REPORTS OF THE COORDINATORS

Overall coordinator's report

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Since the latest overall coordinator's report in Barley Genetics Newsletter Volume 35, no changes of the coordinators have been reported. 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. Please observe some address changes have taken place since the last volume of BGN.

As it became decided at the 9th International Genetic Barley Symposium in Brno, 2004, the current system and trait coordination should continue but with a view towards whole genome coordination. Bill Thomas and Dave Marshall from the Scottish Crop Research Institute, Invergowrie, Dundee, UK, are investigating the potential of modernizing the overall system and integrating all types of current and historic data collections into a single, combined database. They are working on this subject.

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. Also the germplasm part is under revision. The searchable address is: www.untamo.net/bgs

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

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American six-row malting barleys possess an effective and durable resistance against spot blotch. In the variety 'Morex' Steffenson *et al*. (Steffenson *et al*. 1996) had dissected his resistance into a seedlings resistant on chromosome 7H, one major QTL for adult plant resistance on chromosome 1H and one minor QTL for adult plant resistance on chromosome 7H. This was done in a doubled haploid population from the cross 'Steptoe' × 'Morex', and 'Morex' contributet all alleles for resistance. In order to confirm these resistance genes, 'Morex' resistance against spot blotch was investigated in the crosses 'Dicktoe' × 'Morex' and 'Harrington' × 'Morex' (Bilgic *et al*. 2005). Additionally, the experiment in the cross 'Steptoe' × 'Morex' was repeated. While the latter experiment confirmed the QTL found before, no QTL on chromosome 1H was detected in the other two crosses.

The localistion of QTLs for straw-quality characteristics of barley under drought stress was the aim of Grando *et al*. (2005). For this purpose 494 F_7 recombinant inbred lines were scored in two years and two locations for acid detergent fiber (ADF), neutral detergent fiber (NDF), voluntary intake (INT), lignin content (LIC), crude protein (CP) and digestible organic matter in dry matter (OMD). Additionally, in one environment, the percentages of blades, sheaths and stems, respectively (PCB, PCH, PCS) were measured. On chromosome 1H, eight QTLs were found: one for NDF, INT and CP, one for ADF and PCS, one for PCH, two for INT, one for LIC and NDF, one for CP and one for INT and ash content.

Peighambari *et al*. (2005) performed a QTL analysis in 72 doubled haploid lines from the cross Steptoe × Morex for several agronomical traits scored in two years. On chromosome 1H, four different QTLs were detected: one for number of seeds per spike, one for the date of spike inititiation, one for spikes per plant and thousand-seeds-weight and one for date of flowering and date of maturity.

In order to localize QTLs for different disease resistances, Yun *et al*. (2005) analysed 104 F_6-plants from a cross between the *spontaneum*-line OUH602 and the cultivar 'Harrington'. They phenotyped the lines for resistance against powdery mildew, leaf scald, Septoria speckled leaf blotch, net type net blotch and spot blotch. On the short arm of chromosome 1H, they detected one QTL for powdery mildew (at or nearby the position of the *Mla*-locus), one QTL for scald and one QTL for net type net blotch. While the allele conferring resistance for scald and powdery mildew originated from OUH602, 'Harrington' contributed the allele for resistance against net type net blotch.

In an advanced backcross population (BC_2DH) originating from a cross between the *spontaneum* line ISR42-8 and the variety 'Scarlett', von Korff *et al*. (2005) detected QTLs for different disease resistances. On chromosome 1H, they found a major QTL for resistance against powdery mildew, at or near by the *Mla*-locus. The alleles of the *spontaneum*-line reduced disease severity by 51.5%.

Hori *et al*. (2005) presented an alternative approach for advanced backcrosses. They produced both doubled haploid lines and BC_3F_2 lines from a same cross between the Japanese malting barley variety 'Haruna Nijo' and the *spontaneum*-line H605. The linkage map was calculated in the population of doubled haploids and subsequently a QTL analysis was done in both populations for agronomic and phenotypic traits. On the short arm of chromosome 1H, one QTL was found for kernel weight and the number of spikelets per ear in the BC_3F_2. On the long arm of the same chromosome, they detected a QTL for the number of spikelets per ear in the doubled haploids.

In an attempt to find QTL influencing 'none-parasitic leaf spots' (NPLS), Behn *et al*. (2005) analysed 536 DH lines from a cross between the NPLS tolerant barley line 'IPZ 24727' and the variety 'Krona' and compared them with results published before (Behn *et al*. 2004) from a cross with the same *ant* line and the variety 'Barke' (all spring barley varieties). On chromosome 1H, they found a minor QTL NPLS-tolerance in each of the crosses, but on different regions of the chromosome. Additionally, they detected three different QTLs for heading date and two QTLs for plant height on the same chromosome.

Yin *et al* (2005) looked for QTLs representing inputs for a ecophysiological phenology model predicting flowering time in the cross 'Apex' × 'Prisma': f_0 as the minimum number of days from sowing to flowering under optimal conditions,. θ_1 and θ_2 as the development stage for the start and the end of the photoperiod-sensitive phase, respectively, and δ as the parameter characterizing the photoperiod-sensitivity. On chromosome 1H, they found 3 different loci: one for the θ_1, one for f_0 and one for all four parameters.

