance and Al-activated citrate efflux phenotypes that have been mapped on the long arm of chromosome 4H (Wang *et al.*, 2007).

A different study addressed the salt tolerance in barley by analysing single feature polymorphisms (SFPs) and an oligonucleotide pool assay for single nucleotide polymorphisms (SNPs) in the salt tolerant cultivar Golden Promise and intolerant cultivar Maythorpe. Golden Promise has been generated by inducing mutation in the cultivar Maythorpe. The transcriptome analysis indicates that the response of the two genotypes to the salinity stress is quite different.. This study identified 3 haplotype blocks spanning 6.4 cM on chromosome 1H, 23.7 cM on chromosome 4H and 3.0 cM on 5H suggesting that Golden Promise is not isogenic (Walia *et al*., 2007).

A gene encoding the branched-chain amino acid aminotransferase (*HvBCAT-1*) that mapped on chromosome 4H, was identified by using differential mRNA display applied to ABA, drought and cold treated barley seedling shoots. Transcript levels of *Hvbcat-1* increased in response to drought stress. The complementation of a yeast double knockout strain revealed that *HvBCAT-1* can function as the mitochondrial (catabolic) *BCATs in vivo*. This allowed to put forward the hypothesis, that under drought stress conditions, one of the detoxification mechanisms could be associated with degradation of the branched-chain amino acids (Malatrasi *et al*., 2006).

Zhang *et al*. (2006) have reported a novel locus that is required for *Rpg1* gene mediated resistance to the stem rust (*Puccinia graminis f. sp. tritici*) fungus. It was identified by inducing the irradiation mutations in the resistant barley cultivar and selecting for susceptible individuals in the M2 progeny. *Rpg1* gene in one such susceptible mutant plants was found to be intact and the following mutation mapping identified a locus on chromosome 4H, that was named *Rpr1* (*Required for P. graminis resistance*). Several candidate genes or novel markers for this locus were identified by using large scale parallel transcript profiling approach.

Other papers that related to chromosome 4H were describing either characterization and mapping gene families and the candidate genes for certain QTLs (Brueggeman *et al*., 2006;

Skinner *et al*., 2006) or mapping novel QTLs (Friesen *et al*., 2006; Richardson *et al*., 2006; Yan and Chen 2006; von Korff *et al*., 2006).

Thus, Brueggeman *et al*. (2006) reported mapping of members of the serine/threonine kinase-like protein family that encode at least one predicted catalytically active kinase domain. One of them was localized to chromosome 4H. In a different study, allelic nature and map locations of barley homologs to three classes of Arabidopsis low temperature regulatory genes-*CBFs*, *ICE1*, and *ZAT12* were investigated for associations with the LT tolerance QTLs. In the same study, phenotyping of the Dicktoo x Morex (DxM) mapping population under controlled freezing conditions identified three new low temperature tolerance (LT) QTLs on 1H-L, 4H-S, and 4H-L in addition to the previously reported 5H-L Fr-H1 QTL. (Skinner *et al*., 2006).

Barley interaction with the net blotch fungi, *Pyrenophora teres f. teres* (net-type net blotch (NTNB)) and *Pyrenophora teres f. maculata* (spot-type net blotch (STNB)) was studied using a doubled-haploid population derived from the lines SM89010 and Q21861. Major QTLs for NTNB and STNB resistance were located on chromosomes 6H and 4H, respectively (Friesen *et al*., 2006).

Barley and the stripe rust fungus (*Puccinia striiformis f. sp. hordei*) interaction phenotypes, such as latency period, infection efficiency, lesion size and pustule density were mapped using i-BISON lines (intermediate barley near-isogenic lines). The (i-BISON) lines represented disease resistance QTL combined in one-, two-, and three-way combinations in a susceptible background. The 4H QTL allele had the largest effect followed by the alleles on chromosomes1H and 5H (Richardson *et al*., 2006).

In a different study Yan and Chen (2006) reported population of 182 recombinant inbred lines (RILs) (F8) derived from cultivars Steptoe and GZ that was generated to map the resistance to two barley stripe rust fungus strains on the long arm of barley chromosome 4H.

The BC2DH population derived from a cross between the spring barley cultivar Scarlett and the wild barley accession ISR42-8 (*Hordeum vulgare ssp. spontaneum*) was developed to evaluate nine agronomic traits. Favourable ISR42-8 alleles were detected for the yield-related traits that have QTLs on the long arm of chromosome 4H (von Korff *et al*., 2006).

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Coordinator's Report: Chromosome 5H

George Fedak

Eastern Cereals and Oilseeds Research Centre
Agriculture and Agri-Food Canada
Ottawa ON K1A 0C6

e-mail: fedakga@agr.gc.ca

The grain hardness locus (Ha) of barley consists of a cluster of genes located on the short arm of 5H designated as Hina, Hinb-1, Hinb-2 and GSP. Eighty diverse barley genotypes were screened for kernel hardness, ruminant digestibility and haplotypes of the four alleles. The highest level of genetic variation was obtained with GSP followed by Hina, Hinb-2. Hina was significantly related to grain hardness while Hinb-1 and Hinb-2 were significantly associated with dry water digestibility. (Turuspekov *et al*., 2007).

Using the Nure (winter) x Tremois (spring) mapping population, two low temperature QTL were located on the long arm of chromosome 5H. *FrHi* was located in a distal position and *Fr-H2* in a proximal location. The location of the latter coincided with the location of a QTL regulating the accumulation of two COR proteins; COR14b and TMC-Ap3. Six barley genes for the CBF transcription factor have been mapped in a single cluster in this region and they represent candidate genes for Fr-H2. (Francia *et.al*., 2007)
In a related study, Lombda phage libraries were constructed from 2 spring (Morex and Tremois) and two winter (Dicktos, Nure) cultivars. Clones containing CBF genes were sequenced. It was found that the winter varieties have a large duplication at the *Fr-H2* gene resulting in an increased number of CBF genes at this locus. The spring barley Tremois, however, has a significant deletion at this locus. This suggests that the relative numbers of CBF in the cluster contributes to different levels of winterhardiness (Knox *et.al*.,2007).

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Coordinator's Report: Chromosome 7H

Lynn S. Dahleen

USDA-Agricultural Research Service
Fargo, ND 58105, USA

e-mail: DAHLEEN@fargo.ars.usda.gov

Barley gene mapping in 2006 showed a greater emphasis on using candidate gene approaches in addition to standard qualitative and quantitative trait mapping. Increased use of public EST and BAC libraries was evident, providing tools to better understand the barley genome.

Efforts to map morphological genes have continued. Roder *et al.* (2006) mapped the shrunken endosperm gene *seg8* to a 4.6 cM interval near the centromere of chromosome 7H, while Taketa *et al.* (2006) developed a fine map of the naked caryopsis *nud* locus, placing it in a 0.66 cM region. Rostoks *et al*. (2006) found that the barley homolog of the *Arabidopsis HLM1* gene corresponded to the *nec1* locus on chromosome 7H. Allelic variation was uncovered at the locus that causes necrotic spotting of *nec1* plants. Rossini *et al.* (2006) examined candidate rice genes in regions syntenous with markers linked to various barley morphological mutants. On chromosome 7H they found *brh1* candidate genes on rice chromosome 6 and candidates for *suKF-76, suKE-74* (suppressors of Hooded) and *sld4* on rice chromosomes 6 and 8. The low resolution of the barley maps in this region resulted in selection of rather large rice regions and numerous candidate genes. Yan *et al*. (2006) identified the *AtFT* flowering locus as an ortholog of the barley and wheat vernalization gene *VRN3*. The barley gene *VRN-H3* was located on the short arm of chromosome 7H, not chromosome 1H as previously thought based on loose linkage with *BLP*. Szucs *et al*. (2006) mapped genes for photoreceptor gene families and vernalization regulation, and compared their locations to QTL for photoperiod response. The barley ortholog to a wheat flowering repressor, *HvVRT-2* mapped to the short arm of chromosome 7H. This locus coincided with a photoperiod QTL with small effects mapped in the Dicktoo x Morex population. Tondelli *et al*. (2006), using a similar approach, mapped candidate genes for cold or drought response based on sequences identified in other plants. Two orthologs of *Arabidopsis* genes (*AtFRY1* and *AtICE1*) that have a prominent role in cold acclimation were identified on chromosome 7H.

QTL analyses for a variety of traits were reported this year. Chloupek *et al.* (2006) mapped root system size traits in a population segregating for two semidwarf genes, *sdw1* and *ari-e.GP*. On chromosome 7H, they identified a region associated with height, and another region associated with harvest index, plant weight, root system size at grain filling and total root system size. Advanced backcross QTL analysis continued, with von Korff *et al*. (2006) detecting favorable alleles from wild barley in crosses with Scarlett. Out of the 86 QTL identified for 9 traits, the *H. spontaneum* alleles improved performance for 31. QTL for height, heading date, harvest index, lodging at flowering, vegetative dry biomass, thousand grain weight, brittleness and yield were located on chromosome 7H. Li *et al.* (2006), in a similar study of a wild barley x Brenda advanced backcross, found 100 QTL. Chromosome 7H QTL included yield, heading date, height, ear length, spikelets per spike, seed per spike, spikes per plant, thousand grain weight, leaf length, and leaf area loci. Yun *et al.* (2006) also used advanced backcross lines from a cross of *H. spontaneum* with Harrington to validate QTLs for disease resistance loci. A QTL for spot

blotch resistance previously identified in a RIL population was confirmed to be located on chromosome 7H.

Additional disease resistance genes were located in several studies. Cheong *et al*. (2006) located a QTL for adult plant resistance to leaf scald using two populations. One of these QTL was located on the short arm of chromosome 7H. Rossi *et al.* (2006) located QTL for barley strip rust and leaf rust resistance plus a powdery mildew resistance QTL on chromosome 7H. Jafary *et al*. (2006) located genes involved in nonhost immunity to rust pathogens, including four QTL on chromosome 7H controlling reactions to seven rust species. Brueggeman *et al.* (2006) identified five additional members of the *Rpg1* gene family, including one that is closely linked to *Rpg1* on chromosome 7H.

Kilian *et al*. (2006) examine haplotype structure at seven loci, including the *Adh3* and *Waxy* loci on chromosome 7H, to compare sequence diversity between 20 domesticated and 25 wild barleys. As expected, more haplotypes were identified in the wild barley than the domesticated barley. At *Adh3*, wild barley showed 15 haplotypes while domesticated barley had three and at *Waxy*, the wilds had 17 haplotypes compared to 4 in the domesticated barley. This diversity was also evident in nucleotide sequence, with more polymorphic sites in the wild barley than in the domesticated barley. Pickering *et al.* (2006) examined associations between chromosomes in two *H. vulgare* x *H. bulbosum* hybrids. Chromosome 7HS-7H^{b}S associations were higher than the average for other chromosome arms in both hybrids examined.

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Integrating Molecular and Morphological/Physiological Marker Maps

A. Kleinhofs

Dept. Crop and Soil Sciences and
School of Molecular Biosciences
Washington State University
Pullman, WA 99164-6420, USA

e-mail: andyk@wsu.edu

There has been only limited progress in mapping morphological markers during the past year. However, there is a major effort under way in Europe to map the morphological mutant isolines developed by Jerry Franckowiak (for details see http://www.smallgraincereals.org/SGCNewsletterSummer2007.pdf). This effort, when completed, should provide a map of 1000 morphological markers with accurate reference to molecular markers.

A recessive barley stripe rust resistance gene *rpsGZ* (from Grannenlose Zweizeilige) was mapped to chromosome 4H bin9 (Yan and Chen, 2006). This gene cosegregated with several RGAP markers identified in the publication complete with primer information. It is also closely linked to SSR markers EBmac0679 and EBmac0701.

Septoria speckled leaf blotch resistance genes *Rsp1*, *Rsp2*, and *Rsp3* were mapped (Lee and Neate, 2007a). *Rsp2* cosegregated with MWG938 placing it on chromosome 5(1H) bin2. *Rsp3* was closely linked to *Rsp2* on chromosome 5S(1HS). *Rsp2* was flanked by RAPD markers OPBA12314C and OPB17451R at 2.4 and 3.5 cM, respectively. I was not able to locate these to a specific bin. *Rsp1* was mapped to chromosome 3H short arm flanked by RAPD markers OPC2441R (3.0 cM) and UBC285158R (4.3 cM). In addition closely linked DArT markers were also identified. Specific bin location was not possible. The RAPD markers were converted into sequence tagged markers and primer sequences published (Lee and Neate, 2007b).

Aluminum tolerance gene *Alp* was mapped to chromosome 4H bin7 closely linked to ABG715 and cosegregating with several markers including HvMATE (AV942930) which was proposed as a candidate gene for the *Alp* locus (Wang *et al*., 2007)

Five barley *flowering locus T*-like (*FT*-like) genes were mapped (Faure *et al*., 2007). *HvFT1* maps on chromosome 1(7H) between markers AF022725 and Bmac31 closely linked to *VRN-H3* and ABC158 placing it in bin4. *The VRN-H3* gene was previously believed to be located on chromosome 5(1H), but more recently shown to be on chromosome 1(7H) (Yan *et al*., 2006). *HvFT2* was mapped on chromosome 3H between markers Bmac067 and MWG985 placing it in bin6. *HvHT3* was mapped to chromosome 7(5H) cosegregating with PSR162 placing it in bin11. *HvFT4* was mapped to the short arm of chromosome 2H proximal to cMWG663 placing it in bin6. *HvHT5* was mapped to chromosome 4H long arm cosegregating with scsnp20989. It was not possible for me to determine the bin placement.

The naked caryopsis gene (*nud*) has been previously mapped to chromosome 1(7H) bin 7. It has now been mapped at a high resolution (Taketa *et al*., 2006). The closest SCAR marker SKT9, mapped 0.06 cM from the *nud* locus based on 4,760 gametes from 6 mapping populations.

Barley lipoxygenase (Lox-1) thermostability factor was shown to cosegregate with the structural gene *LoxA* (Hirota *et al*., 2006). The *LoxA* and *LoxC* loci were previously mapped to chromosome 4H bin3 and chromosome 7(5H) probably bin 10 (van Mechelen *et al*., 1999).

Barley homologs of large number of Arabidopsis low temperature regulatory genes were mapped assigning either linkage map or chromosome locations to 1 *ICE1*, 2 *ZAT12* and 17 *CBF* homologs (Skinner *et al*., 2006). Eleven of the CBF genes with assigned linkage map positions formed two tandem clusters on 5HL(7L). These were coincident with reported Triticeae low temperature tolerance and *CO R* gene accumulation QTL and suggest that one or more of the *CBF* genes may be candidates for *Fr-H2* QTL.

Bin Assignments for Morphological Map Markers and closest molecular marker

* - indicates that the gene has been cloned
red - indicates that the gene is very accurately mapped with molecular markers
yellow - indicates that it is fairly accurately mapped with molecular markers
blue - indicates that the gene has been approximately mapped mainly using Bulked Segregant Analysis

Chr.1(7H)

BIN1	ABG704		
	*Rpg1	RSB228	Brueggeman *et al*., PNAS 99:9328, ‘02
	Run1		
	Rdg2a	MWG851A	Bulgarelli *et al*., TAG 108:1401, ‘04
	Rrs2	MWG555A	Schweizer *et al*., TAG 90:920, ‘95
	mlt		
	brh1	MWG2074B	Li et al., 8th IBGS 3:72, ‘00
BIN2	ABG320		
	Est5	iEst5	Kleinhofs *et al*., TAG 86:705, ‘93
	fch12	BCD130	Schmierer *et al*., BGN 31:12, ‘01
	*wax	Wax	Kleinhofs BGN 32:152, ‘02
	gsh3	His3A	Kleinhofs BGN 32:152, ‘02
BIN3	ABC151A		
	fch5	ABC167A	Kleinhofs BGN 32:152, ‘02
	Rcs5	KAJ185	Johnson & Kleinhofs, unpublished
	yvs2		
	cer-ze	ABG380	Kleinhofs BGN 27:105, ‘96
BIN4	ABG380		
	wnd		
	*HvFT1	ABC158	Faure *et al*., Genetics 176:599, '07
	VrnH3	ABC158	Yan *et al*., PNAS 103:19581, '06
	Lga	BE193581	Johnson & Kleinhofs, unpublished
	abo7		

BIN5	ksuA1A		
	ant1		
	nar3	MWG836	Kleinhofs BGN 32:152, ‘02
	ert-m		
	ert-a		
BIN6	ABC255		
	ert-d		
	fch8		
	fst3		
	cer-f		
	msg14		
BIN7	ABG701		
	dsp1	cMWG704	Sameri & Komatsuda JARQ 41:195, '07
	msg10		
	rsm1	ABC455	Edwards & Steffenson, Phytopath. 86:184,’96
	sex6		
	seg5		
	seg2		
	pmr	ABC308	Kleinhofs BGN 27:105, ‘96
	mo6b	Hsp17	Soule *et al*., J Her. 91:483, ‘00
	nud	sKT9	Taketa *et al*., Plant Breeding 125:337, '06
	fch4	MWG003	Kleinhofs BGN 27:105, ‘96
BIN8	*Amy2	Amy2	Kleinhofs *et al*., TAG 86:705, ‘93
	lks2	WG380B	Costa *et al*., TAG 103:415, ‘01
	ubs4		
	blx2		
BIN9	RZ242		
	lbi3		
	Rpt4	Psr117D	Williams *et al*., TAG 99:323, ‘99
	xnt4		
	lpa2	?	Larson *et al*., TAG 97:141, ‘98
	msg50		
	Rym2		
	seg4		
BIN10		ABC310B	
	Xnt1	BF626025	Hansson *et al*., PNAS 96:1744, ‘99
	xnt-h	BF626025	Hansson *et al*., PNAS 96:1744, ‘99
BIN11		ABC305	
	Rph3		
	Tha2		Toojinda *et al*., TAG 101:580, ‘00
BIN12		ABG461A	
	Mlf		
	xnt9		
	seg1		
	msg23		
BIN13		Tha	
	Rph19	Rlch4(Nc)	Park & Karakousis Plt. Breed. 121:232. ‘02

Chr.2(2H)

BIN1	MWG844A		
	sbk		
	brh3	Bmac0134	Dahleen *et al*., J. Heredity 96:654, '05
BIN2	ABG703B		
BIN3	MWG878A	gsh6	Kleinhofs BGN 32:152, '02
	gsh1		
	gsh8		
BIN4	ABG318		
	Eam1		
	Ppd-H1	MWG858	Laurie *et al*., Heredity 72:619, '94
	sld2		
	rtt		
	flo-c		
	sld4		
BIN5	ABG358		
	fch15		
	brc1		
	com2		
BIN6	Pox		
	msg9		
	abo2		
	Rph15	P13M40	Weerasena *et al*., TAG 108:712 '04
	rph16	MWG874	Drescher *et al*., 8thIBGS II:95, '00
BIN7	Bgq60		
	yst4	CDO537	Kleinhofs BGN 32:152, '02
	Az94	CDO537	Kleinhofs BGN 32:152, '02
	gai	MWG2058	Börner *et al*., TAG 99:670, '99
	msg33		
	*HvCslF	(barley Cellulose synthase-like)	Burton *et al*., Science 311:1940 '06
	*Bmy2		
	msg3		
	fch1		
BIN8	ABC468		
	Eam6	ABC167b	Tohno-oka *et al*., 8thIBGS III:239, '00
	gsh5		
	msg2		
	eog	ABC451	Kleinhofs BGN 27:105, '96
	abr		
	cer-n		
BIN9	ABC451		
	Gth		
	hcm1		
	wst4		
	*vrs1	MWG699	Komatsuda *et al*., Genome 42:248, '00
BIN10	MWG865		
	cer-g		
	Lks1		
	mtt4		
	Pre2		

	msg27		
BIN11	MWG503		
	Rha2	AWBMA21	Kretschmer *et al*., TAG 94:1060, ‘97
	Ant2	MWG087	Freialdenhoven *et al*., Plt. Cell 6:983, ’94
	*Rar1	AW983293B	Freialdenhoven *et al*., Plt. Cell 6:983, ’94
	fol-a		
	gal	MWG581A	Börner *et al*., TAG 99:670, ‘99
	fch14		
	Pau		
BIN12	ksuD22		
	Pvc		
BIN13	ABC252		
	lig	BCD266	Pratchett & Laurie Hereditas 120:35, ‘94
	nar4	Gln2	Kleinhofs BGN 27:105, ‘96
	Zeo1	cnx1	Costa *et al*., TAG 103:415, ‘01
	lpa1	ABC157	Larson *et al*., TAG 97:141, ‘98
BIN14	ABC165		
BIN15	MWG844B		
	gpa	CDO036	Kleinhofs BGN 27:105, ‘96
	wst7	MWG949A	Costa *et al*., TAG 103:415, ‘01
	MlLa	Ris16	Giese *et al*., TAG 85:897, ‘93
	trp		

Chr. 3(3H)

BIN1	Rph5	ABG070	Mammadov *et al*., TAG 111:1651, ‘05
	Rph6	BCD907	Zhong et al., Phytopath. 93:604, ‘03
	Rph7	MWG848	Brunner *et al*., TAG 101:783, ‘00
BIN2	JS195F	BI958652; BF631357; BG369659	
	ant17		
	sld5		
	mo7a	ABC171A	Soule et al., J. Hered. 91:483, ‘00
	brh8		
BIN3	ABG321		
	xnt6		
BIN4	MWG798B		
	btr1		Senthil & Komatsuda Euphytica 145:215, ‘05
	btr2		Senthil & Komatsuda Euphytica 145:215, ‘05
	lzd		
	alm	ABG471	Kleinhofs BGNL 27:105, ‘96
BIN5	BCD1532		
	abo9		
	sca		
	yst2		
	dsp10		
BIN6	ABG396		
	Rrs1		Graner *et al*., TAG 93: 421 ´96
	Rh/Pt	ABG396	Smilde *et al*., 8th IBGS 2:178, ‘00
	Rrs.B87	BCD828	Williams *et al*., Plant Breed. 120:301, ‘01

	AtpbB		
	abo6		
	xnt3		
	HvHT2	Bmac067	Faure *et al*., Genetics 176:599, '07
	msg5		
	ari-a		
	yst1		
	zeb1		
	ert-c		
	ert-ii		
	cer-zd		
	Ryd2	WG889B	Collins *et al*., TAG 92:858, '96
	*uzu	AB088206	Saisho *et al*., Breeding Sci. 54:409, '04
BIN7	MWG571B		
	cer-r		
BIN8	ABG377		
	wst6		
	cer-zn		
	sld1		
BIN9	ABG453		
	wst1		
BIN10	CDO345		
	vrs4		
	Int1		
	gsh2		
BIN11	CDO113B		
	als		
	sdw1	PSR170	Laurie *et al*., Plant Breed. 111:198, '93
BIN12	His4B		
	sdw2		
BIN13	ABG004		
	Pub	ABG389	Kleinhofs *et al*., TAG 86:705, '93
BIN14	ABC161		
	cur2		
BIN15	ABC174		
	Rph10		
	fch2		
BIN16	ABC166		
	eam10		
	Est1/2/3		
	*rym4	*eIF4E*	Stein *et al*.,Plt. J. 42:912, '05
	*rym5	*eIF4E*	and Kanyuka *et al*., Mol. Plant Path. 6:449, '05
	Est4		
	ant28		

Chr.4(4H)

BIN1	MWG634		
BIN2	JS103.3		
	fch9		

	sln		
BIN3	Ole1		
	Dwf2		Ivandic *et al*., TAG 98:728, ‘99
	*LoxA	MWG011b	van Mechelen *et al*., Plt. Mol. Biol. 39:1283, '99
	LoxB		van Mechelen *et al*., Plt. Mol. Biol. 39:1283, '99
	Lox-1 thermo		Hirota *et al*., Plant breeding 125:231, '06
	Ynd		
	int-c	MWG2033	Komatsuda, TAG 105:85, ‘02
	Zeo3		
	glo-a		
	rym1	MWG2134	Okada et al., Breeding Sci. 54:319, ‘04
BIN4	BCD402B		
	*Kap	X83518	Müller *et al*., Nature 374:727, ‘95
	lbi2		
	zeb2		
	lgn3		
BIN5	BCD808B		
	lgn4		
	lks5		
	eam9		
	msg24		
BIN6	ABG484		
	glf1		
	rym11	MWG2134	Bauer *et al*., TAG 95:1263, ‘97
	Mlg	MWG032	Kurth *et al*., TAG 102:53, ‘01
	cer-zg		
	brh2		
BIN7	bBE54A		
	glf3		
	Alp	HvMATE	Wang *et al*., TAG 115:265 '07
	frp		
	min1		
	blx4		
	sid		
	blx3		
BIN8	BCD453B		
	blx1		
BIN9	ABG319A		
	ert1		
	rpsGZ	EBmac0679	Yan & Chen, TAG 113:529, '06
BIN10	KFP221		
	*mlo	P93766	Bueschges *et al*., Cell 88:695, ‘97
BIN11	ABG397		
BIN12	ABG319C		
	Hsh	HVM067	Costa *et al*., TAG 103:415, ‘01
	Hln		
	*sgh1(ZCCT-H; HvSnf2)		Zitzewitz *et al*., PMB 59:449, ‘05
	yhd1		
BIN13	*Bmy1	pcbC51	Kleinhofs *et al*., TAG 86:705, ‘93
	rym8	MWG2307	Bauer *et al*., TAG 95:1263, ‘97

	rym9	MWG517	Bauer *et al*., TAG 95:1263, ‘97
	Wsp3		

Chr. 5(1H)

BIN1	Tel5P		
	Rph4		
	Mlra		
	Cer-yy		
	Sex76	Hor2	Netsvetaev BGN 27:51, ‘97
	*Hor5	Hor5	Kleinhofs *et al*., TAG 86:705, ‘93
BIN2	MWG938		
	Rsp2	MWG938	Lee & Neate, Phytopath. 97:155, '07
	*Hor2	Hor2	Kleinhofs *et al*., TAG 86:705, ‘93
	Rrs14	Hor2	Garvin *et al*., Plant Breed. 119:193-196, ‘00
	*Mla6	AJ302292	Halterman *et al*., Plt J. 25:335, ‘01
BIN3	MWG837		
	*Hor1	Hor1	Kleinhofs *et al*., TAG 86:705, ‘93
	Rps4		
	Mlk		
BIN4	ABA004		
	Lys4		
BIN5	BCD098		
	Mlnn;		
	msg31;		
	sls;		
	msg4;		
	fch3;		
BIN6	Ica1		
	amo1		
BIN7	JS074		
	clh		
	vrs3		
	Ror1	ABG452	Collins *et al*., Plt. Phys. 125:1236, ‘01
BIN8	Pcr2		
	fst2		
	cer-zi		
	cer-e		
	ert-b		
	MlGa		
	msg1		
	xnt7		
BIN9	Glb1		
	*nec1	BF630384	Rostoks *et al*., MGG 275:159, '06
BIN10	DAK123B		
	abo1		
	Glb1		
BIN11	PSR330		
	*HvFT3	PSR162	Faure *et al*., Genetics 176:599, '07
	PpdH2	PSR162	Laurie *et al*., Genome 38:575, '95
	wst5		

	cud2		
BIN12	MWG706A		
	rlv		
	lel1		
BIN13	BCD1930		
	Blp	ABC261	Costa *et al*., TAG 103:415, '01
BIN14	ABC261		
	fch7		
	trd		
	eam8		

Chr. 6(6H)

BIN1	ABG062		
	*Nar1	X57845	Kleinhofs *et al*., TAG 86:705, '93
	abo15		
BIN2	ABG378B		
	nar8	ABG378B	Kleinhofs BGN 27:105, '96
	nec3		
	Rrs13		
BIN3	MWG652A		
BIN4	DD1.1C		
	msg36		
BIN5	ABG387B		
	nec2		
	ant21		
	msg6		
	eam7		
BIN6	Ldh1		
	rob	HVM031	Costa *et al*., TAG 103:415, '01
	sex1		
	gsh4		
	ant13		
	cul2	Crg4(KFP128)	Babb & Muehlbauer BGN 31:28, '01
	fch11		
	mtt5		
	abo14		
BIN7	ABG474		
BIN8	ABC170B		
BIN9	*Nar7	X60173	Warner *et al*., Genome 38:743, '95
	*Amy1	JR115	Kleinhofs *et al*., TAG 86:705, '93
	*Nir	pCIB808	Kleinhofs *et al*., TAG 86:705, '93
	mul2		
	cur3		
BIN10	MWG934		
	lax-b		
	raw5		
	cur1		
BIN11	Tef1		
BIN12	xnt5		

	Aat2		
BIN13	Rph11	Acp3	Feuerstein *et al*., Plant breed. 104:318, '90
	lax-c		
BIN14	DAK213C		
	dsp9		

Chr. 7(5H)

BIN1	DAK133		
	abo12		
	msg16		
	ddt		
BIN2	MWG920.1A		
	dex1		
	msg19		
	nld		
	fch6		
	glo-b		
BIN3	cud1	ABG705A	
	lys3		
	fst1		
	blf1		
	vrs2		
BIN4	ABG395		
	cer-zj		
	cer-zp		
	msg18		
	wst2		
	Rph2	ITS1	Borovkova *et al*., Genome 40:236, '97
	lax-a	PSR118	Laurie *et al*., TAG 93:81, '96
	com1		
	ari-e		
	ert-g		
	ert-n		
BIN5	Ltp1		
	rym3	MWG028	Saeki *et al*., TAG 99:727, '99
BIN6	WG530		
BIN7	ABC324		
BIN8	ABC302A		
BIN9	BCD926		
	srh	ksuA1B	Kleinhofs *et al*., TAG 86:705, '93
	cer-i		
	mtt2		
	lys1		
	cer-t		
	dsk		
	var1		
	cer-w		
	Eam5		

BIN10	ABG473		
	raw1		
	msg7		
BIN11	MWG514B		
	Rph9/12	ABG712	Borokova *et al*., Phytopath. 88:76, '98
	*Sgh2 (HvBM5A)		Zitzewitz *et al*., PMB 59:449, '05
	*Ror2	AY246906	Collins *et al*., Nature 425:973, '03
	lbi1		
	Rha4		
	raw2		
BIN12	WG908		
	none		
BIN13	ABG496		
	rpg4	ARD5303	Druka *et al*., unpublished
	RpgQ	ARD5304	Druka *et al*., unpublished
BIN14	ABG390		
	var3		
BIN15	ABG463		

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Coordinator's report: Barley Genetic Stock Collection

A. Hang and K. Satterfield
USDA-ARS, National Small Grains Germplasm Research Facility,
Aberdeen, Idaho 83210, USA

e-mail: anhang@uidaho.edu

In 2006, 655 barley genetic stocks were planted in the field and in the greenhouse for evaluation and for seed increase.

