

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

In a couple of months the 11th International Barley Genetic Symposium will take place in Hangzhou southwest of Shanghai, China. Like in the last IBGS, a workshop on “Barley Genetic Linkage Groups, Genome and collections” will be arranged Sunday night April 15th, and I do hope that most of the coordinators have the possibility to participate.

Since the latest overall coordinator's report in Barley Genetics Newsletter Volume 40, I feel very sorry to tell that the coordinator for the “Male sterile genetic collection” Mario Therrien passed away suddenly last September, 2011. He had done large efforts to keep the collection in good conditions, he wanted to regenerate it during summer 2011 but because of bad weather conditions he was not able to do it. There will be no successor for this collection but there are requirements going on to transfer the important collection to the Plant Gene Resources of Canada, Agriculture and Agri-Food Canada in Saskatoon, Saskatchewan. Otherwise no changes of the coordinators took place. Most of the coordinators are continuing and delivered their reports, and I hope they also will do so in the future. Today it is very important to let us know the newest research results as especially the genome investigations are increasing rapidly. We do not only need the to-days information but also publications and informations from the last century.

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 2011 the 120 Male Sterile Genetic isogenic Bowman lines have been planted and tested for segregation in Sweden for incorporation in the Nordic Genetic Resource Center (Nordgen), Alnarp, Sweden. The normal looking plants are harvested plant by plant, during summer 2012 these plants will again be tested for segregation and only the heterozygous plants will be incorporated into the Gene Bank. It has been decided some years ago to establish an International Centre for Barley Genetic Stocks at Nordgen, Alnarp, Sweden.

I also want you to pay attention to another important workshop at the 11th IBGS on Wednesday evening, April 18th, 2012 regarding “Barley Genetic Stocks – Global Use and Potential”. Takao Komatsuda will be the key speaker and several other barley researchers will give some small inputs regarding the importance of the genetic stocks, their use, regeneration, and how they have to be kept available in the future.



List of Barley Coordinators

Chromosome 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>](mailto:jerome.franckowiak@deedi.qld.gpv.au)

Chromosome 3H (3): Luke Ramsey, Cell and Molecular Sciences Group, The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. FAX: +44 1382 562426. E-mail: [<Luke.Ramsey@hutton.ac.uk>](mailto:Luke.Ramsey@hutton.ac.uk)

Chromosome 4H (4): Arnis Druka, Cell and Molecular Sciences Group, The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. FAX: +44 1382 562426. e-mail: [<Arnis.Druka@hutton.ac.uk>](mailto:Arnis.Druka@hutton.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>](mailto:fedakga@AGR.GC.CA)

Chromosome 6H (6): Victoria Carollo Blake, USDA-ARS, Albany, CA, USA. e-mail: [<victoria.blake@ars.usda.gov>](mailto:victoria.blake@ars.usda.gov)

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>](mailto:DAHLEENL@fargo.ars.usda.gov)

Integration of molecular and morphological marker maps: David Marshall, Cell and Molecular Sciences Group, The James Hutton Institute, Invergowrie, Dundee, DD2 5DA, United Kingdom. FAX: 44 1382 562426. e-mail: [<David.Marshall@hutton.ac.uk>](mailto:David.Marshall@hutton.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>](mailto: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>](mailto: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>](mailto:houben@ipk-gatersleben.de)

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>](mailto:houben@ipk-gatersleben.de)

List of Barley Coordinators (continued)

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-1799 Copenhagen V, Denmark. FAX: +45 3327 4708; e-mail: <mats.hansson@carlsberglab.dk>

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>
and

Antonio Michele Stanca: Department of Agricultural and Food Science, University of Modena and Reggio Emilia, Reggio Emilia, Italy. FAX +39 0523 983750, e-mail: michele@stanca.it
and

Valeria Terzi: CRA-GPG, Genomics Research Centre, Via Protaso 302, IT-29017 Fiorenzuola d'Arda (PC), Italy. e-mail: <valeria.terzi@entecra.it>

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>

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

Gunter Backes

**The University of Copenhagen
Faculty of Life Sciences
Department of Agriculture and Ecology
Thorvaldsensvej 40
DK-1871 Frederiksberg C, Denmark**

e-mail: guba@life.ku.dk

Li *et al.* (2010) localised putative Universal Stress Proteins (USP) in barley. The expression of USP is affected by a wide range of internal and external stresses, and it is suggested that these proteins enhance the rate of cell survival during prolonged exposure to stress. The putative USP sequences were obtained by blasting the conserved region of *IMJH* from *Methanococcus jannaschii* against the HarvEST database of barley EST sequences and comparing the results with known USP sequences of *Arabidopsis* and rice. Of the nine putative USP sequences, two were localised on chromosome 1H: BUG-1 in bin 7 and BUG-2 on bin 9/10.

In a study published by Chen *et al.* (2010), NIL and reversed NIL for the QTLs *Rphq2* and *Rphq3*, loci conferring quantitative resistance to barley leaf rust, were infected with urediospores of *Puccinia hordei* and an expression analysis was carried out on custom-made 15 k Agilent arrays. Differentially expressed genes included not only loci within the confidence interval of the two QTLs, but also HvERF4 on 1H bin 9/10, which is known to play a role in defence response. The authors discuss that the genes behind the two resistance QTLs differentially trans-regulate HvERF4, which is then involved in signalling pathways concerning the resistance reaction.

The barley genes *Ppd.H1*, *VRN-H1*, *VRN-H2*, *VRN-H3*, *HvCO1*, *HvCO2*, *HvG1*, *HvFT2*, *HvFT3*, *HvFT4*, all assumed to be related to photoperiod and vernalization, were localised in a BC₂DH population of 301 lines from a cross between the wild barley (*H. vulgare* ssp. *spontaneum*) line ISR42-8 and the spring barley cultivar 'Scarlett' (G.W. Wang *et al.*, 2010). *HvFT3* localized on 1HL-bin14.3. Further, in a QTL analysis for different heading date related traits (on four locations x two years), a minor QTL for heading date was localised at the position of *HvFT3*.

Another QTL study for plant-development related traits including candidate genes (Borràs-Gelonch *et al.*, 2010) revealed QTLs for the rate of tillers per leaf, the phyllochron and the thermal time between sowing and leaf and spikelet initiation in a wider range on 1H stretching from the loci *HvFT3* and *Ppd.H2* (bin 11.2) until *Eam8* (bin 14.3). Further QTLs for thermal days of stem elongation and thermal days of grain filling period were localised near *Eam8*. The analysis was carried out in a population of 118 DH lines from a cross between the two-row spring barleys 'Henni' and 'Meltan' on two locations and two years.

QTLs for resistance against *Septoria* speckled leaf blotch, a disease caused by *Septoria passerinii*, were detected by Yu *et al.* (2010) in a population of recombinant inbred lines from the cross between the resistant line PI 643302 and the susceptible line Zhemongda 7. A mixture

of two isolates was applied in five experiments with three replicates of two plants in a pot. Two major QTLs were found, one of them on 1HS-bin 1-3, explaining 38 to 45% of the phenotypic variation. The authors suspect that the known qualitative resistance gene *Rsp2* might be behind this QTL. The other QTL on 2HL has not been known before.

As it is easier to work in barley than in the hexaploid oat, Lorang *et al.* (2010) analysed sensitivity to victorin, a toxin of *Cochliobolus victoriae*, causing Victoria blight in oat in a doubled haploid (DH) population (93 lines) from the cross of the victorin-sensitive cultivar 'Baroness' and the victorin-insensitive line BCD 47. In two replicated experiments, the detached second and fourth leaf of two plants per DH line were incubated with victorin and differences in the reaction were observed 5 days after incubation. One single major QTL was found on 1H bin 2/3 explaining 79% of the phenotypic variation for this trait.

In order to compare QTLs for malting quality in the European and American barley material, a population of 106 doubled haploid lines from the malting barley cultivars 'Triumph' (Europe) and 'Morex' (USA) was analysed for several malting quality related traits after being grown in five different environments (Elía *et al.*, 2010). On 1H, three different QTLs were identified: one in bin 6/7 explaining 16 to 31% of the phenotypic variation for malt extract, one in bin 7 explaining 13% of the phenotypic variation for soluble N and 18% for fermentability and finally one in bin 9 explaining 23% of the variation for protein content. For these QTLs, 'Morex' showed the higher extract and fermentability, as well as the lower soluble N and protein content. All QTLs were affected by the environment and confirmed the position of QTLs detected before at these positions.

Another quality parameter related to barley processing, viscosity of the slurry from flour during heating and re-cooling, was analysed by Y.W. Wang *et al.* (2010). For this purpose a QTL analysis was carried out in a doubled haploid population of 177 lines from the cross between 'Yerong', a six-rowed feed barley, and 'Franklin', a two-rowed malting barley cultivar, both from Australia. The kernel were derived from three different field environments and four different QTLs were found on 1H, namely in the bins 7-9 (Time to peak viscosity, 14% explained phenotypic variation), bin 12 (range of viscosity breakdown, 13% explained phenotypic variation), bins 10-12 (Viscosity setback, 7% explained phenotypic variation) and bins 12-14 (pasting temperature, 6% explained phenotypic variation).

Tyagi *et al.* (2010) used EST-based transcript-derived markers (TDM) to reanalyse barley green plant regeneration in tissue culture. The map of those markers have been developed on the base of 150 DH lines from the 'Steptoe' x 'Morex' population and included 1596 TDMs (Potokina *et al.*, 2008). In three separate experiments, 71 randomly selected QTLs were analysed for green and albino plants and their regeneration rate. On 1H a QTL for albino plant regeneration was confirmed and the TDM in the respective regions might represent candidate genes for the detected QTLs.

References:

- Borràs-Gelonch, G., G.A. Slafer, A.M. Casas, F. van Eeuwijk, and I. Romagosa. 2010.** Genetic control of pre-heading phases and other traits related to development in a double-haploid barley (*Hordeum vulgare* L.) population. *Field Crops Res.* 119: 36–47.
- Chen, X.W., R.E. Niks, P.E. Hedley, J. Morris, A. Druka, T.C. Marcel, A. Vels, and R. Waugh. 2010.** Differential gene expression in nearly isogenic lines with QTL for partial resistance to *Puccinia hordei* in barley. *BMC Genomics* 11: 629.
- Elía, M., J.S. Swanston, M. Moralejo, A. Casas, A.-M. Pérez-Vendrell, F.J. Ciudad, W.T.B. Thomas, P.L. Smith, S.E. Ullrich, and J.-L. Molina-Cano. 2010.** A model of the genetic differences in malting quality between European and North American barley cultivars based on a QTL study of the cross Triumph x Morex. *Plant Breed.* 129: 280–290.
- Li, W.-T., Y.-M. Wei, J.-R. Wang, C.-J. Liu, X.-J. Lan, Q.-T. Jiang, Z.-E. Pu, and Y.-L. Zheng. 2010.** Identification, localization, and characterization of putative USP genes in barley. *Theor. Appl. Genet.* 121: 907–917.
- Lorang, J., A. Cuesta-Marcos, P.M. Hayes, and T.J. Wolpert. 2010.** Identification and mapping of adult-onset sensitivity to victorin in barley. *Mol. Breed.* 26: 545–550.
- Potokina, E., A. Druka, Z. Luo, R. Wise, R. Waugh, and M. Kearsey. 2008.** Gene expression quantitative trait locus analysis of 16 000 barley genes reveals a complex pattern of genome-wide transcriptional regulation. *Plant J.* 53: 90–101.
- Tyagi, N., L.S. Dahleen, and P. Bregitzer. 2010.** Candidate genes within tissue culture regeneration QTL revisited with a linkage map based on transcript-derived markers. *Crop Sci.* 50: 1697–1707.
- Wang, G.W., I. Schmalenbach, M. von Korff, J. León, B. Kilian, J. Rode, and K. Pillen. 2010.** Association of barley photoperiod and vernalization genes with QTLs for flowering time and agronomic traits in a BC2DH population and a set of wild barley introgression lines. *Theor. Appl. Genet.* 120: 1559–1574.
- Wang, J.M., J.M. Yang, D. McNeil, and M.X. Zhou. 2010.** Mapping of quantitative trait loci controlling barley flour pasting properties. *Genetica* 138: 1191–1200.
- Yu, G.T., J.D. Franckowiak, S.H. Lee, R.D. Horsley, and S.M. Neate. 2010.** A novel QTL for *Septoria* speckled leaf blotch resistance in barley (*Hordeum vulgare* L.) accession PI 643302 by whole-genome QTL mapping. *Genome* 53: 630–636.