By addition lines, Nasuda *et al*. (2005) localised totally 701 EST sequences to the 7 barley chromosomes. Seventy one were assigned to chromosome 1H.

Rostoks *et al*. (2005) presented an integrated map from three populations originating from the crosses 'Steptoe' × 'Morex', 'Lina' × HS92 and 'Oregon Wolfe Barley Dominant' × 'Oregon Wolfe Barley Recessive'. Beside 904 RFLP, SSR, and AFLP markers localized before, the map is enriched by 333 EST unigenes, localized by SNPs, InDels or SSRs within these genes. For many of these unigenes, up- or down-regulation under different stress conditions is presented as well as the localization of the respective homologues in rice. On chromosome 1H, 41 unigenes were localized.

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Coordinator's report: Chromosome 2H (2)

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Gottwald *et al*. (2004) reported on an attempt to isolate the gene controlling a gibberellic-acid insensitive dwarf mutant in barley. The locus was named *sdw3* and is closely linked to RFLP marker MWG2287 on 2HS near the centromere. The gene symbols *gai* and *GA-ins* were used for the mutant in line Hv287 in earlier publications (Börner *et al*., 1999). This region of 2HS is orthologous with a highly conserved region on rice chromosome 7L. ESTs in this region were used to identify three putative GA-related ORFs in rice that might correspond to the *sdw3* locus (Gottwald *et al*., 2004).

Dahleen *et al*. (2005) studied 27 mutants from various sources that were placed in the brachytic (*brh*) group of semidwarf mutants. Based on allelism tests and molecular mapping studies using simple sequence repeat (SSR) markers, the mutants occurred at 18 different loci. Three of the brachytic mutants were located on chromosome 2H: *ert-t* (*brh3.y*), *brh4.j*, and *brh10.l*. Several mutants earlier identified as having a *brh3* phenotype were found to be allelic at the *ert-t* locus. Since the *ert-t* locus symbol was the symbol first published for this locus, it will be the recommended symbol. The *ert-t* locus was positioned near the tip of 2HS distal from SSR marker Bmac0134. The *brh4* locus was positioned near bin 9 of 2HL and *brh10* was position in bins 4 or 5 of 2HS (Dahleen *et al*., 2005).

Hori *et al*. (2005) mapped QTLs for resistance Fusarium head blight (FHB), incited primarily by *Fusarium graminearum*, using recombinant inbred lines (RILs) from a cross between a resistant two-rowed accession 'Russian 6' and a very susceptible six-rowed accession H.E.S. 4 from Afghanistan. Reactions to FHB were determined using a cut spike test where field grown spikes were harvested at anthesis and sprayed with a conidial suspension. The six-rowed spike 1 (*vrs1*) and closed flowering (*cly1*/*Cly2*) loci were mapped on 2HL. Two QTLs for FHB severity were detected on 2HL: one near the *vrs1* locus in bin 10 and one near the *cly1/Cly2* locus in bin 13. Rachis internode length was correlated with FHB severity. Other QTLs found on 2HL included early heading in bin 8, plant height and number fertile rachis nodes (spike length) in bin 10, and rachis internode length near bin 13.

Hori *et al*. (2006) used two-rowed barley accessions from China and Turkey to map QTLs for resistance to FHB. A set of recombinant inbred lines (RILs) was developed with 'Harbin' as the resistant parent and 'Turkey 6' as the susceptible parent. Using the cut spike to test FHB reactions, QTLs for FHB severity were not detected in the bin 7 to 10 region of 2HL. This result suggests that these two-rowed parents were homogeneous for QTLs controlling FHB severity in this region. A QTL for FHB severity was detected on 2HL and positioned near (5.8 cM) the closed flowering (*cly1*/*Cly2*) locus, probably in bin 13. Rachis internode length was correlated with FHB severity in this study.

Horsley *et al*. (2006) reported that chromosome 2HL contains a series of agronomically important traits and QTLs for resistance to FHB and for the accumulation of the toxin deoxynivalenol (DON). 'Foster', a Midwest six-rowed cultivar, was crossed to the resistant

two-rowed accession CIho 4196. RILs were evaluated in 10 field grown tests for FHB and in several tests for DON accumulation and for morphological traits. QTLs for various traits were found primarily on 2HL. QTLs for FHB severity and DON level were in bins 8 and 10 and were named *Qrgz-2H-8* and *Qrgz-2H-10*, respectively. These QTLs have been found in several other studies where FHB resistance was evaluated in crosses between two- and six-rowed cultivars. A QTL for DON was found in bin 2 of 4HS. A QTL for early heading was found in bin 8 of 2HL and is presumably the *Eam6* gene from the six-rowed parent. A QTL for low number of fertile rachis nodes was located in bin 10 near the six-rowed spike 1 (*vrs1*) locus. This QTL probably was identified earlier as the *lin1* locus. One or two QTLs for plant height were also found very close to the *vrs1* locus. Since the genes *Eam6*, *lin1*, and *vrs1* and the QTLs for susceptibility to FHB and shortness were all contributed by the six-rowed cultivar, breeding adapted lines with improved FHB resistance has been difficult in six-rowed barley. QTLs for spike angle and spike density or rachis internode length were located in bin 13 of 2HL. A number of these associations on 2HL were previous reported by Dahleen *et al*. (2003).