Two mapping populations, including SSD F6 seed OSU 11/Harrington and SSD F6 seed OSU 15/Harrington, derived from single seed descent (SSD) of crosses between *Hordeum vulgare subps. Spontaneum* and cultivar "Harrington" obtained from Dr. Pat Hayes, Oregon State University (OSU), were planted in the field for seed increase.

Four necrotic or lesion mimic mutants obtained from Dr. Anders Falk, Biological Research Center, Sweden, were also grown in the greenhouse for observation and for seed increase.

Three hundred forty-five samples of barley genetic stocks were shipped to researchers in 2006.

Coordinator's report: Trisomic and aneuploid stocks

An Hang

USDA-ARS, National Small Grains Germplasm Research Facility,
Aberdeen, Idaho 83210, USA

e-mail: anhang@uidaho.edu

There is no new information about trisomic and aneuploid stocks. Lists of these stocks are available in BGN 25:104. Seed request for these stocks should be sent to the coordinator.

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Coordinator's report: Translocations and balanced tertiary trisomics

Andreas Houben
Institute of Plant Genetics and Crop Plant Research
DE-06466 Gatersleben, Germany

email: houben@ipk-gatersleben.de

Restructured barley chromosomes have been used by Nasuda et al. (2005) to elucidate the function of centromere-localized DNA sequences. The satellite sequences (AGGGAG)(n) and Ty3/gypsy-like retrotransposons are known to localize at the barley centromeres. Using a gametocidal system, which induces chromosomal mutations in barley chromosomes added to common wheat, the authors obtained an isochromosome for the short arm of barley chromosome 7H (7HS) that lacked the barley-specific satellite sequence (AGGGAG)(n). Two telocentric derivatives of the isochromosome arose in the progeny: 7HS* with and 7HS** without the pericentromeric C-band. FISH analysis demonstrated that both truncated telosomes lacked not only the barley-specific centromeric repeats but also any of the known wheat centromeric tandem repeats. Although they lacked these centromeric repeats, both truncated telochromosomes showed normal mitotic and meiotic transmission. Indirect immunostaining revealed that centromere-specific proteins localized at the centromeric region of 7HS*. The authors conclude that the barley centromeric repeats are neither sufficient nor obligatory to assemble kinetochores, and discussed the possible formation of a novel centromere in a barley chromosome.

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.

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Nasuda, S., Hudakova, S., Schubert, I., Houben, A., and Endo, T.R. 2005. Stable barley chromosomes without centromeric repeats. Proc Natl Acad Sci U S A 102: 9842-9847.

Coordinator's report: Autotetraploids

Wolfgang Friedt

Institute of Crop Science and Plant Breeding I.
Justus-Liebig-University, Heinrich-Buff-Ring 26-32
DE-35392 Giessen, Germany

e-mail: wolfgang.friedt@agrar.uni-giessen.de
Fax: +49(0)641-9937429

The collection of barley autotetraploids (exclusively spring types) described in former issues of BGN is maintained at the Giessen Field Experiment Station of our institute. The set of stocks, i.e. autotetraploids (4n) and corresponding diploid (2n) progenitors (if available) have last been grown in the field for seed multiplication in summer 2000. Limited seed samples of the stocks are available for distribution.

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Coordinator's report: *Eceriferum* Genes

Udda Lundqvist

Nordic Gene Bank
P.O. Box 41, SE-230 53 Alnarp, Sweden

e-mail: udda@nordgen.org

Dahleen and Franckowiak (2006) could localize the *eceriferum*-zt locus on chromosome 2HS based on their molecar linkage studies and found linkage in bin 2H-01 d 16.8 distal from the SSR molecular marker Bmac 0134. Surface wax coating on the spike appears slightly reduced with *eceriferum*-zt. The wax code for this mutant gene is + ++ ++ .

No further research work on gene localization has been reported on these collections of *Eceriferum* and *Glossy* genes. All descriptions in Barley Genetics Newsletter (BGN) Volume 26 are valid and still up-to-date. All Swedish *Eceriferum* alleles can be seen in the SESTO database of the Nordic Gene Bank. Descriptions, images and graphic chromosome map displays of the *Eceriferum* and *Glossy* genes are available in the AceDB database for Barley Genes and Barley Genetic Stocks, and they get currently updated. Its address is found by: www.untamo.net/bgs

As my possibilities in searching literature are very limited, I apologize if I am missing any important papers. Please send me notes of publications and reports to include in next year's reports.

Every research of interest in the field of *Eceriferum* genes, 'Glossy sheath' and 'Glossy leaf' genes can be reported to the coordinator as well. Seed requests regarding the Swedish mutants can be forwarded to the coordinator udda@nordgen.org or to the Nordic Gene Bank, www.nordgen.org/ngb, all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov or to the coordinator at any time.

Reference:

Dahleen, L.S. and J.D. Franckowiak. 2006. SSR linkages to eight additional morphological marker traits. Barley Genetic Newsletter 36:12+16.

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Coordinator's report: Nuclear genes affecting the chloroplast

Mats Hansson

**Department of Biochemistry,
Lund University, Box 124,
SE-22100 Lund, Sweden**

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

Barley nuclear mutants deficient in chlorophyll biosynthesis and chloroplast development are 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.

Although the mutations are generally lethal, the large endosperm of barley seeds supports plant growth for several weeks, allowing analysis of the mutants at a seedling stage. This has been utilized in three studies concerning cold acclimation (Svensson *et al*. 2006), photosystem II (Morosinotto *et al*. 2006) and dominance/recessivity in chlorophyll biosynthesis (Axelsson *et al*. 2006), respectively.

Svensson and collaborators (2006) used the Affymetrix Barley1 GeneChip in combination with *albina-e*.16, *albina-f*.17, *xantha-s*.46 and *xantha-b*.12 to assess the effect of the chloroplast on the expression of cold-regulated genes. About 67% of wild-type cold-regulated genes were not regulated by cold in any mutant (chloroplast-dependent cold-regulated genes).They found that the lack of cold regulation in the mutants is due to the presence of signalling pathway(s) normally cold activated in wild type but constitutively active in the mutants, as well as to the disruption of low-temperature signalling pathway(s) due to the absence of active chloroplasts. They also found that photooxidative stress signalling pathway is constitutively active in the mutants. These results demonstrate the major role of the chloroplast in the control of the molecular adaptation to cold.

The barley mutant *viridis-zb*.63 lacks photosystem I and was employed by Morosinotto *et al*. (2006) to mimic extreme and chronic overexcitation of photosystem II. The mutation was shown to reduce the photosystem II antenna to a minimal size of about 100 chlorophylls per photosystem II reaction centre, which was not further reducible. The minimal photosystem II unit was found to consist of a dimeric photosystem II reaction centre core surrounded by monomeric Lhcb4 (chlorophyll protein 29), Lhcb5 (chlorophyll protein 26) and trimeric light-harvesting complex II antenna proteins. This minimal photosystem II unit forms arrays *in vivo*, possibly to increase the efficiency of energy distribution and provide photoprotection. In wild-type plants, an additional antenna protein, chlorophyll protein 24 (Lhcb6), which is not expressed in *viridis-zb*.63, is proposed to associate to this minimal unit and stabilize larger antenna systems when needed. The analysis of the mutant also revealed the presence of two distinct signalling pathways activated by excess light absorbed by photosystem II: one, dependent on the redox state of the electron transport chain, is involved in the regulation of antenna size, and the second, more directly linked to the level of photoinhibitory stress perceived by the cell, participates in regulating carotenoid biosynthesis.

Axelsson *et al*. (2006) studied the enzyme Mg-chelatase, which catalyzes the insertion of Mg^{2+} into protoporphyrin IX at the first committed step of the chlorophyll biosynthetic pathway. It consists of three subunits; I, D and H. The I-subunit belongs to the AAA-protein superfamily (ATPases associated with various cellular activities) that is known to form hexameric ring structures in an ATP-dependant fashion. Dominant mutations in the *Xantha-h* gene, encoding the I-subunit, revealed that it functions in a cooperative manner. Axelsson *et al*. demonstrated that the D-subunit, encoded by *Xantha-g*, forms ATP-independent oligomeric structures and should also be classified as an AAA-protein. Furthermore, the question of cooperativity of the D-subunit was addressed by characterizing *xantha-g*.28, *-g*.37, *-g*.44, *-g*.45 and *-g*.65 at the molecular level. The recessive behavior *in vivo* was explained by the absence of mutant proteins in the barley cell. The identified mutations were constructed in the corresponding gene of *Rhodobacter capsulatus* and the resulting D-proteins were studied *in vitro*. Mixtures of wild-type and mutant *R. capsulatus* D-subunits showed a lower activity as compared to wild-type subunits assayed alone. Thus, the mutant D-subunits displayed a dominant behavior *in vitro* thus revealing cooperativity between the D-subunits in the oligomeric state. Based on these results, they proposed a model where the D-oligomer forms a platform for the stepwise assembly of the I-subunits. The cooperative behavior suggests that the D-oligomer takes an active part in the conformational dynamics between the subunits of the enzyme.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found elsewhere in this issue of BGN and at

http://www.mps.lu.se/fileadmin/mps/People/Hansson/Barley_mutants_web.pdf

Dr. Mats Hansson
Department of Biochemistry
Lund University
Box 124
SE-22100 Lund, SWEDEN
Phone: +46-46-222 0105
Fax: +46-46-222 4534
E-mail: Mats.Hansson@biochemistry.lu.se

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Coordinator's report: The Genetic Male Sterile Barley Collection

M.C. Therrien

Agriculture and Agri-Food Canada
Brandon Research Centre
Box 1000A, RR#3, Brandon, MB
Canada R7A 5Y3
E-mail: MTherrien@agr.gc.ca

The GMSBC has been at Brandon since 1992. If there are any new sources of male-sterile genes that you are aware of, please advice me, as this would be a good time to add any new source to the collection. For a list of the entries in the collection, simply E-mail me at the above adress. I can send the file (14Mb) in Excel format. We continue to store the collection at -20^{o}C and will have small (5 g) samples available for the asking. Since I have not received any reports or requests the last years, there is absolutely no summary in my report.

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Coordinator's report: Ear morphology genes.

Udda Lundqvist

Nordic Gene Bank
P.O. Box 41 SE-230 53 Alnarp, Sweden

e-mail: udda@nordgen.org

A. Michele Stanca and Valeria Terzi

C.R.A., Genomic Research Centre
Via San Protaso 302
29017-Fiorenzuola d'Arda, Italy

e-mail: michele@stanca.it; v.terzi@iol.it

The studies on barley development in these last years have taken advantages both from genetics and genomics approaches. Some barley genes involved in the ear morphology development have been mapped on high density molecular linkage maps and this strategy has been accompanied by candidate gene approaches (Pozzi *et al*., 2002).
In the work of Pozzi *et al*. (2003) 29 genetic loci for which mutant alleles exist were placed on a restriction fragment length polymorphism- amplified fragment length polymorphism (RFLP-AFLP) map. Among the 29 loci considered in the work, some specifically affect ear morphology and assume characteristics proper to phytomers of other regions (like *third outer glume* and *awned palea*) or are characterized by the presence of modified organs (like *liguleless*, *bracteatum*, *triple awned lemma* and *awned lemma*). In Table 1 the map positions individuated by Pozzi *et al.* (2003) for some loci involved in ear morphology are reported.

Table 1. Position of 12 developmental mutant loci in a Proctor X Nudinka AFLP map (from Pozzi et al, 2003), but revised regarding symbols and nomenclature.

Mutant symbol and name	**Map position**	**Closest marker**
adp1, awned palea1	Chr. 3H/27	E3634-8
als1, absent lower laterals1	Chr 3H/28	E4234-11
bra-d.7, bracteatum-d.7	Chr. 1H	E3634-7
dub.1, double seed.1	Chr 5H/66 and 67	E4038-4
hex-v.3, hexastichon-v.3	Chr. 2H/19-21	E4343-7
hex-v.4, hexastichon-v.4	Chr. 2H/19 and 20	E3438-3
int- c.5, intermedium-c.5	Chr. 4H/8	E4143-5
Kap1, Hooded lemma1	Chr. 4H/36 and 37	E4140-1
lks2, short awn2	Chr. 7H/6	E4138-3
lks5, short awn5	Chr. 4H/38	E4143-5
trp1, triple awned lemma1	Chr. 2H/22 and 23	E3644-13
trd1, third outher glume1	Chr.1H/52	E3634-7

The genetics of barley *Hooded* suppression has been studied by Roig *et al*. (2004). The genetic basis of this phenotype is a mutation in the homeobox *Bkn3*. After chemical mutagenesis and

complementation tests, five *suK* (suppressor of K) loci were identified and mapped on chromosomes 5H and 7H.

Comparative genetic studies across species has revealed syntenous conservation in the order of genes and markers along grass chromosomes. Starting from this observation, Rossini *et al.* (2006) used a synteny approach comparing barley and rice genomes to individuate candidate genes for a set of barley developmental mutants.

The gene *vrs1* (*six-rowed spike 1*) responsible for the six-rowed spike in barley has been recently isolated by means of positional cloning by Komatsuda *et al*. (2007). The wild type *Vrs1* gene, present in two-rowed barley, encodes a transcription factor that includes a homeodomain with a closely linked leucine zipper motif. VRS1 protein suppresses lateral rows and give two-rowed spike, whereas a mutation in the homeodomain-leucine zipper of *Vrs1* resulted into loss of function and development of six-rowed phenotype.

The conservation and implementation of the barley morphological mutant collections is essential for future studies, ranging from the use of computer graphic L-system- models to simulate the final morphology of a plant (Buck-Sorlin *et al.*, 2004) to the use of genomic tools for the elucidation of the gene functions.

Regarding the Swedish mutation collection two new additional mutant loci could be mapped based on molecular mapping studies using simple sequences repeat (SSR) markers (Dahleen *et al*. 2005, Dahleen and Franckowiak. 2006).

(1). The *intermedium spike-k* (*int-k*) gene could be localized in the centromeric region of chromosome 7H, closely linked to Bmag0217 and Bmac0162 in bins 6 to 7. This spike mutant has a short and dense spike and the lateral spikelets are enlarged with a pointed apex. Occasionally they have a short awn. The central spikelets are semi-sterile and there is no seed set in the lateral spikelets. Plants have a dense coating of wax surface. They also have significantly reduced height, peduncle length, awn length, kernels per spike, leaf length, kernel weight and yield.

(2). The *erectoides-t* (*ert-t*) gene, one of the dense spike mutant loci, could be localized near the tip of chromosome 2HS, approximately 11.4 cM distal from SSR marker Bmac0134, near the boundary between bins 2H-01 and 2H-02. The spikes of this mutant gene are semicompact, rachis internode length is about 2.7 mm and culm length is about 2/3 of normal. These phenotypic traits plus short awns are inheritated together. Based on general appearance of the plants, *ert-t* can be placed in the brachytic class and by diallelic crosses three earlier identified Brachytic 3 (*brh3*) phenotypes were found to be allelic at the *ert-t* locus (Franckowiak, 2006).

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Coordinator's report: Semidwarf genes

J.D. Franckowiak

Hermitage Research Station
Queensland Department of Primary Industries and Fisheries
Warwick, Queensland 4370, Australia

e-mail: jerome.franckowiak@dpi.qld.gpv.au

The *sdw1* (*denso*) gene for the semidwarfism in barley was shown to be orthologous to the *sd1* of rice based on similar map positions and linkage of both semidwarf genes to RFLP maker R1545 (Zhang *et al*., 2005). Both genes are sensitive to gibberellic acid (GA) treatments and encode a GA_{20}-oxidase mutant (*HV20ox2*), which produces lower levels of GA and causes the dwarf phenotype. Zhang *et al*. (2005) reported that the barley and rice genes shared 88% sequence similarity and 89% amino acid identity.

Yin *et al*. (2005) confirmed that QTLs that lengthening the preflowering duration in the 'Apex'/'Prisma' population of 94 recombinant inbred lines (RILs) were located in the long arms of chromosome 2H and 3H and originated from Prisma. The QTL on 3HL was associated with presence of the *sdw1* gene from Prisma and likely is a pleiotropic effect of *sdw1* gene.

Korff *et al*. (2006) detected the presence of the *sdw1* gene from 'Scarlett' in doubled-haploid lines from the second backcross of Scarlett to *Hordeum vulgare* ssp. *spontaneum* accession ISR42-8. QTLs for plant height were detected also on other chromosomes by Korff *et al*. (2006).

Gruszka *et al*. (2006) reported that a semidwarf mutant 093AR, which was produced by MNU (N-methyl-N-nitrosourea) treatment of variety Aramir, is allelic to the uzu (*uzu1* on chromosome 3HL) dwarfing gene. Their analysis of the DNA sequence of the *HvBRI1* gene of 093AR showed a single-nucleotide substitution of the C to A substitutions at the positions 1760 and 1761. Gruszka et al. (2006) also confirmed that the *uzu1* mutation was an A to G change at position 2612 of the *HvBRI1* gene. Chono *et al*. (2003) previously reported that the mutation resulted in an amino acid change at the highly conserved residue (His-857 to Arg-857) of the kinase domain of BRI1 (brassinosteroids) receptor protein. This change caused reduced sensitivity to BRs and reduced plant height (Chono *et al*., 2003).

References:

Gruszka, D., J. Zbieszczyk, M. Kwasniewski, I. Szarejko and M. Maluszynski. 2006. A new allele in a *uzu* gene encoding brassinosteroid receptor. Barley Genet. Newsl 36:1-2. author: wintergrun@op.pl

Chono, M., I. Honda, H. Zeniya, K. Yoneyama, D. Saisho, K. Takeda, S. Takatsuto, T. Hoshino and Y. Watanabe. 2003. A semidwarf phenotype of barley uzu results from a nucleotide substitution in the gene encoding a putative brassinosteroid receptor. Plant Physiol. 133:1209-1219.

von Korff, M., H. Wang, J. Léon, and K. Pillen. 2006. AB-QTL analysis in spring barley: II. Detection of favourable exotic alleles for agronomic traits introgressed from wild barley (*H. vulgare* ssp. *spontaneum*). Theor. Appl. Genet. 112:1221-1231.

Yin, X., P.C. Struik, F.A. van Eeuwijk, P. Stam, and J. Tang. 2005. QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley J. Exp. Bot. 56(413):967-976.

Zhang, J., X. Yang, P. Moolhuijzen, C. Li, M. Bellgard, R. Lance, and R. Appels. 2005. Towards isolation of the barley green revolution gene. Australian Barley Technical Symposium 2005. http://www.cdesign.com.au/proceedings_abts2005/posters%20(pdf)/poster_li.pdf. Verified 4 July 2007.

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: rislam@waite.adelaide.edu.com

The production of five different disomic addition lines (1Hm, 2Hm, 4Hm, 5Hm and 7Hm) of *Hordeum marinum* chromosomes to Chinese Spring wheat has been reported earlier. It has now been possible to isolate a monosomic addition for chromosome 6Hm. Amphiploids have also been produced between *H. marinum* and more cultivars of commercial wheat (Islam and Colmer, unpublished).

References:

Islam,S; Malik, AI; Islam, AKMR; Colmer TD. 2007. Salt tolerance in a *Hordeum marinum-Triticum aestivum* amphiploid, and its parents. J Experimental Botany (in Press).

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Coordinator's report: Early maturity genes

Udda Lundqvist

Nordic Gene Bank
P-O. Box 41
SE-23 053 Alnarp, Sweden

e-mail: udda@nordgen.org

Not much new research on gene localization has been reported on the Early maturity or Praematurum genes since the latest reports in Barley Genetic Newsletter (BGN) or in the AceDB database for Barley Genes and Barley Genetic Stocks.

During the last years many reports are published on various QTLs detected in populations derived from wild x cultivated barley crosses with the goal of transferring desirable genes into cultivated barley lines.

Korff *et al*. (2006) transferred favourable genes from wild barley to cultivated barleys and made evaluations in backcrosses of a doubled haploid population. A QTL for Early heading was associated with the Early maturity 1 (*Eam1* or *Ppd-H1*) gene in the bin 3 region of 2HS.

Several QTLs were found in crosses between two- and six-rowed cultivars. One QTL for early heading is reported and found in bin 8 of 2HL and is probably the *Eam6* gene from a six-rowed parent (Franckowiak 2006).

All information and descriptions made in the Barley Genetics Newsletter are valid and up-to-date. As my possibilities in searching literature are very limited, I apologize if I am missing any important papers and reports. I would like to call on the barley community to assist me by sending notes of publications and reports to include in next year's report. Descriptions, images and graphic chromosome map displays of the Early maturity or Praematurum genes are available in the AceDB database for Barley Genes and Barley Genetic Stocks. They get currently updated and are searchable under the address: www.untamo.net/bgs

Every research of interest in the field of Early maturity genes can be reported to the coordinator as well. Seed requests regarding the Swedish mutants can be forwarded to the coordinator or directly to the Nordic Gene Bank, www.nordgen.org/ngb, all others to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov or to the coordinator at any time.

References:

Franckowiak, J.D. 2006. Coordinator's report: Chromosome 2H. Barley Genetics Newsletter 36:54-56.

Korff, M. von, H. Wang, J. Léon, and K. Pilen. 2006. AB-QTL analysis in spring barley: II. Detection of favourable exotic alleles for agronomic traits introgressed from wild barley (*Hordeum vulgare ssp. spontaneum*). Theor. Appl. Genet. 112:1221-1231.

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Descriptions of barley genetic stocks for 2007.

Lynn Dahleen,[1], Jerome D. Franckowiak[2], Udda Lundqvist[3]

[1]USDA-ARS, State University Station, P.O. Box 5677,
Fargo, ND 58105-5051, USA
[2] Hermitage Research Station,
Queensland Department of Primary Industries and Fisheries
Warwick, Queensland 4370, Australia
[3]Nordic Gene Bank
P.O. Box 41, SE-230 53 Alnarp, Sweden

In this volume of the Barley Genetics Newsletter, seventy six new and revised Barley Genetic Stock descriptions are published (Table 1). The current list of new and revised BGS descriptions, including those in Table 1, are again presented by BGS number order (Table 2) and by locus symbol in alphabetic order (Table 3) in this issue. Information on the description location, recommended locus name, chromosomal location, previous gene symbols, and the primary genetic stock (GSHO 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), Aberdeen, Idaho 83210, USA. The NGB stocks are held in the Nordic Gene Bank, P.O. Box 41, SE-230 53 Alnap, 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/**

Table 1. A listing of Barley Genetic Stock (BGS) descriptions published in this issue of the Barley Genetics Newsletter, giving recommended locus symbols and names, and stock location information.