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

Nair *et al.* (2010) identified a nucleotide substitution putative microRNA miR172 as DNA change associated with closed flowering caused by the cleistogamy 1 (*cly1*) mutant. Cleavage of a mRNA directed by miR172 was blocked in cleistogamous barley (Nair *et al.*, 2010). Closed flowering is caused by the failure of the lodicules to expand properly at anthesis. The *Cly1* locus was previously mapped by Turuspekov *et al.* (2004) in chromosome 2HL near a dominant gene for dense spike (Sameri *et al.*, 2006).

Druka *et al.* (2011) reported results of a SNP molecular marker analysis of donor parent segments retained in Bowman backcross-derived lines for morphological traits. The donor parents had morphological variants that could be selected for visually during backcrossing. Plants exhibiting the morphological variant were selected in F2 or F3 progenies and again crossed to Bowman. Based on 881 lines with 2 to 9 crosses to Bowman, 426 mutant alleles were associated with specific chromosome segments. Over 25 mutants previously not associated with a specific chromosome retained heterogeneous regions only in chromosome 2H of their Bowman backcross-derived lines (Table 1).

Pourkheirandish and Komatsuda (2010) provide a more detailed history of the evolution of barley based on alleles at the six-rowed spike (*vrs1*) locus on chromosome 2H. DNA sequence analysis revealed that 2 of the 3 variants with a six-rowed spike, *vrs1.a2* and *vrs1.a3*, arose from two-rowed ancestors, *Vrs1.b2* and *Vrs1.b3*, based on a single nucleotide change. The origin of the oldest six-rowed variant, *vrs1.a1*, is unknown. Based on the archaeological literature reviewed, two-rowed barley in Europe disappeared for 1,000 to 3,000 years before reappearing about 1,100 years ago (Pourkheirandish and Komatsuda, 2010). Thus, they speculate that the two-rowed ancestor of most six-rowed barley has been lost.

Jin *et al.* (2010) reported on three QTL that controlling lipoxygenase (LOX) content of barley, which affects foam stability and flavor of beer. Presence of LOX was determined in a doubled haploid (DH) population from a cross between the Australian malting barley Stirling and Canadian malting barley Harrington. The two QTL with a major influence on LOX content were located on 5H near loci, where low LOX levels are associated with pre-harvest sprouting of Harrington. The third QTL with a minor effect on LOX content was located on 2H.

Phenotypic plasticity is defined as the variation in phenotypic traits produced by a genotype in different environments. Lacaze *et al.* (2009) studied this phenomenon in barley based on

simulations and real data. They found that QTL for environmental plasticity were coincident with QTL on 2H for kernel weight, grain protein, and yield.

A study of OWB population was conducted using a newly developed sequence-based marker technology, Restriction site Associated DNA (RAD), which enabled synchronous single nucleotide polymorphism (SNP) marker discovery and genotyping using massively parallel sequencing (Chutimanitsakun *et al.*, 2011). The marker orders in the new map were similar to older maps for the OWB population. Two loci on 2H, six-rowed spike 1 (*vrs1*) and Zeocriton 1 (*Zeo1*), were associated in height, spike length, kernels per spike, 100-kernel weight, and grain yield. Unfavorable alleles were contributed in R.I. Wolfe's Master Dominant Marker Stock, a semidwarf with short, two-rowed spikes (*Zeo1.a* and *Vrs1.t*).

A population of 39 BC₂DH lines from a cross between the wild barley and Scarlett was evaluated for agronomic traits (Schmalenbach *et al.*, 2009). The region of 2HS in which the long day photoperiod response gene (*Ppd-H1* or *Eam1*) is located was associated with early heading, reduced plant height and lodging, fewer kernels per spike, and increased number of spikes m⁻², and increased kernel weights. Correlations between these traits were reported, but the material will be studied further to determine which associations are caused by pleiotropic effects.

The response of barley to waterlogging restricts the production of barley in high rainfall environments. Zhou *et al.* (2010) studied leaf chlorosis after a two-week period of waterlogging and plant survival after eight weeks in lines of two doubled haploid populations. QTL for reduced chlorosis from Chinese line TX9425 and the Australian cultivar Yerong were mapped on 6 of the 7 barley chromosomes. Four regions of 2H were associated with waterlogging responses.

Tolerance to several level of salt stress was determined in plants of the Steptoe/Morex doubled haploid population based on chlorophyll fluorescence and other traits (Aminfar *et al.* (2011). The strongest association reported was between RFLP markers on 2H and chlorophyll fluorescence.

Laws *et al.* (2010) used marker assisted selection (MAS) to transfer tolerance to frost at flowering from Haruna Nijo into South Australian germplasm. The chromosomal segment around the reproductive frost tolerance (RTF) QTL on chromosome 2HL and 5HL were transferred using SSR markers. Whole genome profiling with DArTs (Diversity Array Technology) revealed that many, but not all, of the surviving 34 lines retained both critical regions.

QTL for adult plant resistance to the net form of net blotch, *Pyrenophora teres* f. sp. *teres* were detected in two regions of 2H in three mapping populations (Lehmensick *et al.*, 2007, 2010). The centromeric region of 2H was associated with QTL for resistance from Sloop and WI2875-1 and the short arm of 2H was associated with a QTL from Arapiles.

References:

- Aminfar, Z., M. Dadmehr, B. Korouzhdehi, B. Siasar, and M. Heidari. 2011.** Determination of chromosomes that control physiological traits associated with salt tolerance in barley at the seedling stage. *African Jour. Biotech.* 10 (44):8794-8799.
- Chutimanitsakun, Y., R.W. Nipper, A. Cuesta-Marcos, L. Cistué, A. Corey, T. Filichkina, E.A Johnson, and P.M. Hayes. 2011.** Construction and application for QTL analysis of a Restriction Site Associated DNA (RAD) linkage map in barley. *BMC Genomics* 2011 **12**:4 doi:10.1186/1471-2164-12-4 at: <http://www.biomedcentral.com/1471-2164/12/4>
- Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011.** Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
- Jin, X., S. Harasymow, Y. Bonnardeaux, A. Tarr, A., R. Appels, R. Lance, G. Zhang, and C. Li. 2011.** QTLs for malting flavour component associated with pre-harvest sprouting susceptibility in barley (*Hordeum vulgare* L.). *Jour. Cereal Sci.* 53:149-153.
- Lacaze, X., P. M. Hayes, and A. Korol. 2009.** Genetics of phenotypic plasticity: QTL analysis in barley, *Hordeum vulgare*. *Heredity* 102:163-173.
- Laws, M.R., J.L. Reinheimer, S.J. Coventry, and J.K. Eglinton. 2010.** Introgression and validation of reproductive frost tolerance. pp. 222-229. In: S. Ceccarelli and S. Grandó (eds). *Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt.* ICARDA, PO Box 5466, Aleppo, Syria.
- Lehmensick, A., G.J. Platz, E. Mace, D. Poulsen, and M.W. Sutherland. 2007.** Mapping of adult plant resistance to net form of net blotch in three Australian barley populations. *Austral. J. Agric. Res.* 58:1191-1197.
- Lehmensick, A., M. Sutherland, J.H. Bovill, G.J. Platz, R.B. McNamara, and E. Mace. 2010.** Markers for resistance to three foliar diseases in barley. pp. 278-285. In: S. Ceccarelli and S. Grandó (eds). *Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt.* ICARDA, PO Box 5466, Aleppo, Syria.
- Nair, S.K., N. Wang, Y. Turuspekoy, M. Pourkheirandish, S. Sinsuwongwat, G. Chen, M. Sameri, A. Tagiri, I. Honda, Y. Watanabe, H. Kanamori, T. Wicker, N. Stein, Y. Nagamura, T. Matsumoto, and T. Komatsuda. 2010.** Cleistogamous flowering in barley arises from the suppression of microRNA-guided *HvAP2* mRNA cleavage. *Proc. Natl. Acad. Sci. U.S.A.* 107(1):490-495.
- Pourkheirandish, M., and T. Komatsuda. 2010.** Evolution of barley *vrs1*. pp. 157-165. In: S. Ceccarelli and S. Grandó (eds). *Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt.* ICARDA, PO Box 5466, Aleppo, Syria.

- Roy, J.K., K.P. Smith, G.J. Muehlbauer, S. Chao, T.J. Close, and B.J. Steffenson. 2010.** Association mapping of spot blotch resistance in wild barley. *Mol. Breeding* 26:243-256.
- Sameri, M., K. Takeda, and T. Komatsuda. 2006.** Quantitative trait loci controlling agronomic traits in recombinant inbred lines from a cross of oriental- and occidental-type barley cultivars. *Breed. Science* 56:243-252.
- Schmalenbach, I., J. Léon, and K. Pillen, 2009.** Identification and verification of QTLs for agronomic traits using wild barley introgression lines. *Theor. Appl. Genet.* 118: 483-497.
- Turuspekov, Y., Y. Mano, I. Honda, N. Kawada, Y. Watanabe, and T. Komatsuda. 2004.** Identification and mapping of cleistogamy gene in barley. *Theor. Appl. Genet.* 109:480-487.
- Zhou, M.X., J.Y. Pang, H.B. Li, N.J. Mendham, S. Shahala, and R. Vaillancourt. 2010.** Physiological mechanism and quantitative trait loci associated with waterlogging tolerance in barley. pp. 199-204. In: S. Ceccarelli and S. Grandó (eds). *Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt. ICARDA, PO Box 5466, Aleppo, Syria.*

Table 1. Morphological markers and mutants associated with chromosome 2H based on donor SNPs retained from the donor parent in Bowman backcross-derived lines, data from Druka et al. (2011).

BW no ¹	Allele symbol ²	Locus or mutant name	BGS no. ³	Bow cross ⁴	Chromosome bin position ⁵	SNP markers retained	Map position (cM) ⁶	Prev. loc. ⁷
BW103	cal-a.1	Subjacent hood 1	062	6	2H bin 02	1_0326	16.9	2HS
BW766	sbk1.a	Subjacent hood 1	062	4	2H bin 02	1_1059 to 2_0563	18.0 – 21.9	2HS
BW767	sbk1.b	Subjacent hood 1	062	7	2H bin 02	1_0326 to 1_1059	16.9 – 18.0	2HS
BW682	Rph1.a	Reaction to <i>Puccinia hordei</i> 1	070	6	2H bin 02	1_0326 to 2_1416	16.9 – 22.4	
BW091	brh3.g	Erectoides-t, brachytic 3	566	7	2H bin 02	2_0609 to 1_1059	16.9 – 18.0	2HS
BW094	brh3.y	Erectoides-t, brachytic 3	566	6	2H bin 02	1_0326 to 1_0180	16.9 – 40.1	2HS
BW324	ert-t.55	Erectoides-t	566	7	2H bin 02	1_0326 to 2_0563	16.9 – 21.2	2HS
BW031	ari-u.245	Breviaristatum-u	679	5	2H bin 02/03	2_0609 to 2_1040	16.9 – 35.9	
BW409	gsh6.s	Glossy sheath 6	356	7	2H bin 02	1_0326 to 2_0563	16.9 – 21.2	2HS
BW411	gsh8.ag	Glossy sheath 8	413	5	2H bin 02/05	2_1377 to 1_0919	20.1 – 66.8	2HS
BW404	gsh1.a	Glossy sheath 1	351	7	2H bin 03	2_0562 to 1_0943	22.4 – 34.3	2HS
BW595	mtt7.h	Mottled leaf 7	--	5	2H bin 02/03	1_0326 to 2_0107	16.9 – 33.7	
BW175	cer-zt.389	Eceriferum-zt	437	5	2H bin 02/05	2_0609 to 1_0399	16.9 – 66.8	2HS
BW140	cer-yi.254	Eceriferum-yi	522	4	2H bin 02/10	2_0609 to 1_1533	16.9 – 141.6	Invers.
BW426	int-i.39	Intermedium spike-i	545	6	2H bin 03/05	1_0943 to 2_1304	34.3 – 58.6	
BW280	Eam1.c	Early maturity 1	065	8	2H bin 04/05	1_0216 to 2_0173	47.5 – 75.0	2HS
BW281	Eam1.d	Early maturity 1	065	9	2H bin 05	2_1366 to 2_1261	50.6 – 50.6	2HS
BW282	Eam1.f	Early maturity 1	065	8	2H bin 04/05	1_0216 to 2_1366	47.5 – 48.7	2HS
BW830	sdw3.az	Semidwarf 3	--	1	2H bin 02/06	1_0326 to 1_1061	16.9 - 81.5	2HS
BW759	Rph8.h	Reaction to <i>Puccinia hordei</i> 8	576	6	2H bin 04/06	1_0216 to 1_0342	47.5 – 73.9	
BW686	Rph14.ab	Reaction to <i>Puccinia hordei</i> 14	591	5	2H bin 05/06	2_0173 to 1_0342	63.9 – 73.9	2HS
BW719	Rph15.ad	Reaction to <i>Puccinia hordei</i> 15	096	8	2H bin 05/06	1_0525 to 1_0342	65.0 – 73.9	2HS
BW695	Rph15.ad	Reaction to <i>Puccinia hordei</i> 15	096	6	2H bin 05	1_0891 to 2_1304	54.5 – 66.8	2HS
BW733	Rph15.ad	Reaction to <i>Puccinia hordei</i> 15	096	6	2H bin 05	1_0173 to 1_0919	65.7 – 66.8	2HS
BW124	cer-v.49	Eceriferum-v	414	7	2H bin 05/06	2_1187 to 2_1338	51.6 – 75.0	2HS