The transfer of favorable genes from wild barley to cultivated barley was evaluated in backcross two of a doubled-haploid population by von Korff *et al*. (2006). Early heading and short stature were associated with the early maturity 1 (*Eam1* or *Ppd-H1*) gene in the bin 3 region of 2HS. A second QTL for short stature was found in the bin 7 to 9 region of 2HL. A QTL for lodging resistance was found in bins 12 to 13 of 2HL.

Sameri and Komatsuda (2004) studied heading time in barley using RILs from a cross between a winter six-rowed accession and a spring two-rowed cultivar. Heading times for the RILs were estimated under long-day, short-day, and continuous light conditions. Two QTLs for early heading were detected on 2H under both spring and fall sown conditions, but not under continuous light. The QTL near the centromere from the winter parent, Azumamugi, probably corresponds to the *Eam6* or *eps2S* locus. The QTL on 2HL was also from the winter parent, but at a position not frequently associated with early maturity genes in barley.

Liu *et al*. (2005) identified in barley two full-length cDNA sequences homologous to caleosin, a seed-storage oil-body protein from sesame. The cDNAs, named *HvClo1* and *HvClo2*, are paralogs that cosegregate and were mapped on chromosome 2HL in bin 9 near marker CDO588.. *HvClo1* is expressed during late stages of embryogenesis and is seed specific. *HvClo2* is expressed in endosperm tissues during grain development.

Tondell *et al*. (2006) observed that four of twelve drought tolerance QTLs found on a barley consensus map were associated with regulatory candidate genes that mapped in similar genome positions. One of the four candidate genes is on chromosome 2HL in the bin 9 region.

Rostoks *et al*. (2005) used SNP discovery and linkage analysis to construct an integrated SNP map of more than 300 SNP loci. With the integration of RFLP, AFLP, and SSR markers, the map contained a total of 1,237 loci. Two regions of chromosome 2H were associated with QTLs for seedling tolerance to high salt concentrations.

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Coordinator's Report: Barley Chromosome 3H

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Over the last year there have been a number of publications reporting the mapping of genes and QTL on barley chromosome 3H. The largest number of genes assigned to 3H was the 271 mapped by Cho *et al.* (2006) using transcriptome analysis on the wheat-barley disomic chromosome addition lines. Rostoks *et al*. (2005) mapped 51 genes to 3H as part of a genome–wide SNP discovery programme in which over 300 genes responsive to abiotic stress were mapped, mostly as SNPs. These publications confirmed the close syntenic relationship between barley 3H and rice chromosome 1. This synteny was used by Mammadov *et al*. (2005) to direct the development of 9 EST-derived STS markers that were mapped onto a high resolution map of the leaf rust resistance gene *Rph5* region on 3HS including five that co-segregated with the resistance gene. Hori *et al*. (2005) also published mapping data based on 60 EST derived markers, 7 of which mapped to 3H. These represent a small subset of 163 mapped to 3H by Sato *et al*. (2004), however primer information on the seven is given in Hori *et al*. (2005) allowing the association of EST sequences to the loci.

The mapping of individual genes has also reported in the last year with the barley homologue of GIGANTEA, *HvGI*, mapping to a syntenic position on 3HS (Bin 5-6) (Dunford *et al*., 2005). This gene is the homologue of an *Arabidopsis* flowering time regulator, however its map position does not correspond to the map position of any known flowering time QTL in barley. Skinner *et al*. (2006) reported the mapping of *HvICE2* a homologue of an Arabidopsis low temperature regulatory gene to 3HL (Bin 13-14). However, again, the map position of this candidate gene did not correspond to the position of a known low-temperature tolerance QTL.

The barley homologue of *acsF,* an enzyme involved in chlorophyll biosynthesis, was mapped to the short arm of chromosome 3H through the use of the wheat-barley disomic chromosome addition lines and was shown to be the known mutant *Xantha-l* (Rzeznicka *et al*.,. 2005).

Although much mapping work utilised the growing genomic resources in barley there were reports that used more generic approaches. Thus Mammadov *et al*. (2006) utilised degenerate primers designed to conserved motifs of the NBS region in known resistance genes to isolate 190 resistance gene analogues (RGA) clones from barley genomic DNA and mapped two of them to 3H (Bin 4 and Bin 14) using the Steptoe x Morex DH mapping population. AFLP have been used for detailed mapping of the *btr1/btr2* locus on 3HS (Senthil and Komatsuda, 2005) and some of these have been converted to STS markers (Azhacuvel *et al*., 2006).

Again this year a considerable number of QTL were reported in the literature some of which mapped to 3H. These included an increasing number of reports using recombinant chromosome substation lines to delineate association of quantitative traits with genomic regions (Hori *et al*., 2005, von Korff *et al*., 2005, 2006, Yun *et al*., 2006). Thus von Korff *et al*. (2005) report QTL for powdery mildew resistance on 3HS (Bin 5-6) and on 3HL (Bin 13-15) with the latter interval also housing QTL for resistance to leaf rust and scald. The same population, derived from *H. vulgare spontaneum* introgressions into the spring barley cultivar

Scarlett, has also been assessed for agronomic traits (von Korff *et al*., 2006). Several traits are reported to be associated with regions on chromosome 3H including brittleness of the rachis with a region on 3HS (Bin 3-6) and a large number of traits including height and harvest index with a region on 3HL (Bin 10-16). The authors postulate that these associations could be explained by the segregation of *btr1* and *sdw-1* (denso) respectively in this population. Other QTLs on 3H found in this study do not have obvious candidate genes but are consistent with other studies. Thus a QTL for thousand grain weight found on the distal end of 3HL (Bins 14-15) appears to relate to a similar QTL found by Hori *et al*. (1995) in a doubled haploid population derived from a cross between the cultivar Haruna Nijo and a *Hordeum sponteneum* accession. Other QTL found on populations derived from the same cross include ear length, number of spikelets and culm length (Hori *et al*., 1995).

