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REPORTS OF THE COORDINATORS

Overall coordinator's report

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

e-mail: udda@nordgen.org

Since the latest overall coordinator's report in Barley Genetics Newsletter Volume 38 not many changes of the coordinators took place. As Mark Sutherland, Australia who should take care of the coordination of the disease and pest resistant genes is so engaged with administration work at his university, we had to find a successor. Professor Frank Ordon from Germany is willing to take over. I wish him welcome to our group.

Several research groups world-wide are working with Single Nucleotide Polymorphism (SNP) genotyping and are using induced mutants from different Gene Banks. Good results have already been published in many publications as different reports are dealing with. About 950 different near isogenic lines (NIL) that are established by J.D. Franckowiak, now working in Australia, are an extraordinary source for this genotyping. During the summer of 2009 about half of these lines have been increased and propagated in Sweden in order to incorporate them in the Nordic Genetic Resource Center (Nordgen), Alnarp, Sweden. The other part will be increased during the summer of 2010 in Sweden. It has been decided to establish an International Centre for Barley Genetics Stocks at Nordgen, Sweden.

Some of us had the opportunity to participate the 14th Australian Barley Technical Symposium at the Sunshine Coast of Queensland, Australia, during september 2009. Several sessions dealed with economics production, quality, biotechnology and future research and production in variable environments of malt and feed barley. Also important presentations were on pest and disease resistant problems and the control of biotic and abiotic stresses. It was very interesting to learn that Australia is fighting with complete other breeding problems to release cultivars than what we have to do in Europe. Especially drought is a large problem in the early season of barley cultivation.

List of Barley Coordinators

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

Chromosome 2H (2): Jerry. D. Franckowiak, Hermitage Research Station, Agri-science Queensland, Department of Employment, Economic Development and Innovation, Warwick, Queensland 4370, Australia, FAX: +61 7 4660 3600; e-mail: <jerome.franckowiak@deedi.qld.gpv.au>

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

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

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

Chromosome 6H (6): Victoria Carollo Blake, Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT 59717, USA.e-mail: <vblake@montana.edu>

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

Integration of molecular and morphological marker maps: David Marshall, Genetics Programme, Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. FAX: 44 1382 562426. e-mail: <David.Marshall@scri.ac.uk>

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

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

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

List of Barley Coordinators (continued)

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

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

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

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

Chloroplast genes: Mats Hansson, Carlsberg Research Center, Gamle Carlsberg vej 10, DK-2500 Valby, Copenhagen Denmark. e-mail: <mats@crc.dk>

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

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

Semi-dwarf genes: Jerry D. Franckowiak, Hermitage Research Station, Agri-science Queensland, Department of Employment, Economic Development and Innovation, Warwick, Queensland 4370, Australia, FAX: +61 7 4660 3600; e-mail: < jerome.franckowiak@deedi.qld.gpv.au >

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

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

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

Gunter Backes

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

e-mail: guba@life.ku.dk

A member of the cellulose synthase-like gene family, HvCslF9 was localized to chromosome 1H, bin 7 (Burton *et al*., 2008). The family includes seven genes in barley and there is evidence that the gene is involved in the synthesis of β-glucan.

In a doubled haploid population (100 lines) from a cross between the two-row spring barley line BCD47 and the variety 'Baronesse', on chromosome 1H, bin 3/4, a QTL affecting both heading date (LOD 2.1 – 2.9), photoperiod response (LOD 1.7), physiological maturity (LOD 1.8) and grain filling period (LOD 1.4) was localized (Castro *et al*., 2008). The phenotyping was based on eight field experiments covering three years. Besides, two major QTLs for heading date and physiological maturity explained most of the phenotypic variation.

A QTL for heading date, when sown in autumn in four field experiments, and for short photoperiod, measured in two green house experiments, was localized to 1H, bin 11 (Cuesta-Marcos *et al*., 2008a). The localisation was carried out in 120 doubled haploid lines from a cross between the French two-row cultivars 'Beka' and 'Mogador'. *Ppd-H2* might be a candidate gene for this QTL.

Fifteen small interconnected doubled haploid populations (7 to 20 lines each, adding up to 281 lines in total), were cultivated under the same conditions as the population described in the precedent paragraph. In the field experiments, the heading date was measured, while in the greenhouse experiment, Cuesta-Marcos *et al.* (2008b) determined the number of leaves. Again, on chromosome 1H, bin 11, a QTL, likely representing *Ppd-H2*, affected both traits.

Verhoeven *et al*., 2008 were interested in the habitat-specific selection on heading-date related QTLs. For this purpose, they tested 140 $F_{2:3}$ families from a cross between two wild barley lines (*Hordeum vulgare* ssp. *spontaneum*) originating from two different environments. They tested the lines in different controlled and natural environments and localized relatively large overlapping areas affecting seed weight (measured in field experiments) and relative growth rate (measured in a green house experiment) on chromosome 1H.

In an association study using a population consisting of 83 barley landraces, 44 old genotypes and 65 modern genotypes from within the Mediterranean basin, Pswarayi *et a*l., 2008 detected associations for grain yield in bin 2 and bin 8 of chromosome 1H. The experiment was carried

out in Spain (one year) and Syria (two years) on two locations with high and low yield potential, respectively. Both mentioned associations were detected in the low-yield environment in Syria.

A QTL for coleoptiles elongation under uncovered darkness (LOD 3.9) was found by Takahashi *et al*. (Takahashi *et al*., 2008) on chromosome 1H, bin 14. The authors phenotyped 150 doubled haploid lines from the Harrington/TR306 population in pot experiments.

Ulrich *et al*. (Ullrich *et al*., 2008) analyzed 150 doubled haploid lines from 'Steptoe'/'Morex' for pre-harvest sprouting. They found a QTL for germination percentage on chromosome 1H, bin 14, with an LR of 12. The ears from plants grown in one field and one green house environment were treated for five days in a mist chamber.

In two doubled haploid populations, one including 92 lines from the cross TX0425/'Franklin' and one including 177 lines from the cross 'Yerong'/'Franklin', Li *et al*. (2008) searched for QTLs related to waterlogging tolerance. In TX0425/'Franklin', they detected a QTL for chlorosis after two weeks of waterlogging on chromosome 1H bin 6/7 (LOD 2.8). In the population derived from 'Yerong'/'Franklin' they detected another QTL effecting leaf yellowing after 2 weeks of waterlogging in bin 8/9 (LOD 2.8).

In an greenhouse experiment with well-watered and drought-stress treatments Guo *et al*. (2008) measured different chlorophyll-related traits on 194 recombinant inbred lines originating from a cross between 'Arta' and the wild barley (*Hordeum vulgare* ssp. *spontaneum*) line 41-1. On chromosome 1H, a QTL for initial photosynthesis was discovered in bin 11 (LOD 2.8).

Another experiment dealing with drought related trait was carried out as a field experiment with four Mediterranean locations in two years on 158 recombinant inbred lines from the cross 'Tadmor'/'ER/Apm' (von Korff *et al*., 2008a). Several traits related to drought stress, plant morphology and development were observed. On chromosome 1H, five QTLs were observed: in bin 7 and 8 two QTLs affecting heading date (F-values 12.1 and 20.8, respectively), in bin 9 a QTL affecting spike length (F-value 15.7), in bin 12 a QTL affecting both growth vigour and days to maturity (F-values 19.5 and 31.4, respectively) and in bin 14 a QTL affecting the grain filling period (F-value 20.8).

In an advanced back-cross population (301 BC_2DH lines) originating from a cross between 'Scarlett' and the wild barley (*H. vulgare* ssp. *spontaneum*) line ISR42-8, von Korff *et al*. (2008b) analyzed malting quality traits on kernels harvested from four locations through two years. Six QTLs were detected on chromosome 1H: in bin 3 a QTL for protein content, (F-value 11), in bin 3/4 a QTL for α-amylase activity (F-value 11), in bin 4 a QTL for malt extract (F-value 16.3), in bin 6-8 a QTL for friability and protein content (F-values 153 and 59, respectively), in bin 6-9 a QTL for viscosity, in bin 7 another QTL for malt extract (F-value 45), in bin 10 a QTL for friability and viscosity (F-value 23 and 15, respectively) and in bin 13 another QTL for protein content. For the last-mentioned QTL the wild barley contributed the advantageous allele.

Two major QTLs for resistance against spot blotch, caused by *Cochliobolus sativus*, were localized by Kuldeep *et al*. (2008) on chromosome 1H of barley. One was localized in bin 6/7

(LOD 9.0) and one was localized in bin 6/7 (LOD 18.9). A further QTL was localized on chromosome 7H. The analysis was carried out in field experiments (one location, 3 years) on a population of 200 recombinant inbred lines (F_5 - F_7) from a cross between the resistant line IBON 18 and the susceptible line RD 2508.