BW no ¹	Allele symbol ²	Locus or mutant name	BGS no. ³	Bow cross ⁴	Chromosome bin position ⁵	SNP markers retained	Map position (cM) ⁶	Prev. loc. ⁷
BW185	fch16.117	Chlorina seedling 16	676	5	2H bin 05/06	2_1187 to 2_1338	51.6 - 75.0	
BW562	msg27.ae	Male sterile genetic 27	464	7	2H bin 05/06	2_1366 to 2_1153	50.6 – 69.1	2HL
BW192	com2.g	Compositum 2	071	8	2H bin 05/07	1_0525 to 1_0325	65.0 – 90.5	2HS
BW187	com2.k	Compositum 2	071	3	2H bin 03/07	1_0943 to 1_0996	34.3 – 91.6	
BW239	des3.c	Desynapsis 3	386	6	2H bin 05/08	2_0173 to 2_0528	64.0 – 118.8	
BW864	sld4.d	Slender dwarf 4	100	7	2H bin 04/06	3_1169 to 1_1061	48.4 – 81.5	2HL
BW862	sld2.b	Slender dwarf 2	083	7	2H bin 06/07	1_1493 to 1_0325	76.1 – 90.5	2HS
BW225	cur5.h	Curly 5	231	8	2H bin 05/07	1_1073 to 2_0476	65.7 – 96.5	2HS
BW250	cur5.h & dsk1	Curly 5, Dusky1	231	7	2H bin 06/07	1_0498 to 2_0476	81.4 – 96.5	2HS
BW518	mnd1.a	Many noded dwarf 1	519	9	2H bin 07	1_0638 to 1_0624	86.8 – 96.5	2H
BW565	msg3.cc	Male sterile genetic 3 (sdw)	359	8	2H bin 06/07	1_1493 to 1_1046	76.1 – 96.5	2HS
BW351	fch1.a	Chlorina seedling 1	055	9	2H bin 06/07	1_1493 to 2_0458	76.1 – 96.5	2HS
BW357	fch15.x	Chlorina seedling 15	052	2	2H bin 06/09	2_1338 to 2_0699	75.0 – 126.3	2HS
BW045	ari-g.24	Breviaristatum-g	089	8	2H bin 05/08	2_1187 to 2_0528	51.6 – 118.8	2H
BW768	sca.b (ari-g)	Short crooked awn b	089	4	2H bin 08/09	2_0390 to 1_1435	103.7 – 126.3	
BW800	sdw.aw	Semidwarf aw	--	7	2H bin 05/09	2_1073 to 1_0818	65.7 – 126.3	
BW183	clo.104	Chlorina-104	--	8	2H bin 06/09	1_0498 to 1_1100	81.4 – 135.2	
BW081	brh10.1	Brachytic 10	653	8	2H bin 06/09	1_0498 to 2_0960	81.4 - 120.8	2HS
BW408	gsh5.m	Glossy sheath 5	355	8	2H bin 06/08	1_0498 to 2_0960	81.4 – 113.3	2HL
BW122	cer-s.31	Glossy sheath 5	355	8	2H bin 07/08	1_0748 to 2_0528	95.5 – 118.8	2HL
BW118	cer-n.20	Eceriferum-n	408	8	2H bin 07/08	2_0674 to 2_0528	85.7 – 118.8	2HL
BW412	gsh9.al	Eceriferum-n	408	7	2H bin 06/08	1_1493 to 2_0699	76.1 – 122.0	2HL
BW150	cer-ys.680	Eceriferum-ys	532	5	2H bin 07/11	2_0674 to 1_1250	85.7 – 161.1	2HL
BW001	abr1.a	Accordion basal rachis 1	472	7	2H bin 07/10	2_0674 to 1_1533	85.7 – 141.6	2HL
BW133	cer-yb.200	Eceriferum-yb	445	7	2H bin 07/10	2_0674 to 1_1533	85.7 – 141.6	2HL

Barley Genetics Newsletter (2011) 41:12-53

BW no1	Allele symbol2	Locus or mutant name	BGS no.3	Bow cross4	Chromosome bin position5	SNP markers retained	Map position (cM)6	Prev. loc.7
BW111	cer-g.10	Eceriferum-g	402	7	2H bin 08	1_0317 to 2_0374	98.4 – 104.8	2HL
BW507	mat-b.7	Praematurum-b	578	7	2H bin 07/08	2_0674 to 2_0374	85.7 – 104.8	
BW508	mat-c.19	Praematurum-c	579	6	2H bin 05/09	1_0525 to 1_1100	65.0 – 135.2	2HL
BW058	blf1.a	Broad leaf 1	326	3	2H bin 05/08	1_0525 to 2_1078	65.0 – 118.8	5HL
BW896	viv-a.5	Viviparoides-a	627	4	2H bin 05/08	2_0173 to 2_1251	64.0 - 118.8	
BW346	fch.ae	Chlorina seedling ae	--	5	2H bin 07/11	2_1005 to 2_0923	83.6 - 161.1	
BW569	msg33.x	Male sterile genetic 33	470	7	2H bin 07/08	2_0458 to 2_1251	96.5 – 115.9	2H
BW554	msg2.cb	Male sterile genetic 2	358	7	2H bin 07/08	2_0674 to 2_0585	85.7 – 103.7	2HL
BW394	glo-c.1004	Globosum-c	072	7	2H bin 07/09	2_0387 to 1_1214	90.5 - 133.6	2HL
BW299	eog1.a	Elongated outer glume 1	057	7	2H bin 07/10	1_0147 to 2_0582	90.5 – 119.0	2HL
BW300	eog1.c	Elongated outer glume 1	057	7	2H bin 07/10	1_0147 to 2_0699	90.5 - 126.3	2HL
BW301	eog1.d	Elongated outer glume 1	057	3	2H bin 06/10	1_0498 to 1_1402	81.4 – 119.9	2HL
BW302	eog1.e	Elongated outer glume 1	057	3	2H bin 06/07	1_1493 to 2_0476	76..1 – 96.5	2HL
BW395	glo-d.1006	Curly 4	460	7	2H bin 07/08	2_0674 to 2_0582	85.7 – 119.0	2HL
BW223	cur4.f	Curly 4	460	7	2H bin 07/08	1_0297 to 2_1258	85.7 - 115.0	2HL
BW224	cur4.i	Curly 4	460	7	2H bin 04/08	1_0216 to 2_0833	47.5 - 115.9	2HL
BW812	sdw.l	Semidwarf 1	--	6	2H bin 06/08	1_1493 to 2_0528	76.1 - 119.0	
BW913	wst4.d	White streak 4	056	7	2H bin 06/08	1_1493 to 2_1258	76.1 – 115.0	2HL
BW413	gth1.a	Toothed lemma 1	069	6	2H bin 08/09	2_0528 to 2_1242	118.8 – 133.6	2HL
BW439	acr1.a	Accordion rachis 1	097	7	2H bin 05/08	1_0525 to 2_0582	65.0 – 118.0	2H
BW009	acr1.a	Accordion rachis 1	097	7	2H bin 05/09	1_0525 to 2_0699	65.0 – 126.3	2H
BW167	cer-zk.85	Eceriferum-zk	429	6	2H bin 08	2_0667 to 2_0582	117.7 – 118.8	
BW537	msg.ga	Male sterile genetic ga	--	6	2H bin 08/11	2_1251 to 1_1250	115.9 – 161.1.	
BW313	ert-j.31	Erectoides-j	090	7	2H bin 09/10	3_1205 to 1_1533	139.4 - 141.6	2H
BW490	Lks1.a	Awnless 1 (with gth1.a)	075	6	2H bin 09/10	1_0619 to 1_0287	133.6 – 141.6	2HL
BW491	Lks1.b	Awnless 1	075	7	2H bin 08/09	2_0667 to 1_0287	117.7 – 138.4	2HL
BW607	vrs1, mul2	Six-rowed spike 1	006	7	2H bin 09	2_0781 to 2_0340	135.2 – 138.4	2HL
BW	Allele	Locus or mutant name	BGS	Bow	Chromosome	SNP markers	Map position	Prev.

Barley Genetics Newsletter (2011) 41:12-53

no1	symbol2		no.3	cross4	bin position5	retained	(cM)6	loc.7
BW898	vrs1.a	Six-rowed spike 1	006	8	2H bin 09/10	2_0781 to 2_1351	135.2 – 145.8	2HL
BW899	vrs1.c	Six-rowed spike 1	058	7	2H bin 09/11	2_0781 to 1_1250	135.2 – 161.1	2HL
BW900	Vrs1.t	Six-rowed spike 1	067	8	2H bin 07/10	2_0131 to 2_1351	90.5 – 145.8	2HL
BW904	vrs1.c	Six-rowed spike 1	058	7	2H bin 09/11	1_0952 to 2_0086	122.0 - 158.4	2HL
BW422	Int-d.12	Six-rowed spike 1	006	7	2H bin 09/12	2_0340 to 2_0182	138.4 – 185.5	2HL
BW648	Pre2.b	Purple lemma and pericarp 2	076	9	2H bin 10/11	1_0214 to 1_0352	151.0 – 174.0	2HL
BW020	ant2.h	Anthocyanin-less 2	080	7	2H bin 10/12	1_0214 to 2_0182	151.0 – 185.5	2HL
BW370	fol-a.1	Angustifolium-a	073	7	2H bin 10/11	1_0214 to 1_1250	151.0 – 161.1	2HL
BW086	brh15.u	Brachytic 15	657	5	2H bin 11/12	1_0876 to 2_0182	161.1 – 185.5	
BW602	mtt4.e	Mottled leaf 4	078	7	2H bin 11/12	2_1340 to 2_0182	166.1 – 185.5	2HL
BW580	msg43.br	Male sterile genetic 43	506	7	2H bin 11/13	1_0352 to 2_1459	174.0 – 202.7	
BW571	msg35.dr	Male sterile genetic 35	498	7	2H bin 11/13	1_1118 to 2_0715	180.9 – 213.1	2HL
BW022	ant22.1508	Proanthocyanidin-free 22	604	6	2H bin 11/13	1_0346 to 2_0895	165.0 – 209.9	7HS
BW939	Zeo2.c	Zeocriton 2	614	4	2H bin 12/13	1_0404 to 1_0072	186.6 – 239.8	
BW270	dsp.ax	Zeocriton 2	614	5	2H bin 11/14	2_1184 to 2_0681	178.0 – 247.9	
BW933	Zeo2.d	Zeocriton 2	614	7	2H bin 11/14	1_1118 to 1_0315	180.9 – 224.4	3HS
BW936	Zeo2.j	Zeocriton 2	614	7	2H bin 12/14	2_1370 to 1_1023	199.5 – 224.4	
BW277	(dsp1.a)	Zeocriton 2	614	7	2H bin 13/14	1_0376 to 2_0561	209.9 – 247.9	7HS
BW940	Zeo3.h	Zeocriton 2	184	8	2H bin 13/14	2_1125 to 2_0293	206.2 – 234.6	4HS
BW381	gig1.a	Gigas 1	463	7	2H bin 12/14	1_0780 to 1_0085	189.4 – 247.9	2HL
BW397	gpa1.b	Grandpa 1	059	7	2H bin 12/14	1_1236 to 1_1085	184.5 - 247.9	2HL
BW483	lig1.a	Liguleless 1	060	8	2H bin 12/14	1_0383 to 2_0994	207.2 – 233.4	2HL
BW482	lig1.2	Liguleless 1	060	5	2H bin 13/14	1_0446 to 2_0994	199.5 – 233.4	2HL
BW937	Zeo1.a	Zeocriton 1	082	7	2H bin 13/14	2_0715 to 2_1453	213.1 – 245.7	2HL
BW938	Zeo1.b	Zeocriton 1	082	9	2H bin 13	1_1486 to 2_0590	202.7 – 218.5	2HL
BW322	Ert-r.52	Zeocriton 1	332	8	2H bin 13	2_0715 to 1_0551	213.1 – 221.7	2HL
BW336	fch.aa	Chlorina seedling aa	--	6	2H bin 13/14	2_0590 to 2_0293	218.5 – 234.6	
BW no ¹	Allele symbol ²	Locus or mutant name	BGS no. ³	Bow cross ⁴	Chromosome bin position ⁵	SNP markers retained	Map position (cM) ⁶	Prev. loc. ⁷

BW474	le1.a	Leafy lemma 1	235	4	2H bin 10/14	1_0404 to 2_1346	156.0 – 233.4	1HL
BW475	le1.a	Leafy lemma 1	235	5	2H bin 13	2_1274 to 2_0590	218.5	1HL
BW916	wst7.k	White streak 7	079	7	2H bin 14	2_1346 to 3_1180	233.4 – 245.7	2HL
BW823	sdw.w	Semidwarf w	--	5	2H bin 13/14	2_0715 to 1_0072	213.1 – 239.8	
BW825	sdw.y	Semidwarf y	--	7	2H bin 14	3_0823 to 1_0072	238.7 - 239.8	
BW450	Lax.ag	Laxatum ag	--	7	2H bin 13/14	1_0551 to 1_0085	221.7 – 247.9	

¹Bowman (BW) backcross-derived line number.