BGS no.	Locus symbol* Rec	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol.p.	GSHO no.‡
1	brh1	br, ari-i	7HS	Brachytic 1	37:188	25
2	fch12	f_c, clo-fc	7HS	Chlorina seedling 12	37:190	36
6	vrs1	v, Int-d	2HL	Six-rowed spike 1	37:192	196
7	nud1	n, h	7HL	Naked caryopsis 1	37:195	115
10	lks2	lk2, lk4	7HL	Short awn 2	37:197	1232
22	Rsg1	Grb	7H	Reaction to *Schizaphis gramineum* 1	37:199	1317
32	Rph9	Pa9	5HL	Reaction to *Puccinia hordei* 9	37:201	1601
41	brh7	brh.w	5HS	Brachytic 7	37:203	1687
44	brh16	brh.v	7HL	Brachytic 16	37:204	1686
60	lig1	li, aur-a	2HL	Liguleless 1	37:205	6
79	wst7	rb	2HL	White streak 7	37:207	247
82	Zeo1	Knd	2HL	Zeocriton 1	37:209	1613
85	yst4	yst4	2HL	Yellow streak 4	37:210	2502
87	fch14	f14	2HL	Chlorina seedling 14	37:211	1739
88	Rph2	Pa_2, A	5HS	Reaction to *Puccinia hordei* 2	37:212	1593
96	Rph15	Rph16	2HS	Reaction to *Puccinia hordei* 15	37:214	1586
98	Eam6	Ea6	2HS	Early maturity 6	37:216	
100	sld4	sld.d	7HS	Slender dwarf 4	37:218	2479
101	als1	als	3HL	Absent lower laterals 1	37:219	1065
102	uzu1	uz, u	3HL	Uzu 1 or semi-brachytic 1	37:220	1300
108	alm1	al, ebu-a	3HS	Albino lemma 1	37:222	270
122	Rph5	Pa5, Rph6	3HS	Reaction to *Puccinia hordei* 5	37:224	1597
130	eam10	ea_{sp}	3HL	Early maturity 10	37:226	2504
136	Rph7	Pa7, Pa_5	3HS	Reaction to *Puccinia hordei* 7	37:228	1318
142	brh8	brh.ad	3HS	Brachytic 8	37:230	1671
148	brh14	brh.q	3HL	Brachytic 14	37:231	1682
149	Rpc1		3H	Reaction to *Puccinia coronata* var *hordei* 1	37:232	1601
155	glf1	gl, cer-zh	4HL	Glossy leaf 1	37:233	98
157	brh2	br2, ari-l	4HL	Brachytic 2	37:235	573
178	int-c	i, v5	4HS	Intermedium spike-c	37:237	776
179	Hsh1	Hs	4HL	Hairy leaf sheath 1	37:240	986
185	brh5	brh.m	4HS	Brachytic 5	37:242	1678
186	sld3	sld.e	4HS	Slender dwarf 3	37:243	2480
187	brh9	brh.k	4HS	Brachytic 9	37:244	1676
203	Blp1	B	1HL	Black lemma and pericarp 1	37:245	988
214	eam8	ea_k, mat-a	1HL	Early maturity 8	37:247	765
222	nec1	sp,,b	1HL	Necrotic leaf spot 1	37:251	989
253	cul2	uc2	6HL	Uniculm 2	37:253	531

Table 1 (continued)

BGS no.	Locus symbol* Rec	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol.p.	GSHO no.‡
254	rob1	o, rob-o	6HS	Orange lemma 1	37:255	707
266	ert-e, dsp9	ert-e	6HL	Erectoides-e	37:257	477
306	var1	va	5HL	Variegated 1	37:259	1278
348	Eam5	Ea5	5HL	Early maturity 5	37:260	
349	brh4	brh.j	2HL	Brachytic 4	37:262	1675
350	brh6	brh.s	5HS	Brachytic 6	37:263	1683
377	seg1	se1	7HL	Shrunken endosperm genetic 1	37:264	750
379	seg3	se3	3HS	Shrunken endosperm genetic 3	37:265	752
380	seg4	se4	7HL	Shrunken endosperm genetic 4	37:267	753
396	seg6	se6	3HL	Shrunken endosperm genetic 6	37:268	2467
397	seg7	se7		Shrunken endosperm genetic 7	37:269	2468
437	cer-zt	cer-zt	2HS	Eceriferum-zt	37:270	1527
449	cer-yf	cer-yf		Eceriferum-yf	37:271	1539
455	seg8	seg8	7H	Shrunken endosperm genetic 8	37:272	2469
474	lax-a	lax-a	5HL	Laxatum-a	37:273	1775
516	Rsp2	Sep_2	1HS	Reaction to *septoria passerinii* 2	37:275	2511
517	Rsp3	Sep_3	1HS	Reaction to *septoria passerinii* 3	37:276	2512
518	sdw1	denso	3HL	Semidwarf 1	37:277	2513
546	int-k	int-k	7H	Intermedium spike-k	37:279	1770
547	int-m	int-m		Intermedium spike-m	37:280	1772
566	ert-t	ert-t, brh3	2HS	Erectoides-t	37:281	494
577	Rsg2	Rsg2		Reaction to *Schizaphis gramineum* 2	37:283	2513
586	bra-d		1HL	Bracteatum-d	37:284	1696
593	adp1	adp	3HL	Awned palea 1	37:285	1950
599	ant17	ant17	3HS	Proanthocyanin-free 17	37:286	
617	cul4	uc-5	3HL	Uniculme 4	37:289	2493
623	eli-a	lig-a		Eligulum-a	37:290	
633	mnd6	den-6	5HL	Many noded dwarf 6	37:291	1713
636	tst2	lin2		Tip sterile 2	37:292	1781
653	brh10	brh.l	2HS	Brachytic 10	37:293	1677
654	brh11	brh.n	5HS	Brachytic 11	37:294	1679
655	brh12	brh.o	5HS	Brachytic 12	37:295	1680
656	brh13	brh.p	5HS	Brachytic 13	37:296	1681
657	brh15	brh.u		Brachytic 15	37:297	1685
658	brh17	brh.ab	5HS	Brachytic 17	37:298	1669
659	brh18	brh.ac	5HS	Brachytic 18	37:299	1670
660	nld2			Narrow leafed dwarf 2	37:300	
661	dub1		5HL	Double seed 1	37:301	

* 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.

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

BGS no.	Locus symbol* Rec.	Prev.	Chr. loc.†	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
1	brh1	br, ari-i	7HS	Brachytic 1	37:188	25
2	fch12	f_c, clo-fc	7HS	Chlorina seedling 12	37:190	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	26: 48	40
6	vrs1	v, Int-d	2HL	Six-rowed spike 1	37:192	196
7	nud1	n, h	7HL	Naked caryopsis 1	37:195	115
9	dsp1	l	7HS	Dense spike 1	26: 53	1232
10	lks2	lk2, lk4	7HL	Short awn 2	37:197	566
11	ubs4	u4, ari-d	7HL	Unbranched style 4	26: 56	567
12	des1	lc	7H	Desynapsis 1	26: 57	592
13	des4	des4	7H	Desynapsis 4	26: 58	595
14	des5	des5	7H	Desynapsis 5	26: 59	596
15	blx1	bl	4HL	Non-blue aleurone xenia 1	26: 60	185
16	wax1	wx, glx	7HS	Waxy endosperm 1	26: 61	908
17	fch4	f4, yv	7HL	Chlorina seedling 4	26: 63	1214
18	fch5	f5, yv2	7HS	Chlorina seedling 5	26: 64	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	7HS	Winding dwarf 1	26: 69	2499
24	fst3	fs3	7HS	Fragile stem 3	26: 70	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	26: 73	536
28	ert-a	ert-a	7HS	Erectoides-a	26: 74	468
29	ert-d	ert-d	7HS	Erectoides-d	26: 76	475
30	ert-m	ert-m	7HS	Erectoides-m	26: 78	487
31	sex6	sex6	7HS	Shrunken endosperm xenia 6	26: 80	2476
32	Rph9	Pa9	5HL	Reaction to *Puccinia hordei* 9	37:201	1601
33	ant1	rs, rub-a	7HS	Anthocyanin-less 1	26: 82	1620
34	msg50	msg,,hm	7HL	Male sterile genetic 50	26: 83	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	7HS	Seminudoides 1	32: 78	1602
39	mss2	mss2	7HS	Midseason stripe 2	32: 79	2409

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
40	prm1	prm	7HS	Premature ripe 1	32: 80	2429
41	brh7	brh.w	5HS	Brachytic 7	37:203	1687
42	Pyr1	Pyr1	7HS	Pyramidatum 1	32: 82	1581
43	mov1	mo5	7HL	Multiovary 1	35:185	
44	brh16	brh.v	7HL	Brachytic 16	37:204	1686
51	rtt1	rt	2HS	Rattail spike 1	26: 87	216
52	fch15	or	2HS	Chlorina seedling 15	26: 88	49
53	abo2	a2	2HS	Albino seedling 2	26: 89	70
55	fch1	f, lg	2HS	Chlorina seedling 1	26: 90	112
56	wst4	wst4	2HL	White streak 4	26: 91	568
57	eog1	e, lep-e	2HL	Elongated outer glume 1	26: 92	29
58	vrs1	lr, v^{lr}	2HL	Six-rowed spike 1	26: 94	153
59	gpa1	gp, gp2	2HL	Grandpa 1	26: 95	1379
60	lig1	li, aur-a	2HL	Liguleless 1	37:205	6
61	trp1	tr	2HL	Triple awned lemma 1	26: 97	210
62	sbk1	sk, cal-a	2HS	Subjacent hood 1	32: 83	267
63	yvs1	y_x, alb-c2	2HS	Virescent seedling 1	26: 99	68
64	des7	des7	2H	Desynapsis 7	26:100	598
65	Eam1	Ea, Ppd-H1	2HS	Early maturity 1	26:101	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	26:105	132
69	Gth 1	G	2HL	Toothed lemma 1	26:106	309
70	Rph1	Pa	2H	Reaction to *Puccinia hordei* 1	26:107	1313
71	com2	bir2	2HS	Compositum 2	26:108	1703
72	glo-c	glo-c	2H	Globosum-c	26:109	1329
73	fol-a	fol-a	2HL	Angustifolium-a	26:110	1744
74	flo-c	flo-c	2HS	Extra floret-c	26:111	1743
75	Lks1	Lk	2HL	Awnless 1	26:112	44
76	Pre2	Re2, P	2HL	Red lemma and pericarp 2	26:113	234
77	hcm1	h	2HL	Short culm 1	26:115	2492
78	mtt4	mt,,e, mt	2HL	Mottled leaf 4	26:116	1231
79	wst7	rb	2HL	White streak 7	37:207	247
80	ant2	pr, rub	2HL	Anthocyanin-less 2	26:118	1632
81	gsh7	gs7		Glossy sheath 7	26:119	1759
82	Zeo1	Knd	2HL	Zeocriton 1	37:209	1613
83	sld2	sld2	2HS	Slender dwarf 2	26:121	2491
84	mss1	mss	2H	Midseason stripe 1	26:122	1404
85	yst4	yst4	2HL	Yellow streak 4	37:210	2502
86	fch13	f13		Chlorina seedling 13	26:124	16

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
87	fch14	f14	2HL	Chlorina seedling 14	37:211	1739
88	Rph2	Pa2, A	5HS	Reaction to *Puccinia hordei* 2	37:212	1593
89	ari-g	ari-g, lk10		Breviaristatum-g	26:128	1655
90	ert-j	ert-j	2H	Erectoides-j	26:129	484
91	ert-q	ert-q	2H	Erectoides-q	26:130	1562
92	ert-u	ert-u, br5	2H	Erectoides-u	26:131	496
93	ert-zd	ert-zd, br7	2H	Erectoides-zd	26:132	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	32: 85	1617
98	Eam6	Ea6, Ea	2HS	Early maturity 6	37:216	
99	lin1	s, rin	2HL	Lesser internode number 1	32: 88	2492
100	sld4	sld.d	7HS	Slender dwarf 4	37:218	2479
101	als1	als	3HL	Absent lower laterals 1	37:219	1065
102	uzu1	uz, u	3HL	Uzu 1 or semi brachytic 1	37:220	1300
104	yst1	yst, ys	3HS	Yellow streak 1	26:138	1140
105	xnt3	x_c, vir-l	3HS	Xantha seedling 3	26:139	66
106	abo6	a_c	3HS	Albino seedling 6	26:140	30
107	wst1	wst, wst3	3HL	White streak 1	26:141	159
108	alm1	al, ebu-a	3HS	Albino lemma 1	37:222	270
109	yst2	yst2	3HS	Yellow streak 2	26:144	570
111	dsp10	l_c	3HS	Dense spike 10	26:145	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	26:148	274
115	btr1	bt1	3HS	Non-brittle rachis 1	26:149	1233
116	btr2	bt2	3HS	Non-brittle rachis 2	26:150	842
117	fch2	f2, lg5	3HL	Chlorina seedling 2	26:151	107
118	lnt1	rnt, int-l	3HL	Low number of tillers 1	26:153	833
119	des2	ds	3H	Desynapsis 2	26:154	593
120	zeb1	zb	3HL	Zebra stripe 1	26:155	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	26:159	775
125	lzd1	lzd, dw4	3HS	Lazy dwarf 1	26:161	1787
126	sld1	dw1	3HL	Slender dwarf 1	26:162	2488
127	Pub1	Pub	3HL	Pubescent leaf blade 1	26:163	1576
128	sca1	sca	3HS	Short crooked awn 1	26:164	2439

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
129	wst6	wst,,j	3HL	White streak 6	26:165	2500
130	eam10	ea_{sp}	3HL	Early maturity 10	37:226	2504
131	gra-a	gran-a	3HL	Granum-a	26:167	1757
132	ari-a	ari-a	3HS	Breviaristatum-a	26:168	1648
133	sdw2	sdw-b	3HL	Semidwarf 2	26:169	2466
134	ert-c	ert-c	3HL	Erectoides-c	26:170	471
135	ert-ii	ert-ii	3HL	Erectoides-ii	26:172	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	26:175	
139	nec5	nec5	3H	Necrotic leaf spot 5	26:176	
140	xnt8	xan,,h	3HS	Xantha seedling 8	26:177	582
141	rym5	Ym	3HL	Reaction to Barley yellow mosaic virus 5	32: 90	
142	brh8	brh.ad	3HS	Brachytic 8	37:230	1671
143	sex8	sex.j	3HS	Shrunken endosperm 8	32: 93	2471
144	sld5	sld5	3HS	Slender dwarf 5	32: 94	2483
146	cal-d	cal-d	3H	Calcaroides-d	32: 95	1697
147	mov2	mo	3HS	Multiovary 2	35:190	
148	brh14	brh.q	3HL	Brachytic 14	37:231	1682
149	Rpc1		3H	Reaction to Puccinia *coronata* var. *hordei* 1	37:232	1601
151	fch9	f9	4HS	Chlorina seedling 9	26:178	571
152	Kap1	K	4HS	Hooded lemma 1	26:179	985
155	glf1	gl, cer-zh	4HL	Glossy leaf 1	37:233	98
156	lbi2	lb2, ert-i	4HL	Long basal rachis internode 2	26:183	572
157	brh2	br2, ari-l	4HL	Brachytic 2	37:235	573
158	yhd1	yh	4HL	Yellow head 1	26:185	574
160	min2	en-min		Enhancer of minute 1	26:186	266
161	min1	min	4HL	Semi-minute dwarf 1	26:187	987
163	sgh1	sh1	4HL	Spring growth habit 1	26:188	575
164	Hln1	Hn	4HL	Hairs on lemma nerves 1	26:189	576
165	glf3	gl3, cer-j	4HL	Glossy leaf 3	26:190	577
166	msg25	msg,,r	4HL	Male sterile genetic 25	26:192	744
167	rym1	Ym	4HL	Reaction to barley yellow mosaic virus 1	32: 96	
168	glo-a	glo-a	4HS	Globosum-a	26:194	1328
170	lgn3	lg3	4HL	Light green 3	26:195	171
171	lgn4	lg4, lg9	4HL	Light green 4	26:196	681
172	lks5	lk5, ari-c	4HL	Short awn 5	26:197	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	

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
178	int-c	i, v5	4HS	Intermedium spike-c	37:237	776
179	Hsh1	Hs	4HL	Hairy leaf sheath 1	37:240	986
180	sid1	nls	4HL	Single internode dwarf 1	26:203	2477
181	eam9	ea,,c	4HL	Early maturity 9	26:204	1732
182	flo-a	flo-a		Extra floret-a	26:205	1741
183	Ynd1	Yn	4HS	Yellow node 1	32:98	
184	Zeo3	Zeo.h	4HL	Zeocriton 3	32:99	1611
185	brh5	brh.m	4HS	Brachytic 5	37:242	1678
186	sld3	ant17.567	4HS	Slender dwarf 3	37:243	2480
187	brh9	brh.k	4HS	Brachytic 9	37:244	1676
201	fch7	f7	1HL	Chlorina seedling 7	26:206	4
202	trd1	t, bra-c	1HL	Third outer glume 1	26:207	227
203	Blp1	B	1HL	Black lemma and pericarp 1	37:245	988
207	abo1	a_t	1HL	Albino seedling 1	26:210	51
208	fst2	fs2	1HL	Fragile stem 2	26:211	578
213	Sgh3	Sh3	1HL	Spring growth habit 3	26:212	764
214	eam8	ea_k, mat-a	1HL	Early maturity 8	37:247	765
215	des6	des6	1H	Desynapsis 6	26:216	597
218	Rph4	Pa4	1HS	Reaction to *Puccinia hordei* 4	26:217	1314
220	fch3	f3	1HS	Chlorina seedling 3	26:218	851
221	wst5	wst5	1HL	White streak 5	26:219	591
222	nec1	sp,,b	1HL	Necrotic leaf spot 1	37:251	989
223	zeb3	zb3, zb_c	1HL	Zebra stripe 3	26:221	1451
224	ert-b	ert-b	1HL	Erectoides-b	26:222	470
225	clh1	clh	1HL	Curled leaf dwarf 1	26:223	1212
226	rvl1	rvl	1HL	Revoluted leaf 1	26:224	608
227	sls1	sls	1HS	Small lateral spikelet 1	26:225	2492
228	Sil1	Sil	1HS	Subcrown internode length 1	26:226	1604
229	cud2	cud2	1HL	Curly dwarf 2	26:227	1712
230	glo-e	glo-e	1HL	Globosum-e	26:228	1755
231	cur5	cu5	1HS	Curly 5	26:229	1710
232	Lys4	sex5	1HS	High lysine 4	26:230	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
251	mul2	mul2	6HL	Multiflorus 2	26:232	1394
252	eam7	ea7, ec	6HS	Early maturity 7	26:233	579
253	cul2	uc2	6HL	Uniculm 2	37:253	531
254	rob1	o, rob-o	6HS	Orange lemma 1	37:255	707
255	xnt5	x_n	6HL	Xantha seedling 5	26:237	43

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
257	raw5	r,,e	6HL	Smooth awn 5	26:238	785
258	dsp9	l9, ert-e	6HL	Dense spike 9	26:239	1774
260	fch11	f11	6HL	Chlorina seedling 11	26:240	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	26:243	1707
264	mtt5	mt,,f	6HL	Mottled leaf 5	26:244	2410
265	nec3	nec3	6HS	Necrotic leaf spot 3	26:245	1330
266	ert-e	ert-e, dsp9	6HL	Erectoides-e	37:257	477
267	Rph11	Rph11	6HL	Reaction to *Puccinia hordei* 11	26:247	1589
268	lax-b	lax-b	6HL	Laxatum-b	26:248	1776
269	lys6	lys6	6H	High lysine 6	26:249	1786
270	abo14	alb,,q	6HL	Albino seedling 14	26:250	586
271	abo15	alb,,t	6HS	Albino seedling 15	26:251	
301	fst1	fs	5HL	Fragile stem 1	26:252	629
302	mtt2	mt2	5HL	Mottled leaf 2	26:253	1398
303	var3	va3	5HL	Variegated 3	26:254	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	26:258	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	26:262	1390
314	vrs2	v2	5HL	Six-rowed spike 2	26:263	773
315	vrs3	v3, int-a	1HL	Six-rowed spike 3	26:264	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	26:268	1764
321	srh1	s, l	5HL	Short rachilla hair 1	26:269	27
322	dsk1	dsk	5HL	Dusky 1	26:270	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		Curly lateral 1	26:273	1211
326	blf1	bb	5HL	Broad leaf 1	26:274	1393
327	flo-b	flo-b	5HL	Extra floret-b	26:275	1742
328	ari-e	ari-e	5HL	Breviaristatum-e	26:276	1653
329	ari-h	ari-h	5HL	Breviaristatum-h	26:277	1656
330	ert-g	ert-g, br3	5HL	Erectoides-g	26:278	479

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
331	ert-n	ert-n	5HL	Erectoides-n	26:279	488
332	Ert-r	Ert-r		Erectoides-r	26:280	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	26:283	2402
336	glo-b	glo-b	5HL	Globosum-b	26:284	1326
337	blf2	bb2, nlh	5HL	Broad leaf 2	26:285	1667
338	lys1	lys	5HL	High lysine 1	26:286	1784
339	lys3	sex3	5HL	High lysine 3	26:287	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	28: 30	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	5HL	Yellow streak 5	32:107	2501
347	mnd4	m4	5HL	Many noded dwarf 4	32:108	1798
348	Eam5	Ea5	5HL	Early maturity 5	37:260	
349	brh4	brh.j	2HL	Brachytic 4	37:262	1675
350	brh6	brh.s	5HS	Brachytic 6	37:263	1683
351	gsh1	gs1, cer-q	2HS	Glossy sheath 1	26:292	735
352	gsh2	gs2, cer-b	3HL	Glossy sheath 2	26:294	736
353	gsh3	gs3, cer-a	7HS	Glossy sheath 3	26:296	737
354	gsh4	gs4, cer-x	6HL	Glossy sheath 4	26:298	738
355	gsh5	gs5, cer-s	2HL	Glossy sheath 5	26:300	739
356	gsh6	gs6, cer-c	2HS	Glossy sheath 6	26:302	740
357	msg1	ms1	1HL	Male sterile genetic 1	26:304	1810
358	msg2	ms2	2HL	Male sterile genetic 2	26:306	2371
359	msg3	ms3	2HS	Male sterile genetic 3	26:307	1130
360	msg4	ms4	1H	Male sterile genetic 4	26:308	2392
361	msg5	ms5	3HS	Male sterile genetic 5	26:309	2403
362	msg6	ms6	6HS	Male sterile genetic 6	26:310	2405
363	msg7	ms7	5HL	Male sterile genetic 7	26:311	2406
364	msg8	ms8	5HL	Male sterile genetic 8	26:312	2407
365	msg9	ms9	2HS	Male sterile genetic 9	26:313	2408
366	msg10	ms10	7HS	Male sterile genetic 10	26:314	1811
367	msg11	ms11		Male sterile genetic 11	26:315	1812
368	msg13	ms13		Male sterile genetic 13	26:316	1813
369	msg14	ms14	7HS	Male sterile genetic 14	26:317	1814
370	msg15	ms15		Male sterile genetic 15	26:318	1815

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
371	msg16	ms16	5HS	Male sterile genetic 16	26:319	1816
372	msg17	ms17		Male sterile genetic 17	26:320	1817
373	msg18	ms18	5HL	Male sterile genetic 18	26:321	1818
374	msg19	ms19	5HS	Male sterile genetic 19	26:322	1819
375	msg20	ms20	1H	Male sterile genetic 20	26:323	2372
376	msg21	ms21		Male sterile genetic 21	26:324	2373
377	seg1	se1	7HL	Shrunken endosperm genetic 1	37:264	750
378	seg2	se2	7HS	Shrunken endosperm genetic 2	26:326	751
379	seg3	se3	3H	Shrunken endosperm genetic 3	37:265	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	26:331	741
384	msg23	ms23	7HL	Male sterile genetic 23	26:332	2375
385	msg24	ms24	4HL	Male sterile genetic 24	26:333	2376
386	des3	des3		Desynapsis 3	26:334	594
387	des8	des8		Desynapsis 8	26:335	599
388	des9	des9		Desynapsis 9	26:336	600
389	des10	des10		Desynapsis 10	26:337	601
390	des11	des11		Desynapsis 11	26:338	602
391	des12	des12		Desynapsis 12	26:339	603
392	des13	des13		Desynapsis 13	26:340	604
393	des14	des14		Desynapsis 14	26:341	605
394	des15	des15		Desynapsis 15	26:342	606
395	msg26	msg,,u	7HS	Male sterile genetic 26	26:343	745
396	seg6	se6	3HL	Shrunken endosperm genetic 6	37:268	2467
397	seg7	se7		Shrunken endosperm genetic 7	37:269	2468
399	cer-d	cer-d		Eceriferum-d	26:346	425
400	cer-e	cer-e	1HL	Eceriferum-e	26:347	1518
401	cer-f	cer-f	7HS	Eceriferum-f	26:348	427
402	cer-g	cer-g	2HL	Eceriferum-g	26:349	428
403	cer-h	cer-h		Eceriferum-h	26:351	429
404	cer-i	cer-i	5HL	Eceriferum-i	26:352	430
405	cer-k	cer-k	7HS	Eceriferum-k	26:354	432
406	cer-l	cer-l		Eceriferum-l	26:355	433
407	cer-m	cer-m		Eceriferum-m	26:356	434
408	cer-n	gs9	2HL	Eceriferum-n	26:357	435
409	cer-o	cer-o		Eceriferum-o	26:359	436
410	cer-p	cer-p		Eceriferum-p	26:360	437
411	cer-r	cer-r	3HL	Eceriferum-r	26:361	439

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. † loc.	Locus name or phenotype	Descr. vol. p.	GSHO no. ‡
412	cer-t	cer-t	5HL	Eceriferum-t	26:362	441
413	gsh8	cer-u, gs8	2HS	Glossy sheath 8	26:364	442
414	cer-v	cer-v	2HS	Eceriferum-v	26:366	443
415	cer-w	cer-w	5HL	Eceriferum-w	26:367	1519
417	cer-y	cer-y		Eceriferum-y	26:368	446
418	cer-z	cer-z	7HS	Eceriferum-z	26:369	447
419	cer-za	cer-za	5HL	Eceriferum-za	26:370	1521
420	cer-zb	cer-zb		Eceriferum-zb	26:371	1522
421	cer-zc	cer-zc		Eceriferum-zc	26:372	450
422	cer-zd	cer-zd	3HL	Eceriferum-zd	26:373	451
423	cer-ze	gl5	7HS	Eceriferum-ze	26:374	452
424	cer-zf	cer-zf		Eceriferum-zf	26:376	453
425	cer-zg	cer-zg	4HL	Eceriferum-zg	26:377	454
427	cer-zi	cer-zi	1HL	Eceriferum-zi	26:378	456
428	cer-zj	cer-zj	5HL	Eceriferum-zj	26:379	457
429	cer-zk	cer-zk	2H	Eceriferum-zk	26:381	458
430	cer-zl	cer-zl		Eceriferum-zl	26:382	459
431	cer-zn	cer-zn	3HL	Eceriferum-zn	26:383	1523
432	cer-zo	cer-zo		Eceriferum-zo	26:384	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		Eceriferum-zr	26:387	1525
436	cer-zs	cer-zs		Eceriferum-zs	26:388	1526
437	cer-zt	cer-zt	2HS	Eceriferum-zt	37:270	1527
438	cer-zu	cer-zu		Eceriferum-zu	26:390	1528
439	cer-zv	cer-zv		Eceriferum-zv	26:391	1529
440	cer-zw	cer-zw		Eceriferum-zw	26:392	1530
441	cer-zx	cer-zx		Eceriferum-zx	26:393	1531
442	cer-zy	cer-zy		Eceriferum-zy	26:394	1532
443	cer-zz	cer-zz		Eceriferum-zz	26:395	1533
444	cer-ya	cer-ya	3HS	Eceriferum-ya	26:396	1534
445	cer-yb	cer-yb	2HL	Eceriferum-yb	26:397	1535
446	cer-yc	cer-yc		Eceriferum-yc	26:398	1536
447	cer-yd	cer-yd	3HS	Eceriferum-yd	26:399	1537
448	cer-ye	cer-ye	5HL	Eceriferum-ye	26:400	1538
449	cer-yf	cer-yf		Eceriferum-yf	37:271	1539
450	cer-yg	cer-yg	7HS	Eceriferum-yg	26:402	1540
451	cer-yh	cer-yh	3HS	Eceriferum-yh	26:403	1541
454	blx5	bl5	7HL	Non-blue aleurone xenia 5	26:404	2509
455	seg8	seg8	7H	Shrunken endosperm genetic 8	37:272	2469