The QTL locus *Rphq21* conferring resistance against leaf rust, caused by *Puccinia hordei*, was located on chromosome 1H, bin 5/6 by Marcel *et al*. (2008). The resistance was effective against one out of 4 isolates in the seedling stage of barley. It was localized with an LOD of 3.9 in a population of 103 recombinant inbred lines (F_9) from the cross L94/'Vada'.

Jafary *et al*. (2008) studied non-host resistance in barley against heterologous rust fungi. For this purpose, they infected two different populations of barley with *Puccinia triticina*, *P. persistens*, *P. hordei-murini* and *P. hordei-secalini*. On chromosome 1H, two QTLs conferring resistance against *P. hordei-murini* were localized. In the population consisting of 113 recombinant inbred lines (F_9) from the cross 'SusPtrit'/'Cepada Capa' a QTL in bin 2-4 was detected and in the other population, consisting of 92 doubled haploid lines from the Oregon-Wolfe Barley population, a QTL in bin 6-8 was found.

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Coordinator's report: Chromosome 2H (2)

J.D. Franckowiak

Hermitage Research Station
Agri-science Queensland
Department of Employment, Economic Development and Innovation
Warwick, Queensland 4370, Australia

e-mail: jerome.franckowiak@deedi.qld.gov.au

Three genes [*Ppd-H1* (synonym *Eam1* on 2HS), *HvCO1* (synonym *Vrn-H3* on 7HS), and *HvFT1* (positional associated with *esp7S* on 7HS)] known to play essential roles in the regulation of flowering time under long days in barley were analyzed for nucleotide diversity in a collection of 220 spring barley accessions by Stracke *et al*. (2009). The coding region of *Ppd-H1* was highly diverse, while both *HvCO1* and *HvFT1* showed a rather limited level of diversity. The *Ppd-H1* alleles (the late flowering haplotype was more common than the five early haplotypes combined) were strongly associated with flowering time across four environments, showing a difference of five to ten days between the most extreme haplotypes. The association between flowering time and the variation at *HvFT1* and *HvCO1* was strongly dependent on the haplotype present at *Ppd-H1*.

Karsai *et al*. (2008) examined the interaction of vernalization (*Vrn*) and photoperiod sensitivity (*Ppd*) genes in progenies variable winter and spring growth habits under various thermo- and photoperiods. Alleles at the *Ppd-H1* (*Eam1* on 2HS) locus were found to interact with alleles for spring growth habit at the *Vrn-H1* (*Sgh2* on 5HL) locus. Certain allele combinations at these two loci interacted with alleles at the *Ppd-H2* (1HL) locus under various thermo- and photoperiods to produce short-day photoperiod responses, when the dominant allele at the *Ppd-H1* locus was absent.

Custa-Marcos *et al*. (2009) studied the genetic control of flowering time under Northern Spanish (Mediterranean) conditions using a new population derived from the spring x winter cross Beka x Mogador. A set of 120 doubled haploid lines was evaluated in the field, and under controlled temperature and photoperiod conditions. Genotyping included markers for vernalization candidate genes: HvBM5 (*Vrn-H1* on 5HL), HvZCCT (*Vrn-H2* on 4HL), and HvT SNP22 (*Ppd-H1* on 2HS). Four major QTL, and the interactions between them, accounted for most of the variation in both field (71 to 92%) and greenhouse trials (55 to 86%). These were coincident with the location of the major genes for response to vernalization and a gene for short photoperiod response (*Ppd-H2* on 1HL). A major QTL, near the centromere of chromosome 2H (*Eam6* or *eps2S*), was the most important under autumn sowing conditions. Although it was detected under all conditions, its action seemed dependent on environmental cues. The presence of the winter Mogador allele at the two loci combined with the effect of *Ppd-H2* was found to cause short-day vernalization.

Mittal *et al*. (2008) reported response to Russian wheat aphid (RWA, *Diuraphis noxia* Kurdjumov) infestations was associated with a minor QTL on 2H near marker GBM1523, which explained 6% of the variation. The RWA feeding damage results were based on testing of 191 F_2–derived F_3 families from the cross Morex x STARS-9301B where Morex is a susceptible six-rowed malting barley and STARS-9301B is a selection from RWA-resistant Afghanistan introduction PI 366450.

Roslinsky *et al*. (2007) reported markers for low phytate genes. Seed homozygous for *low phytic acid 1-1* (*lpa1-1*) or *low phytic acid 2-1* (*lpa2-1*) has a 50 and 70% decrease in seed phytate, respectively. These mutations were previously mapped to chromosomes 2HL and 7HL respectively. They converted RFLP marker ABC153 located in the same region of 2H as *lpa1-1* to a sequence-characterized-amplified-region (SCAR) marker. Segregation analysis of the CDC McGwire × Lp422 doubled haploid population confirmed linkage between the SCAR marker and the *lpa1-1* locus with 15% recombination.

Palmer *et al*. (2009) describe archaeobotanical samples of barley found at Qasr Ibrim as having a two-rowed phenotype that is unique to the region of archaeological sites upriver of the first cataract of the Nile. The pictured spike set little or no seed in the lateral spikelets and shows lateral bracts (spikelets) that are typical of intermediates between two- and six-rowed spikes. This phenotype was reported to occur throughout all strata at Qasr Ibrim, which range in age from 3000 to a few hundred years. Palmer *et al*. (2009) extracted ancient DNA from barley samples from the entire range of occupancy of the site and studied the *Vrs1* locus on 2HL that is responsible for row number. They found a genotype that is consistent with the six-rowed condition. These results indicate a six-rowed ancestry for the Qasr Ibrim barley, but a loss of lateral fertility, possibly caused by alleles at the *Int-c* locus. The consistency of this genotype/phenotype discord over time supports a scenario of adoption of this barley type by successive cultures.

Genetic diversity of 33 Qinghai-Tibetan wild barley accessions and 56 landraces collected primarily from other parts of China was evaluated with 52 SSR markers by Gong *et al*. (2009). At the 52 SSR loci, 206 alleles were detected of which 111 were common alleles. Polymorphism information content (PIC) values ranged from 0 to 0.81 with an average of 0.54 for Qinghai-Tibetan wild barley and 0 to 0.79 with an average of 0.49 for landraces. Twenty-four unique alleles were observed in Qinghai-Tibetan wild barley, and the frequency of unique alleles in Qinghai-Tibetan wild barley was about 2.1 times higher than that in the landraces. Only chromosome 2H had more unique alleles in the landraces.

Chen *et al*. (2009b) studied mechanisms for low temperature tolerance in reproductive tissues (LTR tolerance) in barley using Amagi Nijo x WI2585 and Haruna Nijo x Galleon populations. Flowering time and spike morphology traits were associated with the LTR tolerance loci. In spring-type progeny of both crosses, winter alleles at the vernalization response locus on 5HL (*Vrn-H1*) were linked in coupling with LTR tolerance and earlier flowering. In contrast, tolerance on 2HL was coupled with late flowering alleles at a locus named *Flt-2L*. Both chromosome regions influenced chasmogamy/cleistogamy (open/closed florets), although tolerance was associated with cleistogamy at the 2HL locus and chasmogamy at the 5HL locus. LTR tolerance controlled by both loci was accompanied by shorter spikes, fewer florets per spike

on 5HL (possibly *Eam5*) and shorter rachis internodes on 2HL (possibly *Zeo2*). The *Eps-2S* or *Eam6* locus on 2HS segregated in both crosses and influenced spike length and flowering time but not LTR tolerance. Thus, none of the traits was consistently correlated with LTR tolerance.

Chen *et al*. (2009a) identified a major gene-rich region on the end of the long arm of Triticeae group 2 chromosomes that exhibits high recombination frequencies, making it an attractive region for positional cloning. Traits known to be controlled by this region include chasmogamy/cleistogamy, frost tolerance at flowering, grain yield, head architecture, and resistance to Fusarium head blight and rusts. To assist these cloning efforts, detailed genetic maps of barley chromosome 2H, including 61 polymerase chain reaction markers, were constructed. Collinearity with rice occurred in eight distinct blocks, including five blocks in the terminal gene-rich region. Sequencing across 91 gene fragments totaling 107 kb from four barley genotypes revealed the highest single nucleotide substitution and insertion-deletion polymorphism levels in the terminal regions of the chromosome arms.