²Recommended allele symbol.

³Number for the Barley Genetic Stock (BGS) description of the locus.

⁴Number of cross to Bowman for each BW line.

⁵The estimated positions of retained SNP markers based on figures presented in Roy et al. (2010).

⁶Estimated map positions in centiMorgans (cM) from Durka *et al.* (2011).

⁷Chromosome locations based on previous mapping studies.

Coordinator's Report: Barley Chromosome 3H.

L. Ramsay

Cell and Molecular Sciences Group
James Hutton Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK.

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

Over the last year there have been a number of publications reporting the mapping of genes and QTL on barley chromosome 3H. The spontaneous mutation *eibi1.b* in wild barley that has a low capacity to retain leaf water has been mapped to 3H, cloned and shown to encode an ATP-binding cassette (ABC) subfamily G full transporter (*HvABCG31A*) (Chen *et al.* 2011). A novel recessive mutant gene *prbs* that produces branched spikes with irregular multiple rows was found and mapped to 3HS (Huang and Wu, 2011). Another gene mapped to 3HS was the trypsin inhibitor (BTI-CMe) that has been shown to be involved in the improvement of beer haze stability (Ye *et al.* 2011). Tang *et al.* (2011) also mapped *CYP710A8* that encodes sterol C-22 desaturase to chromosome 3H having implicated the gene in the accumulation of stigmaterol.

Mameaux *et al.* (2012) mapped members of the cytokinin oxidase/dehydrogenase gene family to chromosome 3H (*HvCKX2.1*, *HvCKX2.2* and *HvCKX4*). The *eIF4E* gene on the distal end of 3HL has been studied in even greater depth with a signature of positive selection being revealed by Hofinger *et al.* (2011). The *sdw1* semi-dwarfing gene on 3HL has also been the subject of a number of studies (Jia *et al.* 2011b; Kuczynska and Wyka, 2011) and postulated as a candidate gene to QTL found in others (Comadran *et al.* 2011; Malosetti *et al.* 2011) though the functional polymorphism underlying the *denso* allele is as yet unknown.

A number of QTL on 3H have been reported in the last year including a number for resistance to pests and diseases. This included a strong QTL for Fusarium head blight resistance on 3HL in six-rowed germplasm found in a large association genetics study (Massman *et al.* 2011) that corresponds with that found in previous bi-parental studies (see Jia *et al.* 2011a). Other examples include a major QTL for resistance to the root-lesion nematode *Pratylenchus neglectus* (Sharma *et al.* 2011) as well as QTL to scald (Li and Zhou, 2011) and net blotch (Cakir *et al.* 2011). Schweizer and Stein (2011) published a meta-analysis reviewing many disease resistance studies in barley and postulated four meta-QTL on 3H involved in the resistance to multiple diseases. Other 3H QTL reported in this year were for Aluminium tolerance (Navakode *et al.* 2011), forage quality traits (Surber *et al.* 2011), heading date (Comadran *et al.* 2011), resistance to drought (Szira *et al.* 2011) and to waterlogging (Zhou, 2011).

Work on the development of genomic and genetic resources in barley continued with the publication last year of the BAC library resources necessary for the development of a physical map (Schulte *et al.* 2011). Of particular note was the work reported by Sato *et al.* (2011b) of aligning 372 BAC contigs to the 3H genetic map using mapped ESTs. The availability of single nucleotide polymorphisms (SNP) genotyping means that 3H genic molecular markers have been

used to characterize near-isogenic lines containing introgressions on 3H in both a Haruna Nijo and Bowman background (Sato *et al.* 2001a and Druka *et al.* 2011 respectively). The use of SNP genotyping was supplemented by two other approaches published this year in barley. A Restriction Site Associated DNA (RAD) linkage map was constructed using the Oregon Wolfe Barley (OWB) population using a total 436 co-dominant RAD loci derived from next-generation sequencing (NGS) (Chutimanitsakun *et al.* 2011). A further development of a RAD like protocol has allowed for another approach for robust genotyping by sequencing (GBS) that has also been applied to the OWB population mapping 24,186 sequence tags onto the genetic map (Elshire *et al.* 2011). The integration of such approaches with the physical map will mean that barley researchers will likely to be able to use most of the gene space on chromosome 3H, together with the rest of the genome, as a source of genotypic information in future studies.

References:

- Cakir, M., S. Gupta, C. Li, M. Hayden, D.E. Mather, G.A. Ablett, G.J. Platz, S. Broughton, K.J. Chalmers, R. Loughman, M.G.K. Jones, and R.C.M. Lance. 2011.** Genetic mapping and QTL analysis of disease resistance traits in the barley population Baudin x AC Metcalfe. *Crop & Pasture Science* 62: 152-161.
- Chen, G., T.Komatsuda, J.F. Ma, C. Nawrath, M. Pourkheirandish, A. Tagiri, Y.-G. Hu, M. Sameri, X. Li, X. Zhao, Y. Liu, C. Li, X. Ma, A. Wang, S. Nair, N. Wang, A. Miyao, S. Sakuma, N. Yamaji, X. Zheng, and E. Nevo. 2011.** An ATP-binding cassette subfamily G full transporter is essential for the retention of leaf water in both wild barley and rice. *Proc Natl Acad Sci USA* 108:12354-12359.
- Chutimanitsakun, Y., R.W. Nipper, A. Cuesta-Marcos, L. Cistue, A. Corey, T. Filichkina, E.A. Johnson, and P.M. Hayes. 2011.** Construction and application for QTL analysis of a Restriction Site Associated DNA (RAD) linkage map in barley. *BMC Genomics* 12:4.
- Comadran, J., J.R. Russell, A. Booth, A. Pswarayi, S. Ceccarelli, S. Grando, A.M. Stanca, N. Pecchioni, T. Akar, A. Al-Yassin, A. Benbelkacem, H. Ouabbou, J. Bort, F. A. van Eeuwijk, W.T.B. Thomas, and I. Romagosa. 2011.** Mixed model association scans of multi-environmental trial data reveal major loci controlling yield and yield related traits in *Hordeum vulgare* in Mediterranean environments. *Theor Appl Genet* 122:1363-1373.
- Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh, 2011.** Genetic Dissection of Barley Morphology and Development. *Plant Physiology* 155:617-627.
- Elshire, R.J., J.C. Glaubitz, Q. Sun, J.A. Poland, K. Kawamoto, E.S. Buckler, and S.E. Mitchell. 2011.** A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. *PLOS One* 6: e19379.

- Hofinger, B.J., J.R. Russell, C.G. Ross, T. Baldwin, M. Dos Reis, P.E. Hedley, Y. Li, M. Macaulay, R. Waugh, K.E. Hammond-Kosack, and K. Kostya. 2011.** An exceptionally high nucleotide and haplotype diversity and a signature of selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. *Molecular Ecology* 20:3652-3668.
- Huang B.-G. and W.-R. Wu. 2011.** Mapping of Mutant Gene *prbs* Controlling Poly-Row-and-Branched Spike in Barley (*Hordeum vulgare* L.). *Agricultural Sciences in China* 10:1501-1505.
- Jia, H., B.P. Millett, S. Cho, H. Bilgic, W.W. Xu, K.P. Smith, and G.J. Muehlbauer. 2011.** Quantitative trait loci conferring resistance to *Fusarium* head blight in barley respond differentially to *Fusarium graminearum* infection. *Functional & Integrative Genomics* 11:95-102.
- Jia, Q., X.-Q. Zhang, S. Westcott, S. Broughton, M. Cakir, J. Yang, R. Lance, and C. Li. 2011.** Expression level of a gibberellin 20-oxidase gene is associated with multiple agronomic and quality traits in barley. *Theor Appl Genet* 122:1451-1460.
- Kuczynska, A. and T. Wyka. 2011.** The effect of the *denso* dwarfing gene on morpho-anatomical characters in barley recombinant inbred lines. *Breeding Science* 61: 275-280.
- Li, H.B. and M.X. Zhou. 2011.** Quantitative trait loci controlling barley powdery mildew and scald resistances in two different barley doubled haploid populations. *Molecular Breeding* 27:479-490.
- Malosetti, M., F.A. van Eeuwijk, M.P. Boer, A.M. Casas, M. Elia, M. Moralejo, P.R. Bhat, L. Ramsay, and J.-L. Molina-Cano. 2011.** Gene and QTL detection in a three-way barley cross under selection by a mixed model with kinship information using SNPs. *Theor Appl Genet* 122:1605-1616.
- Mameaux, S., J. Cockram, T. Thiel, B. Steuernagel, N. Stein, S. Taudien, P. Jack, P. Werner, J.C. Gray, A.J. Greenland, and W. Powell. 2012.** Molecular, phylogenetic and comparative genomic analysis of the cytokinin oxidase/dehydrogenase gene family in the Poaceae. *Plant Biotechnology Journal* 10:67-82.
- Massman, J., B. Cooper, R. Horsley, S. Neate, R. Dill-Macky, S. Chao, Y. Dong, P. Schwarz, G.J. Muehlbauer, and K.P. Smith. 2011.** Genome-wide association mapping of *Fusarium* head blight resistance in contemporary barley breeding germplasm. *Molecular Breeding* 27:39-454.
- Navakode, S., A.Weidner, R.K.Varshney, U.Lohwasser, U.Scholz, M.S.Roeder, and A.Boerner. 2010.** A Genetic Analysis of Aluminium Tolerance in Cereals. *Agriculturae Conspectus Scientificus* 75:191-196.

- Sato, K., T.J. Close, P. Bhat, M. Munoz-Amatriain, and G.J. Muehlbauer. 2011.** Single Nucleotide Polymorphism Mapping and Alignment of Recombinant Chromosome Substitution Lines in Barley. *Plant and Cell Physiology* 52:728-737.
- Sato, K., Y. Motoi, N. Yamaji, and H. Yoshida. 2011.** 454 sequencing of pooled BAC clones on chromosome 3H of barley. *BMC Genomics* 12:246.
- Schulte, D., R. Ariyadasa, B. Shi, D. Fleury, C. Saski, M. Atkins, P. deJong, C.-C. Wu, A. Graner, P. Langridge, and N. Stein. 2011.** BAC library resources for map-based cloning and physical map construction in barley (*Hordeum vulgare* L.). *BMC Genomics* 12:247.
- Schweizer, P. and N. Stein. 2011.** Large-Scale Data Integration Reveals Co-localization of Gene Functional Groups with Meta-QTL for Multiple Disease Resistance in Barley. *Molecular Plant-Microbe Interactions* 24:1492-1501.
- Sharma, S., S. Sharma, F.J. Kopsisch-Obuch, T. Keil, E. Laubach, N. Stein, A. Graner, and C. Jung. 2011.** QTL analysis of root-lesion nematode resistance in barley: 1. *Pratylenchus neglectus*. *Theor Appl Genet* 122:1321-1330.
- Surber, L., H. Abdel-Haleem, J. Martin, P. Hensleigh, D.Cash, J.Bowman, and T. Blake. 2011.** Mapping quantitative trait loci controlling variation in forage quality traits in barley. *Molecular Breeding* 28:189-200.
- Szira, F., A. Boerner, K. Neumann, K.Z. Nezhad, G. Galiba, and A.F. Balint. 2011.** Could EST-based markers be used for the marker-assisted selection of drought tolerant barley (*Hordeum vulgare*) lines? *Euphytica* 178:373-391.
- Tang, J., K. Ohyama, K. Kawaura, H. Hashinokuchi, Y. Kamiya, M. Suzuki, T. Muranaka, and Y. Ogihara. 2011.** A new insight into application for barley chromosome addition lines of common wheat: achievement of stigmaterol accumulation. *Plant Physiology* 157:1555-1567.
- Ye, L., F. Dai, L. Qiu, D. Sun, and G. Zhang. 2011.** Allelic Diversity of a Beer Haze Active Protein Gene in Cultivated and Tibetan Wild Barley and Development of Allelic Specific Markers. *Journal Of Agricultural And Food Chemistry* 59:7218-7223.
- Zhou, M., 2011.** Accurate phenotyping reveals better QTL for waterlogging tolerance in barley. *Plant Breeding* 130:203-208.