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
460	cur4	cu4, glo-d	2HL	Curly 4	26:406	1708
461	zeb2	zb2, f10	4HL	Zebra stripe 2	26:407	93
462	yst3	yst,,c	3HS	Yellow streak 3	26:409	48
463	gig1	gig, sf	2H?	Gigas 1	26:410	1650
464	msg27	msg,,ae	2HL	Male sterile genetic 27	26:411	2379
465	msg28	msg,,as	6H	Male sterile genetic 28	26:412	2380
466	msg29	msg,,a	5HL	Male sterile genetic 29	26:413	2381
467	msg30	msg,,c	7HL	Male sterile genetic 30	26:414	2382
468	msg31	msg,,d	1HS	Male sterile genetic 31	26:415	2383
469	msg32	msg,,w	7H	Male sterile genetic 32	26:416	2384
470	msg33	msg,,x	2HS	Male sterile genetic 33	26:417	2385
471	msg34	msg,,av	6H	Male sterile genetic 34	26:418	2386
472	abr1	abr	2HL	Accordion basal rachis internode 1	26:419	1563
473	com1	bir1	5HL	Compositum 1	26:420	1702
474	lax-a	lax-a	5HL	Laxatum-a	37:273	1775
475	lax-c	lax-c	6HL	Laxatum-c	26:423	1777
498	msg35	msg,,dr	2HL	Male sterile genetic 35	26:424	2387
499	msg36	msg,,bk	6HS	Male sterile genetic 36	26:425	2388
500	msg37	msg,,hl		Male sterile genetic 37	26:426	2389
501	msg38	msg,,jl		Male sterile genetic 38	26:427	2390
502	msg39	msg,,dm	6H	Male sterile genetic 39	26:428	2391
503	msg40	msg,,ac	6H	Male sterile genetic 40	26:429	2393
504	msg41	msg,,aj		Male sterile genetic 41	26:430	2394
505	msg42	msg,,db	3H	Male sterile genetic 42	26:431	2395
506	msg43	msg,,br		Male sterile genetic 43	26:432	2396
507	msg44	msg,,cx		Male sterile genetic 44	26:433	2397
508	msg45	msg,,dp		Male sterile genetic 45	26:434	2398
509	msg46	msg,,ec		Male sterile genetic 46	26:435	2399
510	msg47	msg,,ep		Male sterile genetic 47	26:436	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	Sep_2		Reaction to *Septoria passerinii* 2	37:275	2511
517	Rsp3	Sep_3		Reaction to *Septoria passerinii* 3	37:276	2512
518	sdw1	denso	3HL	Semidwarf 1	37:277	2513
519	mnd1	m		Many-noded dwarf 1	26:446	253
520	msg48	msg,,jt	2H	Male sterile genetic 48	26:447	2401
521	mtt1	mt	1HS	Mottled leaf 1	26:448	622
522	cer-yi	cer-yi		Eceriferum-yi	26:449	1542

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. † loc.	Locus name or phenotype	Descr. vol. p.	GSHO no. ‡
523	cer-yj	cer-yj		Eceriferum-yj	26:450	1543
524	cer-yk	cer-yk		Eceriferum-yk	26:451	1544
525	cer-yl	cer-yl		Eceriferum-yl	26:452	1545
526	cer-ym	cer-ym		Eceriferum-ym	26:453	1546
527	cer-yn	cer-yn		Eceriferum-yn	26:454	1547
528	cer-yo	cer-yo		Eceriferum-yo	26:455	1548
529	cer-yp	cer-yp		Eceriferum-yp	26:456	1549
530	cer-yq	cer-yq		Eceriferum-yq	26:457	1550
531	cer-yr	cer-yr		Eceriferum-yr	26:458	1551
532	cer-ys	cer-ys		Eceriferum-ys	26:459	1552
533	cer-yt	cer-yt		Eceriferum-yt	26:460	1553
534	cer-yu	cer-yu		Eceriferum-yu	26:461	1554
535	cer-yx	cer-yx		Eceriferum-yx	26:462	1555
536	Cer-yy	Gle1	1HS	Eceriferum-yy	26:463	1556
537	cer-yz	cer-yz		Eceriferum-yz	26:464	1557
538	cer-xa	cer-xa		Eceriferum-xa	26:465	1558
539	cer-xb	cer-xb		Eceriferum-xb	26:466	1559
540	cer-xc	cer-xc		Eceriferum-xc	26:467	1560
541	cer-xd	cer-xd		Eceriferum-xd	26:468	1561
542	Dwf2	Dwf2		Dominant dwarf 2	24:170	
543	int-f	int-f		Intermedium spike-f	26:469	1767
544	int-h	int-h		Intermedium spike-h	26:470	1768
545	int-i	int-i		Intermedium spike-i	26:471	1769
546	int-k	int-k	7H	Intermedium spike-k	37:279	1770
547	int-m	int-m		Intermedium spike-m	37:280	1772
548	Fol-b	Ang		Angustifolium-b	26:474	17
549	Lga1	Log		Long glume awn 1	26:475	835
550	ari-b	ari-b		Breviaristatum-b	26:476	1649
551	ari-f	ari-f		Breviaristatum-f	26:477	1654
552	ari-j	ari-j		Breviaristatum-j	26:478	1658
553	ari-k	ari-k		Breviaristatum-k	26:479	1659
554	ari-m	ari-m		Breviaristatum-m	26:480	1661
555	ari-n	ari-n		Breviaristatum-n	26:481	1662
556	ari-o	ari-o		Breviaristatum-o	26:482	
557	ari-p	ari-p		Breviaristatum-p	26:483	1664
558	ari-q	ari-q		Breviaristatum-q	26:484	1665
559	ari-r	ari-r		Breviaristatum-r	26:485	1666
560	ert-f	ert-f		Erectoides-f	26:486	478
561	ert-h	ert-h		Erectoides-h	26:487	481
562	ert-k	ert-k		Erectoides-k	26:488	485

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr. † loc.	Locus name or phenotype	Descr. vol. p.	GSHO no. ‡
563	ert-l	ert-l		Erectoides-l	26:489	486
564	ert-p	ert-p		Erectoides-p	26:490	490
565	ert-s	ert-s		Erectoides-s	26:491	493
566	ert-t	ert-t, brh3	2HS	Erectoides-t	37:281	494
567	ert-v	ert-v		Erectoides-v	26:493	497
568	ert-x	ert-x		Erectoides-x	26:494	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		Erectoides-za	26:497	501
572	ert-zb	ert-zb		Erectoides-zb	26:498	502
573	ert-zc	ert-zc		Erectoides-zc	26:499	503
574	ert-ze	ert-ze		Erectoides-ze	26:500	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	26:504	1788
579	mat-c	mat-c		Praematurum-c	26:506	1789
580	mat-d	mat-d		Praematurum-d	26:507	1790
581	mat-e	mat-e		Praematurum-e	26:508	1791
582	mat-f	mat-f		Praematurum-f	26:509	1792
583	mat-g	mat-g		Praematurum-g	26:510	1793
584	mat-h	mat-h		Praematurum-h	26:511	1794
585	mat-i	mat-i		Praematurum-i	26:512	1795
586	bra-d	bra-d	1HL	Bracteatum-d	37:284	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	28: 33	757
593	adp1	adp		Awned palea 1	37:285	1618
594	ant3	rub		Anthocyanin-deficient 3	29: 82	1641
595	ant4	ant4		Anthocyanin-deficient 4	29: 83	1642
596	ant5	rs2		Anthocyanin-deficient 5	29: 84	1643
597	ant6	ant6		Anthocyanin-deficient 6	29: 85	1644
598	ant13	ant13	6HL	Proanthocyanin-free 13	29: 86	1624
599	ant17	ant17	3HS	Proanthocyanin-free 17	37:286	
600	ant18	ant18	7HL	Proanthocyanin-free 18	29: 90	1630
601	ant19	ant19		Proanthocyanin-free 19	29: 92	1631
602	ant20	ant20		Anthocyanin-rich 20	29: 93	1633

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
603	ant21	ant21	6H	Proanthocyanin-free 21	29: 94	1634
604	ant22	ant22	7HL	Proanthocyanin-free 22	29: 95	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		Necrotic leaf spot 6	32:112	2424
612	gig2	gig2		Gigas 2	32:113	1750
613	brc1	brc-5	2HS	Branched 1	32:114	
614	Zeo2	Zeo2		Zeocriton 2	32:115	637
615	wxs1	wxs1		Waxy spike 1	32:116	
616	cul3	cul3		Uniculme 3	32:117	2494
617	cul4	uc-5	3HL	Uniculme 4	37:289	2493
618	mnd3	mn3, m3	3H	Many noded dwarf 3	32:119	1797
619	bra-a	bra-a	7HS	Bracteatum-a	32:120	1693
620	cal-b	cal-b	5H	Calcaroides-b	32:121	1697
621	Cal-c	Cal-c	5HL	Calcaroides-c	32:122	1567
622	cal-e	cal-23	5HS	Calcaroides-e	32:123	
623	eli-a	lig-a		Eligulum-a	37:290	
624	ops1	op-3		Opposite spikelets 1	32:125	2427
625	sci-a	sci-3		Scirpoides 1	32:126	
626	scl-a	scl-6		Scirpoides leaf-a	32:127	
627	viv-a	viv-5		Viviparoides-a	32:128	2498
628	sex7	sex.i	5HL	Shrunken endosperm 7	32:129	2470
629	mtt6	mtt6		Mottled leaf 6	32:130	2411
630	Ari-s	ari-265		Breviaristatum-s	32:131	
631	brh3	brh.g, ert-t		Brachytic 3	32:132	1672
632	mnd5	mnd5		Many noded dwarf 5	32:133	
633	mnd6	den-6	5HL	Many noded dwarf 6	37:291	1713
634	pmr2	nec-50		Premature ripe 2	32:135	2421
635	nec7	nec-45		Necroticans 7	32:136	2420
636	tst2	lin2		Tip sterile 2	37:292	1781
637	nar1	nar1	6HS	NADH nitrate reductase-deficient 1	35:194	
638	nar2	nar2	5HL	NADH nitrate reductase-deficient 2	35:195	
639	nar3	nar3	7HS	NADH nitrate reductase-deficient 3	35:196	
640	nar4	nar4	2HL	NADH nitrate reductase-deficient 4	35:197	
641	nar5	nar5	5HL	NADH nitrate reductase-deficient 5	35:198	
642	nar6	nar6	2HL	NADH nitrate reductase-deficient 6	35:199	

Table 2 (continued)

BGS no.	Locus symbol* Rec.	Prev.	Chr.† loc.	Locus name or phenotype	Descr. vol. p.	GSHO no.‡
643	nar7	nar7	6HL	NADH nitrate reductase-deficient 7	35:200	
644	nar8	nar8	6HS	NADH nitrate reductase-deficient 8	35:201	
645	bsp1	bsp1		Bushy spike 1	35:202	
646	ovl2	ovl2		Ovaryless 2	35:204	
647	tst1	tst1		Tip sterile 1	35:205	
648	mov4	mo8		Multiovary 4	35:206	
649	asp1	asp1		Aborted spike 1	35:207	
650	sun1	sun1		Sensitivity to *Ustilago nuda* 1	35:208	
651	lam1	lam1		Late maturity 1	35:209	
652	ylf1	ylf1		Yellow leaf 1	35:210	
653	brh10	brh.l	2HS	Brachytic 10	37:293	1677
654	brh11	brh.n	5HS	Brachytic 11	37:294	1679
655	brh12	brh.o	5HS	Brachytic 12	37:295	1680
656	brh13	brh.p	5HS	Brachytic 13	37:296	1681
657	brh15	brh.u		Brachytic 15	37:297	1685
658	brh17	brh.ab	5HS	Brachytic 17	37:298	1669
659	brh18	brh.ac	5HS	Brachytic 18	37:299	1670
660	nld2			Narrow leafed dwarf 2	37:300	
661	dub1		5HL	Double seed 1	37:301	

* 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, Idaho, 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, and original cultivars.

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
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	32:85	Burma Girl
adp1	adp	593	3HL	Awned palea 1	37:285	Unknown cultivar
alm1	al	108	3HS	Albino lemma 1	37:222	Russia 82
als1	als	101	3HL	Absent lower laterals 1	37:219	Montcalm
ant1	rs	33	7HS	Anthocyanin-less 1	26:82	Bonus
ant2	pr	80	2HL	Anthocyanin-less 2	26:118	Foma
ant3		594		Anthocyanin-deficient 3	29:82	Bonus
ant4		595		Anthocyanin-deficient 4	29:83	Foma
ant5		596		Anthocyanin-deficient 5	29:84	Bonus
ant6		597		Anthocyanin-deficient 6	29:85	Foma
ant13		598	6HL	Proanthocyanidin-free 13	29:86	Foma
ant17		599	3HS	Proanthocyanidin-free 17	37:286	Nordal
ant18		600	7HL	Proanthocyanidin-free 18	29:90	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	7HS	Proanthocyanidin-free 22	29:95	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

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
ari-a		132	3HS	Breviaristatum-a	26:168	Bonus
ari-b		550		Breviaristatum-b	26:476	Bonus
ari-e		328	5HL	Breviaristatum-e	26:276	Bonus
ari-f		551		Breviaristatum-f	26:477	Bonus
ari-g		89		Breviaristatum-g	26:128	Bonus
ari-h		329	5HL	Breviaristatum-h	26:277	Foma
ari-j		552		Breviaristatum-j	26:478	Bonus
ari-k		553		Breviaristatum-k	26:479	Bonus
ari-m		554		Breviaristatum-m	26:480	Bonus
ari-n		555		Breviaristatum-n	26:481	Bonus
ari-o		556		Breviaristatum-o	26:482	Bonus
ari-p		557		Breviaristatum-p	26:483	Foma
ari-q		558		Breviaristatum-q	26:484	Kristina
ari-r		559		Breviaristatum-r	26:485	Bonus
Ari-s	ari-265	630		Breviaristatum-s	32:131	Kristina
asp1		649		Aborted spike 1	35:207	Steptoe
blf1	bb	326	5HL	Broad leaf 1	26:274	Bonus
blf2	bb2	337	5HL	Broad leaf 2	26:285	Hannchen
Blp1	B	203	1HL	Black lemma and pericarp 1	37:245	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	7HS	Bracteatum-a	32:120	Bonus
bra-d		586	1HS	Bracteatum-d	37:284	Foma
brc1	brc-5	613	2HS	Branched 1	32:114	
brh1	br	1	7HS	Brachytic 1	37:188	Himalaya
brh2	br2	157	4HL	Brachytic 2	37:235	Svanhals
brh3	brh.g, ert-t	631		Brachytic 3	32:132	Birgitta
brh4	brh.j	349	5HS	Brachytic 4	37:262	Birgitta
brh5	brh.m	185	4HS	Brachytic 5	37:242	Birgitta
brh6	brh.s	350	5HS	Brachytic 6	37:263	Akashinriki
brh7	brh.w	41	5HS	Brachytic 7	37:203	Volla
brh8	brh.ad	142	3HS	Brachytic 8	37:230	Birgitta
brh9	brh.k	187	4HS	Brachytic 9	37:244	Birgitta
brh10	brh.l	653	2HS	Brachytic 10	37:293	Birgitta
brh11	brh.n	654	5HS	Brachytic 11	37:294	Birgitta
brh12	brh.o	655	5HS	Brachytic 12	37:295	Birgitta

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
brh13	brh.p	656	5HS	Brachytic 13	37:296	Birgitta
brh14	brh.q	148	3HL	Brachytic 14	37:231	Akashinriki
brh15	brh.u	657		Brachytic 15	37:297	Julia
brh16	brh.v	44	7HL	Brachytic 16	37:204	Korál
brh17	brh.ab	658	5HS	Brachytic 17	37:298	Morex
brh18	Brh.ac	659	5HS	Brachytic 18	37:299	Triumph
bsp1		645		Bushy spike 1	35:203	Morex
btr1	bt	115	3HS	Non-brittle rachis 1	26:149	A 222
btr2	bt2	116	3HS	Non-brittle rachis 2	26:150	Sakigoke
cal-b		620	5H	Calcaroides-b	32:121	Bonus
Cal-c		621	5HL	Calcaroides-c	32:122	Bonus
cal-d		146	3H	Calcaroides-d	32:95	Foma
cal-e		622	5HS	Calcaroides-e	32:123	Semira
cer-d		399		Eceriferum-d + ++ ++	26:346	Bonus
cer-e		400	1HL	Eceriferum-e -/+ ++ ++	26:347	Bonus
cer-f		401	7HS	Eceriferum-f + + ++	26:348	Bonus
cer-g		402	2HL	Eceriferum-g + + ++	26:349	Bonus
cer-h		403		Eceriferum-h - ++ ++	26:351	Bonus
cer-i		404	5HL	Eceriferum-i - ++ ++	26:352	Bonus
cer-k		405	7HS	Eceriferum-k + ++ ++	26:354	Bonus
cer-l		406		Eceriferum-l + ++ ++	26:355	Bonus
cer-m		407		Eceriferum-m +/++ + ++	26:356	Bonus
cer-n	gs9	408	2HL	Eceriferum-n - - ++ & - +/- ++	26:357	Bonus
cer-o		409		Eceriferum-o -/+ ++ ++	26:359	Bonus
cer-p		410		Eceriferum-p ++ ++ +	26:360	Bonus
cer-r		411	3HL	Eceriferum-r +/- + ++	26:361	Bonus
cer-t		412	5HL	Eceriferum-t +/- ++ ++	26:362	Bonus
cer-v		414	2HS	Eceriferum-v +/- ++ ++	26:366	Bonus
cer-w		415	5HL	Eceriferum-w +/- ++ ++	26:367	Bonus
cer-y		417		Eceriferum-y + +/++ ++	26:368	Bonus
cer-z		418	7HS	Eceriferum-z - - ++	26:369	Bonus
cer-za		419	5HL	Eceriferum-za ++ ++ -	26:370	Foma
cer-zb		420		Eceriferum-zb - ++ ++	26:371	Bonus
cer-zc		421		Eceriferum-zc +/- ++ ++	26:372	Bonus
cer-zd		422	3HL	Eceriferum-zd ++ ++ -	26:373	Bonus
cer-ze	gl5	423	7HS	Eceriferum-ze ++ ++ -	26:374	Bonus
cer-zf		424		Eceriferum-zf ++ ++ +	26:376	Bonus
cer-zg		425	4HL	Eceriferum-zg ++ ++ +	26:377	Foma
cer-zi		427	1HL	Eceriferum-zi + + ++	26:378	Bonus

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
cer-zj		428	5HL	Eceriferum-zj ++ ++ -	26:379	Bonus
cer-zk		429	2H	Eceriferum-zk + + +/-	26:381	Bonus
cer-zl		430		Eceriferum-zl - - ++	26:382	Bonus
cer-zn		431	3HL	Eceriferum-zn +/- ++ ++	26:383	Foma
cer-zo		432		Eceriferum-zo - ++ ++	26:384	Foma
cer-zp		433	5HL	Eceriferum-zp ++ ++ -	26:385	Bonus
cer-zq		434		Eceriferum-zq ++ ++ -	26:386	Foma
cer-zr		435		Eceriferum-zr +/- ++ ++	26:387	Foma
cer-zs		436		Eceriferum-zs + ++ ++	26:388	Foma
cer-zt		437	2HS	Eceriferum-zt + ++ ++	37:270	Foma
cer-zu		438		Eceriferum-zu - + ++	26:390	Bonus
cer-zv		439		Eceriferum-zv - - -	26:391	Foma
cer-zw		440		Eceriferum-zw + + ++	26:392	Foma
cer-zx		441		Eceriferum-zx + + ++	26:393	Bonus
cer-zy		442		Eceriferum-zy ++ ++ +	26:394	Bonus
cer-zz		443		Eceriferum-zz ++ ++ -	26:395	Bonus
cer-ya		444	3HS	Eceriferum-ya ++ ++ -	26:396	Bonus
cer-yb		445	2HL	Eceriferum-yb ++ ++ -	26:397	Bonus
cer-yc		446		Eceriferum-yc - ++ ++	26:398	Bonus
cer-yd		447	3HS	Eceriferum-yd - ++ ++	26:399	Bonus
cer-ye		448	5HL	Eceriferum-ye ++ ++ -	26:400	Foma
cer-yf		449		Eceriferum-yf ++ ++ +	37:271	Bonus
cer-yg		450	7HS	Eceriferum-yg - - -	26:402	Carlsberg II
cer-yh		451	3HS	Eceriferum-yh - ++ ++	26:403	Bonus
cer-yi		522		Eceriferum-yi ++ ++ -	26:449	Foma
cer-yj		523		Eceriferum-yj ++ ++ -	26:450	Bonus
cer-yk		524		Eceriferum-yk + + ++	26:451	Bonus
cer-yl		525		Eceriferum-yl - - ++	26:452	Bonus
cer-ym		526		Eceriferum-ym - - -	26:453	Bonus
cer-yn		527		Eceriferum-yn + + ++	26:454	Kristina
cer-yo		528		Eceriferum-yo ++ ++ +	26:455	Bonus
cer-yp		529		Eceriferum-yp ++ ++ +	26:456	Bonus
cer-yq		530		Eceriferum-yq ++ ++ -	26:457	Kristina
cer-yr		531		Eceriferum-yr -/+ + ++	26:458	Foma
cer-ys		532		Eceriferum-ys ++ ++ -	26:459	Bonus
cer-yt		533		Eceriferum-yt - ++ ++	26:460	Bonus
cer-yu		534		Eceriferum-yu ++ ++ -	26:461	Bonus
cer-yx		535		Eceriferum-yx + + ++	26:462	Foma
Cer-yy	Gle1	536	1HS	Eceriferum-yy - ++ ++	26:463	Bonus
cer-yz		537		Eceriferum-yz + + ++	26:464	Bonus

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
cer-xa		538		Eceriferum-xa ++ ++ -	26:465	Foma
cer-xb		539		Eceriferum-xb - ++ ++	26:466	Bonus
cer-xc		540		Eceriferum-xc + + ++	26:467	Bonus
cer-xd		541		Eceriferum-xd + + ++	26:468	Bonus
clh1	clh	225	1HL	Curled leaf dwarf 1	26:223	Hannchen
com1	bir1	473	5HL	Compositum 1	26:420	Foma
com2	bir2	71	2HS	Compositum 2	26:108	CIMMYT freak
crl1	cl	325		Curly lateral 1	26:273	Montcalm
crm1	cm	305	5HL	Cream seedling 1	26:256	Black Hulless
cud1	cud	324	5HL	Curly dwarf 1	26:272	Akashinriki
cud2		229	1HL	Curly dwarf 2	26:227	Akashinriki
cul2	uc2	253	6HL	Uniculm 2	37:253	Kindred
cul3		616		Uniculme 3	32:117	Donaria
cul4	uc-5	617	3HL	Uniculme 4	37:289	Bonus
cur1	cu1	262	6HL	Curly 1	26:242	48-cr cr-17
cur2	cu2	114	3HL	Curly 2	26:148	Choshiro
cur3	cu3	263	6HL	Curly 3	26:243	Akashinriki
cur4	cu4	460	2HL	Curly 4	26:406	Asahi 5
cur5	cu5	231	1HS	Curly 5	26:229	Glenn
ddt1	ddt	317	5HS	Reaction to DDT 1	26:266	Spartan
des1	lc	12	7H	Desynapsis 1	26:57	Mars
des2	ds	119	3H	Desynapsis 2	26:154	Husky
des3		386		Desynapsis 3	26:334	Betzes
des4		13	7H	Desynapsis 4	26:58	Betzes
des5		14	7H	Desynapsis 5	26:59	Betzes
des6		215	1H	Desynapsis 6	26:216	Betzes
des7		64	2H	Desynapsis 7	26:100	Betzes
des8		387		Desynapsis 8	26:335	Betzes
des9		388		Desynapsis 9	26:336	Betzes
des10		389		Desynapsis 10	26:337	Betzes
des11		390		Desynapsis 11	26:338	Betzes
des12		391		Desynapsis 12	26:339	Betzes
des13		392		Desynapsis 13	26:340	Betzes
des14		393		Desynapsis 14	26:341	Betzes
des15		394		Desynapsis 15	26:342	Ingrid
dex1	sex2	311	5HS	Defective endosperm xenia 1	26:260	BTT 63-j-18-17
dsk1	dsk	322	5HL	Dusky 1	26:270	Chikurin-Ibaraki 1
dsp1	l	9	7HS	Dense spike 1	26:53	Honen 6
dsp9	l9, ert-e	258	6HL	Dense spike 9	26:239	Akashinriki

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
dsp10	l_c	111	3HS	Dense spike 10	26:145	Club Mariout
dub1		661	6HL	Double seed 1	37:301	Bonus
Dwf2		542		Dominant dwarf 2	24:170	Klages/Mata
Eam1	Ea	65	2HS	Early maturity 1	26:101	Estate
Eam5	Ea5	348	5HL	Early maturity 5	37:260	Higuerilla*2/ Gobernadora
eam6	Ea6, Ea	98	2HS	Early maturity 6	37:216	Morex
eam7	ea7	252	6HS	Early maturity 7	26:233	California Mariout
eam8	ea_k, ert-o	214	1HL	Early maturity 8	37:247	Kinai 5
eam9	ea,,c	181	4HL	Early maturity 9	26:204	Tayeh 8
eam10	ea_{sp}	130	3HL	Early maturity 10	37:226	Super Precoz
eli-a	lig-a	623		Eligulum-a	37:290	Foma
eog 1	e	57	2HL	Elongated outer glume 1	26:92	Triple Bearded Club Mariout
ert-a	ert-6	28	7HS	Erectoides-a	26:74	Gull
ert-b	ert-2	224	1HS	Erectoides-b	26:222	Gull
ert-c	ert-1	134	3HL	Erectoides-c	26:170	Gull
ert-d	ert-7	29	7HS	Erectoides-d	26:76	Gull
ert-e	dsp9	266	6HL	Erectoides-e	37:257	Bonus
ert-f	ert-18	560		Erectoides-f	26:486	Bonus
ert-g	ert-24	330	5HL	Erectoides-g	26:278	Bonus
ert-h	ert-25	561		Erectoides-h	26:487	Bonus
ert-ii	ert-79	135	3HL	Erectoides-ii	26:172	Bonus
ert-j	ert.31	90	2H	Erectoides-j	26:129	Bonus
ert-k	ert-32	562		Erectoides-k	26:488	Bonus
ert-l	ert-12	563		Erectoides-l	26:489	Maja
ert-m	ert-34	30	7HS	Erectoides-m	26:78	Bonus
ert-n	ert-51	331	5HL	Erectoides-n	26:279	Bonus
ert-p	ert-44	564		Erectoides-p	26:490	Bonus
ert-q	ert-101	91	2H	Erectoides-q	26:130	Bonus
Ert-r	Ert-52	332		Erectoides-r	26:280	Bonus
ert-s	ert-50	565		Erectoides-s	26:491	Bonus
ert-t	brh3	566	2HS	Erectoides-t	37:281	Bonus
ert-u	ert-56	92	2H	Erectoides-u	26:131	Bonus
ert-v	ert-57	567		Erectoides-v	26:493	Bonus
ert-x	ert-58	568		Erectoides-x	26:494	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		Erectoides-za	26:497	Bonus
ert-zb	ert-132	572		Erectoides-zb	26:498	Bonus