Guo *et al*. (2008) analyzed the quantitative trait loci (QTL) controlling chlorophyll content and chlorophyll fluorescence in RILs developed from the cross between 'Arta' and *Hordeum spontaneum* 41-1. Five traits, chlorophyll content, and four chlorophyll fluorescence parameters, namely initial fluorescence (F_o), maximum fluorescence (F_m), variable fluorescence (F_v), and maximum quantum efficiency of PSII (F_v/F_m) which are related to the activity of the photosynthetic apparatus, were measured under well-watered and drought stress conditions at post-flowering stage. QTL analysis identified a total of nine and five genomic regions, under well watered and drought stress conditions, respectively. No common QTL was detected except one for chlorophyll content. The desirable QTL under drought were from Arta. A QTL for F_v/F_m, which is related to the drought tolerance of photosynthesis, was identified on 2H at 116 cM. In addition, another QTL for F_v/F_m was also located on 2H at 135.7 cM. Guo *et al*. (2008) suggest that two major loci on 2H are involved in the development of functional chloroplast at post-flowering stage for drought tolerance of photosynthesis in barley under drought stress

To understand genetic patterns of the morphological and physiological traits in flag leaf of barley, a DH population derived from Yerong (six-rowed) x Franklin (two-rowed) was used by Xue *et al*. (2008) to determine QTL controlling length, width, length/width, and chlorophyll content of flag leaves. A total of 9 QTL showing significantly additive effect were detected in 8 intervals on 5 chromosomes. The variation of individual QTL ranged from 1.9 to 20.2%. For chlorophyll content expressed as SPAD value, 4 QTL were identified on chromosomes 2H, 3H and 6H; for leaf length and width, 2 QTL located on chromosomes 5H and 7H, and 2 QTL located on chromosome 5H were detected; and for length/width, 1 QTL was detected on chromosome 7H. The two QTL for chlorophyll content detected on 2H were at different positions than those reported by Guo *et al*. (2008).

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Coordinator's Report: Barley Chromosome 3H (3)

Luke Ramsay

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

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

Over the last year there have been a number of publications reporting the mapping of genes and QTL on barley chromosome 3H. These included a number of publications that took advantage of available genomic resources to map at high density across the whole genome using the high throughput SNP genotyping. Close *et al.* (2009) summarised the development of SNP genotyping using the Illumina GoldenGate assay including a consensus map with 484 gene derived SNPs on 3H. The use of this genotyping platform also under-pinned the map with 123 genic SNPs on 3H presented by Sato and Takeda (2009) of a doubled haploid population derived from Haruna Nijo x H602 (*H. v.* ssp *spontaneum*). This population was also used by Sato *et al*. (2009) to map genes serially resulting in a genetic map with 444 ESTs mapped to 3H. The development of high density gene based maps has enabled detailed analysis of the co-linearity of chromosome 3H with the syntenic rice chromosome 1 (Thiel *et al*. 2009) and also underpins analysis of genetical genomics experiments (Druka *et al.* 2008). Other developments of relevance to mapping of chromosome 3H are the progress made in the development of a physical map of the barley genome (Schulte *et al*. 2009) and the integration of this with the genetic map (Close *et al.* 2009, Sakai *et al.* 2009).

In comparison to genome wide studies, other reports have concentrated on the mapping of members of gene families of particular interest in barley. Thus Demetriou *et al*. (2009) report the mapping of HvHDAC2-2 (a member of the plant specific HD2 family of histone deacetylases) to the long arm of 3H (cosegregating with ABG004 in bin 13) and Kikuchi *et al.* 2009) mapping two members of the PEBP (phosphatidylethanolamine-binding protein) gene family, similar to FLOWERING LOCUS T (FT) in Arabidopsis, to 3H, HvMFT1 mapping distally in bin 1 and HvFt2 mapping to bin 6.

In the analysis of the (1,3)-beta-D-glucan synthase gene family in barley by Schober *et al.* (2009) two genes HvGSL6 and HvGSL7 were mapped to bin 6 using the Clipper x Sahara population. Emebiri (2009) reported a QTL for beta-glucanase activity in bin 6 in a VB9524 x ND11231*12 population as well as a QTL for wort beta glucan content on the long arm of 3H. A QTL for friability was also found in the region of bins 6 and 7 by Laido *et al.* (2009) in the doubled haploid population Nure x Tremois. Other malting quality QTL were reported by Wei *et al.* (2009) with a QTL for Beta amylase activity in the central region and QTL for grain total protein and protein fraction content on the distal end of the long arm using a population derived from a cross between CM72 and Gairdner. The distal end of 3HL (Bins13-16) was also implicated as controlling Kolbach index (soluble/total protein) in an analysis of introgression lines derived from backcrosses of ISR 42-8 (*H. v.* ssp *spontaneum*) x Scarlett (Schmalenbach and Pillen 2009).

In an approach integrating proteomic and genetic approaches, Finnie *et al.* (2009) mapped differences in seed protein profiles using a population derived from a Scarlett x Meltan cross. Two protein groups were mapped to 3H; one, D1, relating to a 17 kDa small heat shock protein mapped to the top of the short arm, whereas the other (J1, with unknown identity) mapped near HVM 27 in bin 6.

During the last year QTL on 3H were also reported for resistance to pests and diseases. The major QTL on 3HL conferring Russian wheat aphid resistance previously found in a cross between the resistant STARS-9301B and Morex (Mittal *et al*. 2008) was also found in a cross between another resistance cultivar STARS-9577B and Morex (Mittal *et al*. 2009). Li *et al*. (2009) reported a major QTL for resistance to crown rot, caused by Fusarium *spp*., in a cross between the resistant landrace TX9425 and Franklin. This QTL, designated as *Qcrs.cpi-3H*, mapped slightly distal to Bmag0606 on 3HL and was coincident with one of two plant height QTL on 3HL in the same population though it is unclear whether which of these relates to the *denso*/*sdw1* locus which is segregating in the population (Li *et al.* 2009).

Jia *et al.* 2009 mapped a giberellic acid-20 oxidase to the long arm of 3H using a doubled haploid population derived from a Baudin x AC Metcalfe cross. Given its co-incidence with a QTL for plant height in the same cross and the genes homology to *sd1* in rice the authors suggest that the gene is a good candidate for *sdw1/denso*. Other reports of genes on 3H included that of Dabbert *et al.* (2009) who mapped a low-tillering mutant; absent lower laterals (*als*) on the long arm of chromosome 3H in bin 11 using an F_2 population derived form a cross between Bowman-*als* and Morex and that of Chen *et al.* (2009) who mapped a drought hyper sensitive cuticle mutant eibi1 to 3H bin 6 co-segregating with the EST AV918546 in two mapping populations.

In addition several new reports of QTL on 3H for agronomic characters were published during this reporting period. Cuesta-Marcos *et al*. (2009) and Inostroza *et al*. (2009) both reported QTL for grain yield in the region of bins 13-14 although neither study used crosses in which the *sdw/denso* mutation was present (Beka x Mogador and Harrington x Caeserea 26-24 (*H. v*. ssp. *spontaneum*) respectively). The *sdw/denso* mutation was however postulated as a candidate gene for some of the QTL reported in studies using a BC2DH population (Bauer *et al*. 2009) or derived introgression lines (Schmalenbach and Pillen, 2009, Schmalenbach *et al.* 2009) derived from a cross between ISR 42-8 (*H. v*. ssp *spontaneum*) and Scarlett. These QTL included those for grain sieving fraction > 2.5mm (Schmalenbach and Pillen, 2009), plant height (Bauer *et al*. 2009, Schmalenbach *et al.* 2009), days to heading (Bauer *et al*. 2009, Schmalenbach *et al.* 2009) and grain yield (Bauer *et al*. 2009). These studies also included QTL on 3H unassociated with the *sdw1* region including those for days to heading, plant height, grain yield, thousand grain weight and ears/m^2 (Bauer *et al*. 2009) and grains per ear (Schmalenbach *et al.* 2009). In a study evaluating the phenotypic plasticity of grain yield and thousand kernel weight using data from multiple environments, Lacaze *et al* (2009) found QTL for the primary traits on 3H in both the Harrington x Morex and Steptoe x Morex populations and in the latter QTL for the plasticity trait around BCD828 in bin 6.

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Coordinator's Report: Chromosome 4H (4)

Arnis Druka

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

e-mail: Arnis.Druka@scri.sari.ac.uk

Several papers that mention genes and QTLs specifically on chromosome 4H have been published in 2008 - 2009.

Schober *et al*., 2009 reports transcription patterns of members of the callose synthase gene family from barley (*Hordeum vulgare*). The fragments of six barley (1,3)-beta-d-glucan synthase-like (GSL) cDNAs were obtained by PCR amplification using primers designed to barley expressed sequence tag (EST) sequences. The HvGSL genes, designated HvGSL2 to HvGSL7, were mapped to individual loci that were distributed across the barley genome on chromosomes 3H, 4H, 6H and 7H. The HvGSL1 gene has been isolated and characterised previously. Transcript levels for all the genes were analysed by quantitative real-time PCR in a range of barley tissues and organs, at various developmental stages. High levels of transcript for many of the HvGSL genes were detected in endosperm during the early stages of grain development, when cellularisation of the endosperm was occurring and it is likely that many of the genes participate in this process. Transcripts of HvGSL1 and HvGSL5 mRNAs were significantly more abundant than other GSL mRNAs in the roots of young seedlings, while HvGSL7 mRNA was detected at relatively high levels along the length of two week old shoots.