Other studies that report QTL on 3H include those for agronomic characters discovered using the Steptoe x Morex mapping population reported by Peighambari *et al*. (2005). The QTL found on 3H include those for date of flowering, date of maturity, plant height and spike length (Peighambari *et al*., 2005). In an extensive study on straw quality characteristics reported by Grando *et al*. (2005) the QTL reported on 3H include those for acid detergent fibre, lignin content, voluntary intake and digestible organic matter (Grando *et al*., 2005).

In addition to the work reported in von Korff *et al*. (2005) other disease resistance QTL have been reported on 3H in the last year. Bilgic *et al*. (2005) found a total of four QTL for seedling (Bins 4-6 and 11-12) and adult resistance (Bins 2-4 and 9-11) to spot blotch in a study comparing resistance expression in four populations. The authors postulate that the seedling and adult resistances could relate to the same underlying QTL and note that the resistance mapped to 3HS does not correspond to anything reported previously (Bilgic *et al*., 2005). Yun *et al*. (2005) report a net blotch QTL on 3H (Bin 6) shown in a RIL population derived from a cross between H. *vulgare spontaneum* (OUH602) and the cultivar Harrington. This QTL was confirmed in a RCSL population derived from the same cross (Yun *et al*., 2006).

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Coordinators Report: Chromosome 5H(7)

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Winterhardiness in winter barley is controlled by regulatory elements of photoperiod sensitivity and vernalization response combined with the physical trait of low temperature tolerance. Of the six photoreceptors mapped on two mapping populations, only one, *HvPhyC*, coincided with a photoperiod response QLT on chromosome 5HL (Szucs *et al*., 2006). The vernalization locus *VRN-H1* (*HvBM5A*) whose expression is regulated by photoperiod has been mapped on chromosome 5HL and is closely linked to *HvPhyC*.

Reproductive frost tolerance is the ability of reproductive organs to tolerate low temperatures. A QTL on chromosome 5H for tolerance to frost-induced floret sterility and frost-induced grain damage was identified in three mapping populations (Reinheimer *et al.*, 2004). This locus is located close to the vrn-H1 locus on chromosome 5H and has been associated with the locus giving a response at both vegetative and reproductive developmental stages.

Seed dormancy is an important trait that can prevent preharvest sprouting and regulate germination during the malting process. A major seed dormancy QLT was detected on chromosome 5H plus two others on chromosome 1H in a mapping population derived from crossing the Japanese malting cultivar Haruna Nijo x H602 (*H. spontaneum – dormant*) (Sato *et al*., 2006). Seven EST markers were localized in the vicinity of the QLT on chromosome 5H.

Identification of QTL resistance to Fusarium Head Blight (FHB) continues to be a challenging exercise. Chromosome 5H appears to be a lesser contributor of FHB resistance QTL. For example, in recombinant inbred populations derived from two-rowed crosses of Harbin (R) x Turkey 6 (HR), resistance QTL were located on all chromosomes except 5H (Hori *et al*., 2006). However, in an RI population derived from Russia 6 (HR) x HES4 (HS), which was mapped with 1,255 markers, two pulative resistance loci were located on chromosome 2H and one on 5H (Takeda, 2004).

Of more general interest to barley geneticists are the assembly of a high density microsatellite consensus map and the sequencing of the barley chloroplast genome. The consensus microsatellite or SSR map was assembled by combining the information from six independent mapping populations. It consists of 784 unique microsatellite loci from 696 primers spanning 1,137.6 cM with an average density of one SSR marker every 1.45 cM (Varshney *et al*., 2006).

The chloroplast genome of barley consists of 136,462 bp, including a large single copy region of 80,600 bp, a small single copy region of 12,704 bp, plus a pair of inverted repeats of 21,597 bp. The genome consists of 104 genes, including 70 peptide-encoding genes, plus 30 tRNA and 4 rRNA genes that are duplicated in the inverted repeat (Saski et al., 2006). This genome is practically identical to other cereal chloroplast genomes, indicating that such genomes are highly conserved.

