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REPORTS OF THE COORDINATORS

Overall coordinator's report

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

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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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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

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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. 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

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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

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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

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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

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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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Barley Genetics Newsletter (2007) 37: 105-153

Coordinator's report: Barley Genetic Stock Collection

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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

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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

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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.

Reference:

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

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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.

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Coordinator's report: *Eceriferum* Genes

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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

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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

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New references:

Axelsson, E., A. Sawicki, S. Nilsson, I. Schröder, S. Al-Karadaghi, R. D. Willows and M. Hansson. 2006. Recessiveness and dominance in barley mutants deficient in Mg-chelatase subunit D, an AAA protein involved in chlorophyll biosynthesis. Plant Cell 18: 3606-3616.

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Svensson, J.T., C. Crosatti, C. Campoli, R. Bassi, A. Michele Stanca, T.J. Close, and L. Cattivelli. 2006. Transcriptions analysis of cold acclimation in barley *albina* and xantha mutants. Plant Physiol. 141: 257-270.

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.

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Coordinator's report: Ear morphology genes.

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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

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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).

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Coordinator's report : Wheat-barley genetic stocks

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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).

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Coordinator's report: Early maturity genes

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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.

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