REPORTS OF THE COORDINATORS

Overall coordinator's report

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First of all I have to inform the barley community the sad news that our dear friend Robert (Bob) Nilan passed away in Pullman, Washington State, USA, October 7th, 2015, with him USA and the whole barley community has lost a pioneer within plant breeding and plant genetic research especially barley. One of his proudest achievements during his long career was the establishment of the International Barley Genetics Symposia (IBGS) that are still taking place. The first symposium was organized 1963, in Wageningen, the Netherlands, but the second IBGS, Bob had the pleasure and opportunity to organize himself in Pullman, USA, 1969. He could participate in 10 of the symposia, but unhappily he was not able to make it to the eleventh in China, 2012, because of health troubles. He greatly contributed to establish the Barley Genetics Newsletter where the first issue appeared in 1971 and with this issue BGN has been published for 45 years. You can read more in the memorium written in this BGN 45:1-3.

In a few weeks the 12th International Barley Genetic Symposium will take place in Minneapolis, in the midwest of the United States, June 26-30, 2016. I do hope that many of the barley community people have the possibility to participate in this important event. Like in the last symposium in Hangzhou, China, 2012, a workshop on "Barley Genetic stocks, there Use and Potential" will be organized Tuesday evening, June 28th. Several important topics will be discussed, i.e. Developmental Mutants in Barley, Characterization and Use. The future of publishing Barley Genetics Newsletter will be a very important discussion topic. There will not be a special workshop for the coordination for several important barley mutant collections as we had in previous meetings, these discussions will get included in the above mentioned workshop as a special topic.

Since the last overall coordinator's report in BGN 44 not too many exciting news have happened. Again, no research report has been received for this issue. Once again I want to stress the importance of publishing short research notes after having been published in high level journals. The barley community should gain very much what different barley research groups are working on and receiving new results to investigate the whole barley genome.

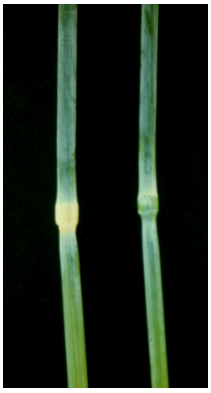
In this volume, BGN 45, again one hundred and twenty-two stock descriptions are described, revised or updated with latest research results and citied literature. They are listed in table 1, additionally also tables 2 and 3, with BGS numbers in order (table 2) and in alphabetic order of the recommended locus names and symbols (table3) are again published to make it easy for barley researchers to find gene descriptions. The construction of the 'International Database for Barley Genes and Barley Genetic Stocks' is happily proceeding fast and will be presented in a modern and easy to handle version. Hopefully it will be ready for demonstration at the IBGS in June 2016..

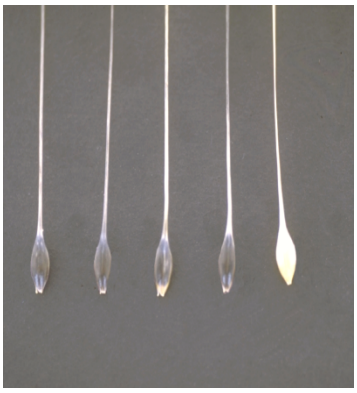
Some different barley genetic stock characters.







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Barley Genetic Stocks (GSHO – Genetic Stocks (*Hordeum*) in the USDA-ARS National Small Grains Collection

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GSHO Distributions – January 1, 2015 to March 24, 2016.
A total of 1,115 GSHO accession samples were distributed in 63 separate requests to scientists in 10 countries (Australia, China, Czech Republic, Germany, Japan, Republic of Korea, Morocco, Poland, United Kingdom, and United States).

Voucher Images
High resolution scans of kernels of most GSHO accessions have been attached to the accession records as voucher images. They are viewable on the GRIN-Global search page: https://npgsweb.ars-grin.gov/gringlobal/search.aspx

New Accessions
Dr. Andris Kleinhofs has donated additional mutant stocks and GSHO numbers have been assigned as follows.