Coordinator's Report: Chromosome 4H

Arnis Druka

Cell and Molecular Sciences Group
The James Hutton Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK.

e-mail: Arnis.Druka@hutton.ac.uk

In 2011, specifically in relation to barley chromosome 4H Ramsay *et al.* showed that *int-c* gene is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1 (Tb1)* and identified 17 coding mutations in barley *Tb1* correlated with lateral spikelet fertility phenotypes. In barley, domestication process has resulted in two different cultivated types, two-rowed and six-rowed forms. Both derived from the wild two-rowed ancestor. Archaeo-botanical evidence indicated the origin of six-rowed barley early in the domestication of the species, some 8,600-8,000 years ago. Variation at *six-rowed spike 1 (vrs1)* is sufficient to control this phenotype. However, phenotypes imposed by *vrs1* alleles are modified by alleles at the *intermedium-c (int-c)* locus. Identification of the *int-c* gene should promote detailed molecular and cellular studies on lateral spikelet development in barley. general, barley papers published in 2011 with relevance to chromosome 4H mapping. Thus, Sato *et al.* identified 100 genes that have been mapped to different regions of barley chromosome.

There were several other, more 4H and have SNP polymorphisms between the malting barley cultivar 'Haruna Nijo' and the food barley cultivar 'Akashinriki'. The SNPs were also used to genotype 98 BC(3)F(4) recombinant chromosome substitution lines (RCSLs) developed from the same cross (Haruna Nijo/Akashinriki). These data were used to create graphical genotypes for each line and thus estimate the location, extent and total number of introgressions from Akashinriki in the Haruna Nijo background. The 35 selected RCSLs sample most of the Akashinriki food barley genome, with only a few missing segments. These resources bring new alleles into the malting barley gene pool from food barley. Also, a diversity analysis on a set of 37 barley accessions was conducted as part of this paper.

Russell *et al* published genotyping data set of 448 geographically matched landrace and wild barley accessions from the Fertile Crescent. Each accession was genotypes with >1000 known, genetically mapped gene-based SNPs. Landrace and wild barley categories were clearly genetically differentiated, but a limited degree of secondary contact was evident. Significant chromosome-level differences in diversity between barley types were observed around genes known to be involved in the evolution of cultivars. The region of Jordan and southern Syria, compared with the north of Syria, was supported by SNP data as a more likely domestication origin. These data provide evidence for hybridization as a possible mechanism for the continued adaptation of landrace barley under cultivation, indicating regions of the genome that may be subject to selection processes and suggesting limited origins for the development of the cultivated crop.

Liu *et al.* reported exciting new approach to screen systematically BAC libraries for specific gene sequences. Agilent 44K mRNA expression microarrays were probed with BAC DNA pools. As a result, 1390 BAC clones for 3040 barley genes were identified. The approach represents a cost-effective, highly parallel alternative to traditional addressing methods. By coupling the gene-to-BAC address data with gene-based molecular markers, thousands of BACs can be anchored directly to the genetic map, thereby generating a framework for orientating and ordering genes.

Mayer *et al.* published a novel approach to gene mapping that incorporated above-mentioned array hybridization (see Liu *et al.*), together with chromosome sorting, next-generation sequencing and systematic exploitation of conserved synteny with model grasses was used to assign ~86% of the estimated ~32,000 barley (*Hordeum vulgare*) genes to individual chromosome arms. Using a series of bioinformatically constructed genome zippers that integrate gene indices of rice (*Oryza sativa*), sorghum (*Sorghum bicolor*), and *Brachypodium distachyon* in a conserved synteny model, putative linear order of 21,766 barley genes was proposed. This included 2529 known barley unigenes that were assigned to chromosome 4H.

Druka *et al.* published construction of a collection of 881 backcross-derived lines containing mutant alleles that induce a majority of the morphological and developmental variation described in barley. After genotyping these lines with up to 3,072 single nucleotide polymorphisms, comparison to their recurrent parent defined the genetic location of 426 mutant alleles to chromosomal segments, each representing on average <3% of the barley genetic map. Thirty nine of these lines had a single introgression mapped to barley chromosome 4H.

References:

- Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, R. Waugh. 2011.** Genetic dissection of barley morphology and development. *Plant Physiol.* 2011 Feb;155(2):617-27.
- Liu, H., J. McNicol, M. Bayer, J.A. Morris, L. Cardle, D.F. Marshall, D. Schulte, N. Stein, B.J. Shi, S. Taudien, R. Waugh, P.E. Hedley. 2011.** Highly parallel gene-to-BAC addressing using microarrays. *Biotechniques.* 2011 Mar;50(3):165-74.
- Mayer, K.F., M. Martis, P.E. Hedley, H. Simková, H. Liu, J.A. Morris, B. Steuernagel, S. Taudien, S. Roessner, H. Gundlach, M. Kubaláková, P. Suchánková, F. Murat, M. Felder, T. Nussbaumer, A. Graner, J. Salse, T. Endo, H. Sakai, T. Tanaka, T. Itoh, K. Sato, M- Platzer, T. Matsumoto, U. Scholz, J. Dolezel, R. Waugh, and N. Stein. 2011.** Unlocking the barley genome by chromosomal and comparative genomics. *Plant Cell.* 2011 Apr;23(4):1249-63.
- Ramsay, L, J. Comadran, A. Druka, D.F. Marshall, W.T. Thomas, M. Macaulay, K. MacKenzie, C. Simpson, J. Fuller, N. Bonar, P.M. Hayes, U. Lundqvist, J.D. Franckowiak, T.J. Close, G.J. Muehlbauer, and R. Waugh. 2011.** *INTERMEDIUM-*

C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1*. *Nat Genet.* 2011 Feb;43(2):169-72.

Russell, J., I.K. Dawson, A. J. Flavell, B. Steffenson, E. Weltzien, A. Booth, S. Ceccarelli, S. Grando, and R. Waugh. 2011. Analysis of >1000 single nucleotide polymorphisms in geographically matched samples of landrace and wild barley indicates secondary contact and chromosome-level differences in diversity around domestication genes. *New Phytol.* 2011 Jul;191(2):564-78.

Sato, K., T.J. Close, P. Bhat, M. Muñoz-Amatriain, and G.J. Muehlbauer. 2011. Single nucleotide polymorphism mapping and alignment of recombinant chromosome substitution lines in barley. *Plant Cell Physiol.* 2011 May;52(5):728-37.

Coordinator's Report: Chromosome 6H (6)

Victoria Carollo Blake

USDA-ARS, Albany, CA, USA

e-mail: victoria.blake@ars.usda.gov

Near-isogenic barley lines differing in the alleles at the GPC-6H locus were analyzed by Parrott *et al.*, (2011) for differences in the timing of anthesis and whole-plant senescence. They found that in the high-GPC germplasm, pre-anthesis plant development was enhanced. This was more evident under short day conditions than long day conditions and the allelic difference was negated by vernalization.

A major gene for resistance to Australian net type net blotch (NTNB) was mapped to the centromeric region of 6H using SSR markers by Gupta *et al.* (2011). F1-derived double haploid populations of 'WPG8412 x Stirling', 'WPG8412 x Pompadour' and 'Stirling x Pompadour' were tested with two Australian NTNB isolates, 97NB1 and NB73. Authors suggest there are at least three closely-linked genes or alleles in this complex locus.

A dehydrin, *dhn4*, was cloned from the 6H chromosome of a Tibetan hulless barley and transformed into tobacco by *Agrobacterium*. (Wang, *et al.*, 2011).

References:

- Gupta, S., C. Li, R. Loughman, M. Cakir, S. Westcott, and R. Lance. 2011.** Identifying genetic complexity of 6H locus in barley conferring resistance to *Pyrenophora teres f. teres*. *Plant Breeding* 130:423-429.
- Parrott, D.L., E.P. Downs, and A.M. Fischer. 2011** Control of barley (*Hordeum vulgare* L.) development and senescence by the interaction between a chromosome six grain protein content locus, day length and vernalization. *J. Exp. Botany*. doi: 10.1093/jxb/err360.
- Wang, J.-H., K.-L. Chen, H.-W. Li, J. He, B. Guan, J.-B. Du, and J.-J. Liu. 2011.** Tibetan hulless barley dehydrin, *dhn4*, cloning and transforming into tobacco. *J. Agric. Env. Intl. Devel.* 103:173-184.

Coordinator's Report: Chromosome 7H

Lynn S. Dahleen

USDA-Agricultural Research Service
Fargo, ND 58102, USA

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

Mapping research and marker development continued in 2010, with many additions to genes and QTL on chromosome 7H.

Abdel-Haleem *et al.* (2010 a, b) evaluated F₅-derived families from a cross between a hulled and hull-less genotype for a variety of feed-related traits. They found major QTL for acid detergent fiber and starch tightly linked or pleiotropic to the *nud1* gene near the middle of 7H, with an r^2 as high as .47. This loci was significant in both irrigated and rain-fed environments. Another QTL associated with starch was located on the short arm of 7H, but only was detected in the irrigated and combined environment analyses (Abdel-Haleem *et al.* 2010a). This second QTL also was associated with *in sacco* dry matter digestibility and particle size, again only in the irrigated and combined environment analyses (Abdel-Haleem *et al.* 2010 gb).

Basal host resistance to powdery mildew was examined by Aghnoum *et al.* (2010) in six mapping populations. Their combined map of 6990 markers was used to locate seedling and adult plant resistance QTL. Chromosome 7H contained two seedling QTL and one adult plant QTL located on the short arm. The first, Rbgq20, was coincident with the *mlt* locus. Five of the 22 ESTs upregulated with *Blumeria graminis* inoculation were located on chromosome 7H and two were in QTL for resistance. Silvar *et al.* (2010) mapped QTL for powdery mildew resistance in an inbred line derived from the Spanish landrace SBCC97. All four mildew isolates showed the same two QTL on chromosome 7H, one on the short arm (likely *mlt*) and one on the long arm (likely *Mlf*), which explained up to 45% of the variation in disease reaction. This is the first time a single cultivated barley line contained both QTL, providing adapted material for breeding programs.

Further functional characterization of *Rpg1*, the stem rust resistance gene on the short arm of chromosome 7H, was conducted by Nirmala *et al.* (2010). They show that the Rpg1 protein is quickly phosphorylated when exposed to fungal elicitors from avirulent *Puccinia graminis*. This phosphorylation was essential for a resistance response. Research continues to better understand the mechanism of resistance in this gene.

Beattie *et al.* (2010) used association mapping to locate loci for malt quality and disease resistance in 91 elite 2-rowed Canadian malting barley cultivars. Loci associated with alpha amylase, diastatic power, friability, protein, and net form net blotch were located on chromosome 7H. The candidate gene *GAmyb* binding protein was associated with the alpha amylase locus and one friability locus, and limit dextrinase was associated with one of the diastatic power loci. A C-terminal protease/peptidase was associated with the second friability locus. These associations, once confirmed, will provide additional markers for molecular

breeding to fix the favorable alleles in breeding populations. The genetic differences in malting quality between European and North American malting quality standard cultivars was studied by Elia *et al.* (2010). They used a 462 marker linkage map to locate QTL for multiple traits. Chromosome 7H contained loci for protein content, malt extract, diastatic power, and fermentability. The QTL for extract had not been found in previous studies. These QTL provide opportunities for breeders to exploit other elite germplasm not traditionally used to improve malting quality traits.