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
ert-zc	ert-149	573		Erectoides-zc	26:499	Bonus
ert-zd	ert-159	93	2H	Erectoides-zd	26:132	Bonus
ert-ze	ert-105	574		Erectoides-ze	26:500	Bonus
fch1	f	55	2HS	Chlorina seedling 1	26:90	Minn 84-7
fch2	f2	117	3HL	Chlorina seedling 2	26:151	28-3398
fch3	f3	220	1HS	Chlorina seedling 3	26:218	Minn 89-4
fch4	f4	17	7HL	Chlorina seedling 4	26:63	Montcalm
fch5	f5	18	7HS	Chlorina seedling 5	26:64	Gateway
fch6	f6	313	5HL	Chlorina seedling 6	26:262	Himalaya
fch7	f7	201	1HL	Chlorina seedling 7	26:206	Smyrna
fch8	f8	5	7HS	Chlorina seedling 8	26:48	Comfort
fch9	f9	151	4HS	Chlorina seedling 9	26:178	Ko A
fch11	f11	260	6HL	Chlorina seedling 11	26:240	Himalaya
fch12	f_c	2	7HS	Chlorina seedling 12	37:190	Colsess
fch13	f13	86		Chlorina seedling 13	26:124	Niggrinudum
fch14	f14	87	2HL	Chlorina seedling 14	37:211	Shyri
fch15	or	52	2HS	Chlorina seedling 15	26:88	Trebi IV
flo-a		182		Extra floret-a	26:205	Foma
flo-b		327	5HL	Extra floret-b	26:275	Foma
flo-c		74	2HS	Extra floret-c	26:111	Foma
fol-a		73	2HL	Angustifolium-a	26:110	Proctor
Fol-b	Ang	548		Angustifolium-b	26:474	Unknown
fst1	fs	301	5HL	Fragile stem 1	26:252	Kamairazu
fst2	fs2	208	1HL	Fragile stem 2	26:211	Oshichi
fst3	fs3	24	7HS	Fragile stem 3	26:70	Kobinkatagi 4
gig1	gig	463	2H?	Gigas 1	26:410	Tochigi Golden Melon
gig2		612		Gigas 2	32:113	ND12463
glf1	gl	155	4HL	Glossy leaf 1 ++ ++ -	37:233	Himalaya
glf3	gl3	165	4HL	Glossy leaf 3 ++ ++ -	26:190	Goseshikoku
glo-a		168	4HS	Globosum-a	26:194	Proctor
glo-b		336	5HL	Globosum-b	26:284	Villa
glo-c		72	2H	Globosum-c	26:109	Villa
glo-e		230	1HL	Globosum-e	26:228	Foma
glo-f		342	5HL	Globosum-f	26:291	Damazy
gpa1	gp	59	2HL	Grandpa 1	26:95	Lyallpur
gra-a	gran-a	131	3HL	Granum-a	26:167	Donaria
gsh1	gs1	351	2HS	Glossy sheath 1 - - ++	26:292	CIho 5818
gsh2	gs2	352	3HL	Glossy sheath 2 - - ++	26:294	Atlas
gsh3	gs3	353	7HS	Glossy sheath 3 - - ++	26:296	Mars

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
gsh4	gs4	354	6HL	Glossy sheath 4 - - ++	26:298	Gateway
gsh5	gs5	355	2HL	Glossy sheath 5 + - ++	26:300	Jotun
gsh6	gs6	356	2HS	Glossy sheath 6 - - ++	26:302	Betzes
gsh7	gs7	81		Glossy sheath 7 - - ++	26:119	Akashinriki
gsh8	cer-u	413	2HS	Glossy sheath 8 + + ++	26:364	Bonus
Gth1	G	69	2HL	Toothed lemma 1	26:106	Machine (Wexelsen)
hcm1	h	77	2HL	Short culm 1	26:115	Morex
Hln1	Hn	164	4HL	Hairs on lemma nerves 1	26:189	Kogane-mugi
Hsh1	Hs	179	4HL	Hairy leaf sheath 1	37:240	Kimugi
int-b		320	5HL	Intermedium spike-b	26:268	Bonus
int-c	i	178	4HS	Intermedium spike-c	37:237	Gamma 4
int-f		543		Intermedium spike-f	26:469	Foma
int-h		544		Intermedium spike-h	26:470	Kristina
int-i		545		Intermedium spike-i	26:471	Kristina
int-k		546	7H	Intermedium spike-k	37:279	Kristina
int-m		547		Intermedium spike-m	37:280	Bonus
Kap1	K	152	4HS	Hooded lemma 1	26:179	Colsess
lam1		651		Late maturity 1	35:209	Steptoe
lax-a		474	5HL	Laxatum-a	37:273	Bonus
lax-b		268	6HL	Laxatum-b	26:248	Bonus
lax-c		475	6HL	Laxatum-c	26:423	Bonus
lbi1	lb	308	5HL	Long basal rachis internode 1	26:258	Wisconsin 38
lbi2	lb2	156	4HL	Long basal rachis internode 2	26:183	Montcalm
lbi3	lb3	27	7HL	Long basal rachis internode 3	26:73	Montcalm
lel1	lel	235	1HL	Leafy lemma 1	32:103	G7118
Lfb1	Lfb	343	5HL	Leafy bract 1	28:30	Montcalm
Lga1	Log	549		Long glume awn 1	26:475	Guy Mayle
lgn3	lg3	170	4HL	Light green 3	26:195	No 154
lgn4	lg4	171	4HL	Light green 4	26:196	Himalaya / Ingrescens
lig1	li	60	2HL	Liguleless 1	37:205	Muyoji
lin1	s, rin	99	2HL	Lesser internode number 1	32:88	Natural occurence
Lks1	Lk	75	2HL	Awnless 1	26:112	*Hordeum inerme*
lks2	lk2	10	7HL	Short awn 2	37:197	Honen 6
lks5	lk5	172	4HL	Short awn 5	26:197	CIho 5641
lnt1	lnt	118	3HL	Low number of tillers 1	26:153	Mitake

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
lys1	lys	338	5HL	High lysine 1	26:286	Hiproly
lys3	sex3	339	5HL	High lysine 3	26:287	Bomi
Lys4	sex5	232	1HS	High lysine 4	26:230	Bomi
lys6		269	6H	High lysine 6	26:249	Bomi
lzd1	lzd	125	3HS	Lazy dwarf 1	26:161	Akashinriki
mat-b		578		Praematurum-b	26:504	Bonus
mat-c		579		Praematurum-c	26:506	Bonus
mat-d		580		Praematurum-d	26:507	Bonus
mat-e		581		Praematurum-e	26:508	Bonus
mat-f		582		Praematurum-f	26:509	Bonus
mat-g		583		Praematurum-g	26:510	Bonus
mat-h		584		Praematurum-h	26:511	Bonus
mat-i		585		Praematurum-i	26:512	Bonus
min1	min	161	4HL	Semi-minute dwarf 1	26:187	Taisho-mugi
min2	en-min	160		Enhancer of minute 1	26:186	Kaiyo Bozu
mnd1	m	519		Many-noded dwarf 1	26:446	Mesa
mnd3	m3	618	3H	Many noded dwarf 3	32:119	Montcalm
mnd4	m4	347	5HL	Many noded dwarf 4	32:108	Akashinriki
mnd5		632		Many noded dwarf 5	32:133	C2-95-199
mnd6	den-6	633	5HL	Many noded dwarf 6	37:291	Bonus
mov1	mo6b	43	7HL	Multiovary 1	35:185	Steptoe
mov2	mo7a	147	3HS	Multiovary 2	35:190	Steptoe
mov3	mo-a	234	1H	Multiovary 3	32:102	Akashinriki
mov4		648		Multiovary 4	35:206	Steptoe
msg1		357	1HL	Male sterile genetic 1	26:304	CIho 5368
msg2		358	2HL	Male sterile genetic 2	26:306	Manchuria
msg3		359	2HS	Male sterile genetic 3	26:307	Gateway
msg4		360	1H	Male sterile genetic 4	26:308	Freja
msg5		361	3HS	Male sterile genetic 5	26:309	Carlsberg II
msg6		362	6HS	Male sterile genetic 6	26:310	Hanna
msg7		363	5HL	Male sterile genetic 7	26:311	Dekap
msg8		364	5HL	Male sterile genetic 8	26:312	Betzes
msg9		365	2HS	Male sterile genetic 9	26:313	Vantage
msg10		366	7HS	Male sterile genetic 10	26:314	Compana
msg11		367		Male sterile genetic 11	26:315	Gateway
msg13		368		Male sterile genetic 13	26:316	Haisa II
msg14		369	7HS	Male sterile genetic 14	26:317	Unitan
msg15		370		Male sterile genetic 15	26:318	Atlas/2*Kindred
msg16		371	5HS	Male sterile genetic 16	26:319	Betzes
msg17		372		Male sterile genetic 17	26:320	Compana

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
msg18		373	5HL	Male sterile genetic 18	26:321	Compana
msg19		374	5HS	Male sterile genetic 19	26:322	CIho 14393
msg20		375	1H	Male sterile genetic 20	26:323	Hannchen
msg21		376		Male sterile genetic 21	26:324	Midwest Bulk
msg22		383	7H	Male sterile genetic 22	26:331	Glacier/Compana
msg23		384	7HL	Male sterile genetic 23	26:332	Betzes
msg24		385	4HL	Male sterile genetic 24	26:333	Betzes
msg25		166	4HL	Male sterile genetic 25	26:192	Betzes
msg26		395	7HS	Male sterile genetic 26	26:343	Unitan
msg27		464	2HL	Male sterile genetic 27	26:411	Firlbecks III
msg28		465	6H	Male sterile genetic 28	26:412	York
msg29		466	5HL	Male sterile genetic 29	26:413	Ackermans MGZ
msg30		467	7HL	Male sterile genetic 30	26:414	Compana
msg31		468	1HS	Male sterile genetic 31	26:415	51Ab4834
msg32		469	7H	Male sterile genetic 32	26:416	Betzes
msg33		470	2HS	Male sterile genetic 33	26:417	Betzes
msg34		471	6H	Male sterile genetic 34	26:418	Paragon
msg35		498	2HL	Male sterile genetic 35	26:424	Karl
msg36		499	6HS	Male sterile genetic 36	26:425	Betzes
msg37		500		Male sterile genetic 37	26:426	Clermont
msg38		501		Male sterile genetic 38	26:427	Ingrid
msg39		502	6H	Male sterile genetic 39	26:428	CIho 15836
msg40		503	6H	Male sterile genetic 40	26:429	Conquest
msg41		504		Male sterile genetic 41	26:430	Betzes
msg42		505	3H	Male sterile genetic 42	26:431	Betzes
msg43		506		Male sterile genetic 43	26:432	Betzes
msg44		507		Male sterile genetic 44	26:433	HA6-33-02
msg45		508		Male sterile genetic 45	26:434	RPB439-71
msg46		509		Male sterile genetic 46	26:435	Hector
msg47		510		Male sterile genetic 47	26:436	Sel 12384CO
msg48		520	2H	Male sterile genetic 48	26:447	Simba
msg49		335	5HL	Male sterile genetic 49	26:283	ND7369
msg50		34	7HL	Male sterile genetic 50	26:83	Berac
mss1	mss	84	2H	Midseason stripe 1	26:122	Montcalm
mss2		39	7HS	Midseason stripe 2	32:79	ND11258
mtt1	mt	521	1HS	Mottled leaf 1	26:448	Montcalm
mtt2	mt2	302	5HL	Mottled leaf 2	26:253	Montcalm
mtt4	mt,,e	78	2HL	Mottled leaf 4	26:116	Victorie
mtt5	mt,,f	264	6HL	Mottled leaf 5	26:244	Akashinriki
mtt6		629		Mottled leaf 6	32:130	ND6809

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
mul2		251	6HL	Multiflorus 2	26:232	Montcalm
nar1		637	6HS	NADH ntrate reductase-deficient 1	35:194	Steptoe
nar2		638	5HL	NADH ntrate reductase-deficient 2	35:196	Steptoe
nar3		639	7HS	NADH ntrate reductase-deficient 3	35:197	Winer
nar4		640	2HL	NADH ntrate reductase-deficient 4	35:198	Steptoe
nar5		641	5HL	NADH ntrate reductase-deficient 5	35:199	Steptoe
nar6		642	2HL	NADH ntrate reductase-deficient 6	35:200	Steptoe
nar7		643	6HL	NADH ntrate reductase-deficient 7	35:201	Steptoe
nar8		644	6HS	NADH ntrate reductase-deficient 8	35:202	Steptoe
nec1		222	1HL	Necrotic leaf spot 1	37:251	Carlsberg II
nec2		261	6HS	Necrotic leaf spot 2	26:241	Carlsberg II
nec3		265	6HS	Necrotic leaf spot 3	26:245	Proctor
nec4		138	3H	Necrotic leaf spot 4	26:175	Proctor
nec5		139	3H	Necrotic leaf spot 5	26:176	Diamant
Nec6	Sp	611		Necrotic leaf spot 6	32:112	Awnless Atlas
nec7	nec-45	635		Necroticans 7	32:136	Kristina
nld1	nld	323	5HL	Narrow leafed dwarf 1	26:271	Nagaoka
nld2		660		Narrow leafed dwarf 2	37:300	Steptoe
nud1	n, nud	7	7HL	Naked caryopsis 1	37:195	Himalaya
ops1	op-3	624		Opposite spikelets 1	32:125	Bonus
ovl1		176	4H	Ovaryless 1	35:191	Kanto Bansei Gold
ovl2		646		Ovaryless 2	35:204	Harrington
pmr1	pmr	40	7HS	Premature ripe 1	32:80	Glenn
pmr2	nec-50	634		Premature ripe 2	32:135	Bonus
Pre2	Re2	76	2HL	Red lemma and pericarp 2	26:113	Buckley 3277
Pub1	Pub	127	3HL	Pubescent leaf blade 1	26:163	Multiple Dominant
Pvc1	P_c	68	2HL	Purple veined lemma 1	26:105	Buckley 2223-6
Pyr1		42	7HS	Pyramidatum 1	32:82	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	26:238	Akashinriki
raw6	r6	334	5HL	Smooth awn 6	26:282	Glenn

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
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	26:217	Gull
Rph5	Pa5	122	3HS	Reaction to *Puccinia hordei* 5	37:224	Magnif 102
Rph6	Pa6	575	3HS	Reaction to *Puccinia hordei* 6	26:501	Bolivia
Rph7	Pa7	136	3HS	Reaction to *Puccinia hordei* 7	37:228	Cebada Capa
Rph8	Pa8	576		Reaction to *Puccinia hordei* 8	26:502	Egypt 4
Rph9	Pa9	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

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
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	Sep_2	516		Reaction to *Septoria passerinii* 2	37:275	PI 70837
Rsp3	Sep_3	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	26:224	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	32:83	Tayeh 13
sca1	sca	128	3HS	Short crooked awn 1	26:164	Akashinriki
sci-a	sci-3	625		Scirpoides-a	32:126	Bonus
scl-a	scl-6	626		Scirpoides leaf-a	32:127	Foma
sdw1	sdw	518	3HL	Semidwarf 1	37:277	M21
sdw2	sdw-b	133	3HL	Semidwarf 2	26:169	Mg2170
seg1	se1	377	7HL	Shrunken endosperm genetic 1	37:264	Betzes
seg2	se2	378	7HS	Shrunken endosperm genetic 2	26:326	Betzes
seg3	se3	379	3H	Shrunken endosperm genetic 3	37:265	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	37:268	Ingrid
seg7	se7	397		Shrunken endosperm genetic 7	37:269	Ingrid

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
seg8		455	7H	Shrunken endosperm genetic 8	37:272	60Ab1810-53
sex1	lys5	382	6HL	Shrunken endosperm xenia 1	26:330	Compana
sex6		31	7HS	Shrunken endosperm xenia 6	26:80	K6827
sex7	sex.i	628	5HL	Shrunken endosperm xenia 7	32:129	I90-374
sex8	sex.j	143	6HS	Shrunken endosperm xenia 8	32:93	I89-633
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	26:203	Akashinriki
Sil1	Sil	228	1HS	Subcrown internode length 1	26:226	NE 62203
sld1	dw-1	126	3HL	Slender dwarf 1	26:162	Akashinriki
sld2		83	2HS	Slender dwarf 2	26:121	Akashinriki
sld3	ant-567	186	4HS	Slender dwarf 3	37:243	Manker
sld4		100	7HS	Slender dwarf 4	37:218	Glacier
sld5		144	3HS	Slender dwarf 5	32:94	Indian Dwarf
sls1	sls	227	1HS	Small lateral spikelet 1	26:225	Morex
smn1	smn	38	7HS	Seminudoides 1	32:225	Haisa
snb1	sb	26	7HS	Subnodal bract 1	26:72	L50-200
srh1	s	321	5HL	Short rachilla hair 1	26:269	Lion
sun1		650		Sensitivity to *Ustilago nuda* 1	35:208	Steptoe
trd1	trd	202	1HL	Third outer glume 1	26:207	Valki
trp1	tr	61	2HL	Triple awned lemma 1	26:97	CIho 6630
tst1		647		Tip sterile 1	35:205	Steptoe
tst2	lin2	636		Tip sterile 2	37:292	Donaria
ubs4	u4	11	7HL	Unbranched style 4	26:56	Ao-Hadaka
uzu1	uz	102	3HL	Uzu 1 or semi brachytic 1	37:220	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	26:254	Montcalm
viv-a	viv-5	627		Viviparoides-a	32:128	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

Table 3 (continued)

Locus symbol*		BGS	Chr.	Locus name or phenotype	Descr.	Parental cultivar
Rec.	Prev.	no.	loc.†		vol. p.	
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	26:264	Hadata 2
vrs4	v4	124	3HL	Six-rowed spike 4	26:159	MFB 104
wax1	wx	16	7HS	Waxy endosperm 1	26:61	Oderbrucker
wnd1	wnd	23	7HS	Winding dwarf 1	26:69	Kogen-mugi
wst1	wst	107	3HL	White streak 1	26:141	CIho 11767
wst2		304	5HL	White streak 2	26:255	Manabe
wst4		56	2HL	White streak 4	26:91	Kanyo 7
wst5		221	1HL	White streak 5	26:219	Carlsberg II
wst6	wst,,j	129	3HL	White streak 6	26:165	Akashinriki
wst7	rb	79	2HL	White streak 7	37:207	GS397
Xnt1	X_a	25	7HL	Xantha seedling 1	26:71	Akanshinriki
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	26:185	Kimugi
yhd2	yh2	592		Yellow head 2	28:34	Compana
ylf1		652		Yellow leaf 1	35:210	Villa
Ynd1	Yn	183	4HS	Yellow node 1	32:98	Morex
yst1	yst	104	3HS	Yellow streak 1	26:138	Gateway
yst2		109	3HS	Yellow streak 2	26:144	Kuromugi 148/ Mensury C
yst3	yst,,c	462	3HS	Yellow streak 3	26:409	Lion
yst4		85	2HL	Yellow streak 4	37:210	Glenn
yst5		346	5HL	Yellow streak 5	32:107	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	26:155	Mars
zeb2	zb2	461	4HL	Zebra stripe 2	26:407	Unknown
zeb3	zb3	223	1HL	Zebra stripe 3	26:221	Utah 41
Zeo1	Knd	82	2HL	Zeocriton 1	37:209	Donaria
Zeo2		614		Zeocriton 2	32:115	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 1, Brachytic 1, *brh1*

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

Previous nomenclature and gene symbolization:
Brachytic = *br* (10, 12).
Breviaristatum-i = *ari-i* (5, 8).
Dwarf x = *dx1* (6).

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

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

Origin of mutant:
A spontaneous mutant in Himalaya (CIho 1312) (10, 12).

Mutational events:
brh1.a in Himalaya (12); *brh1.c* (GSHO 229) in Moravian (PI 539135) (13); *ari-i.38* (NGB 115888, GSHO 1657) in Bonus (PI 189763) (8, 14); *brh1.e* (GSHO 1690) in Aramir (PI 467786) (14); *brh1.f* (*dx1*, GSHO 1422) in Domen (CIho 9562) (6); *brh1.t* (OUM136, GSHO 1691) in Akashinriki (PI 467400, OUJ659); *brh1.x* (7125, DWS1224, GSHO 1692) in Volla (PI 280423); *brh1.z* (Hja80001) in Aapo; *brh1.aa* (Hja80051) in a Hja80001 cross (4, 7); and *brh1.ae* (FN53) in Steptoe (CIho 15229) (4).

Mutant used for description and seed stocks:
brh1.a in Himalaya (GSHO 25); *brh1.a* in Bowman (PI 483237)*7 (GSHO 1820); *ari-i.38* in Bowman*6 (GSHO 1821); *brh1.e* in Bowman*7 (GSHO 1822); *brh1.t* in Bowman*7 (GSHO 1823); *brh1.x* in Bowman*7 (GSHO 1824); *brh1.z* in Bowman*7 (GSHO 2179).

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Prepared:
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Revised:
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J.D. Franckowiak. 1997. BGN 26:44.
J.D. Franckowiak and L. S. Dahleen. 2007. BGN 37:188-189.

BGS 2, Chlorina seedling 12, *fch12*

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

Previous nomenclature and gene symbolization:
Chlorina seedling-c = f_c (3).
Chlorina seedling-fc = *clo-fc* (7).

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

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

Origin of mutant:
A spontaneous mutant in Colsess (CIho 2792) (3).

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

Mutant used for description and seed stocks:
fch12.b in Colsess (GSHO 36); *fch12.b* in Bowman (PI 483237)*7 (GSHO 1826).

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Prepared:

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Revised:
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J.D. Franckowiak and A. Hang. 1997. BGN 26:45.
J.D. Franckowiak. 2007. BGN 37:190-191.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

vrs1.a1 in most six-rowed cultivars (1, 10, 22); *vrs1.a2* in Dissa and Valenci (10), *vrs1.a3* in Natsudaikon Mugi (OUK735) (10), *Vrs1.b* in wild barley (10), *Vrs1.b2* in Pamella Blue (OUH630) (10), *Vrs1.b3* in Bonus (PI 189763) (10), *Vrs1.t* in a few two-rowed cultivars (10, 22); *vrs1.c* or *lr* in Nudihaxtoni (PI 32368) (12, 19); *Vrs1.d* in Svanhals (PI 5474) (22); 23 induced mutants from programs in Belgium, Germany, and Hungary (2); *hex-v.3* (NGB 115545), *-v.4* (NGB 115546), *-v.6* (NGB 115547), *-v.7* (NGB115548), *-v.8* (NGB 115549), *-v.9* (NGB 115550), *-v.10* (NGB 115551), *-v.11* (NGB 115552), *-v.12* (NGB 115553), *-v.18* (NGB 115559), *-v.44* (NGB 115581), *-v.45* (NGB 115582), *-v.46* (NGB 115583), *-v.47* (NGB 115584), *-v.48* (NGB 115585), in Bonus, *-v.13* (NGB 115554), *-v.14* (NGB 115555), *-v.15* (NGB 115556), *-v.16* (NGB 115557), *-v.17* (NGB 115558), *-v.19* (NGB 115560), *-v.21* (NGB 115562), *-v.22* (NGB 115563), *-v.23* (NGB 115564), *-v.24* (NGB 115565), *-v.25* (NGB 115566), *-v.26* (NGB 115567), *-v.27* (NGB 115568), *-v.28* (NGB 115569), *-v.29* (NGB 115570), *-v.30* (NGB 115571), *-v.31* (NGB 115572), *-v.35* (NGB 115574) in Foma (CIho 11333), *-v.20* (NGB 115561) in Ingrid (CIho 10083), *-v.33* (NGB 115573), *-v.36* (NGB 115575), *-v.38* (NGB 115576), *-v.39* (NGB 115577), *-v.41* (NGB 115578), *-v.42* (NGB 115579), *-v.43* (NGB 115580) in Kristina (NGB 1500) (5, 14); *hex-v.49* (NGB 115586) in Bonus, *-v.50* (NGB 115587), *-v.51* (NGB 115588) in Sv 79353, *-v.52* (NGB 119353) in Golf (PI 488529) (13); *Int-d.11* (NGB 115429), *-d.12* (NGB 115430), *-d.22* (NGB 115440), *-d.24* (NGB 115442), *-d.28* (NGB 115446), *-d.36* (NGB 115454) in Foma, *-d.40* (NGB 115458), *-d.41* (NGB 115459), *-d.50* (NGB 115468), *-d.57* (NGB 115475), *-d.67* (NGB 115485), *-d.68* (NGB 115486), *-d.69* (NGB 115487) in Kristina (5, 15); *Int-d.73* (NGB 115491), *-d.80* (NGB 115498), *-d.82* (NGB 115500) in Bonus, *-d.93* (NGB 115511), *-d.94* (NGB 115512), *-d.96* (NGB 115514), *-d.97* (NGB 115515), *-d.100* (NGB 115518) in Hege (NGB 13692) (13); *vrs1.o* (*v1b*) in New Golden (16).

Mutant used for description and seed stock:

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

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22. Woodward, R.W. 1949. The inheritance of fertility in the lateral florets of the four barley groups. Agron. J. 41:317-322.

Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:49-50.
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:192-194.

BGS 7, Naked caryopsis 1, *nud1*

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

Previous nomenclature and gene symbolization:
Naked caryopsis = *k* (14).
Naked caryopsis = *s* (21).
Naked caryopsis = *n* (6, 9).
Hulless = *h* (10).

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

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

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

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

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

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Barleys: a phenotypically polymorphic doubled-haploid population. Theor. Appl. Genet. 103:415-424.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. BGN 1:110.

Revised:

J.D. Franckowiak and T. Konishi. 1997. BGN 26:51-52.

J.D. Franckowiak. 2007. BGN 37:195-196.

BGS 10, Short awn 2, *lks2*

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

Previous nomenclature and gene symbolization:
Short awn = *a* (15, 16).
Short awn = *lk* (14).
Short awn 2 = lk_1 (7).
Short awn 2 = *lk2* (11).
Short awn 4 = *lk4* (2, 5).

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

Description:
Awns of both central and lateral spikelets are reduced to about 3/5 of the long awned type. Texture of the short awn is finer and more flexible than that of the long awn, especially in non-uzu genotypes (13, 14). The awn length of heterozygotes in some crosses is shorter that of the normal parent. Other plant characteristics are apparently unaltered by the *lks2.b* gene.