Comadran *et al*., 2009 reported population structure and genome-wide linkage disequilibrium (LD) analysis in 192 *Hordeum vulgare* accessions providing a comprehensive coverage of past and present barley breeding in the Mediterranean basin by using 50 nuclear microsatellite and 1,130 DArT(R) markers. Both clustering and principal coordinate analyses clearly sub-divided the sample into five distinct groups centred on key ancestors and regions of origin of the germplasm. For given genetic distances, large variation in LD values was observed, ranging from closely linked markers completely at equilibrium to marker pairs at 50 cM separation still showing significant LD. Mean LD values across the whole population sample decayed below r (2) of 0.15 after 3.2 cM. By assaying 1,130 genome-wide DArT((R)) markers it was demonstrated that, after accounting for population substructure, current genome coverage of 1 marker per 1.5 cM except for chromosome 4H with 1 marker per 3.62 cM is sufficient for whole genome association scans. It was also shown, that by identifying associations with powdery mildew that map in genomic regions known to have resistance loci, associations can be detected in strongly stratified samples provided population structure is effectively controlled in the analysis.

Schmalenbach and Pillen 2009 reported a malting quality quantitative trait locus (QTL) study using a set of 39 wild barley introgression lines (hereafter abbreviated with S42ILs). Each S42IL harbors a single marker-defined chromosomal segment from the wild barley accession 'ISR 42-8'

(*Hordeum vulgare ssp. spontaneum*) within the genetic background of the elite spring barley cultivar 'Scarlett' (*Hordeum vulgare ssp. vulgare*). The aim of the study was (1) to verify genetic effects previously identified in the advanced backcross population S42, (2) to detect new QTLs, and (3) to identify S42ILs exhibiting multiple QTL effects. For this, grain samples from field tests in three different environments were subjected to micro malting. Subsequently, a line x phenotype association study was performed with the S42ILs in order to localize putative QTL effects. A QTL was accepted if the trait value of a particular S42IL was significantly ($P < 0.05$) different from the recurrent parent as a control, either across all tested environments or in a particular environment. For eight malting quality traits, altogether 40 QTLs were localized, among which 35 QTLs (87.5%) were stable across all environments. Six QTLs (15.0%) revealed a trait improving wild barley effect. Out of 36 QTLs detected in a previous advanced backcross QTL study with the parent BC(2)DH population S42, 18 QTLs (50.0%) could be verified with the S42IL set. For the quality parameters alpha-amylase activity and Hartong 45 degrees C, all QTLs assessed in population S42 were verified by S42ILs. In addition, eight new QTL effects and 17 QTLs affecting two newly investigated traits were localized. Two QTL clusters harboring simultaneous effects on eight and six traits, respectively, were mapped to chromosomes 1H and 4H. In future, fine-mapping of these QTL regions will be conducted in order to shed further light on the genetic basis of the most interesting QTLs.

Netsvetaev 2008 report mapping peroxidase activity. Identical specimens were separated by electrophoresis in two gels to detect and fix peroxidase isozymes. Both gels were stained by Coomassie brilliant blue for detecting proteins. One gel was previously incubated for detecting peroxidase activity. The differences in electrophoretic patterns between the gels indicate the zones of peroxidase activity. It has been shown that locus Prx 6H, controlling a low-mobility grain peroxidase (PRX 6H), is localized to barley chromosome 6. Two loci, Alb 4H and Alb 7H, controlling the biosyntheses of water-soluble proteins of barley endosperm, were localized to chromosomes 4 and 7. It has been demonstrated that barley culture is polymorphic at multiple molecular forms of peroxidase.

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Coordinator's report: Chromosome 5H (7).

George Fedak

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada, ECORC
Ottawa, ON, Canada K1A OCA

e-mail: George.Fedak@AGR.GC.CA

For this coordinator's report, the abstracts of the proceedings of the Plant and Animal Genome Conference for the years 2009 (volume XVII) and 2010 (volume XVIII) were screened.

Cellulose synthase-like CslF genes have been implicated in the biosynthesis of (1,3:1,4) beta-D-glucans. Seven CslF genes have already been isolated from barley. Four of these genes have been mapped to a single locus on chromosome 2H in a region corresponding to a major QTL for grain glucan content. The other CslF genes map to chromosomes 1H, 5H, and 7H (Fincher *et al*., 2010).

Flow cytometric chromosome sorting can be used to dissect the barley genome to chromosome 1H and the arms of chromosomes 2H to 7H. These aliquots can be used for sequencing and physical mapping. Of the 1536 genes examined using flow sorted material, 1329 were assigned to specific chromosome arms, confirming the chromosome/arm locations of these genes (Bhat, *et al*., 2009).

Association mapping, using SNP markers, was used to identify barley lines with spot blotch resistance. A major gene was found on chromosome 7H. Markers were also associated with spot blotch resistance on chromosomes 2H, 3H and 5H (Zhou *et al*., 2009).

FrH2 is one of two major QTLs, located on chromosome 5H, and affecting freezing tolerance and winter hardiness of barley. FR1 is hypothesized to be due to a pleiotropic effect of Vrn-1. FR2 spans a cluster of CBF genes; these loci are genetically and functionally linked. There are 14 genes encoding CBF (C repeat binding factors), that map coincidently with FrH2. It is not known if the FrH2 QTL is the result of a single CBF or a subset of these genes. In the first step of mapping FrH2, recombinants between 7 of the 14 CBF genes have been identified and showed that the cluster spans 81 cM. A BAC library is now being screened with 6CBF genes with the aim of constructing a single contig containing FrH2 (Francia *et al*., 2010).

Stem rust race TTKS (Ug99) will also attack barley. This race is capable of attacking 70% of wheat and barley cultivars globally. To find resistance loci, an association mapping approach was used, on 761 breeding lines using 1927 SNP markers. Of the 761 lines tested, 19 were found to be resistant. Three markers were found to be significantly associated with resistance to TTKS. Two of the markers were located on the long arm of chromosome 5H and one on the short arm of 2H (Zhou *et al*., 2010).

As part of the US National Barley Cap project, a subset of 96 advanced lines from the Virginia Tech. winter barley program were phenotyped for 11 agronomic traits and association mapping conducted with 2933 SNP markers. Significant SNPs were identified for many traits. Net blotch resistance was identified on chromosomes 2H, 3H and 5H with R2 values ranging from 6 to 8% (Liu *et al*., 2010).

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Coordinator's Report: Chromosome 6H (6)

Victoria Carollo Blake

Montana State University
Bozeman, MT 59717 USA

e-mail: vblake@montana.edu

Breeding efforts to improve barley for rainfed/dryland conditions have been a focus of several groups. Among those with results on 6H was a study by Inostroza, *et al*. who tested recombinant chromosome substitution lines in four locations in Chile and the US with varying water availability. Four regions on 6H were found to be significant for yield, two of which were significant at P<0.001. Another study to identify QTL associated to Mediterranean dryland conditions (Von Korff, *et al*.) revealed several loci on 6H in a RIL population derived from ER/Apm and Tadmor including days to maturity, grain yield, lodging and plant height. Agronomic performance was tested over four years in a rainfed environment in four locations in Syria and Lebanon.

In pathology studies, Jafary *et al*. evaluated two mapping populations and the OWB population for resistance to four heterologous rust species. They found diverse genes conferring resistance and mapped six overlapping QTLs to 6H. Wagner *et al.* identified a minor QTL for *Rhynchosporium secalis* near the centromeric region of 6H. The authors reported that this region was relevant for a stress reaction but did not indicate the potential of candidate genes for *R. secalis* resistance.

Malting quality studies identified six SNPs resulting in four haplotypes for the α-amylase gene *amy1* (Matthies, *et al*.). These SNPs were discovered in a collection of 117 European varieties, have varying degrees of influence on malting quality and have all been converted to high-throughput markers.

New GrainGenes maps that included Chromosome 6H were included in the following Map_Data sets.

1) Barley, Abiotic QTL Consensus. These abiotic QTL, assembled as part of the plan to place all reported barley QTL into GrainGenes, were placed on the maps published as part of the 'Barley, Consensus 2005, SNP' map set from Rostocks. *et al*. See Table 1 for a list of QTL placed on this map.

2) Barley, OWB, OPA2009. This map set adds OPA and DArT markers to the Oregon Wolfe Barley maps with previously described malt-quality QTL aligned (Szucs *et al*., 2009). See Table 1 for a list of QTL placed on this map.