Haseneyer *et al.* (2010) used association mapping to locate regions associated with a variety of agronomic and quality traits in a population of 224 spring barley accessions from around the world. While they only used 45 EST-SSR markers, they found trait associations with a number of markers, including starch content and plant height on chromosome 7H, which had been previously identified in bi-parental crosses.

Rapacz *et al.* (2010) examined freezing tolerance and cold acclimation of the photosynthetic apparatus in a set of 28 winter barley genotypes. They found two significant markers on chromosome 7H, one associated with quenching excitation energy of photosystem II in photochemical processes, and the other associated with maximum quantum yield of PSII. Large environmental effects were observed, suggesting further tests under controlled conditions will be needed to better understand frost resistance. Wang *et al.* (2010) examined allelic variation in photoperiod and vernalization genes involved in control of flowering time to better understand underlying mechanisms. Chromosome 7H contains VRN-H3 (HvFT1) and HvCO1. They found that VRN-H3 was located in one of the three QTL for flowering time on chromosome 7H and also was associated with grains/ear, height, and yield. HvCO1 was associated with heading date, harvest index, and yield. The results of this study help us better understand regulation of flowering time.

Salinity in soils is an increasing problem around the world. Shavnakov *et al.* (2010) used saline hydroponic culture to locate a gene for salinity exclusion in a cross between the best shoot Na⁺ excluder spontaneous accession CPI-71284-48 and the intermediate excluder Barque-73. Resistance in the CPI line was controlled by a locus named *HvNax3* located on the short arm of chromosome 7H. Several candidate genes were identified by comparison with syntenous regions of rice and Brachypodium.

Yu *et al.* (2010) mapped QTL for height, heading data, and rachis internode length in a population derived from the semi-dwarf line Zau7 and a tall breeding line from North Dakota. Two height QTL were located on chromosome 7H, including one that was detected in all environments. This locus did not affect heading date or rachis internode length, and reduced plant height by approximately one fourth. The QTL, named *Qph-7H*, may be useful in breeding shorter barley cultivars with less lodging.

Von Korff *et al.* (2010) examined epistatic interactions between exotic alleles from *H. spontaneum* introgressed into Scarlett barley for the traits heading date, plant height, and yield. They found one marker on chromosome 7H interacted with a 2H marker for heading date, three markers on 7H interacted with markers on 1H, 3H and 5H for height, and two chromosome 7H markers interacted with markers on 1H and 3H for yield. These epistatic effects need to be

considered for gene cloning and marker-assisted selection. Synteny between barley and *Brachypodium distachyon* was evaluated by Drader and Kleinhofs (2010) along with positions of disease resistance genes. The short arm of barley chromosome 7H showed synteny with *Brachypodium* contig Super_1 while the long arm was syntenous with Super_0. A high degree of colinearity among markers was evident. An ortholog for *Rpg1* was located in *Brachypodium* and several candidate genes for *Rcs5* were identified.

Li *et al.* (2010) created a high density composite map from doubled haploid lines of four populations, two derived from anther culture, and then looked at marker segregation to identify any distortion in the individual and combined maps. The composite map contained 2,111 unique loci. Segregation distortion was more common in the anther culture derived populations, with as many as 14.3% of the markers on chromosome 7H showing distortion. Three of the four populations showed the same region of markers with distorted segregation around the centromere of chromosome 7H, indicating the method of doubled haploid line development was not the cause of the distortion. Varshney *et al.* (2010) evaluated diversity in 223 *H. vulgare* and *H. spontaneum* genotypes from 30 countries with SNP and SSR markers. Polymorphism information content (PIC) of the six SNP markers on chromosome 7H ranged from 0.21 to 0.50. The seven SSRs on chromosome 7H showed between 3 and 17 alleles with PIC values ranging from 0.26 to 0.85. Data from the full set of markers was used to examine genetic relationships and trends in genetic diversity.

Wheat-barley addition lines have been useful in a variety of genetic studies. Szakacs and Molnar-Lang (2010) report on the development of new addition lines including the 7H disomic addition from the winter barley 'Igri' into a winter wheat variety. This line is taller than the wheat parent, has longer spikes, lower grain yield, an increase in the number of tillers, and a significant decrease in fertility. The 7H disomic addition was very stable, with 96.4% transmission to progeny. These addition lines will continue to be of use for barley and wheat geneticists.

References:

- Abdel-Haleem, H., J. Bowman, M. Giroux, V. Kanazin, H. Talbert, L. Surber, and T. Blake. 2010a.** Quantitative trait loci of acid detergent fiber and grain chemical composition in hulled x hull-less barley population. *Euphytica* 172:405-418.
- Abdel-Haleem, H., J.G.P. Bowman, V. Kanazin, L. Surber, H. Talbert, P.M. Hayes, and T. Blake. 2010b.** Quantitative trait loci for dry matter digestibility and particle size traits in two-rowed x six-rowed barley population. *Euphytica* 172:419-433.
- Aghnoum, R., T.C. Marcel, A. Johrde, N. Pecchioni, P. Schweizer, and R.E. Nix. 2010.** Basal host resistance of barley to powdery mildew: connecting quantitative trait loci and candidate genes. *MPMI* 23:91-102.
- Beattie, A.D., M.J. Edney, G.J. Scoles, and B.G. Rossnagel. 2010.** Association mapping of malting quality data from western Canadian two-row barley cooperative trials. *Crop Sci.* 50:1649-1663.

- Drader, T. and A. Kleinhofs, 2010.** A synteny map and disease resistance gene comparison between barley and the model monocot *Brachypodium distachyon*. *Genome* 53:406-417.
- Elia, M., J.S. Swanston, M. Moralejo, A. Casas, A.-M. Perez-Vendrell, F.J. Ciudad, W.T.B. Thomas, P.L. Smith, S.E. Ullrich, and J.-L. Molina-Cano. 2010.** A model of the genetic differences in malting quality between European and North American barley cultivars based on a QTL study of the cross Triumph x Morex. *Plant Breed.* 129:280-290.
- Haseneyer, G., S. Stracke, C. Paul, C. Einfeldt, A. Broda, H.-P. Piepho, A. Graner, and H.H. Geiger. 2010.** Population structure and phenotypic variation of a spring barley world collection set up for association studies. *Plant Breeding* 129:271-279.
- Li, H., A. Kilian, M. Zhou, P. Wenzl, E. Huttner, N. Mendham, L. McIntyre, and R.E. Vaillancourt. 2010.** Construction of a high-density composite map and comparative mapping of segregation distortion regions in barley. *Mol. Genet. Genomics* 284:319-331.
- Nirmala, J., T. Drader, X. Chen, B. Steffenson, and A. Kleinhofs. 2010.** Stem rust spores elicit rapid Rpg1 phosphorylation. *MPMI* 23:1635-1642.
- Rapacz, M., M. Tyrka, M. Gut, and W. Mikulski. 2010.** Associations of PCR markers with freezing tolerance and photosynthetic acclimation to cold in winter barley. *Euphytica* 175:293-301.
- Shavrukov, Y., N.K. Gupta, J. Miyazaki, M.N. Baho, K.J. Chalmers, M. Tester, P. Langridge, and N.C. Collins. 2010.** *HvNax3* – a locus controlling shoot sodium exclusion derived from wild barley (*Hordeum vulgare* ssp. *spontaneum*). *Funct. Integr. Genomics* 10:277-291.
- Silvar, C., H. Dhif, E. Igartua, D. Kopahnke, M.P. Gracia, J.M. Lasa, F. Ordon, and A.M. Casas. 2010.** Identification of quantitative trait loci for resistance to powdery mildew in a Spanish barley landrace. *Mol. Breeding* 25:581-592.
- Szakacs, E. and M. Molnar-Lang. 2010.** Identification of new winter wheat – winter barley addition lines (6HS and 7H) using fluorescence *in situ* hybridization and the stability of the whole ‘Martonvasari 9 kr1’ – ‘Igri’ addition set. *Genome* 53:35-44.
- Varshney, R.K., M. Baum, P. Guo, S. Grando, S. Ceccarelli, and A. Graner. 2010.** Features of SNP and SSR diversity in a set of ICARDA barley germplasm collection. *Mol. Breeding* 26:229-242.
- von Korff, M., J. Leon, and K. Pillen. 2010.** Detection of epistatic interactions between exotic alleles introgressed from wild barley (*H. vulgare* ssp. *spontaneum*). *Theor. Appl. Genet.* 121:1455-1464.

Wang, G., I. Smalenbach, M. von Korff, J. Leon, B. Kilian, J. Rode, and K. Pillen. 2010. Association of barley photoperiod and vernalization genes with QTLs for flowering time and agronomic traits in a BC₂DH population and a set of wild barley introgression lines. *Theor. Appl. Genet.* 120:1559-1574.

Yu, G.T., R.D. Horsley, B. Zhang, and J.D. Franckowiak. 2010. A new semi-dwarfing gene identified by molecular mapping of quantitative trait loci in barley. *Theor. Appl. Genet.* 120:853-861.

**Barley Genetic Stocks Collection
(GSHO – Genetic Stocks-*Hordeum*)**

**USDA-ARS National Small Grains Collection
1691 S. 2700 W.
Aberdeen, Idaho 83210, USA**

Curator: Harold Bockelman

e-mail: harold.bockelman@ars.usda.gov

Additions

GSHO 10001 – 13070 were added in the past year. These accessions represent mapping populations generated during the four years of the Barley CAP (Coordinated Agricultural Project). Unfortunately, inventories of these accessions are very low and thus not available for distribution. Details of the project and participants are available at this URL: <http://www.barleycap.org>.

Regenerations

During the 2010-2011 greenhouse season a total of 71 GSHO accessions were regenerated.

Distributions

In the past year a total of 1246 samples in 36 separate requests were distributed to scientists in 12 countries.

GRIN

All GSHO accessions are described on the Germplasm Resources Information Network (GRIN) online at <http://www.ars-grin.gov/npgs>.

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

Farre and colleagues (2011) described a novel statistical-genetic approach for the construction of linkage maps in populations obtained from reciprocal translocation heterozygotes of barley (*Hordeum vulgare* L.). Using standard linkage analysis, translocations usually lead to 'pseudo-linkage': the mixing up of markers from the chromosomes involved in the translocation into a single linkage group. Close to the translocation breakpoints recombination is severely suppressed and, as a consequence, ordering markers in those regions is not feasible. The novel strategy presented in this paper is based on (1) disentangling the "pseudo-linkage" using principal coordinate analysis, (2) separating individuals into translocated types and normal types and (3) separating markers into those close to and those more distant from the translocation breakpoints. The methods make use of a consensus map of the species involved. The final product consists of integrated linkage maps of the distal parts of the chromosomes involved in the translocation {Farre, 2011 #14099}.

Colleagues from Kyoto (Japan) used two gametocidal (Gc) chromosomes 2C and 3C(SAT) to dissect barley chromosome 4H added to common wheat. The Gc chromosome induced chromosomal structural rearrangements in the progeny of the 4H addition line of common wheat carrying the monosomic Gc chromosome. They established 60 dissection lines of common wheat carrying single rearranged 4H chromosomes. The rearranged 4H chromosomes had either a deletion or a translocation or a complicated structural change. The breakpoints were distributed in the short arm, centromere and the long arm at a rough ratio of 2:2:1. Based on the PCR result, a cytological map of chromosome 4H was constructed with 18 regions separated by the breakpoints of the rearranged chromosomes. Thirty-seven markers were present in the short arm and 56 in the long arm, and about 70% of the markers were present in no more than the distal 25.6% and 43.1% regions of the short and long arms, respectively. The authors reconstructed a genetic map using 38 of the 93 markers that was used to construct the cytological map of chromosome 4H. The order of the markers on the genetic map was almost the same as that on the cytological map. On the genetic map, no markers were available in the pericentromeric region, but on the cytological map, 14 markers were present in the proximal region, and one of the markers was in the centromeric region of the short arm {Sakata, 2010 #14100}.

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

References:

- Farre, A., L.L. Benito, L. Cistue, J.H. de Jong, L. Romagosa, and J. Jansen. 2011.** Linkage map construction involving a reciprocal translocation. *Theor Appl Genet* 122, 1029-1037.
- Sakata, M., S. Nasuda, and T.R. Endo. 2010.** Dissection of barley chromosome 4H in common wheat by the gametocidal system and cytological mapping of chromosome 4H with EST markers. *Genes Genet Syst* 85, 19-29.