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Coordinator's Report: Chromosome 7H

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2005 brought many reports of various QTLs detected in populations derived from wild x cultivated barley crosses, with the goal of transferring desirable genes into elite breeding lines. Hori *et al.* (2005b) located QTLs for glume length, rachis-internode length, dormancy after five and ten weeks, ear length and kernel weight on chromosome 7H in a population derived from a cross with *H. vulgare* ssp. *spontaneum* (accession H602). An examination of straw quality QTLs (Grando *et al*. 2005) located several loci on chromosome 7H, for traits acid detergent fiber, lignin content, voluntary intake, and percentage of sheaths by weight of the air-dried straw sample. They used a RIL population derived from *H. vulgare* ssp. *spontaneum* accession 41-1. Li *et al*. (2005) determined QTLs for yield, yield components and malting quality in an advanced backcross population with *H. vulgare* ssp. *spontaneum* accession HS213. Five QTLs were located on chromosome 7H, for heading date, ear length, spikelet number per spike, protein content and friability. QTLs involved in dormancy and desiccation tolerance were located in *H. vulgare* ssp. *spontaneum* accession Wadi Qilt genotype 23-39 (Zhang *et al*. 2005a). Loci for maximum germination rate under drought stress, and minimum and maximum revival after drought stress were located on chromosome 7H. A new dominant scald resistance gene, *Rrs15* derived from *H. vulgare* ssp. *spontaneum* (accession CPI 77132 Caesarea plant 38), was located on the long arm of chromosome 7H, near the SSR marker HVM49 (Genger *et al*. 2005). In another study using *H. vulgare* ssp. *spontaneum* (accession OUH602), Yun *et al.* (2005) identified a new resistance locus on chromosome 7H for spot blotch (*Rcs2-4*). This gene was located on the short arm of the chromosome in a cluster of genes for resistance to fungal diseases. A third disease resistance study with *H. vulgare* ssp. *spontaneum* (accession ISR42-8) used advanced backcross QTL analysis and located two resistance loci on chromosome 7H, one for powdery mildew (QPm.S42-7H.a) and one for leaf rust (QLr.S42-7H.a), both on the long arm (von Korff *et al*. 2005).

Additional studies located genes and QTLs from cultivated crosses. Emebiri *et al*. (2005b) examined disease resistance in a two-rowed barley population segregating for malting quality traits. The only locus on chromosome 7H, identified by QTL and classical linkage analyses, was for stem rust resistance, likely *Rpg1*. Adult and seedling resistance to spot blotch in Morex was compared in four doubled haploid populations by Bilgic *et al*. (2005). They found that the locus on chromosome 7H, presumably *Rcs5*, was consistently identified for both seedling and adult plant resistance, while loci on other chromosomes were not found in all four populations. Hori *et al*., (2005a) located QTLs for Fusarium head blight resistance from the cultivar Russia 6, along with QTLs for spike morphology. They located QTLs for rachis-internode length and heading date on chromosome 7H.

In a cross between two low protein parents, Emebiri *et al*. (2005a) located QTLs for grain protein content on five chromosomes. The one on chromosome 7H significantly reduced protein in six of the eight environments tested and was not associated with QTLs for yield, height or heading date. Peighambari *et al*. (2005) tested the Steptoe x Morex doubled haploid population for agronomic traits in Iran. Only two QTLs were located on chromosome 7H, for date of spike initiation and 1000 seed weight. Dahleen *et al*. (2005) characterized and located

genes for 27 brachytic semidwarf mutants using SSR markers on near-isogenic lines. One of the new mutants, *brh.v*, was located on chromosome 7H, and the *brh1.z* allele mapped to the expected location of the previously mapped *brh1* locus.

One study has looked at expanding our selection of molecular markers for barley. Zhang *et al*. (2005b) tested 98 EST-SSR markers derived from wheat sequences in barley. They found that 50.4% of the markers amplified sequences in barley. When they examined some of the amplified sequences in more detail, most had repeats similar to those in wheat.

Additional mapping and marker work can be found in proceedings from various meetings, like the North American Barley Researchers Workshop, held in Red Deer Alberta last July.

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Integrating Molecular and Morphological/Physiological Marker Maps

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Updates to barley morphological/physiological genetic map and gene cloning include publication of the cloning and characterization of the barley *Nec1* locus encoding a cyclic nucleotide-gated ion channel gene (Rostoks *et al.* 2006). The previously reported *rym4* locus coding for the eukaryotic translation initiation factor 4E has been published (Kanyuka *et al.* 2005).

The barley spring vs. winter growth habit candidate genes were cloned and characterized (Von Zitzewitz *et al.* 2005). The *sgh1* locus, renamed *Vrn-H2* to conform with the wheat nomenclature, maps to chromosome 4 (4H) bin 12 approximately 8 cM proximal to *Bmy1* and co-segregating with the *HvSnf2* gene. The *sgh1 (Vrn-H2)* locus, represented by the *ZCCT-H* gene cluster, encodes a dominant transcription factor flowering repressor. Accession numbers of the two closely related candidate genes are AY485977 (*ZCCT-Ha*) and AY485978 (*ZCCT-Hb*). The *Sgh2* locus, renamed *Vrn-H1* to conform to the wheat nomenclature is located on chromosome 7 (5H) bin 11 between markers *Dhn2* and BCD265C (unfortunately designated BCD265B in Zitzewitz *et al*.). However, the gene, designated *HvBM5A*, has been cloned and the sequence is available (AY750995 genomic and AY785826 cDNA cv. Morex sequences, respectively). *HvBM5A* encodes a MADS-box transcription factor. A closely related gene, *HvBM5B*, maps to chromosome 5 (1H) bin 07 closely linked to ABG452. It is proposed that *HvBM5B* represents *Sgh3*, renamed *Vrn-H3* in the wheat nomenclature.

The *Vrs1* gene has been cloned (Komatsuda, Plant & Animal Genome XIV, Abstract W13 p10). Although details have not yet been published, the *Vrs1* locus was reported to encode a homeobox gene.