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

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

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

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14. Takahashi, R., J. Yamamoto, S. Yasuda, and Y. Itano. 1953. Inheritance and linkage studies in barley. Ber. Ohara Inst. landw Forsch. 10:29-52.
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Prepared:

R. Takahashi. 1972. BGN 2:176.

Revised:

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

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

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

Previous nomenclature and gene symbolization:
Greenbug resistance = *Grb* (8).
Resistance to *Schizaphis graminum* Rondani (greenbug) = *Rsg,,a* (3).
Inheritance:
Monofactorial dominant (2, 3, 9).
Located in chromosome 7H [1] (4).
Description:
Resistant seedlings infested with greenbugs (aphids) are not killed, while susceptible seedlings are killed, eight weeks after infestation by the buildup of the greenbug population (2, 3, 4). The resistance provided by Post 90 (PI 549081), having the *Rsg1.a* gene, to most *S. graminum* biotypes was commonly 2 to 3 readings on a 1 to 9 scale (7). Accessions with the *Rsg1.a* gene conferred resistance to most, but not all greenbug populations (5).
Origin of mutant:
Natural occurrence in Bozu Omugi (OUJ028, PI 87181), Derbent (PI 76504), and Kearney (PI 539126, CIho 7580) (1, 3).
Mutational events:
Rsg1.a in Bozu Omugi, Derbent, Kearney, Dobaku (PI 87817), and CIho 5087 (PI 82683) (3, 7).
Mutant used for description and seed stocks:
Rsg1.a in Bozu Omugi (GSHO 1317); *Rsg1.a* in Post 90 (PI 549081) from Will () (5).
References:
1. Atkins, I.M., and R.G. Dahms. 1945. Reaction of small-grain varieties to greenbug attack. USDA Tech. Bull. 901.
2. Gardenshire, J.H. 1965. Inheritance and linkage studies on greenbug resistance in barley (*Hordeum vulgare* L.). Crop Sci. 5:28-29.
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Prepared:

J.G. Moseman. 1976. BGN 6:119.
Revised:
J.D. Franckowiak. 1997. BGN 26:68.
J.D. Franckowiak. 2007. BGN 37:199-200.

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

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

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 9 = Pa_9 (3, 7, 8).
Resistance to *Puccinia hordei* Otth 9 = *Pa9* (2).
Resistance to *Puccinia hordei* 12 = *Rph12* (1, 2, 9).

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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Prepared:

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

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

Revised:

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

BGS 41, Brachytic 7, *brh7*

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

Previous nomenclature and gene symbolization:
Brachytic-w = *brh.w* (3).
Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 5HS [7S] (1), approximately 4.6 cM proximal from SSR marker Bmac0113 in bin 5H-04 (1).
Description:
Plants are about 5/6 of normal height and awns are about 3/4 of normal length. The rachis internodes are slightly shorter than normal for Bowman. The seedling leaf of *brh7* plants is short and wide and leaf blades are wider than those of normal sibs. The Bowman line with *brh7* showed less lodging than Bowman. Although the kernels of *brh7* plants seem plumper and more globose shaped than those from normal sibs, the primary difference is a 10 to 15% reduction in kernel length. Kernel weights and grain yields of the *brh7* line are slightly lower than those of normal Bowman (1, 2).
Origin of mutant:
An induced mutant in Volla (PI 280423) (4).
Mutational events:
brh7.w in Volla (7101, DWS1211) (4, 5).
Mutant used for description and seed stocks:
brh7.w in Volla (GSHO 1687); *brh7.w* in Bowman (PI 483237)*7 (GSHO 1943).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. (Unpublished).
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Prepared:
J.D. Franckowiak. 2002. BGN 32:81.
Revised:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:203.

BGS 44, Brachytic 16, *brh16*

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

Previous nomenclature and gene symbolization:
Brachytic-v = *brh.v* (2).

Inheritance:
Monofactorial recessive (2, 3).
Located in chromosome 7HL [1L] (1), approximately 7.4 cM proximal from SSR marker Bmag0135 in bin 7H-13 (1).

Description:
Plants are less than 2/3 of normal height and awns are about 3/4 of normal length in the Bowman backcross-derived line. The peduncle is about 2/3 normal length. The rachis internodes are slightly shorter than normal. The tip of the spike has a fascinated appearance because spikelets are very close together. The seed yield of the Bowman line with *brh16* was less than 1/3 of Bowman's yield. Since kernels per spikes and kernel size were not reduced, much of the yield loss was probably associated with reduced tillering (1). The original introduction (HE 2816) contained two dwarf mutants, but only *brh16.v* gene was isolated in the Bowman backcross-derived line.

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

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

Mutant used for description and seed stocks:
brh16.v in HE 2816/Bowman (GSHO 1686); *brh16.v* in Bowman (PI 483237)*7 (GSHO 2177).

References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Váša, M. 1986. (Personal communications).

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

BGS 60, Liguleless 1, *lig1*

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

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

Inheritance:
Monofactorial recessive (9).
Located in chromosome 2HL (6, 9, 10); about 25.1 cM distal from the *mtt4* (mottled leaf 4) locus (2); and near AFLP marker E3633-1 in subgroup 21 of the Proctor/Nudinka map (7).

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

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

Mutational events:
lig1.my as Muyoji (OUL007) (9); *lig1.ky* in Koyo (PI 190819)*, lig1.a1* (OUM001), *lig1.a2* in Akashinriki (PI 467400, OUJ659); *lig1.c1, lig1.c2, lig1.c3, lig1.c4* in Chikurin Ibaraki 1 (OUJ030, CIho 7370) (5); *aur-a.1* (*lig1.b1*) (NGB 114359), *aur-a.2* (*lig1.b2*) (NGB 114360), *aur-a.7* (*lig1.b7*) (NGB 114365), *aur-a.8* (*lig1.b8*) (NGB 114366), *aur-a.9* (*lig1.b9*) (NGB 114367) in Bonus (PI 189763), *aur-a.3* (*lig1.b3*) (NGB 114361), *aur-a.4* (*lig1.b4*) (NGB 114362)*, aur-a.5* (*lig1.b5*) (NGB 114363), *aur-a.6* (*lig1.b6*) (NGB 114364), *aur-a.10* (*lig1.b10*) (NGB 114368) in Foma (CIho 11333) (5); *aur-a.11* (NGB 114369)*, aur-a.12* (NGB 114370, NGB 114371) in Kristina, *aur-a.13* (NGB 114372)*, aur-a.14* (NGB 114373) in Bonus, *aur-a.15* (NGB 119377) in Golf (PI 488529) (6); *lig1.2* in Bonus, found in *eli-2* (eligulum-2) (NGB 115389) stock as the second mutant (2).

Mutant used for description and seed stocks:
lig1.my as Muyoji (GSHO 6); *lig1.my* in Bowman (PI 483237)*8 (GSHO 1930); *lig1.2* in Bowman*5 (2).

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. BGN 1:120.

Revised:

J.D. Franckowiak, U. Lundqvist, T. Konishi. 1997. BGN26:96.
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:205-206.

BGS 79, White streak 7, *wst7*

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

Previous nomenclature and gene symbolization:
Ribbon grass = *rb* (6).
White streak-k = *wst,,k* (10).
White streak-B = *wst,,B* (8).

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

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

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

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

Mutant used for description and seed stocks:
wst7.k in an unknown cultivar (GSHO 247); *wst7.k* from R.I. Wolfe's Multiple Recessive Marker Stock in Bowman (PI 483237)*7 (GSHO 1935).

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Prepared:

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

Revised:

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

BGS 82, Zeocriton 1, *Zeo1*

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

Previous nomenclature and gene symbolization:
"Kurz und dicht" = *Knd* (6).
Inheritance:
Monofactorial incomplete dominant (5).
Located in chromosome 2HL, about 9.2 cM distal from the *lig1* (liguleless 1) locus (4), in bin 2H-13 about 7.3 cM distal from RFLP marker cnx1 (1).
Description:
Plants heterozygous for *Zeo1* have short culms, compact spikes, and wide kernels. Homozygotes have shorter culms (short peduncle), very compact spikes, large outer glumes with long awns, and reduced fertility. Generally, the spike emerges from the side of the sheath in homozygotes. Although the name *zeocriton* is used for this gene, this gene is not from Spratt, the dense ear type described by Engledow (2).
Origin of mutant:
An X-ray induced mutant in Donaria (PI 161974) (5).
Mutational events:
Zeo1.a in Donaria (Mut 2657) (5); *Zeo1.b,* received as "Kurz und dicht" and placed in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1614), was probably derived from Mut 2657 (3, 6).
Mutant used for description and seed stocks:
Zeo1.a in Donaria (GSHO 1613); *Zeo1.a* in Bowman (PI 483237)*5 (GSHO 1931); *Zeo1.b* in Bowman*9 (GSHO 1932).
References:
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Prepared:
J.D. Franckowiak and R.I. Wolfe. 1997. BGN 26:120.
J.D. Franckowiak. 2007. BGN 37:209.

BGS 85, Yellow streak 4, *yst4*

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (2).
Located in chromosome 2HL, near the *vrs1* (six-rowed spike 1) locus (2), in bin 2H-07 near RFLP marker CDO537 (3).
Description:
Plants have a yellow-green color with numerous, vertical yellow streaks in the leaves. The yellow-green color is retained until maturity, but the yellow streaks may be difficult to observe after heading. Plant vigor and height are reduced, heading is delayed, and seed yields are low.
Origin of mutant:
A sodium azide induced mutant in Glenn (CIho 15769) (1).
Mutational events:
yst4.d in Glenn (DWS1059) (2).
Mutant used for description and seed stocks:
yst4.d in Glenn (GSHO 2502); *yst4.d* in Bowman (PI 483237)*7 (GSHO 1922).
References:
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Prepared:
J.D. Franckowiak. 1997. BGN 26:123.
Revised:
J.D. Franckowiak. 2007. BGN 37:210.

BGS 87, Chlorina seedling 14, *fch14*

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

Previous nomenclature and gene symbolization:
Chlorina seedling 14 = *f14* (2).
Inheritance:
Monofactorial recessive (2, 4).
Located in chromosome 2HL (2), probably between the *vrs1* (six-rowed spike 1) and the *ant2* (anthocyanin-less 2) loci (2), likely in bin 2H-11 (3, 4).
Description:
Seedlings have a pale yellow-green color. The leaves gradually become greener starting at the tip of the leaf blade, and mutant plants are indistinguishable in color from normal sibs at heading (2). When grown in the field, plants produce slightly thinner kernels with about a 10% reduction in kernel weight (1).
Origin of mutant:
A spontaneous mutant in Shyri (Lignee 640//Kober/Teran 78) from Ecuador (2).
Mutational events:
fch14.w in Shyri (2, 5).
Mutant used for description and seed stocks:
fch14.w in Shyri (GSHO 1739); *fch14.w* in Bowman (PI 483237)*6 (GSHO 1911).
References:
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2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
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Prepared:
J.D. Franckowiak. 1997. BGN 26:125.
Revised:
J.D. Franckowiak. 2007. BGN 37:211.

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

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

Previous nomenclature and gene symbolization:
Resistance to *Puccinia anomala* Rostr = *Pa* (2).
Resistance to *Puccinia hordei* Otth 2 = Pa_2 (9, 15).
Resistance to *Puccinia hordei* A = A (8, 9).

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

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

Origin of mutant:
Natural occurrence in Peruvian (CIho 935) and several other cultivars (2, 4, 6, 12, 15, 16).

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

Mutant used for description and seed stocks:
Rph2.b in Peruvian (GSHO 1593); *Rph2.b* in Bowman (PI 483237)*3 (GSHO 2320); *Rph2.t* from Rika 1 in Bowman*8 (GSHO 2321).

References

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Prepared:
Y. Jin and J.D. Franckowiak. 1997. BGN 26:126-127.
Revised:
J.D. Franckowiak. 2007. BGN 37:212-213.

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

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

Previous nomenclature and gene symbolization:
Rph16 = Reaction to *Puccinia hordei* 16 (6, 9).

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

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

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

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

Mutant used for description and seed stocks:
Rph15.ad in selection from a cross to Bowman (GSHO 1586); *Rph15.ad* in Bowman*8 (GSHO 2330).

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Prepared:

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

Revised:

J.D. Franckowiak. 2005. BGN 35:186.
J.D. Franckowiak. 2007. BGN 37:214-215.

BGS 98, Early maturity 6, *Eam6*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Revised:

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

BGS 100, Slender dwarf 4, *sld4*

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

Previous nomenclature and gene symbolization:
Slender dwarf d = *sld.d* (2).
Inheritance:
Monofactorial recessive (5, 6).
Located in chromosome 7HS [5S] (4), near AFLP marker E 4134-2 in subgroup 6 of the Proctor/Nudinka map (4).
Description:
Plants with the *sld4.d* gene have reduced vigor and are light green in color during early stages of growth (6). The *sld4.d* mutant is apparently very environmentally sensitive in the Bowman derived line. Plants can vary from less than 1/2 to 3/4 of normal height and heading can be delayed over 10 days in certain environments. The number of fertile spikelets per spike varies from 2/3 normal to near normal. Depending on the delay in heading, kernels vary from very thin to near normal. Grain yield of the Bowman backcross-derived line can vary from very low to nearly normal (1).
Origin of mutant:
A neutron induced mutant in Two-row Glacier (5). (Glacier is available as CIho 6976.)
Mutational events:
sld4.d in Two-row Glacier (80-T-5899-2-13, DWS1368) (2, 3, 5).
Mutant used for description and seed stocks:
sld4.d in Two-row Glacier (GSHO 2479); *sld4.d* in Bowman (PI 483237)*7 (GSHO 1880).
References:
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5. Ramage, R.T., and P. Curtis. 1981. A light green, dwarf mutant located on chromosome 2. Barley Genet. Newsl. 11:37-38.
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Prepared:
J.D. Franckowiak. 2002. BGN 32:89.
Revised:
J.D. Franckowiak. 2007. BGN 37:218.

BGS 101, Absent lower laterals 1, *als1*

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

Previous nomenclature and gene symbolization:
Absent lower laterals = *als* (2).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 3HL (2, 3, 5, 6), about 31.2 cM distal from the *uzu1* (uzu 1) locus (2), about 39.7 cM proximal from the *cur2* (curly 2) locus (3), and near AFLP marker E4234-11 in subgroup 28 of the Proctor/Nudinka map (4).
Description:
Lateral spikelets at the base of the spike fail to develop or are partially developed. Tillers are large, coarse, and stiff, and only 1 or 2 tillers are produced in the six-rowed stock. The plants resemble those of the (*cul2*) uniculm 2 mutant (2). Plants of the Bowman backcross-derived line commonly produce 3 to 5 tillers with short spikes; and seed yields are very low (1).
Origin of mutant:
A gamma-ray induced mutant in Montcalm (CIho 7149) (2).
Mutational events:
als1.a in Montcalm (Alb Acc 281) (2).
Mutant used for description and seed stocks:
als1.a in Montcalm (GSHO 1065); *als1.a* in Bowman (PI 483237)*7 (GSHO 1990).
References:
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Prepared:
T. Tsuchiya and T.E. Haus. 1971. BGN 1:123.
Revised:
J.D. Franckowiak. 1997. BGN 26:135.
J.D. Franckowiak. 2007. BGN 37:219.

BGS 102, Uzu 1, *uzu1*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (8, 9, 11). These organs are often reduced in length and increased in width. Changes in organ length are temperature sensitive, but heading date and maturity are unaltered. The coleoptile of uzu plants shows a prominent projection or hook near the apex. Sometimes the coleoptile of the mutant shows a V-shaped notch on the side opposite from the projection. Thus, the apex of the coleoptile has two notches, one on each side (9, 13, 14). The temperature sensitive reduction in culm length of *uzu1.a* plants ranges from less than 15% in cool environments to over 75% in warm ones. Chono et al. (1) reported that the *uzu1.a* or *HVBRI1* gene is caused by a mutation that changed a highly conserved residue of the kinase domain of *BRI1* (*Arabidopsis* BR-insensitive 1) (brassinosteroids) receptor protein from His-857 to Arg-857.

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

1. Chono, M., I. Honda, H. Zeniya, K. Yoneyama, D. Saisho, K. Takeda, S. Takatsuto, T. Hoshino and Y. Watanabe. 2003. A semidwarf phenotype of barley uzu results from a nucleotide substitution in the gene encoding a putative brassinosteroid receptor. Plant Physiol. 133:1209-1219.

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36:25-38. [In Japanese.]
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7. So, M., S. Ogura, and Y. Imai. 1919. [A linkage group in barley.] J. Sci. Agric. Soc. Jpn. 208:1093-1117. [In Japanese.]
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Prepared:

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

Revised:

T. Tsuchiya. 1984. BGN 14:92.
J.D. Franckowiak and T. Konishi. 1997. BGN 26:136-137.
J.D. Franckowiak. 2007. BGN 37:220-221.

BGS 108, Albino lemma 1, *alm1*

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

Previous nomenclature and gene symbolization:
Albino lemma = *al* (9).
Eburatum = *ebu-a* (3).

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

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

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

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

Mutant used for description and seed stocks:
alm1.a in Russia 82 (GSHO 270); *alm1.a* in Bowman (PI 483237)*8 (GSHO 1953).

References:

1. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. Theor. Appl. Genet. 103:415-424.
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6. Lundqvist, U. (Unpublished).
7. Moriya, I., and R. Takahashi. 1980. Linkage studies of three barley mutants. Barley Genet. Newsl. 10:47-51.
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thick and stiff culms. Barley Genet. Newsl. 3:45-47.
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Prepared:

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

Revised:

T. Tsuchiya. 1980. BGN 10:111.
J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:143.
J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:222-223.

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

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

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 5 = Pa_5 (6, 7).
Resistance to *Puccinia hordei* B = *B* (5).
Resistance to *Puccinia hordei* Otth = X (5, 6).
Resistance to *Puccinia hordei* Otth = Pa_x (6).
Resistance to *Puccinia hordei* 6 = *Rph6.f* (11).

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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resistance gene *Rph5* in barley. Crop Sci. 43:388-393.
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7. Roane, C.W., and T.M. Starling. 1970. Inheritance of reaction to *Puccinia hordei* in barley. III. Genes in the cultivars Cebada Capa and Franger. Phytopathology 60:788-790.
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11. Zhong, S., R.J. Effertz, Y. Jin, J.D. Franckowiak, and B.J. Steffenson. 2003. Molecular mapping of the leaf rust resistance gene *Rph6* in barley and its linkage relationships with *Rph5* and *Rph7*. Phytopathology 93:604-609.

Prepared:

C.W. Roane. 1976. BGN 6:122.
J.D. Franckowiak and Y. Jin. 1997. BGN 26:501, as BGS 575, Reaction to *Puccinia hordei* 6, *Rph6*.

Revised:

J.D. Franckowiak and Y. Jin. 1997. BGN 26:157.
J.D. Franckowiak and B.J. Steffenson. 2005. BGN 35:188.
J.D. Franckowiak. 2007. BGN 37:224-225.

BGS 130, Early maturity 10, *eam10*

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

Previous nomenclature and gene symbolization:
Early maturity sp = ea_{sp} (8).

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

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

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

Mutational events:
eam10.m in Super Precoz 2H plus a dominant maturity enhancer (4, 5, 7);
eam10.m in Amber Nude without the enhancer (4).

Mutant used for description and seed stocks:
eam10.m in Super Precoz 2H (GSHO 2504); *eam10.m* in Amber Nude (GSHO 2505); *eam10.m* from Super Precoz in Bowman (PI 483237)*5.

References:
1. Börner, A., G.H. Buck-Sorlin, P.M. Hayes, S. Malyshev, and V. Korzun. 2002. Molecular mapping of major genes and quantitative trait loci determining flowering time in response to photoperiod in barley. Plant Breed. 121:129-132.
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5. Franckowiak, J.D. (Unpublished).
6. Gallagher, L.W. (Unpublished).
7. Gallagher, L.W., A.A. Hafez, S.S. Goyal, and D.W. Rains. 1994. Nuclear mutations affecting chloroplastic pigments of photoperiod-insensitive barley. Plant Breed. 113:65-70.
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31:256-261.

Prepared:

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

Revised:

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

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

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

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth y = *Pay* (7).
Resistance to *Puccinia hordei* Otth 5 = Pa_5 (10).
Resistance to *Puccinia hordei* Otth 7 = *Pa7* (8).

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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Prepared:

J.D. Franckowiak and Y. Jin. 1997. BGN 26:173.

Revised:

J.D. Franckowiak. 2007. BGN 37:228-229.

BGS 142, Brachytic 8, *brh8*

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

Previous nomenclature and gene symbolization:
Brachytic-ad = *brh.ad* (3).

Inheritance:
Monofactorial recessive (3, 5, 6).
Located in chromosome 3HS (4), near the *btr1* (non-brittle rachis 1) locus based on linkage drag (4), about 26.3 cM proximal from SSR marker HVM60 in bin 3H-08 (1).

Description:
In the Bowman backcross-derived line, *brh8* plants are 3/4 to 5/6 of normal height and awns are 2/3 to 3/4 of normal length. The peduncle is 3/4 normal length. The seedling leaf of *brh8* plants is shorter and wider than those of normal sibs and the leaf blades are slightly wider. Kernels of *brh8* plants are shorter than that of normal sibs and their weights are nearly15% lower. Heading dates are 2 or 3 days later, spikes have 3 to 4 more kernels, and rachis internodes are about 20% shorter. Grain yield is nearly normal (1, 2).

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

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

Mutant used for description and seed stocks:
brh8.ad in Birgitta (GSHO 1671); *brh8.ad* in Bowman (PI 483237)*8 (GSHO 1944).

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

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

BGS 148, Brachytic 14, *brh14*

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

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

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 3HL (2), approximately 24.9 cM proximal from SSR marker Bmac0029 in bin 3H-15 (2).

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

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

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

Mutant used for description and seed stocks:
brh14.q in Akashinriki (GSHO 1682); *brh14.q* in Bowman (PI 483237)*6 (GSHO 2175).

References:
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2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
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Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:231.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial dominant (3).
Located in chromosome 3H centromeric region (1), approximately 2.5 cM from RAPD marker OPO08-700 (1).
Description:
Crown rust of barley was identified as a new disease of barley in North America (2). In seedling tests, resistant cultivars exhibited necrotic or chlorotic flecks (0; to ; infection types) at infection sites and no sporulation (3). Adult plant reactions of Hor2596 were resistant to moderately resistant (3). Hor 2596 is one of the differential lines for barley leaf rust (caused by *Puccinia hordei*), see BGS 032, *Rph9.i* (reaction to *Puccinia hordei* 9). The F1 plants from the Bowman/Hor2596 cross exhibited slightly higher infection types (1,2 reaction) than the resistant parent (3).
Origin of mutant:
Natural occurrence in Abyssinian (Hor 2596, CIho 1234) (3).
Mutational events:
Rpc1.a in Hor 2596 (3).
Mutant used for description and seed stocks:
Rpc1.a in Hor 2596 (GSHO 1601) (3).
References:
1. Agrama, H.A., L. Dahleen, M. Wentz, Y, Jin, and B. Steffenson. 2004. Molecular mapping of the crown rust resistance gene *Rpc1* in barley. Phytopathology 94:858-861.
2. Jin, Y., and B. Steffenson. 1999. *Puccinia coronata* var. *hordei* nov.: morphology and pathogenicity. Mycologia 91:877-884.
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Prepared:
Y. Jin and J.D. Franckowiak. 2007. BGS 37:232.

BGS 155, Glossy leaf 1, *glf1*

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

Previous nomenclature and gene symbolization:
Waxless bloom on leaves = *w1* (11).
Glossy = *gl* (9).
Glossy leaves = *gl* (16).
Glossy leaf = *gl* (15).
Glossy seedling *2* = *gl2* (3, 9).
Eceriferum-zh = *cer-zh* (4).

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

Description:
Surface wax coating on the leaf blade appears absent from the seedling stage to near maturity, and leaves have a shiny appearance (wax code ++ ++ -) (4). Plants are semidwarf, relatively weak, and late in heading. The stock in the Bonus is highly sterile (4), but the Bowman backcross-derived line has nearly complete fertility. The lack of surface waxes reduces the ability of growing germ tube of certain fungi to find the stomata openings (10).

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

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

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

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Prepared:

T.E. Haus and T. Tsuchiya. 1971. BGN 1:141 as BGS 155, Glossy seedling, *gl*; and BGN 1:145 as BGS 159, Glossy seedling 2, *gl2*.

U. Lundqvist. 1975. BGN 5:144 as BGS 426, Eceriferum-zh, *cer-zh*.

Revised:

T. Tsuchiya. 1980. BGN 10:114 as BGS 155, Glossy seedling, *gl*; and BGN 10:116 as BGS 159, Glossy seedling 2, *gl2*.

U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:181-182.

U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:233-234.

BGS 157, Brachytic 2, *brh2*

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

Previous nomenclature and gene symbolization:
Brachytic 2 = *br2* (9).
Breviaristatum-l = *ari-l* (4, 5).

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

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

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

Mutational events:
brh2.b in Svanhals (Kmut 28, OUM283) (8); *ari-l.3* (NGB 115848) in Bonus (PI 189763) (5); *ari-l.132* (NGB 115942) in Foma (CIho 11333) (6); *ari-l.135* (NGB 115945), *-l.145* (NGB 115956), *-l.214* (NGB 116023), *-l.237* (NGB 116047) in Foma, *-l.257* (NGB 116066) in Kristina (NGB 1500) (5).

Mutant used for description and seed stocks:
brh2.b in Svanhals (GSHO 573); *ari-l.3* in Bonus (GSHO 1660); *brh2.b* in Bowman (PI 483237)*7 (GSHO 2016); *ari-l.3* in Bowman*7 (GSHO 2017).

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Barley Genet. Newsl. 1:51-58.
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Prepared:

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

Revised:

T. Tsuchiya. 1980. BGN 10:115.
J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:184.
J.D. Franckowiak and L. S. Dahleen. 2007. BGN 37:235-236.

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

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

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Prepared:

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

Barley Genetics Newsletter (2007) 37: 188-301

Revised:

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

BGS 179, Hairy leaf sheath 1, *Hsh1*

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

Previous nomenclature and gene symbolization:
Hairy leaf sheath = *Hs* (7).
Inheritance:
Monofactorial dominant (4, 5, 6).
Located in chromosome 4HL (6), over 8.7 cM proximal from the *yhd1* (yellow head 1) locus, and over 22.5 cM distal from the *mlo* (reaction to *Erysiphe graminis hordei*-o) locus (3, 5), in bin 4H-12 about 1.1 cM proximal from RFLP marker HVM067 (2).
Description:
Short hairs (1 to 3 mm) are scattered or in rows on leaf sheaths of the basal part of the plant. The density of hairs varies considerably among cultivars and with changes in growing conditions. With few exceptions, no hairs are observed on the sheath of upper leaves (4, 5). Heterozygotes and smooth awned cultivars seem to have fewer hairs.
Origin of mutant:
Natural occurrence in a few cultivars and in some accessions of *Hordeum vulgare* subsp *spontaneum* (1, 5, 6).
Mutational events:
Hsh1.a introduced into cultivated barley from its wild progenitor (5).
Mutant used for description and seed stocks:
Hsh1.a in Kimugi (OUL012, GSHO 986) (5, 6); *Hsh1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)*10 (GSHO 2026).
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2. Costa, J.M., A. Corey, M. Hayes, C. Jobet, A. Kleinhofs, A. Kopisch-Obusch, S.F. Kramer, D. Kudrna, M. Li, O. Piera-Lizaragu, K. Sato, P. Szues, T. Toojinda, M.I. Vales, and R.I. Wolfe. 2001. Molecular mapping of the Oregon Wolfe Barleys: a phenotypically polymorphic doubled-haploid population. Theor. Appl. Genet. 103:415-424.
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Prepared:

R. Takahashi. 1972. BGN 2:184 as BGS 158.
Revised:
J.D. Franckowiak and T. Konishi. 1997. BGN 26:202.
J.D. Franckowiak. 2007. BGN 37:240-241.