3) Barley, Agronomic QTL Consensus. Agronomic QTL, placed on the maps published as part of the 'Barley, Consensus 2005, SNP' map set from Rostocks. *et al*. See Table 1 for a list of QTL placed on this map.

4) Barley OPA123, Consensus. This map set contains 1943 OPA SNP markers, hundreds of which are on 6H. This map was provided as a personal communication from Tim Close and will be updated in 2009.

Table 1. 6H QTL placed onto curated consensus maps on GrainGenes

QTL	Trait	GrainGenes Map Data	Original Reference
QAa.ChHa-6H	alpha-Amylase activity	Barley, OWB, OPA2008	Coventry SJ *et al*., 2003
QAa.StMo-6H	alpha-Amylase activity	Barley, OWB, OPA2008	Hayes P *et al*., 1993
QAa.HaTR-6H	alpha-Amylase activity	Barley, OWB, OPA2008	Mather DE *et al*., 1997
QBoss.ClSa-6H	Boron sensitivity (whole shoot)	Barley, Abiotic QTL Consensus	Jefferies SP *et al*., 1999
QHd.BlKy-6H	Days to heading	Barley, Agronomic QTL Consensus	Bezant J *et al.*, 1996
QHd.StMo-6H	Days to heading	Barley, Agronomic QTL Consensus	Hayes P *et al*., 1993
QHd.IgTr-6H.1	Days to heading	Barley, Agronomic QTL Consensus	Laurie DA *et al*., 1995
QHd.IgTr-6H.2	Days to heading	Barley, Agronomic QTL Consensus	Laurie DA *et al*., 1995
QDp.StMo-6H	Diastatic Power	Barley, OWB, OPA2008	Hayes P *et al*., 1993
QDp.HaTR-6H	Diastatic Power	Barley, OWB, OPA2008	Mather DE *et al*., 1997
QSpsm.TyVo-6H	Spikes per area	Barley, Agronomic QTL Consensus	Kjaer B *et al.*, 1996
QEv.HaTR-6H	Extract viscosity	Barley, OWB, OPA2008	Mather DE *et al*., 1997
QFcd.HaTR-6H	Fine coarse difference	Barley, OWB, OPA2008	Mather DE *et al*., 1997
QGms.HaTR-6H	Germination speed	Barley, Agronomic QTL Consensus	Mano Y *et al*., 1997
QHsh.IgDa-6H	Head shattering	Barley, Agronomic QTL Consensus	Backes G *et al.*, 1995
QHt.IgDa-6H	Height	Barley, Agronomic QTL Consensus	Backes G *et al.*, 1995
QHt.StMo-6H	Height	Barley, Agronomic QTL Consensus	Hayes P *et al*., 1993
QKps.BlKy-6H	Kernels per spike	Barley, Agronomic QTL Consensus	Bezant J *et al*., 1997
QLg.IgDa-6H	Lodging	Barley, Agronomic QTL Consensus	Backes G *et al.*, 1995

QLg.StMo-6H	Lodging	Barley, Agronomic QTL Consensus	Hayes P *et al*., 1993
QMe.StMo-6H	Malt extract	Barley, OWB, OPA2008	Hayes P *et al*., 1993
QPgw.BlKy-6H	Plant grain weight	Barley, Agronomic QTL Consensus	Bezant J *et al*., 1997
QLr.HaTR-6H	Reaction to leaf rust	Barley, Pathology QTL, Consensus*	Spaner D *et al*. 1998
QNb.HaTR-6H	Reaction to net blotch	Barley, Pathology QTL, Consensus	Spaner D *et al*. 1998
QNb.StMo-6H.1	Reaction to net blotch	Barley, Pathology QTL, Consensus	Steffenson B *et al.*, 1996
QNb.StMo-6H.2	Reaction to net blotch	Barley, Pathology QTL, Consensus	Steffenson B *et al.*, 1996
QPm.IgDa-6H	Reaction to Powdery mildew	Barley, Pathology QTL, Consensus	Backes G *et al.* 1996
QScd.IgDa-6H.1	Reaction to scald	Barley, Pathology QTL, Consensus	Backes G *et al.*, 1995
QScd.IgDa-6H.2	Reaction to scald	Barley, Pathology QTL, Consensus	Backes G *et al.*, 1995
QScd.HaTR-6H	Reaction to scald	Barley, Pathology QTL, Consensus	Spaner D *et al*. 1998
QSsg.StMo-6H	Salt sensitivity at germination	Barley, Abiotic QTL Consensus	Mano Y *et al*., 1997
QSss.StMo-6H	Salt sensitivity in seedlings	Barley, Abiotic QTL Consensus	Mano Y *et al*., 1997
QSgw.BlKy-6H.1	Spike grain weight	Barley, Agronomic QTL Consensus	Bezant J *et al*., 1997
QSgw.BlKy-6H.2	Spike grain weight	Barley, Agronomic QTL Consensus	Bezant J *et al*., 1997
QStb.IgDa-6H	Stem breaking	Barley, Agronomic QTL Consensus	Backes G *et al.*, 1995
QTw.BlKy-6H	Test weight	Barley, OWB, OPA2008	Bezant J *et al*., 1997
QTw.HaMo-6H.1	Test weight	Barley, OWB, OPA2008	Marquez-Cedillo LA *et al.* 2000
QTw.BlE2-6H.2	Test weight	Barley, OWB, OPA2008	Thomas W *et al.* 1995
QTw.HaTR-6H	Test weight	Barley, OWB, OPA2008	Tinker NA *et al.* 1995
QTil.TyVo-6H	Top internode length	Barley, Agronomic QTL Consensus	Kjaer B *et al.* 1995
QYld.IgDa-6H	Yield	Barley, Agronomic QTL Consensus	Backes G *et al.*, 1995
QYld.BlKy-6H	Yield	Barley, Agronomic QTL Consensus	Bezant J *et al*., 1997
QYld.StMo-6H	Yield	Barley, Agronomic QTL Consensus	Hayes P *et al*., 1993

QTL not placed on Consensus maps

QTL	Trait	Original Reference
QC13.LiHS-6H.1	C13 content	Ellis RP *et al.* 1997
QC13.LiHS-6H.2	C13 content	Ellis RP *et al.* 1997
QN15c.LiHS-6H	Nitrogen 15 content	Ellis RP *et al.* 1997
QTw.BlE2-6H.1	Test weight	Thomas W *et al.* 1995
QTw.HaMo-6H.2	Test weight	Marquez-Cedillo LA *et al.* 2000

*Map on GrainGenes pending

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Barley Genetics Newsletter (2009) 39:24-76

Coordinator's Report: Chromosome 7H (1)

Lynn S. Dahleen

USDA-Agricultural Research Service
Fargo, ND 58105, USA

e-mail: Lynn.dahleen@ars.usda.gov

Mapping research continued to provide additional markers, QTL and gene locations in 2008. Potokina *et al.* (2008) used the Barley GeneChip to map transcript derived markers (TDMs) and expression QTL for 16,000 barley genes in embryo-derived tissue from germinating seed of the Steptoe x Morex mapping population. They added 243 TDMs and 3673 expression QTL to the chromosome 7H map. These gene-specific markers should be useful to define the genetic control behind traits of interest. Kota *et al.* (2008) sequenced 437 expressed sequence tag (EST)-derived gene fragments in seven cultivars, including the parents of three mapping populations. Single nucleotide polymorphisms (SNPs) and insertion/deletion (InDel) polymorphisms were mapped, including 35 markers on chromosome 7H, and the SNP markers were converted to cleaved amplified polymorphism (CAP) assays. These markers showed 2 to 6 haplotypes and 1 to 28 SNPs from the 35 sequences. Varshney *et al.* (2008) screened 50 simple sequence repeat (SSR) and 50 SNP markers on six diverse barley genotypes from ICARDA and six parents from mapping populations to identify a core set of highly polymorphic markers. Four SSR and four SNP markers were selected for chromosome 7H. Two of the SNPs could be identified by CAP assays, one by InDel and the final one by pyrosequencing. Each marker identifies a single locus, gives high quality amplification, and was highly polymorphic among the diverse genotypes tested.