Coordinator's report: *Eceriferum* genes

**Udda Lundqvist
Nordic Genetic Resource Center (Nordgen)
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. Unhappily the revised descriptions from the last issue of BGN 40 are not updated in the Untamo database but will be hopefully done during 2012. They can also be searched through the Triticeaea 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). Many of them are increased during summer 2010 and 2011 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 (Druka *et al.*, 2011). All Near Isogenic Lines are incorporated into the Nordic Genetic Resource Center (Nordgen) and are available for every research in barley. Descriptions of many of these genes are revised in volume BGN 40 and also in this issue. Please have a look there.

Every research of interest in this field and literature references are very useful to report to the coordinator as well. Seed requests of the original Swedish material can be forwarded to the coordinator udda@nordgen.org or to the Nordic Genetic Resource Center (Nordgen) www.nordgen.org. All original *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.

Reference:

- Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010,** Genetic Dissection of barley morphology and development. *Plant Physiology* 155:617-627.

Coordinator's Report: Disease and Pest Resistance Genes

Tina Lange & 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

In the table below you will find papers published in 2010-2011 extending last year's list of information available on molecular markers for major resistance genes in barley published in Barley Genetics Newsletter 40.

List of papers published on mapped major resistance genes in barley updated until August 31, 2011.

Resistance gene	Chromosomal location	Reference
<i>Puccinia hordei</i>		
<i>Rph20</i>	5HS	Hickey <i>et al.</i> 2011
<i>Puccinia striiformis</i>		
<i>YrpstY1</i>	7H	Sui <i>et al.</i> 2010
<i>Ustilago nuda</i>		
<i>N.N.</i>	3H	Menzies <i>et al.</i> 2010
<i>Pyrenophora teres</i>		
<i>rpt.r, rpt.k</i>	6HL	Liu <i>et al.</i> 2010
<i>Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV, BaMMV-2)</i>		
<i>rym4, rym5</i>	3HL	Sedláček <i>et al.</i> 2010

References:

- Hickey, L.T., W. Lawson, G.J. Platz, M. Dieters, V.N. Arief, S. Germán, S. Flechter, R.F. Park, D. Singh, S. Pereyra, and J. Franckowiak. 2011.** Mapping *Rph20*: a gene conferring adult plant resistance to *Puccinia hordei* in barley. *Theor Appl Genet* 123:55-68.
- Liu, Z., J.D. Faris, M.C. Edwards, and T.L. Friesen. 2010.** Development of Expressed Sequence Tag (EST)-based Markers for Genomic Analysis of a Barley 6H Region
- Menzies, J.G., B.J. Steffenson, and A. Kleinhofs. 2010.** A resistance gene to *Ustilago nuda* in barley is located on chromosome 3H. *Can. J. Plant Pathol.* 32(2):247-251.
- Séčlatek, T., P. Mařík, and J. Chrpová. 2010.** Development of CAPS Marker for Identification of *rym4* and *rym5* Alleles Conferring Resistance to the Barley Yellow Mosaic Virus Complex in Barley. *Czech J. Genet. Plant Breed.* 46(4):159-163.
- Sui, X., Z. He, Y. Lu, Z. Wang, and X. Xia. 2010.** Molecular mapping of a non-host resistance gene *YrpstY1* in barley (*Hordeum vulgare* L.) for resistance to wheat stripe rust. *Hereditas* 147:176-182.

Coordinator's report: Nuclear genes affecting the chloroplast

Mats Hansson

**Carlsberg Laboratory,
Gamle Carlsberg Vej 10,
DK-1799 Copenhagen V,
Denmark**

E-mail: mats.hansson@carlsberglab.dk

Barley mutants deficient in chlorophyll biosynthesis and chloroplast development are easily distinguished from wild type plants by their deviant color. Chlorophyll mutants have been called *albina*, *xantha*, *viridis*, *chlorina*, *tigrina* and *striata seedlings* depending on their color and color 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.

Richter *et al.* (2010) address the question of down-regulation of 5-aminolevulinic acid (ALA) biosynthesis in plants upon transition from light to dark. The formation of ALA is the first committed step in tetrapyrrole biosynthesis leading to the end products chlorophyll, heme, siroheme and phytychromobilin. The formation of ALA is the major regulatory step and the

pathway control prevents the accumulation metabolic intermediates and avoids photo-oxidative damage. The barley mutant *tigrina-d.12* has a relaxed synthesis of ALA in the dark and therefore accumulates an excess of protochlorophyllide. Richter *et al.* (2010) show that the dark repression of ALA formation relies rather on rapid post-translational regulation in response to accumulating protochlorophyllide than on changes in nuclear gene expression.

Yuan *et al* (2010) study the protochlorophyllide oxidoreductase (POR) of the chlorophyll biosynthetic pathway. In angiosperms, POR catalyzes the conversion of protochlorophyllide *a* to chlorophyllide *a* in a light dependant reaction. *Nanchong Yellow Barley (NYB)* is the only POR-less mutant known in barley and was induced by ⁶⁰Co γ -ray treatment. The chloroplast of *NYB* contains fewer thylakoids and grana than the wild type (WT), with a lower total Chl content and a higher Chl *a* / *b* ratio in mature leaves. When *NYB* was hybridized with the WT, the ratio of character segregation was 3 : 1, and the ratio of the test cross was 1 : 1. Therefore, the yellowish color of *NYB* leaves is most probably controlled by a recessive nuclear gene. However, no mutation was found in the *porB* gene encoding PORB. Further, both PORA and PORB proteins were decreased in the mutant, but not at the transcriptional level or at the translational level. It was suggested that *NYB* might be deficient in import of PORA and PORB into the chloroplasts.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found in Barley Genetics Newsletter issue 37 (2007):37-43 and is also linked from

<http://www.carlsberglab.dk/professors/Hansson/Pages/default.aspx>

New references:

Richter, A., E. Peter, Y. Pörs, S. Lorenzen, B. Grimm and O. Czarnecki. 2010. Rapid dark repression of 5-aminolevulinic acid synthesis in green barley leaves. *Plant Cell Physiol.* 51: 670-681.

Yuan, M., S. Yuan, Z.-W. Zhang, F. Xu, Y.-E. Chen, J.-B. Du and H.-H. Lin. 2010. Putative mutation mechanism and light responses of a protochlorophyllide oxidoreductase-less barley mutant *NYB*. *Plant Cell Physiol.* 51: 1361-1371.

Coordinator's report: Early maturity and Praematurum genes

Mats Hansson and Udda Lundqvist

**Carlsberg Laboratory, Gl Carlsberg vej 10
DK-1799 Copenhagen V, Denmark**

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

**[e-mail: mats.hansson@carlsberglab.dk](mailto:mats.hansson@carlsberglab.dk)
udda@nordgen.org**

The demand for early maturity has grown for several decades and became an important goal for plant breeding. Time to flowering has an important impact on yield and has been a key trait in the domestication of crop plants. Early maturity material has been collected for different geographic regions and climate conditions, today a critical issue in times of global warming. Many different early maturity or Praematurum mutants collected in different parts of the world are incorporated in Genebanks. Only in Scandinavia more than 1000 such mutants have been isolated, their phenotypes have been described, analysed genetically and used in plant breeding. In 1961, the Swedish cultivar 'Mari' with the special *mat-a.8* gene was the very first induced early barley mutant to be released as cultivar into commercial production. 'Mari' extended the range of two-row spring barley cultivation as a result of its photoperiod insensitivity. Since its release, 'Mari' or its derivatives have been used extensively across the world to facilitate short-season adaptation and further geographic range extension. By exploiting the extended historical collection of early flowering mutants, we identified Praematurum-a (*Mat-a*) mutant, the gene responsible for this key adaptive phenotype, as a homolog of the *Arabidopsis thaliana* circadian clock regulator *Early flowering 3 (Elf3)*. We characterized 87 induced *mat-a* mutant lines and identified more than 20 different *mat-a* alleles that had clear mutations leading to the defective putative ELF3 protein. Expression analysis of *HvElf3* and *Gigantea* in mutant and wild type plants demonstrated the flowering pathway, leading to the early phenotype. Alleles of *Mat-a* are therefore important and demonstrate a high breeding value in barley, but probably also in many other day-length sensitive crop plants.

Reference:

Zakhrabekova, S., S.P. Gough, I. Brauman, A.H. Müller, J. Lundqvist, K. Ahmann, Ch. Dockter, I. Matyszczak, M. Kurowska, A. Druka, R. Waugh, A. Graner, N. Stein, B. Steuernagel, U. Lundqvist, and M. Hansson. 2012. Induced mutations in circadian clock regulator *Mat-a* facilitated short-season adaptation and range extension in cultivated barley. Proc Natl Acad Sci USA, manuscript accepted, (in press)

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 six disomic addition lines (1Hm, 2Hm, 4Hm, 5Hm, 6Hm, 7Hm) of *Hordeum marinum*-Chinese Spring wheat has been reported earlier. It has also been possible to isolate four disomic addition lines (2Hm, 3Hm, 5Hm and 7Hm) of a different accession of *H. marinum* to Westonia commercial wheat. The *H. marinum*-wheat amphiploids produced maintain higher $K^+ : Na^+$ and suffer less leaf injury than wheat parents in saline conditions.

Reference:

Munns, Rana, RA. James, AKMR. Islam, and T.D. Colmer,TD 2011. *Hordeum marinum*-wheat amphiploid maintain higher $K^+ : Na^+$ and suffer less leaf injury than wheat parents in saline conditions. Submitted to Plant and Soil (in press).

Coordinator's report: ear morphology genes.

A.Michele Stanca
Faculty of Agricultural and Food Science, University of Modena and Reggio Emilia,
Reggio Emilia, Italy

e-mail; michele@stanca.it

Valeria Terzi
CRA-GPG, Genomics Research Centre, Fiorenzuola d'Arda, Italy

e-mail: valeria.terzi@entecra.it

Barley is predominantly self-pollinated, even though much of its pollen is released only after the anthers have been exerted; this is because the stigmas become receptive before anther exertion and are able to capture sufficient self pollen not to require fertilization by windborne nonself pollen. The exertion of the anthers is so pronounced in some wild barleys that their rate of outcrossing is higher than that of cultivated barley.

Natural variants of barley have been described in which the palea and lemma remain tightly closed throughout the period of pollen release. Such closed flowering is known as cleistogamy. The size of the lodicule in the cleistogamous flower is typically smaller than that in the noncleistogamous type. The cleistogamous state in barley is recessive, under the control of a single gene at the *cleistogamy 1 (cly1)* locus, which maps to the long arm of chromosome 2H.

Nair *et al.*, 2010 have isolated *cleistogamy 1 (Cly1)* by positional cloning and show that it encodes a transcription factor containing two AP2 domains and a putative microRNA *miR172* targeting site, which is an ortholog of *Arabidopsis thaliana AP2*. The expression of *Cly1* was concentrated within the lodicule primordia. They conclude that the *miR172*-derived down-regulation of *Cly1* promotes the development of the lodicules, thereby ensuring noncleistogamy, although the single nucleotide change at the *miR172* targeting site results in the failure of the lodicules to develop properly, producing the cleistogamous phenotype.

On this subject Brown and Bregitzer, 2011 demonstrated that *Ds-miR172* mutants show abnormal spikelets development including the conversion of glumes to partially developed florets in apical regions of spikes. Basal regions of the spike show an abnormal branching phenotype resulting from indeterminate spikelet meristem development, with each branch consisting of multiple, abnormal spikelets and other floral organs in place of a single spikelet. This phenotype is similar to *ts4* in maize, the only other known mutation affecting a *miR172* ortholog.

Barley possesses three single-flowered spikelets at each node (meristematic junction) of the rachis, with the three spikelets produced alternately on opposite sides. When all three spikelets

are fertile, the spike (inflorescence) appears to have six rows of grains, but if the two outer lateral spikelets at each node are sterile, then the spike is two rowed. The two-rowed state is ancestral, being found in the wild progenitor of cultivated barley (*Hordeum vulgare* ssp. *spontaneum*), where the sterile spikelets form part of the seed dispersal mechanism. The development of six-rowed spikes is controlled by *VRS1*, a homeodomain-leucine zipper I-class homeobox gene on barley chromosome 2H, which is also associated with differences in plant architecture, in particular, the amount of tillering (basal branching), where a reduction in the number of tillers per plant and thus spikes per plant largely compensates for the increase in number of grains per spike. The wildtype *Vrs1.b* allele encodes a transcriptional repressor that inhibits the development of fertile lateral spikelets and results in a two-rowed phenotype. Loss of function of *VRS1* has occurred independently several times during barley domestication and results in the complete conversion of the sterile laterals into fully developed fertile spikelets.