The cloned morphological/physiological genes represent excellent anchor points for the morphological/physiological barley map since the genes themselves can be used as reference points in mapping populations. There should be ample future opportunities for the identification of other barley genes by homology to the model dicot and monocot plants.

The leaf rust resistance gene *Rph5* was mapped at a high resolution and shown to co-segregate with ABG070 and five ESTs (Mammadov *et al.* 2005). *Rph5* was mapped previously, but this publication provides a high-resolution map and many different closely linked molecular markers.

The location of the non-brittle rachis genes btr1/btr2 was further refined (Senthil and Komatsuda, 2005). However, all of the new markers are AFLP and difficult to integrate with the morphological map.

Molecular mapping located 18 brachytic (*brh*) loci to five of the seven barley chromosomes, albeit with low resolution (Dahleen *et al.* 2005). (The nomenclature of the new loci used here

is that proposed by Dahleen *et al*. for the actual alleles used for mapping see the original paper). The *brh1* and locus was previously mapped with high resolution to chromosome 1 (7H) bin01 and *brh2* was mapped to chromosome 4 (4H) bin 05. Other loci mapping on chromosome 4 (4H) were *brh5* and *brh9*, but lack of flanking markers makes it difficult to determine their bin locations. The same problem exists for *brh3*, *brh4*, and *brh10* loci mapped to chromosome 2 (2H), however *brh3* probably is in bin01. The loci *brh8* and *brh14* were mapped to chromosome 3(3H). A large number of loci were mapped to the short arm of chromosome 7 (5H) including *brh6, brh7, brh11, brh12, brh13, brh17, brh18*. The locus *brh16* was mapped on the long arm of chromosome 1 (7H). Although the sparse markers and lack of flanking markers makes it impossible to reliably place these loci in chromosome bins, they do provide a starting point for those wishing to map these genes more precisely.

The *H. spontaneum* derived leaf scald resistance gene *Rrs15* was mapped to chromosome 1 (7H) long arm 11,5 cM from HVM49 (Genger *et al.* 2005). Since HVM49 is located in bin 12 and the direction of the linkage was not indicated, *Rrs15* could be in bin 11 or 13. The isozyme marker *Acp2* was linked to *Rrs15* at 17.7 cM.

The barley cytoplasmic male sterility restorer gene *Rfm1* was mapped to chromosome 6 (6H) short arm (Murakami *et al.* 2005). Closely linked AFLP markers were identified, however I was not able to assign the locus to a bin.

A very clever use of rice synteny and Arabidopsis was used to identify a cellulose synthase-like (*CslF*) gene cluster as candidates responsible for mediating the cell wall (1,3;1,4)-B-D-glucan syntesis (Burton *et al.* 2006). The work was initiated from the map location of a major QTL for (1,3;1,4)-B-D-glucan content of un-germinated barley grains on chromosome 2 (2H). This QTL is located between the markers *Adh8* bin 6 and ABG019 bin 7 with the peak closer to ABG019. Therefore, I have assigned the *CslF* locus to 2 (2H) bin 7. I believe this is the first example of a map-based cloning of a QTL in barley.

Please advise me of any additions or corrections to this information.

Bin Assignments for Morphological Map Markers and closest molecular marker

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		
	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 (in press)
	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	CDO673	Heun *et al*., Genome 34:437, ‘91
	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
	Rpt4	Psr117D	Williams *et al*., TAG 99:323, ‘99
	ubs4		
	blx2		
BIN9	RZ242		
	lbi3		
	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 BGN 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		
	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
	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		
	frp		
	min1		
	blx4		
	sid		
	blx3		
BIN8	BCD453B		
	blx1		
BIN9	ABG319A		
	ert1		
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		
	*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
	*Sgh3	(HvBM5B)	Zitzewitz *et al*., PMB 59:449, ‘05
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		

	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		

BIN markers are indicated
* - indicates the gene has been cloned

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Coordinator's report: Barley Genetic Stock Collection

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In 2005, 373 barley genetic stocks were planted in the field and in the greenhouse for evaluation and for seed increase.

Four mapping populations including SSD F6 OSU 1/Harr, SSD F6 OSU 2/Harr, SSD F6 OSU 11/Harr and SSD F6 OSU 15/Harr derived from crosses between *Hordeum vulgare subps. Spontaneum* with the cultivar "Harrington" and 142 *H. spontaneum* introgression lines BC2 S1 and BC2 S5 were obtained from Dr. Pat Hayes, OSU and maintained at Aberdeen. Two populations, SSD F6 OSU 1/Harr and SSD F6 2/Harr were planted in the field for seed increase.

One hundred thirty-two samples of barley genetic stocks were shipped to researchers in 2005.

Coordinator's report: Trisomic and aneuploid stocks

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

Coordinator's report: Autotetraploids

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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.

Coordinator's report: The Genetic Male Sterile Barley Collection

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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.