Disease resistance QTL were evaluated in a variety of populations. Sato *et al.* (2008) mapped QTL for FHB resistance in five two-rowed populations derived from crosses with Harbin 2-row as one of the parents. One locus on chromosome 7H was identified in three of the populations, with the Harbin 2-row allele contributing to susceptibility. Wagner *et al.* (2008) examined scald resistance in two populations, Igri (*rrs1*) x Triton (*Rrs1*) and Post x Vixen (both *rrs1*). Three QTL were present in the first population, including *Rrs1* on chromosome 2H and a minor QTL from Triton on the long arm of chromosome 7H that explained about 20% of the variation for scald reaction. This is probably *Rrs2*. A minor QTL from Vixen was located on the short arm of chromosome 7H that explained about 10% of the variation. Both of these loci are in regions where multiple resistance genes have been located. Grewal *et al*. (2008a and b) examined markers for both the net and spot forms of net blotch. QTL analysis of a cross between CDC Dolly (susceptible) and TR251 (resistant) located several loci, including one on chromosome 7H that provided resistance to both forms. They also tested markers linked to net blotch resistance in Australian germplasm for their utility in Canadian breeding materials. QTL analysis of a Chebec x Harrington population located a major QTL for seedling resistance on chromosome 7H, in the same position as *Rpt4*. This QTL is not of much use in Canadian germplasm because it is not effective against the common spot form of net blotch prevalent in Canada.

Lehmensiek *et al*. (2008) added a covered smut resistance gene, *Ruh.7H*, to the Alexis x Sloop linkage map, linked to the RFLP marker ABG704. They identified an EST-based codominant PCR marker between *Ruh.7H* and ABG704. They then used high resolution melting (HRM) procedures to locate two additional SNP markers to the telomere of chromosome 7HS. The HRM technique allowed mapping of single base changes without sequencing. Schmalenbach *et al.* (2008) developed a set of 59 introgression lines in Scarlett, each containing a chromosomal segment of *Hordeum vulgare* ssp. *spontaneum* accession ISR42-8. They tested the lines for reaction to powdery mildew and leaf rust. A powdery mildew resistance QTL was located on chromosome 7H in three potentially overlapping introgression lines. A QTL for leaf rust resistance was located in one of the introgression lines. Both QTL were previously identified in the BC_2DH population used to derive the introgression lines (von Korff *et al*. 2008b).

Mirlohi *et al*. (2008) examined allelic variability of the *Rpg1* stem rust resistance locus in eight Swiss landraces and eight wild barley accessions compared to the Morex allele to investigate diversity and possible origins of the gene. Only one Swiss landrace contained an intact and functional *Rpg1*. The other lines had a GTT InDel, evidence of unequal recombination, or lacked all or part of the locus which resulted in susceptibility to stem rust. No other functioning alleles were found at the locus. Jafari *et al*. (2008) mapped genes for non-host resistance to four leaf rust pathogens that infect wall barley, meadow barley, wheat grass or wheat, in a cross between SusPtrit x Cebada Capa and the Oregon Wolfe barley DH population. These were compared to locations of non-host resistance genes identified in SusPtrit x Vada. Chromosome 7H contained QTL for immunity to *Puccinia triticina*, *P. hordei-murini*, and *P. persistens*, from both Vada and SusPtrit. The locations often corresponded to map positions of defense gene homolog-based markers.

Positional cloning was used by Taketa *et al*. (2008) to identify the gene responsible for hull adherence at the *nud* locus. Markers that cosegregated or were closely linked to *nud* were used to identify overlapping BAC clones containing the locus. *Nud* was identified as an ethylene response factor family transcription factor that controls lipid biosynthesis and thus hull adherence. Lines without hull adherence (*nud*) had a 17 kb deletion in the transcription factor and lack a lipid layer between the hull and developing caryopsis. Evidence from their study indicates a single mutation deleting *Nud* was selected and spread across the world to domesticate barley. Jestin *et al.* (2008) identified QTL for aleurone thickness and cell layer number from a cross between Erhard Frederichen (3-4 cell layers) and Criolla Negra (2 cell layers). One of the three QTL located near the center of chromosome 7H explained 12-15% of the variation in cell layer number and thickness. As the aleurone is rich in minerals and vitamins, a thicker aleurone may provide improved nutrition for barley consumers. Burton *et al.* (2008) located seven members of the cellulose synthase-like (*CslF*) genes which are involved in β-glucan biosynthesis in barley. One of these genes, *HvCslF6*, was located on chromosome 7H, near locations where QTL for grain β-glucan have been found. *HvCslF6* mRNA was more abundant than transcripts of the other *CslF* genes in barley in most tissues examined, but especially in the developing barley coleoptile and endosperm.

Several studies examined traits that affect quality. QTL for preharvest sprouting were located on most chromosomes by Ullrich *et al*. (2008). One of these was on chromosome 7H, between the Brz and Amy2 loci. This QTL influenced preharvest sprouting and germination percent in both

the greenhouse and field. Von Korff *et al*. (2008a) located QTL for malting quality from *H. vulgare* ssp. *spontaneum* advanced backcrosses. On chromosome 7H, they found one QTL for fine-grind malt extract, three for friability and one for Hartong 45°C. Only one of the favorable alleles on chromosome 7H came from the wild parent. QTL involved in β-glucan levels were examined by Li *et al*. (2008) in a cross between CDC Bold and TR251. A major QTL near the centromere of chromosome 7H was detected in all three years of the study, which explained up to 39% of the variation for β-glucan. Another chromosome 7H QTL was detected on the long arm in one year which explained 12.7% of the variation. Both low β-glucan alleles came from CDC Bold.

Three studies verified QTL in locations previously reported for heading and anthesis dates on chromosome 7H (Cuesta-Marcos *et al*. 2008a and b; Castro *et al.* 2008). Most of these QTL had minor effects, except for one major QTL located by Cuesta-Marcos *et al*. (2008a) which explained up to 14% of the variation in heading date.

With drought conditions becoming more prevalent in many barley growing areas, several studies mapped QTL associated with adaption to dry conditions. Takahashi *et al*. (2008) located QTL for elongation of the coleoptile and first internode of deep-seeded barley. A major QTL was found for first internode elongation on chromosome 7H. Four QTL with small effects were also located on chromosome 7H, two for coleoptile elongation and two for first internode elongation. Von Korff *et al*. (2008c) examined QTL associated with dryland adaptation in a cross between Tadmor and ER/Apm. A main effect QTL for grain yield was located on the end of the long arm of chromosome 7H. They also found three QTL x environment interactions on chromosome 7H, two for grain yield and one for heading date. A set of 192 genotypes were grown in wet and dry environments in seven countries for two years in a study by Comadran *et al*. (2008). They identified a large number of marker-grain yield associations, including nine potential QTL on chromosome 7H. These three studies provide linkages for marker-assisted selection and a start at identifying candidate genes to define pathways involved in drought tolerance.

Two studies examined marker allele changes in breeding programs over time. Condon *et al*. (2008) tested regional ancestors, parental lines and cultivar candidates from the University of Minnesota breeding program with 71 markers, 12 of which were on chromosome 7H. In most cases, allele number decreased over time, especially around Rpg1, a spot blotch locus from NDB112 and the major malt quality QTL on the short arm of 7H. Three of the chromosome 7H loci were fixed in the cultivar candidate group from 1988-1998. Pswarayi *et al*. (2008) examined allele frequencies at marker loci linked to QTL in 188 landraces and old and modern cultivars mostly from the Mediterranean area. Three of the chromosome 7H markers were associated with yield QTL. For each of these loci, alleles associated with higher yield were present at a higher frequency in modern cultivars than in the landraces. Both of these studies emphasize the concerns about reduced genetic variability in modern cultivars and the need to examine older germplasm for traits that can improve adaptation.

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Integration of molecular and morphological marker maps

No report received

Barley Genetic Stock Center

No report received

Trisomic and aneuploid stocks

No report received

Coordinator's report: Translocations and balanced tertiary trisomics

Andreas Houben

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

email: houben@ipk-gatersleben.de

Dimitrova and colleagues (Sofia, Bulgaria) studied the ribosomal RNA gene expression in barley lines with modulated activity of nucleolus organizers (NORs) caused by three different types of chromosomal rearrangements. The lack of the whole rRNA gene cluster residing in chromosome 6H of the homozygous deletion line T-35 led to a compensatory effect in the expression of the single NOR remained on chromosome 511, resulting in increased rRNA transcription. The enhanced rRNA gene transcription in this line was accompanied by an increased rate of transcript elongation. The repositioning by translocation of NOR of chromosome 5H to the long non-satellite arm of chromosome 6H did not cause any alterations in the "run-on" transcription, as indicated by the activity of RNA polymerase 1, and in the susceptibility of rDNA chromatin to DNase I digestion, thus suggesting that the chromosome reconstruction did not affect the number of active rRNA genes involved in transcription. No alterations were also observed in segment tetraploid D-2946, which contained a duplication of medial region of satellite arm of chromosome 6H (Dimitrova *et al*., 2008).

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

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Dimitrova, A.D., E.D. Ananiev, L.M. Stoilov, and K.I. Gecheff. 2008. Ribosomal RNA Gene Expression in Reconstructed Barley Karyotypes. Cr Acad Bulg Sci 61, 1159-1168.