Mutation studies conducted in cultivated two-rowed barley show that the phenotypic effect of *Vrs1.b* can be modified by up to ten independent *INTERMEDIUM* (*INT*) genes distributed throughout the barley genome that, when homozygous, generate either a partial or a complete six-rowed phenotype. Furthermore, natural quantitative variation in the size and fertility of the lateral spikelets has also been observed, particularly in progenies of two- by six-rowed crosses. Genetic studies indicate that this quantitative variation is largely due to the effect of alleles of *INT-C* on chromosome 4H. *Int-c.a* in two-rowed cultivars (*Vrs1.b*, *Int-c.a*) causes enlarged, partially male fertile, lateral spikelets. This intermediate state between the standard two- and six-rowed forms is characteristic of the Intermedium phenotype. *INT-C* is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1* (*TBI*) and identifies 17 coding mutations in barley *TBI* correlated with lateral spikelet fertility phenotypes (Ramsay *et al.*, 2011).

Spike morphology is associated with row type, grain density, spike length and grain number and is a target of central importance in crop improvement. Indeed, breeding for ideal plant architecture (IPA) has been proposed as a means to enhance the yield potential of existing elite varieties.

Spike density in barley is under the control of several major genes, as documented previously by genetic analysis of a number of morphological mutants. One such class of mutants affects the rachis internode length leading to dense or compact spikes and the underlying genes were designated *dense spike* (*dsp*).

The gene was allocated by high-resolution bi-parental mapping to a 0.37 cM interval between markers SC57808 (*Hv_SPL14*)–CAPSK06413 residing on the short and long arm at the genetic centromere of chromosome 7H, respectively. This region putatively contains more than 800 genes as deduced by comparison with the collinear regions of barley, rice, sorghum and *Brachypodium*, Classical map-based isolation of the gene *dsp.ar* thus will be complicated due to the unfavorable relationship of genetic to physical distances at the target locus (Shahinnia *et al.*, 2012). In the same position of *dsp.ar* Taketa *et al.*, 2011 have mapped *dsp.1*. The same Authors have positioned *lks.2* (short awns) on chromosome 7. Positional cloning of *lks.2* is in progress.

The spike morphology variation among wild *Hordeum* species - *H. spontaneum*, *H. pusillum*, *H. murinum* and *H. bulbosum* – as well as the evolution of the barley six-rowed spike based on the

effect of HD-ZIP transcription factor are described by Sakuma *et al.* (2011). In addition mutants of the ear are also described in the paper by Saisho and Takeda, 2011.

A novel locus *thresh-1*, derived from *Hordeum spontaneum*, which controls threshability, has been identified and mapped on chromosome 1H. The recessive wild barley allele confers a difficult to thresh phenotype, suggesting that *thresh-1* played an important role during barley domestication. Using a S42IL-HR population, *thresh-1* was fine-mapped within a 4.3cM interval that was predicted to contain candidate genes involved in regulation of plant cell wall composition. The set of wild barley introgression lines and derived high-resolution populations are ideal tools to speed up the process of mapping and further dissecting QTL, which ultimately clears the way for isolating the genes behind QTL effects (Schmalenbach *et al.*, 2011).

NGS Illumina platform is routinely used to exploit induced variation and to dissect quantitative traits. Extensive and well-characterized collections of ear morphological and developmental mutants have been assembled that represent a valuable resource for exploring a wide range of complex and fundamental biological processes, with the final aim to explore the potential of mutants in crop improvement (Druka *et al.*, 2010, 2011).

References

- Brown, R. H. and P. Bregitzer. 2011.** A *Ds* Insertional Mutant of a Barley *miR172* Gene. Results in Indeterminate Spikelet Development. *Crop Science* 51: 1664-1672.
- Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, J. Guzy-Wrobelska, L. Ramsay, I. Druka, I. Grant, M. Macaulay, V. Vendramin, F. Shahinnia, R. Radoic, K. Houston, D. Harrap, B. Thomas, L. Cardle, D. Marshall, M. Morgante, N. Stein, and R. Waugh. 2010.** Exploiting induced variation to dissect quantitative traits in barley. *Biochem Soc Trans* 38: 683–688.
- Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011.** Genetic Dissection of Barley Morphology and Development. *Plant Physiology* 155: 617–627
- Nair, S. K., N. Wang, Y. Turuspekov, M. Pourkheirandish, S. Sinsuwongwat, G. Chen, M. Sameri, A. Tagiri, I. Honda, Y. Watanabe, H. Kanamori, T. Wicker, N. Stein, Y. Nagamura, T. Matsumoto, and T. Komatsuda. 2010.** Cleistogamous flowering in barley arises from the suppression of microRNA-guided *HvAP2* mRNA cleavage. *PNAS* 107 (1): 490–495.
- Ramsay, L., J. Comadran, A. Druka, D.F. Marshall, W.T.W. Thomas, M. Macaulay, K. MacKenzie, C. Simpson, J. Fuller, N. Bonar, P.M. Hayes, U. Lundqvist, J.D. Franckowiak, T.J. Close, G.J. Muehlbauer, and R. Waugh. 2011.** *INTERMEDIUM-C*, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1*. *Nature Genetics* 43: 169-173.

- Saisho, D. and K. Takeda. 2011.** Barley: Emergence as a New Research Material of Crop Science. *Plant Cell Physiol* 52(5): 724–727
- Sakuma, S., B. Salomon, and T. Komatsuda. 2011.** The Domestication Syndrome Genes Responsible for the Major Changes in Plant Form in the Triticeae Crops. *Plant Cell Physiol* 52(5): 738–749.
- Schmalenbach, I., T.J. March, T. Bringezu, R. Waugh, and K. Pillen. 2011.** High-Resolution Genotyping of Wild Barley Introgression Lines and Fine-Mapping of the Threshability Locus *thresh-1* Using the Illumina GoldenGate Assay. *G3* 1: 187-196.
- Shahinnia, F., A. Druka, J. Franckowiak, M. Morgante, R. Waugh, and N. Stein. 2012.** High resolution mapping of *Dense spike-ar* (*dsp.ar*) to the genetic centromere of barley chromosome 7H. *Theor Appl Genet* 124:373–384.
- Taketa, S., T. You, Y. Sakurai, S. Miyake, and M. Ichii. 2011.** Molecular mapping of the short awn 2 (*lks2*) and dense spike 1 (*dsp1*) genes on barley chromosome 7H. *Breed Sci* 61:80

Coordinator's report: Semidwarf genes

Jerry 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 new mutant at the *uzu 1* (*uzu1*) locus in chromosome 3H was identified by Gruszka *et al.* (2011). The mutant 093AR was selected after a mutagenic treatment of seeds of the cv. Aramir with N-methyl-N-nitrosourea. Under field conditions in Poland, plant height in both the 093AR and an *uzu* line was reduced by about 30%. Gruszka *et al.* (2011) found two base pair substitutions in the DNA sequence of barley *HvBR11* gene, encoding leucine-rich repeats receptor kinase (LRR-RK), which participates in brassinosteroid (BR) signaling. These substitutions are at a different position in *HvBR11* gene than the substitution reported by Chono *et al.*, 2003.

The semidwarf, brittle stem mutants, *fst2* (fragile stem 2) alleles, were shown to have reduced levels of crystalline cellulose in their culms compared with their parental lines (Kokubo *et al.*, 1991). The maximum flexural load (Newtons) required to bend the midpoint of each internode was 2 to 3 times lower for the mutants compared to their parents (Kokubo *et al.*, 1991; Burton *et al.*, 2010). A custom-designed microarray used by Burton *et al.*, 2010 revealed a marked decrease in the transcript levels of mRNA for the *HvCesA4* cellulose synthase gene. Sequencing of the *HvCesA4* gene revealed the presence of a 964-bp solo long terminal repeat of a Copia-like retroelement in the first intron of the *HvCesA4* gene, which interferes with transcription of or processing of the mRNA from the *HvCesA4* gene (Burton *et al.*, 2010).

Malosetti *et al.*, 2011 advocated using mixed models including genetic relatedness, or 'kinship' information for QTL detection in populations where selection forces operated. The model used detected fewer QTL and likely provided fewer false detections. From a three way cross, Candela/915006//Plaisant, 161 recombinant inbred lines were selected for study. Candela and Plaisant contributed the semidwarf 1 (*sdw1*) gene and line 915006 contributed the brevistaratum-e (*ari-e.GP*) gene, which produced QTL peaks associated with SNP markers 1_0867 on 3H and 2_1239 on 5H, respectively. Two additional plant height QTL having major effects on plant height were identified on 2H and 7H, associated with SNP marker 1_0191 and 2_0307, respectively (Malosetti *et al.*, 2011). Candela and Plaisant were donors of QTL for reduced height at both of these locations.

A newly developed sequence-based marker technology, Restriction site Associated DNA (RAD), which enabled synchronous single nucleotide polymorphism (SNP) marker discovery and genotyping using massively parallel sequencing, was used to study the Oregon Wolfe Barley (OWB) population (Chutimanitsakun *et al.*, 2011). The marker orders in the new map were similar to older maps for the OWB population. One semi-dwarfing gene, Zeocriton 1 (*Zeo1*), and

the six-rowed spike 1 (*vrs1*) gene were associated height, spike length, kernels per spike, 100-kernel weight, and grain yield. Unfavorable alleles were contributed by R.I. Wolfe's Master Dominant Marker Stock, a semidwarf with short, two-rowed spikes (*Zeol.a* and *Vrs1.t*).

Polok and Zieinski, 2011 visualized the gain and the loss of transposon insertion sites following mutagenic treatment of the cultivars, Brenda and Scarlett. Activities of *BARE-1* retrotransposon and *Tpo1*-like DNA transposon from the CACTA superfamily were analyzed in ten barley mutants. The result suggested the parents and mutant lines can not considered near-isogenic lines. Differences existed among both cultivars and transposons for transposon activities and morphology suggesting different mechanisms shaped the mutant architecture. *BARE-1* was mainly responsible for new insertions while the *Tpo1*-like caused equally insertions and deletions. Some of the morphological difference among the 10 lines studied included plant height.

References:

- Burton, R.A., G. Ma, U. Baumann, A.J. Harvey, N.J. Shirley, J. Taylor, F. Pettolino, A. Bacic, M. Beatty, C.R. Simmons, K.S. Dhugga, J.A. Rafalski, S.V. Tingey, and G.B. Fincher. 2010.** A customized gene expression microarray reveals that the brittle stem phenotype fs2 of barley is attributable to a retroelement in the HvCesA4 Cellulose Synthase Gene 1. *Plant Physiol.* 153:1716-1728.
- Chutimanitsakun, Y., R.W. Nipper, A. Cuesta-Marcos, L. Cistué, A. Corey, T. Filichkina, E.A Johnson, and P.M. Hayes. 2011.** Construction and application for QTL analysis of a Restriction Site Associated DNA (RAD) linkage map in barley. *BMC Genomics* 2011 12. :4 doi:10.1186/1471-2164-12-4 at: <http://www.biomedcentral.com/1471-2164/12/4>.
- Chono, M., I. Honda, H. Zeniya, K. Yoneyama, D. Saisho, K. Takeda, S. Takatsuto, T. Hoshino, and Y. Watanabe. 2003.** A semidwarf phenotype of barley uzu results from a nucleotide substitution in the gene encoding a putative brassinosteroid receptor. *Plant Physiol.* 133:1209-1219.
- Gruszka, D., I. Szarejko, and M. Maluszynski. 2011.** New allele of HvBRI1 gene encoding brassinosteroid receptor in barley. *J. Appl. Genet.* 52:257-268.
- Kokubo, A., N. Sakurai, S. Kuraishi, and K. Takeda. 1991.** Culm brittleness of barley (*Hordeum vulgare* L.) mutants is caused by smaller number of cellulose molecules in cell wall. *Plant Physiol.* 97:509-514.
- Malosetti, M., F.A. van Eeuwijk, M.P. Boer, A.M. Casas, M. Elía, M. Moralejo, P.R. Bhat, L. Ramsay, and J.-L. Molina-Cano. 2011.** Gene and QTL detection in a three-way barley cross under selection by a mixed model with kinship information using SNPs. *Theor. Appl. Genet.* 122:1605-1616.
- Polok, K., and R. Zieinski. 2011.** Mutagenic treatment induces high transposon variation in barley (*Hordeum vulgare* L.). *Acta Agric. Slovenica*, 97:179-188.