BGS 185, Brachytic 5, *brh5*

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

Previous nomenclature and gene symbolization:
Brachytic-m = *brh.m* (3).

Inheritance:
Monofactorial recessive (3, 5).
Located in chromosome 4HS (4), near the *int-c* (intermedium spike-c) locus (4), about 13.0 cM proximal from SSR marker Bmac0310 near the boundary between bins 4H-06 and 4H-07 (1).

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

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

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

Mutant used for description and seed stocks:
brh5.m in Birgitta (GSHO 1678); *brh5.m* in Bowman (PI 483237)*7 (GSHO 2001).

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

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

BGS 186, Slender dwarf 3, *sld3*

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

Previous nomenclature and gene symbolization:
Anthocyanin-free = *ant-567* (5).
Proanthocyanidin-free 17.567 = *ant17.567* (4).
Slender dwarf e = *sld.e* (3).

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

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

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

Mutational events:
sld3.e in *ant17.567* (DWS1050) (1).

Mutant used for description and seed stocks:
sld3.e in Bowman/*ant17.567* (GSHO 2480); *sld3.e* in Bowman (PI 483237)*7 (GSHO 1998).

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

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

BGS 187, Brachytic 9, *brh9*

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

Previous nomenclature and gene symbolization:
Brachytic-k = *brh.k* (3).
Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 4HS (1), about 11.7 cM distal from SRR marker Bmac0310 in bin 4H-06 (1).
Description:
Culms and peduncles are about 3/4 normal length and awns are 3/4 to 5/6 of normal length. Rachis internodes are slightly shorter than those of normal sibs. Seedling leaves of *brh9* plants are relatively short. The kernels of *brh9* plants are shorter and kernel weight are about 20% lower than those of normal sibs. Grain yields averaged less than 1/2 normal (1, 2); however, plants appeared nearly normal when grown in Dundee, Scotland (2). The *brh9.k* gene was found to non-allelic at *brh5* locus, which is located in the same region of 4HS (1).
Origin of mutant:
A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).
Mutational events:
brh9.k in Birgitta (17:14:4, DWS1006) (4, 5).
Mutant used for description and seed stocks:
brh9.k in Birgitta (GSHO 1676); *brh9.k* in Bowman (PI 483237)*6 (GSHO 2170).
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. BGN 37:244.

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

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

Previous nomenclature and gene symbolization:
Black lemma and caryopsis = *B* (6).
Black pericarp = *Bk* (1).
Black lemma and pericarp = *B* (7).

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

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

Origin of mutant:
Natural occurrence in several cultivars (6, 7).

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

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

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Prepared:

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

Revised:

J.D. Franckowiak and U. Lundqvist. 1997. BGN 26:209.
J.D. Franckowiak. 2007: BGN 37:245-246.

BGS 214, Early maturity 8, *eam8*

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

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

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

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

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

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

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

Mutant used for description and seed stocks:

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

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Prepared:

S. Yasuda. 1972. BGN 2:198.

Revised:

J.D. Franckowiak, U. Lundqvist, T. Konishi, and L.W. Gallagher. 1997. BGN 26:213-215.

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

BGS 222, Necrotic leaf spot 1, *nec1*

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

Previous nomenclature and gene symbolization:
Mutant no. 10 (2).
Parkland spot = *sp,,b* (1).

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

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

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

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

Mutant used for description and seed stocks:
nec1.a in Carlsberg II (GSHO 989); *nec1.a* from R.I. Wolfe's Chromosome 5 Marker Stock in Bowman (PI 483237)*7 (GSHO 2052).

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

Prepared:

J. Jensen. 1981. BGN 11:101.

Revised:

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

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

BGS 253, Uniculm 2, *cul2*

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

Previous nomenclature and gene symbolization:
Uniculm 2 = *uc2* (8).
Inheritance:
Monofactorial recessive (8).
Located in chromosome 6HL (4, 6), about 1.3 cM distal from the *gsh4* (glossy sheath 4) locus (3, 5), about 11.4 cM from the *msg36* (male sterile genetic 36) locus (3, 5), about 2.2 cM proximal from the *rob1* (orange lemma 1) locus (3, 4, 5), about 8.8 cM from RFLP markers cMWG679 and ABG458 (1), and about 6.2 cM from AFLP marker E4343-10 in subgroup 54 of the Proctor/Nudinka map (7).
Description:
The *cul2* plants have a single elongated culm (stem), the stem is much greater in diameter than normal, and plants are usually earlier than normal (8). The *cul2* plants initiate vegetative axillary meristems, but tillers fail to develop (1). Irregular placement of some spikelets and male fertility in lateral spikelets occur in the original stock (5) and in the Bowman backcross-derived line (1). Yield of uniculm plants is not restored when grown under high plant populations (2). Double mutant combinations with most other mutants that affect tiller number resulted in a uniculm vegetative phenotype (1).
Origin of mutant:
A thermal neutron induced mutant in Kindred (CIho 6969) (8).
Mutational events:
cul2.b in Kindred (GBC379) (5), *cul2.k* (*unc*^{k}) in an unknown cultivar from the Max-Planck-Institut für Züchtungsforschung (7).
Mutant used for description and seed stocks:
cul2.b in Kindred (GSHO 531, CIho 115530); *cul2.b* in Bowman (PI 483237)*4 (GSHO 2074); *cul2.b* plus *rob1.a* from sel 79Cal in Bowman*8 (GSHO 2075).
References:
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loci hosting 29 developmental mutants. Heredity 90:390-396.
8. Shands, R.G. 1963. Inheritance and linkage of orange lemma and uniculm characters. Barley Newsl. 6:35-36.

Prepared:

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

Revised:

J.D. Franckowiak. 1997. BGN 26:234.
J.D. Franckowiak. 2007. BGN 37:253-254.

BGS 254, Orange lemma 1, *rob1*

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

Previous nomenclature and gene symbolization:
Orange lemma = *pl* (14).
Orange lemma = *br* (1, 2).
Orange lemma = *o* (15).
Robiginosum-o = *rob-o* (6).

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

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

Origin of mutant:
A spontaneous mutant in CIho 5649 (15).

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

Mutant used for description and seed stocks:
rob1.a in CIho 5649 (GSHO 707); *rob1.a* in Bowman (PI 483237)*8 (GSHO 2069).

References:
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Prepared:

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

Revised:

J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997. BGN 26:235-236.
J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:255-256.

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

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

Previous nomenclature and gene symbolization:
Erectoides-17 = *ert-17* (2).
Dense spike = *la* (4).
Dense spike 9 = *l9* (4).

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

Description:
Spikes are very compact with rachis internode length values from 1.2 to 1.5 mm. Plants are about 2/3 normal height. Partial fertility and reduced vigor are noted among *ert-e* mutants. The peduncle is very short and spikes often emerge from the side of the flag sheath (7, 9). A large deficiency of mutant plants is frequently noted in segregating populations (7). Spike density decreases greatly when plants are treated with GA_3 as the flag leaf emerges (10). The mutant *ert-e.17* is allelic to mutant *dsp9.i* (dense spike 9, see BGS 258) (1).

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

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

Mutant used for description and seed stocks:
ert-e.17 in Bonus (GSHO 477); *ert-e.17* in Bowman (PI 483237)*6 (GSHO 2091); *dsp9.i* in Akashinriki (GSHO 1774); *dsp9.i* in Bowman (PI 483237)*7 (GSHO 2090).

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

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

Revised as BGS 258:

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

Revised:

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

BGS 306, Variegated 1, *var1*

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

Previous nomenclature and gene symbolization:
Variegated = *va* (4).
Inheritance:
Monofactorial recessive (4).
Located in chromosome 5HL [7L] (4), about 4.6 cM proximal from the *raw1* (smooth awn 1) locus (3. 4), in bin 5H-09 about 29.2 cM proximal from the *Rph9* (reaction to *Puccinia hordei* 9) locus (1).
Description:
Narrow white stripes develop on young leaves, but they are not as well defined than those of white streak 7 (*wst7*). White stripes are visible on the foliage and stems of older plants (3). When sown in plots, selections homozygous for the *var1.a* gene have a whitish cast until heading (2). The Bowman backcross-derived line for *var1* shows slightly delayed heading and may be slightly shorter (2).
Origin of mutant:
A gamma-ray induced mutant in Montcalm (CIho 7149) (4).
Mutational events:
var1.a in Montcalm (Alb Acc 311) (4).
Mutant used for description and seed stocks:
var1.a in Montcalm (GSHO 1278); *var1.a* in Bowman (PI 483237)*7 (GSHO 2121).
References:
1. Borovkova, I.G., Y. Jin, and B.J. Steffenson. 1998. Chromosomal location and genetic relationship of leaf rust resistance genes *Rph9* and *Rph12* in barley. Phytopathology 88:76-80.
2. Franckowiak, J.D. (Unpublished).
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Prepared:
T.E. Haus and T. Tsuchiya. 1971. BGN 1:165.
Revised:
J.D. Franckowiak. 1997. BGN 26:257.
J.D. Franckowiak. 2007. BGN 37:259.

BGS 348, Early maturity 5, *Eam5*

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

Previous nomenclature and gene symbolization:
Early maturity = *Ea* (5, 8).
Early maturity 3 = *Ea3* (2, 3).
Early maturity 5 = *Ea5* (4).
Early maturity 8 = *Ea8* (6).

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

Description:
Plants with the *Eam5* gene head 3 to 10 days earlier than normal sibs under short-day conditions (1, 5). Early heading is commonly associated a shorter stature compared to normal sibs. The slight reduction in height is also observed under long-day conditions. Peduncles and rachis internodes are slightly shortened (1). The *Eam5* gene appears to be the common early maturity gene present in winter sown spring barley cultivars used in China and Japan; and it is present in the ICARDA/CIMMYT barley lines developed in Mexico. Complex interactions with other genes conditioning photoperiod response have been observed (1, 9). Takahashi and Yasuda (7) classified plants that were about 10 days earlier than normal spring barley as having the *Sgh2.II* (spring growth of habit 2, grade 2) gene, but an earliness factor closely linked to the rough awn gene was earlier identified in spring barley (8).

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

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

Mutant used for description and seed stocks:
Eam5.x in CMB85-533; *Eam5.x* in Bowman (PI 483237)*6 (GSHO 3424).

References:
1. Franckowiak, J.D. (Unpublished).
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Prepared:
J.D. Franckowiak. 2002. BGN 32:109.
Revised:
J.D. Franckowiak and G. Yu. 2007. BGN 37:260-261.

BGS 349, Brachytic 4, *brh4*

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

Previous nomenclature and gene symbolization:
Brachytic-j = *brh.j* 4, 5).

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 2HL (3), about 14.1 cM distal from SSR marker EBmac0850 in bin 2H-08 (1).

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

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

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

Mutant used for description and seed stocks:
brh4.j in Birgitta (GSHO 1675); *brh4.j* in Bowman (PI 483237)*7 (GSHO 2130).

References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
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Prepared:
J.D. Franckowiak. 2002. BGN 32:110.

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

BGS 350, Brachytic 6, *brh6*

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

Previous nomenclature and gene symbolization:
Brachytic-r = *brh.r* (3).
Brachytic-s = *brh.s* (3).

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

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

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

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

Mutant used for description and seed stocks:
brh6.r in Akashinriki (GSHO 1683); *brh6.r* in Bowman (PI 483237)*7 (GSHO 2132).

References:
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7. Konishi, T. 1977. Effects of induced dwarf genes on agronomic characters in barley. p. 21-38. *In* Use of dwarf mutations. Gamma-Field Symposium No. 16.

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

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

BGS 377, Shrunken endosperm genetic 1, *seg1*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se1* (4).
Inheritance:
Monofactorial recessive (3).
Located in chromosome 7HL [1L] (3), linked to the *msg23* (male sterile genetic 23) locus (5).
Description:
Seed is long and thin and the 100-kernel weight is about 33% of normal. Good stands can be established in the field if optimum environmental conditions prevail during germination and emergence (3, 5). This mutant is associated with an increase in percentage lysine in the protein (5). Tannins are not deposited in *seg1* chalazal cell central vacuoles, but rather appeared to cause cytoplasmic disorganization and cell death (1). Light microscopy revealed that *seg1* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (2).
Origin of mutant:
A spontaneous mutant in Betzes (PI 129430) (3).
Mutational events:
seg1.a in Betzes (3, 4).
Mutant used for description and seed stocks:
seg1.a in Betzes (GSHO 750); *seg1.a* in Bowman (PI 483237)*7 (GSHO 1852).
References:
1. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1984. Development of tannin vacuoles in chalazal and seed coat of barley in relation to early chalazal necrosis in the seg1 mutant. Planta 161:540-549.
2. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
3. Jarvi, A.J. 1970. Shrunken endosperm mutants in barley, *Hordeum vulgare*. Ph.D. Thesis. Montana State Univ., Bozeman.
4. Jarvi, A.J., and R.F. Eslick. 1971. BGS 377, Normal vs. shrunken endosperm, *se1*. Barley Genet. Newsl. 1:190.
5. Jarvi, A.J., and R.F. Eslick. 1975. Shrunken endosperm mutants in barley. Crop Sci. 15:363-366.
Prepared:
A.J. Jarvi and R.F. Eslick. 1971. BGN 1:190.
Revised:
R.F. Eslick. 1976. BGN 6:135.
T. Tsuchiya. 1980. BGN 10:124.
J.D. Franckowiak. 1997. BGN 26:325.
J.D. Franckowiak. 2007. BGN 37:264.

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BGS 379, Shrunken endosperm genetic 3, *seg3*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se3* (5).
Proanthocyanidin-free 17 = *ant17* (3).

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

Description:
Seed size is reduced to about 33% of normal when grown under field conditions. Seeds are long and thin similar to those from *seg1* plants; seeds are viable and good stand establishment is possible (6). Light microscopy revealed that *seg3* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (2). The mutant *ant17.148* is an allele at the *seg3* locus (3); thus, all mutants at the proanthocyanidin-free 17 (*ant17*) locus might be alleles at the shrunken endosperm genetic 3 locus. Alleles at the *seg3* locus that have been examined in the Bowman genetic background showed a variable reduction in kernel weight: *ant17.148* and *seg3.c* about 1/3 normal and *ant17.567* about 3/4 normal (3). The *seg3* locus was named before the *ant17* locus, but many more mutants were identified at the *ant17* locus. Therefore, see BGS 599 for a complete listing of *ant1*7 mutants.

Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (4).

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

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

References:
1. Boyd, P.W., and D. E. Falk. 1990. (Personal communications).
2. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
3. Franckowiak, J.D. (Personal communications).
4. Jarvi, A.J. 1970. Shrunken endosperm mutants in barley, *Hordeum vulgare*. Ph.D. Thesis. Montana State Univ., Bozeman.
5. Jarvi, A.J., and R.F. Eslick. 1971. BGS 379, Normal vs. shrunken endosperm, *se3*. Barley Genet. Newsl. 1:191.
6. Jarvi, A.J., and R.F. Eslick. 1975. Shrunken endosperm mutants in barley. Crop Sci. 15:363-366.

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

Revised:

R.F. Eslick. 1976. BGN 6:137.
T. Tsuchiya. 1980. BGN 10:126.
J.D. Franckowiak. 1997. BGN 26:327.
J.D. Franckowiak and U. Lundqvist. 2007. BGN 37:265-266.

BGS 380, Shrunken endosperm genetic 4, *seg4*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se4* (3).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 7HL [1L] (2), over 34.0 cM from the centromere (4).
Description:
Under field conditions in the original mutant, seed size is reduced to about 38% of normal and seed set is about 50% of normal. Stand establishment is poor under field conditions (2, 4). Endosperms of *seg4* were characterized by progressively distorted, disorganized growth, but the quantity of endosperm tissue at maturity varied from severely reduced to near normal (1). The stock described in the 1997 revision was incorrect and was in fact a mixture with GSHO 755 (BGS 382, shrunken endosperm xenia 1, *sex1*), which was identified by Dr. Marion Röder, IPK, Gatersleben.
Origin of mutant:
A spontaneous mutant in Compana (PI 539111) (2).
Mutational events:
seg4.d in Compana (2, 3).
Mutant used for description and seed stocks:
seg4.d in Compana (GSHO 753).
References:
1. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
2. Jarvi, A.J. 1970. Shrunken endosperm mutants in barley, *Hordeum vulgare*. Ph.D. Thesis. Montana State Univ., Bozeman.
3. Jarvi, A.J., and R.F. Eslick. 1971. BGS 380, Normal vs. shrunken endosperm, *se4*. Barley Genet. Newsl. 1:192.
4. Jarvi, A.J., and R.F. Eslick. 1975. Shrunken endosperm mutants in barley. Crop Sci. 15:363-366.
Prepared:
A.J. Jarvi and R.F. Eslick. 1971. BGN 1:192.
Revised:
R.F. Eslick. 1976. BGN 6:138.
T. Tsuchiya. 1980. BGN 10:127.
J.D. Franckowiak. 1997. BGN 26:328.
J.D. Franckowiak. 2007. BGN 37:267.

BGS 396, Shrunken endosperm genetic 6, *seg6*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se6* (3).
Inheritance:
Monofactorial recessive (2).
Located in chromosome 3HL (4).
Description:
Seed size is reduced, but the degree reduction is affected by environment. Seed weights of 25, 50, and 75% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (4). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg6.g* plants can be used to establish stands under field conditions (4). Light microscopy revealed that *seg6* mutants exhibited premature termination of grain filling because of the necrosis and crushing of the chalazal and nucellar projection of the pericarp early during grain filling (1).
Origin of mutant:
A spontaneous mutant in Ingrid (CIho 10083) (3).
Mutational events:
seg6.f in an unknown hybrid, *seg6.g* in Ingrid (3).
Mutant used for description and seed stocks:
seg6.g in Ingrid (GSHO 2467); *seg6.g* in Bowman (PI 483237)*4 (GSHO 1975).
References:
1. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
2. Ramage, R.T. 1983. Chromosome location of shrunken endosperm mutants *seg6g* and *seg8k*. Barley Genet. Newsl. 13:64-65.
3. Ramage, R.T., and R.F. Eslick. 1975. BGS 396, Shrunken endosperm, xenia, *se6*. Barley Genet. Newsl. 5:114.
4. Ramage, R.T., and J.F. Scheuring. 1976. Shrunken endosperm mutants *seg6* and *seg7*. Barley Genet. Newsl. 6:59-60.
Prepared:
R.T. Ramage and R.F. Eslick. 1975. BGN 5:114.
Revised:
R.T. Ramage and R.F. Eslick. 1976. BGN 6:141.
T. Tsuchiya. 1980. BGN 10:130.
R.T. Ramage. 1983. BGN 13:115.
J.D. Franckowiak. 1997. BGN 26:344.
J.D. Franckowiak. 2007. BGN 37:268.

BGS 397, Shrunken endosperm genetic 7, *seg7*

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

Previous nomenclature and gene symbolization:
Shrunken endosperm = *se7* (4).

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

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

Origin of mutant:
A spontaneous mutant in Ingrid (CIho 10083) (3).

Mutational events:
seg7.h in Ingrid (4).

Mutant used for description and seed stocks:
seg7.h in Ingrid (GSHO 2468); *seg7.h* in Bowman (PI 483237)*3 (GSHO 2352).

References:
1. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
2. Franckowiak, J.D. (Unpublished).
3. Ramage, R.T., and R.F. Eslick. 1975. BGS 397, Shrunken endosperm, xenia, *se7*. Barley Genet. Newsl. 5:115.
4. Ramage, R.T., and J.F. Scheuring. 1976. Shrunken endosperm mutants *seg6* and *seg7*. Barley Genet. Newsl. 6:59-60.

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

Revised:
R.T. Ramage and R.F. Eslick. 1976. BGN 6:142.
T. Tsuchiya. 1980. BGN 10:131.
J.D. Franckowiak. 1997. BGN 26:345.
J.D. Franckowiak. 2007. BGN 37:269.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (3).
Location in chromosome 2HS (1), in bin 2H-01 about 16.8 distal from SSR marker Bmac0134 (1).
Description:
Surface wax coating on the spike appears slightly reduced (wax code + ++ ++) (3). The reduction in the surface wax seemed greater in plants selected from the backcrosses to Bowman (wax code +/- ++ ++).
Origin of mutant:
An ethyl methanesulfonate and neutron induced mutant in Foma (CIho 11333) (2).
Mutational events:
cer-zt.389 (NGB 111276)*, -zt.479* (NGB 111367) in Foma (2).
Mutant used for description and seed stocks:
cer-zt.389 in Foma (GSHO 1527); *cer-zt.389* in Bowman (PI 483237)*2 (GSHO 2205).
References:
1. Dahleen, L.S., and J.D. Franckowiak. 2006. SSR linkages to eight additional morphological marker traits. Barley Genet. Newsl. 36:12-16.
2. Lundqvist, U. (Unpublished).
3. Lundqvist, U., and D. von Wettstein. 1971. Stock list for the eceriferum mutants. Barley Genet. Newsl. 1:97-102.
Prepared:
U. Lundqvist. 1975. BGN 5:155.
Revised:
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:389.
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:270.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (3).
Location is unknown.
Description:
Surface wax coating on the leaf blade is reduced (wax code ++ ++ +) (3). In the Bowman backcross-derived line, mutant plants have pale green leaves, heading is delayed by several days, and plants are slightly shorter (1).
Origin of mutant:
A neutron induced mutant in Bonus (PI 189763) (2).
Mutational events:
cer-yf.652 (NGB 111540), *-yf.804* (NGB 111692) in Bonus (3).
Mutant used for description and seed stocks:
cer-yf.652 in Bonus (GSHO 1539); *cer-yf.652* in Bowman (PI 483237)*3 (GSHO 2212).
References:
1. Franckowiak, J.D. (Unpublished).
2. Lundqvist, U. (Unpublished).
3. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. Barley Genet. Newsl. 3:110-112.
Prepared.
U. Lundqvist. 1975. BGN 5:167.
Revised:
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:401.
Revised:
U. Lundqvist. 2007. BGN 37:271.

BGS 455, Shrunken endosperm genetic 8, *seg8*

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (2).
Located in chromosome 7H [1] (4).
Description:
Seed size is reduced and maturity is delayed. Seed weights of 24, 23, and 27% of normal are reported for plants grown in the field in Arizona, in the field in Montana, and in the greenhouse in Arizona, USA, respectively (4). Pollen mother cell meiosis and pollen fertility are normal. Seed from *seg8.k* plants can be used to establish stands under field conditions (4). Endosperms of *seg8* developed as two-filled lateral lobes with no central endosperm lobe, resulting in a distinct dorsal crease (1).
Origin of mutant:
A spontaneous mutant in 60Ab1810-53 (CIho 15686) (3).
Mutational events:
seg8.k in 60Ab1810-53 (3, 4).
Mutant used for description and seed stocks:
seg8.k in 60Ab1810-53 (GSHO 2469); *seg8.k* in Bowman (PI 483237)*5 (GSHO 1854).
References:
1. Felker, F.C., D.M. Peterson, and O.E. Nelson. 1985. Anatomy of immature grains of eight material effect shrunken endosperm barley mutants. Amer. J. Bot. 72:248-256.
2. Ramage, R.T. 1983. Chromosome location of shrunken endosperm mutants *seg6g* and *seg8k*. Barley Genet. Newsl. 13:64-65.
3. Ramage, R.T., and C.L. Crandall. 1981. BGS 453, Shrunken endosperm, *seg8*. Barley Genet. Newsl. 11:103.
4. Ramage, R.T., and C.L. Crandall. 1981. Shrunken endosperm mutant *seg8*. Barley Genet. Newsl. 11:34.
Prepared:
R.T. Ramage and C.L. Crandall. 1981. BGN 11:103 as BGS 453.
Revised:
R.T. Ramage. 1983. BGN 13:116 as BGS 453.
T. Tsuchiya. 1983. BGN 13:117. BGS number changed to BGS 455.
J.D. Franckowiak. 1997. BGN 26:405.
J.D. Franckowiak. 2007. BGN 37:272.

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

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

Previous nomenclature and gene symbolization:
Laxatum-01 = *lax-01* (3, 6, 11).
Laxatum-a = *lax-a*^{01} (12).

Inheritance:
Monofactorial recessive (7, 11).
Located in chromosome 5HL [7L] (7, 10), about 2.4 cM proximal from the *ari-e* (breviaristatum-e) locus (5, 14), and about 3.1 cM from the *ert-g* (erectoides-g) locus (5, 12, 13).

Description:
Florets have five anthers with two developing from transformed lodicules (3, 15); however, the extra anthers are deficient in having two rather than four microsporangia (1). The grain is thin and angular and caryopses are exposed between the lemma and palea. The awn has a very wide base, without a distinct notch in the lemma attachment region. Rachis internodes are 13% longer than normal. Tillers arise at oblique angles giving isolated plants an appearance of a tufty growth habit (6). Treatment of leaves after tillering with GA_3 increases rachis internode length (15).

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

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

Mutant used for description and seed stocks:
lax-a.8 in Bonus (GSHO 1775); *lax-a.8* in Bowman (PI 483237)*7 (GSHO 2103).

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

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

Prepared:
H.E.B. Larsson and U. Lundqvist. 1986. BGN 16:57.
Revised:
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:421-422.
Revised:
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:273-274.

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

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

Previous nomenclature and gene symbolization:
Resistance to *Septoria passerinii* Sacc = Sep_2 (1, 2).
Inheritance:
Monofactorial incomplete dominant (2).
Location in chromosome 1HS [5S] (3), about 3.9 cM from the *Rsp3 (*reaction to *Septoria passerinii* 3) locus (2), cosegregation with SCAR marker E-ACT/M-CAA-170a and close to the *Rsp3* locus (3), about 17.6 cM proximal from marker RFLP Act8 (3).
Description:
The *Rsp2.b* gene conditions a high level of resistance to a single spore culture of *Septoria passerinii* isolated in Minnesota, USA. Pycnidia are observed in some, but not all lesions, on all F_1 plants (2).
Origin of mutant:
Natural occurrence in accession CIho 4780 (PI 70837) (2).
Mutational events:
Rsp2.b in PI 70837.
Mutant used for description and seed stocks:
Rsp2.b in PI 70837 (GSHO 2511).
References:
1. Moseman, J.G. 1972. Report on genes for resistance to pests. Barley Genet. Newsl. 2:145-147.
2. Rasmusson, D.C., and W.E. Rogers. 1963. Inheritance of resistance to septoria in barley. Crop Sci. 3:161-163.
3. Zhong, S., H. Toubia-Rahme, B.J. Steffenson, and K.P. Smith. 2006. Molecular mapping and marker-assisted selection of genes for septoria speckled leaf blotch resistance in barley. Phytopathology 96:993-999.
Prepared:
D.C. Rasmusson. 1988. BGN 18:85 as BGS 466.
Revised:
J.D. Franckowiak. 1997. BGN 26:442.
J.D. Franckowiak. 2007. BGN 37:275.