Coordinator's report: Autotetraploids

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

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

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

Coordinator's report: The Genetic Male Sterile Barley Collection

M.C. Therrien

Agriculture and Agri-Food Canada
Brandon Research Centre
Box 1000A, RR#3, Brandon, MB
Canada R7A 5Y3

E-mail: MTherrien@agr.gc.ca

The Genetic Male Sterile Barley Collection 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 address. I can send the file (14Mb) in Excel format. We continue to store the collection at -20°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.

Barley Genetics Newsletter (2009) 39:24-76

Coordinator´s Report: Disease and Pest resistance genes

Frank Ordon

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

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

Since the advent of molecular techniques in barley research and breeding in the beginning of the 1990s a lot of major resistance genes have been mapped or even isolated. The following table aims at giving an overview on these resistance genes without claiming to be exhaustive for the genes mentioned or references cited. In the future, this table will be updated every second year. Therefore, everyone is welcome to sent missing information on already published genes or information on newly published papers to the above mentioned e-mail address. A similar overview for resistance QTL mapped in barley will be prepared for the next BGN issue.

List of mapped major resistance genes in barley based on Graner (1996a), Graner et al. (2000a), Friedt and Ordon (2008), modified and updated.

Resistance gene	**Chromsomal location**	**Reference(s)**
Powdery mildew (Blumeria graminis)		
Mlo	4HL	Hinze et al. 1991, Büschges et al. 1997, Tacconi et al. 2006
Mlg	4HL	Görg et al. 1993, Kurth et al. 2001, Korell et al. 2008
Mla	1HS	Schüller et al. 1992, Schwarz et al. 1999,2002, Wei et al. 1999, Zhou et al. 2001, Haltermann et al. 2001, 2004, 2006, Repkova et al. 2009
mlt	7HS	Schoenfeld et al. 1996
Mlj	5HL	Schoenfeld et al. 1996
Mlf	7HL	Schoenfeld et al. 1996
MlLa	2HL	Hilbers et al. 1992, Giese et al. 1993, Mohler and Jahoor 1996
Mlh	6H	Hilbers, cit Graner et al. 1996a
Ml^{Hb}	2HS	Pickering et al. 1995, Graner et al. 1996b
Ml(TR)	5H	Falak et al. 1999
Mlh	6HS	Hilbers, cit Graner et al. 1996a
Mli	1HL	Jahoor, cit Graner et al. 1996a
Puccinia graminis		
Rpg1	7HS	Horvath et al. 1995, Penner et al. 1995, Han et al. 1999, Brueggemann et al. 2002, 2006, Mirlohi et al. 2008
rpg4	5HL	Borovkova et al. 1995, Kilian et al. 1997, Brueggeman et al. 2008, 2009, Steffenson et al. 2009

Rpg5	5HL	Brueggeman et al. 2008, 2009, Steffenson et al. 2009
rpg6	6HS	Fetch et al. 2009
Puccinia hordei		
Rph2	5HS	Borovkova et al. 1997
Rph3	7HS	Park et al. 2003
Rph4	1H	Collins et al. 2001, Park et al. 2003, Brüggemann et al. 2009
Rph5	3H	Mammadov et al. 2003, 2005, 2007, Brüggemann et al. 2009
Rph7	3HS	Graner et al. 2000b, Brunner et al. 2000, 2003, Scherer et al. 2005, Mammadov et al. 2007
Rph9	5HL	Borovkova et al. 1998
Rph12	5HL	Borovkova et al. 1998, Park et al. 2003
Rph14	2HS	Golegaonkar et al. 2009
Rph15	2HS	Weerasena et al. 2004
Rph16	2HS	Ivandic et al. 1998, Perovic et al. 2004
Rph19	7HL	Park & Karakousis 2002
Puccinia striiformis		
rpsGZ	4H	Pahalawatta & Chen 2005, Yan & Chen 2006,
Rynchosporium secalis		
Rh (Rrs1)	3HL	Graner & Tekauz 1996, Penner et al. 1996, Reitan et al. 2002, Genger et al. 2003
Rhy	3HL	Barua et al. 1993
Rh2(Rrs2)	7HS	Schweizer et al. 1995, Schmidt et al. 2001, Wagner et al. 2008, Hanemann et al. 2009
Rrs4	4HL	Patil et al. 2003
Rrs13	6HS	Abbott et al. 1995
Rrs14	1H	Garvin et al. 2000
Rrs15	7HL	Genger et al. 2005, Wagner et al. 2008
$Rrs16^{Hb}$	4HS	Pickering et al. 2006
Pyrenophora teres		
Pt.a	3HL	Graner et al. 1996a
Pt.d	2HS	Graner & Tekauz, unpubl., cit. Graner et al. 2000a
Ppt4	7H	Williams et al. 2004
Rpt5	6H	Manninen et al. 2006
Rpt6	5H	Manninen et al. 2006
rpt.r	6H	Abu Qamar et al. 2008, also cf. Friesen et al. 2006, Grewal et al. 2008
rpt.k	6H	Abu Qamar et. al. 2008, also cf. Friesen et al. 2006, Grewal et al. 2008
Cochliobolus sativus		
Rcs5	7HS	Steffenson et al. 1996, Drader et al. 2009
Typhula incarnata		
Ti	1HS	Graner et al. 1996a
Pyrenophora graminea		
Rdg1	2HL	Thomsen et al. 1997
Rdg2	7HS	Tacconi et al. 2001, Bulgarelli et al. 2004
Heterodera avenae		

Ha2	2HS	Kretschmer et al. 1997, Dayteg et al. 2008
Ha4	5HL	Barr et al. 1998
Barley stripe mosaic virus (BSMV)		
Rsm	7HS	Edwards & Stephenson 1996
Barley yellow dwarf virus (BYDV)		
Ryd2	3HL	Collins et al. 1996, Paltridge et al. 1998, Ford et al. 1998
Ryd3	6H	Niks et al. 2004
Ryd4^{Hb}	3HL	Scholz et al. 2009
Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV)		
rym1	4HL	Okada et al. 2004
rym3	5HS	Saeki et al. 1999, Werner et al. 2003a
rym4	3HL	Graner & Bauer 1993, Ordon et al. 1995, Weyen et al. 1996, Stein et al. 2005, Kanyuka et al. 2005, Werner et al. 2005, Stracke et al. 2007, Tyrka et al. 2008
rym5	3HL	Graner et al. 1999a, Pellio et al. 2005, Stein et al. 2005, Kanyuka et al. 2005, Stracke et al. 2007, Tyrka et al. 2008
rym7	1HS	Graner et al. 1999b
rym8	4HL	Bauer et al. 1997
rym9	4HL	Bauer et al. 1997, Werner et al. 2000, Werner et al. 2005
rym10	3HL	Graner et al. 1995
rym11	4HL	Bauer et al. 1997, Nissan-Azzous et al. 2005, Werner et al. 2005
rym12	4HL	Graner et al. 1996a
rym13	4HL	Werner et al. 2003b, Humbroich et al. 2009
Rym14^{Hb}	6HS	Ruge et al. 2003
rym15	6H	Le Gouis et al. 2004
Rym16^{Hb}	2HL	Ruge-Wehling et al. 2006

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Coordinator's report: *Eceriferum* genes

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

e-mail: udda@nordgen.org

No research work on gene localization has been reported on *Eceriferum* and *Glossy* genes. All descriptions in Barley Genetics Newsletter (BGN) Volume 26 and later issues are valid and up-to-date. They are also available in the International Database for Barley Genes and Barley Genetic Stocks, the Untamo database www.untamo.net/bgs .They can also be searched through the Triticeae database GrainGenes.

All the genes have been backcrossed to a common genetic background, the cultivar Bowman, by J.D. Franckowiak, Australia and are available as Near Isogenic Lines (NIL). About half of them are increased during summer 2009 for incorporation into the Nordic Genetic Resource Center (Nordgen), Sweden. The second half is going to be increased during the season of 2010. These lines are extraordinary valuable for gene mapping, valuable molecular genetical analyses of cloned mutant genes, Single Nucleotide Polymorphism (SNP) genotyping and provides a detailed understanding of the genetic composition of the barley genome. It is the idea to incorporate all Near Isogenic Lines into the Nordic Genetic Resource Center (Nordgen).