Coordinator's report: Translocations and balanced tertiary trisomics

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Chromosome 5H of *Hordeum vulgare* carries a gene(s) that accelerates heading in a wheat background. To introduce the early heading gene(s) of barley into the wheat genome, the Japanese scientists S. Taketa and colleagues attempted to induce homoeologous recombination between wheat and 5H chromosomes by 5B nullisomy. A nullisomic 5B, trisomic 5A, monosomic 5H plant (2n = 42) was produced from systematic crosses between aneuploid stocks of wheat group 5 chromosomes. Twelve plants (1.8%) were selected as putative wheat-barley 5H recombinants. Cytological analyses using fluorescence in situ hybridization and C-banding revealed that 6 of the progeny lines are true homoeologous recombinants between the long arms of chromosomes 5D and 5H. The 6 cytologically confirmed recombinant lines included only 2 types (3 lines each), which were reciprocal products derived from exchanges at the same distal interval defined by two flanking markers. One type had a small 5HL segment translocated to the 5DL terminal, and the other type had a small terminal 5DL segment translocated to the 5HL terminal. In the latter type, the physical length of translocated barley segments slightly differed among lines.

There were no requests for samples of balanced tertiary trisomics or tranlocation lines. 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.

Reference:

Taketa, S, T. Awayama , M. Ichii, M. Sunakawa, T. Kawahara, and K. Murai. 2005. Molecular cytogenetic identification of nullisomy 5B induced homoeologous recombination between wheat chromosome 5D and barley chromosome 5H. Genome 48: 115-124.

Coordinator's report: *Eceriferum* Genes

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No research work on gene localization has been reported on the collections of *Eceriferum* and *Glossy* genes since the latest reports in Barley Genetics Newsletter (BGN). All information and descriptions done in Barley Genetics Newsletter (BGN) Volume 26 are valid and still up-to-date. The database of the Swedish collection has been updated during the last months and will soon be searchable within International European databases. All Swedish *Eceriferum* alleles can be seen in the SESTO database of the Nordic Gene Bank. 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. 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

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@ngb.se or 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, anhang@uida.edu or to the coordinator at any time.

Coordinator's report: Nuclear genes affecting the chloroplast

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Chlorophyll biosynthesis is a process involving approximately 20 different enzymatic steps. One of the least understood enzymatic steps is formation of the isocyclic ring, which is a characteristic feature of all chlorophyll molecules. In chloroplasts this is an aerobic reaction catalyzed by Mg-protoporphyrin IX monomethyl ester cyclase. Barley mutants were employed to study this enzyme (Rzeznicka et al. 2005). An *in vitro* assay for the aerobic cyclase reaction required both membrane-bound and soluble components from the chloroplasts. Extracts from barley mutants at the *Xantha-l* and *Viridis-k* loci showed no cyclase activity. Fractionation of isolated plastids by Percoll gradient centrifugation showed that both *xantha-l* and *viridis-k* mutants are defective in

components associated with chloroplast membranes. The evidence suggests that the aerobic cyclase requires at least one soluble and two membrane-bound components. The *Xantha-l* gene was located to the short arm of barley chromosome 3H. The gene was further cloned and sequenced and the mutations *xantha-l.*35, *-l.81* and *–l.*82 were characterized at the DNA level. The study connected for the first time biochemical and genetic data as it demonstrated that *Xantha-l* encodes a membrane-bound cyclase subunit.

The stock list and genetic information presented in the Barley Genetics Newsletter 21: 102-108 is valid and up-to-date. Requests for stocks available for distribution are to be either sent to:

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Lund University
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Nordic Gene Bank
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FAX: +46-40-536650
www.nordgen.org/ngb

Reference:

Rzeznicka, K., C. J. Walker, T. Westergren, G. C. Kannangara, D. von Wettstein, S. Merchant, S. P. Gough, and M. Hansson. 2005. *Xantha-l* encodes a membrane protein subunit of the aerobic Mg-protoporphyrin IX monomethyl ester cyclase in the chlorophyll biosynthetic pathway. Proc. Natl. Acad. Sci. USA 102:5886-5891.

Coordinator's report: Ear morphology genes

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No new research on gene localization or descriptions on different morphological genes have been reported since the latest reports in Barley Genetics Newsletter (BGN) or in the AceDB database for Barley Genes and Genetic Stocks.. All descriptions made in the BGN volumes 26, 28, 29, 32 and 35 are still up-to-date and valid. The databases of the Swedish Ear morphology genes are currently updated and will be searchable within International European databases in the future. All different types and characters with its many alleles of the Swedish ear morphology genes are found in the SESTO database of the Nordic Gene Bank. Also, a survey list of the different Swedish ear morphology genes are published in the last volume of Barley Genetics Newsletter, BGN 35:150-154. As my possibilities in searching literature are very limited, I apologize if I am missing any important reports or papers. 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 reports. Descriptions, images and graphic chromosome map displays of the Ear morphology genes are also 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 Ear morphology genes can be reported to the coordinator as well. Seed requests regarding the Swedish mutants can be forwarded to the coordinator udda@ngb.se or 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, anhang@uida.edu or to the coordinator at any time.