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

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

Previous nomenclature and gene symbolization:
Resistance to *Septoria passerinii* Sacc = Sep_3 (1, 2).
Inheritance:
Monofactorial incomplete dominant (2).
Location in chromosome 1HS [5S] (3), about 3.9 cM from the *Rsp2 (*reaction to *Septoria passerinii* 2) locus (2), cosegregation with SCAR marker E-ACT/M-CAA-170a and close to the *Rsp2* locus (3), about 17.6 cM proximal from marker RFLP Act8 (3).
Description:
The *Rsp3.c* gene conditions a high level of resistance to a single spore culture of *Septoria passerinii* isolated in Minnesota, USA. Infection occurs on F_1 seedlings, but is limited to a few lesions (2).
Origin of mutant:
Natural occurrence in selection II-51-43 from a Feebar/Kindred cross (CIho 10644) (2).
Mutational events:
Rsp3.c in CIho 10644.
Mutant used for description and seed stocks:
Rsp3.c in CIho 10644 (GSHO 2512).
References:
1. Moseman, J.G. 1972. Report on genes for resistance to pests. Barley Genet. Newsl. 2:145-147.
2. Rasmusson, D.C., and W.E. Rogers. 1963. Inheritance of resistance to septoria in barley. Crop Sci. 3:161-163.
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Prepared:
D.C. Rasmusson. 1988. BGN 18:86 as BGS 467.
Revised:
J.D. Franckowiak. 1997. BGN 26:443.
J.D. Franckowiak. 2007. BGN 37:276.

BGS 518, Semidwarf 1, *sdw1*

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

Previous nomenclature and gene symbolization:

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

Inheritance:

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

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

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

References:

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3. Boulger, M.C., R.G. Sears, and W.E. Kronstad. 1982. An investigation of the association between dwarfing sources and gibberellic acid response in barley. p. 550-553. *In* M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.)

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Prepared:

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

Revised:

J.D. Franckowiak. 1997. BGN 26:444-445.
J.D. Franckowiak. 2007. BGN 37:277-278.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (3).
Located in chromosome 7H [1] (2) in the centromeric region closely linked to markers Bmag0217 and Bmac0162 in bins 6 to 7 (2).
Description:
The spike is short and dense in the original mutant. Lateral spikelets are enlarged and the apex is pointed, and they occasionally have a short awn. Seed set does not occur in lateral spikelets and the central spikelets are semi-sterile (3). Plants of the original stock have a dense coating of surface waxes. In the Bowman backcross-derived line, plants are small and weak (about 1/2 normal height) and have short spikes (1/2 normal), reduced awn length (3/4 normal), and very poor seed set. Awns of plants in the derived line are semi-rough, but F1 hybrids with Bowman have semismooth awns (1).
Origin of mutant:
An ethyl methanesulfonate induced mutant in Kristina (NGB 1500) (3).
Mutational events:
int-k.47 in Kristina (3).
Mutant used for description and seed stocks:
in-k.47 in Kristina (GSHO 1770, NGB 115465); *int-k.47* in Bowman (PI 483237)*6.
References:
1. Franckowiak, J.D. (Unpublished).
2. Dahleen, L.S., and J.D. Franckowiak. 2006. SSR Linkages to Eight Additional Morphological Marker Traits. Barley Genet. Newsl. 36:12-16.
3. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. Hereditas 108:13-26.
Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:472.
Revised:
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:279.

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (4).
Location is unknown.
Description:
The spike is very short and has irregular rachis internode lengths. Lateral spikelets are enlarged and pointed, but they do not set seed. Spikelet density at the base of the spike is increased. Rachis internodes at the tip of the spike are very short, and the spike appears to have two or three fused or fasciated terminal spikelets. Tillering of *int-m* plants is increased (1, 4) and heading is slightly earlier (4).
Origin of mutant:
A sodium azide induced mutant in Bonus (PI 189763) (3).
Mutational events:
int-m.85 (NGB 115503) in Bonus (3); *int-m.la* (GSHO 1773) in Lamont (PI 512036) (2).
Mutant used for description and seed stocks:
int-m.85 in Bonus (GSHO 1772); *int-m.85* in Bowman (PI 483237)*7 (GSHO 2273); *int-m.la* in Bowman (PI 483237)*5 (GSHO 2274).
References:
1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley uniculm 2 (*cul2*) mutant. Theor. Appl. Genet. 106:846-857.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).
4. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. Hereditas 108:13-26.
Prepared:
U. Lundqvist and J.D. Franckowiak. 1997. BGN 26:473.
Revised:
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:280.

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

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

Previous nomenclature and gene symbolization:
Erectoides-55 = *ert-55* (7).
Brachytic 4 = *br4* (10).
Brachytic-g = *brh.g* (3).
Brachytic 3 = *brh3* (4).
Brachytic-i = *brh.i* (3).
Brachytic-y = *brh.y* (3).

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

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

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

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

Mutant used for description and seed stocks:
ert-t.55 in Bonus (GSHO 494); *ert-t.55* in Bowman (PI 483237)*7 (GSHO 2257); *brh3.g* in Birgitta (GSHO 1672); *brh3.g* in Bowman*7 (GSHO 2167); *brh3.y* in Bowman*6 (GSHO 2178).

References:
1. Börner, A. 1996. GA response in semidwarf barley. Barley Genet. Newsl. 25:24-26.
2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. BGN 24:56-59.
4. Franckowiak. 2002. BGS 631, Brachytic 3, *brh3*. BGN 32:132.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
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Prepared:

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

Revised:

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

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

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial dominant (1).
Location is unknown.
Description:
Resistant seedlings infested with greenbugs (aphids) are not killed or severely stunted by a buildup of the greenbug population, but susceptible seedlings are killed or severely stunted (1, 4). The resistance provided by PI 426756 (4 to 5 readings on a 1 to 9 scale) to most *S. graminum* biotypes was less effective than that provided the *Rsg1.a* gene in Post 90 (PI 549081) (2 to 3 readings) (3). PI 426756 was confirmed to provide resistance (2 to 3 readings) to the TX1 isolate of *S. graminum*, which produces a susceptible reaction (9 reading) on Post 90 (2).
Origin of mutant:
Natural occurrence in Joa (PI 426756) (1, 4).
Mutational events:
Rsg2.b in PI 426756 (1).
Mutant used for description and seed stocks:
Rsg2.b in PI 426756 (GSHO 2513).
References:
1. Merkle, O.G., J.A. Webster, and G.H. Mogen. 1987. Inheritance of a second source of greenbug resistance in barley. Crop Sci. 27:241-243.
2. Porter, D.R., J.D. Burd, and D.W. Mornhinweg. 2007. Differentiating greenbug resistance genes in barley. Euphytica 153:11-14.
3. Porter, D.R., and D.W. Mornhinweg. 2004. Characterization of greenbug resistance in barley. Plant Breed. 123:493-494.
4. Webster, J.A., and K.J. Starks. 1984. Sources of resistance in barley to two biotypes of greenbug *Schizaphis graminum* (Rondani), Homoptera: Aphididae. Protect. Ecol. 6:51-55.
Prepared:
J.D. Franckowiak. 1997. BGN 26:503.
Revised:
J.D. Franckowiak. 2007. BGN 37:283.

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

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

Previous nomenclature and gene symbolization:
None.

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

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

Origin of mutant:
An ethylene imine induced mutant in Foma (CIho 11333) (3).

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

Mutant used for description and seed stocks:
bra-d.7 in Foma (GSHO 1696); *bra-d.7* in Bowman (PI 483237)*3 (GSHO 2185).

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

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

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

BGS 593, Awned palea 1, *adp1*

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

Previous nomenclature and gene symbolization:
Awned palea = *adp* (1).
Inheritance:
Monofactorial recessive (1, 2).
Located in chromosome 3HL (2), about 5.8 cM distal from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (2).
Description:
This mutant was isolated as a partially female sterile plant with abnormal spikes. The palea is elongated to form two awns (2), which are derived from two fused bracts that form the palea (3). Pistils are often transformed into leafy buds and result in low female fertility and greatly reduced seed set. Two of the anthers appear normal and the third is deformed to some extent (1). Pollen fertility is good (1).
Origin of mutant:
A spontaneous mutant in an inbred line (1).
Mutational events:
adp1.a in an unknown inbred line (1).
Mutant used for description and seed stocks:
adp1.a in a selection, with the *eog1.a* (elongated outer glume 1) gene from Svalöfs Guldkorn 91 [AHOR 226, a mutant of Gull (CIho 1145, GSHO 466)] (1), crossed to the unknown line (GSHO 1618); *adp1.a* in Bowman*5 (GSHO 1950).
References:
1. Ahokas, H. 1977. A mutant of barley: Awned palea. Barley Genet. Newsl. 7:8-10.
2. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (Hordeum vulgare) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. Heredity 90:390-396.
3. Williams, R.F. 1975. The Shoot Apex and Leaf Growth. Cambridge University Press, Cambridge.
Prepared:
J.D. Franckowiak. 1998. BGN 28:34.
Revised:
J.D. Franckowiak. 2007. BGN 37:285.

BGS 599, Proanthocyanidin-free 17, *ant17*

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

Previous nomenclature and symbolization:
None.

Inheritance:
Monofactorial recessive (4, 5).
Located in chromosome 3HS (1), it has been shown that *ant17.148* is an allele at the *seg3* (shrunken endosperm genetic 3, see BGS 379) locus (2).

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

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

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

ant17.408 in KMJ 326 (5); ant17.410, 17.447 in Catrin (5); ant17.421 in VBS 18707 (5); ant17.422, 17.423, 17.424, 17.426 in NZ 3789 (5); ant17.432 in NZ 1836-3 (5); ant17.438, 17.439 in NZ 732.01 (5); ant17.440 in Nordal (5); ant17.450 in Ca 601427 (5); ant17.453, 17.455, 17.457, 17.458 in Ackermann 1734/5 (5); ant17.462 in Pamela (5); ant17.469, 17.470 in Grit (PI 548764, NGB 13685) (5); ant17.475 in Zenit (PI 564447, NGB 13686) (5); ant17.476 in Zenit (6); ant17.480 in Secobra 9709 (5); ant17.501 in Advance (CIho 15804) (4); ant17.504 in Karla (CIho 15860) (4); ant17.506, 17.507, 17.508, 17.509 in OR 9114 (4); ant17.515, 17.516, 17.518 in WA9037-75 (4); *ant17.520* in WA9044-75 (4); *ant17.530* in Morex (CIho15773) (4); *ant17.537*, *17.595*, *17.619*, *17.620* in Advance (5); *ant17.560*, *17.561*, *17.563*, *17.565*, *17.567* in Manker (CIho 15549) (5); *ant17.597* in Morex (6); *ant17.598* in Morex (5); *ant17.600* in S 80351 (5); *ant17.601* in Moravian 111 (CIho 15812) (5); *ant17.604* in Harrington (6); *ant17.612* in Andre, (PI 469107) (5); *ant17.624* in Klages (CIho 15478) (5); *ant17.625* in Robust (M36, PI 476976) (5); *ant17.630* in Azure (CIho 15865) (13); *ant17.636*, *17.658* in Cougbar (PI 496400) (13); *ant17.637* in 8892-78 (13); *ant17.661* in Crest (PI 561409) (13); *ant17.1502*, *17.1505*, *17.1519* in Amagi-Nijo (4); *ant17.1510*, *17.1511* in Haruna- Nijo (4); *ant17.1515* in Nirakei 61 (4); *ant17.1537* in Nirakei 62 (5); *ant17.1544* in Nirakei 63 (5); *ant17.1534* in Nirasaki-Nijo 14 (5); *ant17.2022*, *17.2067* in Natasha (PI 592171) (6); *ant17.2084* in Hege 694/82 (9); *ant17.2106* in Ca 708912 (8); ant17.5019 in Sonja (PI 302047) (9); *ant17.5024* in Ackermann 72/27/4 (6); *ant17.5028* in Trigger (PI 473541) (9); *ant17.5034* in Kaskade (9); *ant17.5035*, *17.5036*, *17.5037* in Video (6); *ant17.5038*, *17.5039*, *17.5040*, *17.5042* in Sonja (6); *ant17.5044* in Ackermann 27/220/8 (6).

Mutant used for description and seed stock:

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

References:

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2. Franckowiak, J.D. (Personal communications).
3. Jende-Strid, B. 1978. Mutation frequencies obtained after sodium azide treatments in different barley varieties. Barley Genet. Newsl. 8:55-57.
4. Jende-Strid, B. 1984. Coordinator's report: Anthocyanin genes. Barley Genet. Newsl. 14:76-79.
5. Jende-Strid, B. 1988. Coordinator's report: Anthocyanin genes. Stock list of ant mutants kept at the Carlsberg Laboratory. Barley Genet. Newsl. 18:74-79.
6. Jende-Strid, B. 1991. Coordinator's report: Anthocyanin genes. Barley Genet. Newsl. 20:87-88.
7. Jende-Strid, B. 1993. Genetic control of flavonoid biosynthesis in barley. Hereditas 119:187-204.
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13. Ullrich, S., and J. Cochran. 1998. (Personal communications).

Prepared:

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

Revised:

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

BGS 617, Uniculme 4, *cul4*

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

Previous nomenclature and gene symbolization:
Uniculme-5 = *uc-5* (3).

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

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

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

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

Mutant used for description and seed stocks:
cul4.5 in Bonus (GSHO 2493, NGB 115063); *cul4.5* in Bowman (PI 483237)*7 (GSHO 2361).

References:
1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley uniculm2 (*cul2*) mutant. Theor. Appl. Genet. 106:846–857.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
4. Lundqvist, U. (Unpublished).
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Prepared:
J.D. Franckowiak and U. Lundqvist. 2002. BGN 32:118.

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

BGS623, Eligulum-a, *eli-a*

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

Previous nomenclature and gene symbolization:
Eligulum-a = *lig-a* (2).
Eligulum-3 = *eli-3* (4).
Inheritance:
Monofactorial recessive (2).
Location is unknown.
Description:
Plants do not have ligules in the junction between the sheath and leaf blade, auricles are rudimentary and asymetrically displaced. Plants are about 2/3 of normal height and have very wide leaves (3, 4). The peduncle is short and spike emergence from the sheath of the flag leaf is poor. Spikes have a compact arrangement of spikelets and are extremely compacted near the tip (1, 3). The culm breaks very easily just below the nodes. The Bowman backcross-derived lines have glume awns that are nearly twice as long as those of Bowman, but the lemma awns are about 2/3 of normal (1).
Origin of mutant:
An ethylene imine induced mutant in Foma (CIho 11333) (2, 3).
Mutational events:
eli-a.2 (NGB 115389), *eli-a.3* (NGB 115390), *-a.7* (NGB 115392), *-a.9* (NGB 115393), *-a.10* (NGB 115394) in Foma (3); *eli-a.11* (NGB 115395), *-a.14* (NGB 115397) in Kristina (NGB 1500); *eli-a.15* (NGB 115398), *-a.16* (NGB 151399) in Bonus (PI 189763 (4), *-a.216* (FN216) in Steptoe (CIho 15229) (1, 3).
Mutant used for description and seed stocks:
eli-a.3 in Foma (NGB 115390); *eli-a.3* in Bowman (PI 483237)*3.
References:
1. Franckowiak, J.D. (Unpublished).
2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.
3. Kleinhofs, A. (Unpublished).
4. Lundqvist, U. (Unpublished).
Prepared:
U. Lundqvist and J.D. Franckowiak. 2002. BGN 32:126.
Revised:
J.D. Franckowiak and A. Kleinhofs. 2005. BGN 35:192.
Revised:
U. Lundqvist and J.D. Franckowiak. 2007. BGN 37:290.

BGS 633, Many noded dwarf 6, *mnd6*

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

Previous nomenclature and gene symbolization:
Densinodosum-6 = *den-6* (3, 4).

Inheritance:
Monofactorial recessive (4).
Located in chromosome 5HL [7L] (5), near AFLP marker E3743-3 in subgroup 65 of the Proctor/Nudinka map (5).

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

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

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

Mutant used for description and seed stocks:
mnd6.6 in Bonus (GSHO 1713), *mnd6.6* in Bowman (PI 483237)*7 (GSHO 2235).

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

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

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

BGS 636, Tip sterile 2, *tst2*

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (4).
Location is unknown.
Description:
Spikes of *tst2.b* plants are 1/4 to 1/2 of normal length because seed set fails in the upper portion of the spike. Slow or poor development of the spike reduces both the number of rachis internodes and number of fertile spikelets (1, 4). Most spikes of the Bowman backcross-derived line set less than 10 seeds. Plants are shorter than are normal sibs because peduncles fail to elongate normally. Both rachis internode length and awn length are reduced in *tst2* plants (1).
Origin of mutant:
An X-ray induced mutant in Donaria (PI 161974) (3, 4).
Mutational events:
tst2.b in Donaria (Mut. 2249, DWS1337) (2, 3).
Mutant used for description and seed stocks:
tst2.b in Donaria (GSHO 1781); *tst2.b* in Bowman (PI 483237)*5 (GSHO 2280).
References:
1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
3. Scholz, F. 1956. Mutationsversuche an Kulturpflanzen. V. Die Vererbung zweier sich variabel manifestierender Übergangsmerkmale von bespelzter zu nackter Gerste bei röntgeninduzierten Mutanten. Kulturpflanze 4:228-246.
4. Scholz, F., and O. Lehmann. 1958. Die Gaterslebener Mutanten der Saatgerste in Beziehung zur Formenmannigfaltigkeit der Art *Hordeum vulgare* L.s.l.I. Kulturpflanze 6:123-166.
Prepared:
J.D. Franckowiak and U. Lundqvist. 2002. BGN 32:137.
Revised:
J.D. Franckowiak. 2005. BGN 35:193. (Locus symbol was changed from *lin2*.)
J.D. Franckowiak. 2007. BGN 37:292.

BGS 653, Brachytic 10, *brh10*

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

Previous nomenclature and gene symbolization:
Brachytic-l = *brh.l* (3).
Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 2HS (1), approximately 12.9 cM distal from SSR marker Bmac0850 in bin 2H-08 (1).
Description:
Plants are about 3/4 normal height and peduncles are over 3/4 normal length. Awns are about 3/4 of normal length. Rachis internodes are slightly shorter than those of normal sibs, but the number of fertile rachis nodes is increased by over 2. Seedling leaves of *brh10* plants are relatively short. Kernels of the Bowman *brh10* line are shorter (7.3 vs. 9.6 mm) and about 20% lighter than those of Bowman. Plants have and erect growth habit and grain yields averaged 20% less than those of Bowman (1, 2).
Origin of mutant:
A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).
Mutational events:
brh10.l in Birgitta (17:15:2, DWS1007) (4, 5).
Mutant used for description and seed stocks:
brh10.l in Birgitta (GSHO 1677); *brh10.l* in Bowman (PI 483237)*7 (GSHO 2171).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator’s report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).
Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:293.

BGS 654, Brachytic 11, *brh11*

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

Previous nomenclature and gene symbolization:
Brachytic-n = *brh.n* (3).
Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 5HS [7S] (1), about 6.7 cM proximal from SSR marker Bmac0113 in bin 5H-04 (1).
Description:
Plants are 2/3 to 3/4 normal height and peduncles are 3/4 to 5/6 normal length. The length of the rachis internodes is about 3/4 as long as those of normal sibs. Seedling leaves of *brh11* plants are relatively short. Kernels of the Bowman *brh11* line are shorter (7.2 vs. 9.6 mm) and about 25% lighter than those of Bowman. Plants have an erect growth habit and grain yields of the *brh11* line averaged less than 1/2 of those for Bowman (1, 2).
Origin of mutant:
A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).
Mutational events:
brh11.n in Birgitta (17:19:2, DWS1011) (4, 5).
Mutant used for description and seed stocks:
brh11.n in Birgitta (GSHO 1679); *brh11.n* in Bowman (PI 483237)*6 (GSHO 2172).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator’s report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).
Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:294.

BGS 655, Brachytic 12, *brh12*

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

Previous nomenclature and gene symbolization:
Brachytic-o = *brh.o* (3).
Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 5HS [7S] (1), approximately 13.5 cM distal from SSR marker Bmag0387 in bin 5H-03 (1).
Description:
Plants are 2/3 to 3/4 of normal height. Awns and peduncles are about 3/4 normal length. The length of the rachis internodes is about 3/4 of normal sibs. Seedling leaves of *brh12* plants are relatively short. Kernels of the Bowman *brh12* line are shorter (7.9 vs. 9.6 mm) and about 20% lighter than those of Bowman. Grain yields of the *brh12* line averaged slightly more than 1/2 of those for Bowman (1, 2).
Origin of mutant:
A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).
Mutational events:
brh12.o in Birgitta (17:20:2, DWS1012) (4, 5).
Mutant used for description and seed stocks:
brh12.o in Birgitta (GSHO 1680); *brh12.o* in Bowman (PI 483237)*7 (GSHO 2173).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator’s report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).
Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:295.

BGS 656, Brachytic 13, *brh13*

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

Previous nomenclature and gene symbolization:
Brachytic-p = *brh.p* (3).

Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 5HS [7S] (1), approximately 8.7 cM distal from SSR marker Bmag0387 in bin 5H-03 (1).

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

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

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

Mutant used for description and seed stocks:
brh13.p in Birgitta (GSHO 1681); *brh13.p* in Bowman (PI 483237)*6 (GSHO 2174).

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

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

BGS 657, Brachytic 15, *brh15*

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

Previous nomenclature and gene symbolization:
Brachytic-u = *brh.u* (3).
Inheritance:
Monofactorial recessive (2, 3).
Location is unknown (1).
Description:
Plants have numerous tillers with small leaves, spikes, and kernels. Prior to heading plants appear to be grassy culms similar to those produced by the *sld2* (slender dwarf 2) and *sld4* (slender dwarf 4) mutants, but heading is not drastically delayed. Culms and peduncles are about 1/2 normal length. Awns and rachis internodes are slightly shorter than those of normal sibs. Leaf blades are narrow and about 1/2 normal length. Mutant plants headed 2 to 3 days later than normal sibs. No lodging was observed. Spikes of *brh15* plants had nearly 4 fewer kernels than those of Bowman. Kernels of the Bowman *brh15* line are slightly shorter (8.6 vs. 9.6 mm), thinner (3.4 vs. 3.8 mm), and about 30% lighter than those of Bowman. The grain yield of the *brh15* line averaged about 2/3 of that recorded for Bowman (1, 2).
Origin of mutant:
A N-methyl-N-nitrosourea induced mutant in Julia (PI 339811) (5, 6).
Mutational events:
brh15.u in Julia (409 JK, DWS1156) (4, 6).
Mutant used for description and seed stocks:
brh15.u in 409 JK/Bowman (GSHO 1685); *brh15.u* in Bowman (PI 483237)*5 (GSHO 2176).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Micke, A. and M. Maluszynski, M. 1984. List of semi-dwarf cereal stocks. *In* Semi-dwarf Cereal Mutants and Their Use in Cross-breeding II. IAEA-TECDOC-307. IAEA, Vienna.
6. Szarejko I., M. Maluszynski, M. Nawrot, and B. Skawinska-Zydron, 1988. Semi-dwarf mutants and heterosis in barley. II. Interaction between several mutant genes responsible for dwarfism in barley. p. 241-246. *In* Semi-dwarf Cereal Mutants and their Use in Cross-breeding III. IAEA- TECDOC-455, IAEA, Vienna.
Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:297.

BGS 658, Brachytic 17, *brh17*

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

Previous nomenclature and gene symbolization:
Semidwarf mutant = Mo4 (5).
Brachytic-ab = *brh.ab* (3).

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

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

Origin of mutant:
A sodium azide induced mutant in Morex (CIho 15773) (6).

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

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

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

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

BGS 659, Brachytic 18, *brh18*

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

Previous nomenclature and gene symbolization:
Brachytic-ac = *brh.ac* (3).
Inheritance:
Monofactorial recessive (3, 4).
Located in chromosome 5HS [7L] (1), approximately 9.2 cM distal from SSR marker Bmac0163 in bin 5H-01(1).
Description:
Plants are about 2/3 normal height and awns are less than 2/3 of normal length. Peduncles are slightly coiled and about 5/6 the length of those of normal sibs. Rachis internodes are about 20% shorter than those of Bowman. Seedling leaves of *brh18* plants are relatively short. Kernels of *brh18* plants are similar in weight to those of Bowman, but slightly shorter. Lodging is reduced, but grain yields averaged slight more than 1/2 of those for Bowman (1, 2).
Origin of mutant:
An induced mutant backcrossed into Triumph (CIho 11612, GSHO 2465) (5).
Mutational events:
brh18.ac in mo6/4*Triumph (402B, DWS1277) (4, 5).
Mutant used for description and seed stocks:
brh18.ac in Mo6/4*Triumph (GSHO 1670); *brh18.ac* in Bowman (PI 483237)*6 (GSHO 2182).
References:
1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. Barley Genet. Newsl. 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator’s report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
5. Falk, D. 1985. (Personal communications).
Prepared:
J.D. Franckowiak and L.S. Dahleen. 2007. BGN 37:299.

BGS 660, Narrow leafed dwarf 2, *nld2*

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

Previous nomenclature and gene symbolization:
None.
Inheritance:
Monofactorial recessive (1, 2).
Location is unknown.
Description:
Mutant plants have narrow, dark green leaves, which are erect with well-developed midribs. Auricles degenerate to tiny projections, but ligules are normal. Stem internodes are short, and the upper ones are curved. Spikelets are relatively narrow and small, and seed set may be low. Kernels of the Bowman *nld2* line are thinner (3.2 vs. 3.8 mm) and about 35% lighter than those of Bowman (1). Plants are 1/2 to 1/3 of normal height, the spike commonly emerges from the side of the sheath before anthesis. Awns of the *nld2.b* line are similar in length to those of Bowman. The *nld2.b* Bowman line is more vigorous than *nld1.a* in Christchurch, New Zealand and in North Dakota greenhouse nurseries, but *nld1.a* was more vigor in the Dundee, Scotland nursery. Seed yields are generally less than 20% of those of Bowman (1).
Origin of mutant:
A fast neutron induced mutant in Steptoe (CIho 15229) (2).
Mutational events:
nld2.b in Steptoe (2).
Mutant used for description and seed stocks:
nld2.b in Steptoe; *nld2.b* in Bowman (PI 483237)*6.
References:
1. Franckowiak, J.D. (Unpublished).
2. Kleinhofs, A. (Unpublished).
Prepared:
J.D. Franckowiak and A. Kleinhofs. 2007. BGN 37:300.

BGS 661, Double seed 1, *dub1*

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

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

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

Description:

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

Origin of mutant:

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

Mutational events:

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

Mutant used for description and seed stocks:

dub1.1 (NGB 114331) in Bonus (2).

References:

1. Lundqvist, U. (Unpublished).

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

Prepared:

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