Every research of interest in this field and literature references are very useful to report to the coordinator as well. Seed requests of the Swedish material can be forwarded to the coordinator udda@nordgen.org or to the Nordic Genetic Resource Center (Nordgen) www.nordgen.org All Glossy genes can be requested 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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Coordinator's report: Nuclear genes affecting the chloroplast

Mats Hansson

Carlsberg Laboratory,
Gamle Carlsberg Vej 10,
DK-2500 Valby,
Copenhagen, Denmark

E-mail: mats@crc.dk

Barley mutants deficient in chlorophyll biosynthetic genes obtain a yellow or pale green phenotype. Occasionally they accumulate the substrate of the enzyme affected by the mutation. This accumulation can often be very pronounced if the plant is fed with 5-aminolevulinic acid, which is a chlorophyll biosynthetic precursor. Since the accumulated compound is a fingerprint of the mutated gene, it can be used in the classification of chlorophyll mutants. Anker Kristiansen et al. (2009) has developed a method involving multi-photon microscopy for *in vivo* detection of chlorophyll biosynthetic precursors in seedling plants. Barley mutants *xantha-f*.10 and *tigrina-d*.12 were involved in the study. In contrast to traditional methods, the described technique is non-destructive and the plant can be rescued for further studies.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found in Barley Genetics Newsletter (BGN) 37:37-43 and at http://www.mps.lu.se/fileadmin/mps/People/Hansson/Barley_mutants_web.pdf

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Coordinator's report: Ear morphology genes

Valeria Terzi

CRA-GPG Genomic Research Centre
Via San Protaso 302
IT-29017 Fiorenzuola d'Arda (PC), Italy

e-mail: valeria.terzi@entecra.it
and

A. Michele Stanca

Faculty of Agricultural Science, UNIMORE-Reggio Emilia, Italy

e-mail: michele@stanca.it

Research on Ear Morphology Genes has been limited in the last few years. However, results on barley spike morphology and its relationship on the origin, genetic resources and cloning *Nud* gene are reported.

The origin of six-rowed with brittle rachis-*agriocrithon*- has been studied to define whether such *agriocrithon* is wild or hybrid in nature. A cross allelism test confirmed that the six-rowed brittle barley was controlled by the *vrs1* locus. *Agriocrithon* does not appear to represent genuinely wild population but more probably originated from hybridization between *Hordeum spontaneum* and six-rowed cultivated barley (Tanno and Takeda, 2004).

A study was carried out to reveal morphological variation of spike shape, type and colour. A set of 39 Simple Sequence Repeats (SSR) markers was used to explore the genetic diversity of the Eritrean barley collected from small-scale farmer's field. Base on the SSR data, individual farmers fields were found to possess 97.3% of the genetic variation present in the Eritrean barleys (Backes *et al*. 2009).

The typical barley cultivars have caryopses with adhering hulls at maturity known as covered or hulled barley. Few cultivars are a free-threshing variant called naked or hulless barley. The covered/naked caryopsis is controlled by a single locus (*nud*) on chromosome arm 7HL. The gene has been positional cloned and the gene expression is localized to the testa. The gene has homology to the *Arabidopsis WIN1/SHN1* transcription factor gene, which is involved in the lipid biosynthesis pathway. In barley the hulled caryopsis is controlled by an Ethylene Response Factor (ERF) family transcription factor gene regulating lipid biosynthesis pathway (Taketa *et al*. 2008).

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Coordinator's report: Wheat-barley genetic stocks

A.K.M.R. Islam

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

e-mail: rislam@waite.adelaide.edu.au

The production of five different disomic addition lines (IHm, 2Hm, 4Hm, 5Hm and 7Hm) of *Hordeum marinum* chromosomes to Chinese Spring wheat has been reported earlier. It has now been possible to isolate disomic addition line 6Hm and work is in progress to isolate the remaining 3Hm addition line. It has also been possible to produce amphiploid of *H. marinum* with commercial wheats, both common (spring and winter habits) and durum in several combinations.(Islam and Colmer, unpublished).

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Coordinator's report: Semidwarf genes

J.D. Franckowiak

Hermitage Research Station
Agri-science Queensland
Department of Employment, Economic Development and Innovation
Warwick, Queensland 4370, Australia

e-mail: jerome.franckowiak@deedi.qld.gov.au

A progeny of recombinant inbred lines from a cross of two Japanese barley varieties was used to study the inheritance of culm and culm internode lengths (Sameri *et al*., 2009). An unexpected QTL for reduced culm length (qCUL on 7HL), which affected mainly the length of the third and fourth culm internodes, was contributed by the variety Kanto Nakate Gold (OUJ518). This QTL was associated with reduced lodging in two experiments. A near-isogenic line (culm length 62.9 to 73.4 cm) in an Azumamugi background, carrying a chromosome segment containing the qCUL allele from Kanto Nakate Gold, was significantly shorter than its recurrent parent (82.9 to 89.4 cm). The F2 generation from the next backcross segregated for plant height in a Mendelian monogenic ratio. The qCUL locus was shown to be tightly linked (1.2 cM) with the codominant STS marker ABG608.

Using the DNA sequence of rice mutants at the gibberellin (GA) insensitive dwarf 1 (*Gid1*) locus, a GA receptor, Chandler *et al*. (2008) demonstrated that the putative orthologue from barley is the GA sensitivity 1 (*gse1*) locus. Of 35 *gse1* mutants evaluated, 16 carried different unique nucleotide substitutions in this sequence. Study of maximal daily elongation rate (LER_{max}) of the first leaf of germinated grains with different GA treatments revealed considerable variation in LER_{max} values, which related closely to the degree of dwarfing observed during plant growth. The *gse1* mutants and their GA responses were previous described by Chandler and Robertson (1999). The *gsela* mutant was characterized by low alpha-amylase levels, but the mutant was responsive to GA treatments (Chandler and Robertson, 1999). The study of individual *gse1* mutants demonstrated some response differences among the *gse1* mutants examined (Chandler *et al*., 2008).

Comparative genomic analysis revealed that the *sdw1*/*denso* (semidwarf 1 on 3HL) locus is in the syntenic region of the rice semidwarf gene *sd1* on chromosome 1 (Jia *et al*., 2009). The *sd1* gene encodes a gibberellic acid (GA)-20 oxidase enzyme. The ortholog of rice *sd1* was isolated from barley using polymerase chain reaction. The barley and rice genes showed a similar gene structure consisting of three exons and two introns. Both genes share 88.3% genomic sequence similarity and 89% amino acid sequence identity. A single nucleotide polymorphism (SNP) was identified in intron 2 between barley varieties Baudin and AC Metcalfe with Baudin known to contain the *sdw1* gene. The single nucleotide polymorphism (SNP) marker was mapped to chromosome 3H in a doubled haploid population of Baudin × AC Metcalfe.

Crown rot (CR, *Fusarium pseudograminearum*) resistance observed in the Chinese land race TX9425 based on seedling evaluations was found to be conditioned by a major QTL (Li *et al*.,

2009). Using a doubled haploid progeny of TX9425/Franklin cross, Li *et al*. (2009) mapped a QTL, designated as Qcrs.cpi-3H, near the centromere on the long arm of chromosome 3H. Its effect is highly significant, accounting for up to 63.3% of the phenotypic variation with a LOD value of 14.8. The location of Qcrs.cpi-3H was coincident with a major QTL (the *uzu1* gene) for reduced plant height. When the effect of PH was accounted for by covariance analysis, the Qcrs.cpi-3H QTL remained highly significant, accounting for over 40% of the phenotypic variation. The effects of the *uzu1* gene on plant height were stronger in the warmer of the two environments tested. The plant height QTL associated with the *sdw1* gene from Franklin was detected only in the cooler environment.

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Coordinator's report: Early maturity and Praematurum genes

Udda Lundqvist

Nordic Genetic Resource Center
P-O. Box 41
SE-23 053 Alnarp, Sweden

e-mail: udda@nordgen.org

Not much research work on gene localization has been reported on the Early maturity or *Praematurum* genes. All descriptions in Barley Genetics Newsletter (BGN) Volume 26 and later issues are valid and still up-to-date. They are also available in the International Database for Barley Genes and Barley Genetic Stocks, the Untamo database www.untamo.net/bgs . They can also be searched through the Triticeae database GrainGenes.

All Early maturity and *Praematurum* genes have been backcrossed to a common genetic background, the cultivar Bowman, by J.D. Franckowiak, Australia and are available as Near Isogenic Lines (NIL). All of them have been increased during summer 2009 for incorporation into the Nordic Genetic Resource Center (Nordgen), Sweden. These lines are extraordinary valuable for gene mapping, valuable molecular genetical analyses of cloned mutant genes, Single Nucleotide Polymorphism (SNP) genotyping and provides a detailed understanding of the genetic composition of the barley genome. There is made a decision to incorporate all Near Isogenic Lines into the Nordic Genetic Resource Center (Nordgen), Sweden. It is also planned to get the Nordic Genetic Resource Center as an International Barley Center for barley stocks and distribution world-wide.

Every research of interest in this field and literature references are very useful to report to the coordinator as well. Seed requests regarding the Swedish mutant alleles can be forwarded to the coordinator udda@nordgen.org or directly to the Nordic Genetic Resource Center (Nordgen), www.nordgen.org/ngb, all others can be requested to the Small Grain Germplasm Research Facility (USDA-ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov or to the coordinator at any time.