Coordinator's report: Semidwarf genes

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Dahleen *et al*. (2005) studied 27 mutants from various sources that were placed in the brachytic (*brh*) group of semidwarf mutants. The mutants were backcrossed into 'Bowman' prior to this study to facilitate allelism studies and their phenotypic characterization. The traits studied included plant height; awn, peduncle, and rachis internode length; leaf width and length; lodging; kernels per spike; grain yield; and kernel weight. Based on allelism tests and molecular mapping studies using simple sequence repeat (SSR) markers, the mutants occurred at 18 different loci. Eight of the loci had been identified in previous studies and ten were new loci. Using small F2 populations, SSR markers were mapped within 30 cM of all loci except the *brh15.u* mutant. The brachytic mutants were located as follows: *ert-t* (*brh3.y*), *brh4.j*, and *brh10.l* on chromosome 2H; *brh8.ad* and *brh14.q* on 3H; *brh2* (*ari-l.3*), *brh5.m*, and *brh9.k* on 4H; *brh6.r*, *brh7.w*, *brh11.o*, *brh12.p*, *brh17.ab*, and *brh18.ac* on 5H; and *brh1.z* and *brh16.v* on 7H. The positional information suggested that one or two clusters of brachytic loci may exist on 5H. Three of five loci that were positioned earlier by linkage drag (Franckowiak, 1995) were found in a similar position base on the SSR mapping data.

All of the *brh* mutants as evaluated in Bowman backcross-derived lines were shorter than Bowman with an average height of 64.8 cm vs. 87.9 for Bowman (Dahleen *et al*. 2005). All of the *brh* lines had shorter awns and most had shorter peduncles and smaller kernels. Some of the *brh* lines had shorter rachis internodes and short leaf blades. The majority of the *brh* lines, 16 of 27, had lower grain yields than Bowman. Although none of the *brh* lines was superior to Bowman, the *brh4*, *brh6*, and *brh8* mutants seemed to be the most promising ones for further agronomic evaluation.

Horsley *et al*. (2006) reported that the main plant height QTLs in a 'Foster'/CIho 4196 mapping population were near the *vrs1* locus on 2HL. Dahleen *et al*. (2003) reported a plant height QTL in the same region of 2H from a study of two- by six-rowed cross, ND9712//Foster/Zhedar 2. The association between plant height and the six-rowed phenotype was first reported as a linkage by Miyake and Imai in 1922 and has been reported often since then (Franckowiak 1997). The locus symbol *hcm1* is currently recommended. Horsley *et al*. (2006) provided some evidence that more than one factor for reduced plant height is associated with the *vrs1* locus in the Foster/CIho 4196 cross. They reported also that they did not recover any short plants with a two-rowed spike type from a large F2 population. Thus, it is still not clear whether the *hcm1* locus exists or the six-rowed allele (*vsr1.a*) at *vrs1* locus has a pleiotropic effect on plant height in warm environments.

Honda *et al*. (2003) found that treatment of barley near-isogenic lines with the brassinosteroid (BR) growth regular caused leaf blade rolling in normal barley and most barley semidwarf mutants. However, detached leaf blade segments from dark grown plants with the *uzu1* gene did not unroll after treatment in the leaf unroll test. In a subsequent study, Chono *et al*. (2003) demonstrated that the response of *uzu1* mutants to BR was caused by a base pair substitution in the *Hordeum vulgare* BR-insensitive 1 (*HvBR11*) gene and an amino acid change in a

highly conserved residue in the kinase domain of the BR-receptor protein. The *uzu1* lines have a missense mutation in the *HvBR11* gene.

Gottwald *et al*. (2004) reported that a gibberellic-acid insensitive dwarf mutant, first described by Favret *et al*. (1976), is closely linked to RFLP marker MWG2287 on 2HS near the centromere. The proposed locus symbol for the GA insensitive mutant is *sdw3*, which replaced the symbols *gai* and *GA-ins* used in earlier publications. The suggested allele symbol is *sdw3.az* for the Hv287 line derived from the M.C. 90 mutant induced in M.C. 20. This region of 2HS is orthologous with a highly conserved region on rice chromosome 7L. ESTs in this region were used to identify three putative GA-related ORFs in rice that might correspond to the *sdw3* locus. (Gottwald *et al*. 2004).

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Favret, E.A., G.C. Favret, and E.M. Malvarez. 1976. Genetic regulatory mechanisms for seedling growth in barley. p. 37-41. p. 181-189. *In* H. Gaul (ed.). Barley Genetics III. Proc. Third Int. Barley Genet. Symp., Garching, 1975. Verlag Karl Thiemig, München.

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Honda, I., H. Zeniya, K. Yoneyama, M. Chono, S. Kaneko, and Y. Watanaba. 2003. *Uzu* mutation in barley (*Hordeum vulgare* L.) reduces leaf unrolling response to brassinole. Biosci. Biotechnol. Biochem. 67:1194-1197.

Horsley, R.D., D. Schmierer, C. Maier, D. Kudrna, C.A. Urrea, B.J. Steffenson, P.B. Schwarz, J.D. Franckowiak, M.J. Green, B. Zhang, and A. Kleinhofs. 2006. Identification of QTLs associated with Fusarium head blight resistance in barley accession CIho 4196. Crop Sci. 46:145-156.

Coordinator's report: Early maturity genes

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No 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. 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, anhang@uidaho.edu or to the coordinator at any time.

Coordinator's report : Wheat-barley genetic stocks

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The production of five different monosomic addition lines of *Hordeum marinum* chromosomes to Chinese Spring wheat has been reported earlier. It has now been possible to isolate five disomic addition lines (1Hm, 2Hm, 4Hm, 5Hm and 7Hm) from them and work is in progress to isolate the two remaining (3Hm and 6Hm) addition lines. Apart from the production of *H. marinum* x CS wheat amphiploid, it has also been possible to produce amphiploid with commercial wheats, both common and durum (Islam and Colmer, unpublished).