Table 1.

GSHO Number	Mutant name	Symbol
3671	Multiovary 5.o	mov5.o
3672	Multiovary 4.m	mov4.m
3673	Multiovary.n	mov.n
3674	Short awn 6.q	lks6.q
3675	Unbranched style 5.e	ubs 5.e
3676	Unbranched style 5.f	ubs5.f
3677	Uniculme 3.m	cul3.m
3678	Low number of tillers 1.b	Int1.b
3679	Waxy spike 1.b	wxs1.b
3680	Waxy spike 1.c	wxs1.c
3681	Waxy spike 1.d	wxs1.d
3682	Albino lemma 1.d	alm1.d

Table 1 continued.

GSHO number	Mutant name	Symbol
3683	Albino lemma 1.e	alm1.e
3684	Fenoxaprop-p-ethyl reaction 1	fxp1
3685	Single internode dwarf 1.c	sid1.c
3686	Many noded dwarf 7.h	mnd7.h
3687	Ovaryless 3.c	ovl3.c
3688	Male sterile genetic.ou	msg.ou
3689	Male sterile genetic.ov	msg.ov
3690	Male sterile genetic.ow	msg.ow
3691	Male sterile genetic.ox	msg.ox
3692	Male sterile genetic.oy	msg.oy

Coordinator's report: Translocations and balanced tertiary trisomics

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The 3HS.3BL spontaneous Robertsonian translocation obtained from the progenies of wheat-barley (Chinese Spring x Betzes) hybrids backcrossed with wheat line Mv9kr1 was transferred into the modern Martonvasar wheat cultivar Mv Bodri by Tukosi *et al.* (2014). The translocation was identified with molecular cytogenetic methods. Fluorescence in situ hybridization using barley subtelomeric (HvT01) and centromere-specific [(AGGGAG)4] repetitive DNA probes confirmed that the complete barley chromosome arm was involved in the Robertsonian translocation. The wheat-specific repetitive DNA probes identified the presence of the whole wheat genome, except the short arm of the 3B chromosome. Genotypes homozygous for the centric fusion were selected, after which morphological analysis was performed on the plants and the yield components were measured in the field during two consecutive vegetative seasons. The introgression of the 3HS.3BL translocation into the modern wheat cultivar Mv Bodri significantly reduced the plant height due to the incorporation of the dwarfing allele RhtD1b. The presence of the 3HS.3BL translocation in the Mv9kr1 and Mv Bodri wheat background improved tillering and seeds per plant productivity in field experiments carried out in Martonvasar and Keszthely, Hungary.

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:

Turkosi E, A. Farkas, N:R. Aranyi, B. Hoffmann, V. Toth, and M. Molnar-Lang. (2014) Improvement of the agronomic traits of a wheat-barley centric fusion by introgressing the 3HS.3BL translocation into a modern wheat cultivar. Genome 57 (11-12):601-607.

Coordinator's Report: Desynaptic Genes

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The status of this genetic stock collection described in BGN 42 did not change.
No work was published describing the application of one of the desynaptic mutants.

However, a novel method suitable to quantify recombination events in barley was described by Dreissig *et al.* (2015). The authors investigated the feasibility of using flow-sorted haploid nuclei, Phi29 DNA polymerase-based whole-genome-amplification (WGA) and multi-locus KASP-genotyping to measure meiotic crossovers in individual barley pollen grains. To demonstrate the proof of concept, 24 gene-based physically mapped single nucleotide polymorphisms were used to genotype the WGA products of 50 single pollen nuclei. The number of crossovers per chromosome, recombination frequencies along chromosome 3H and segregation distortion were analysed and compared to a doubled haploid (DH) population of the same genotype. The number of crossovers and chromosome wide recombination frequencies show that this approach is able to produce results that resemble those obtained from other methods in a biologically meaningful way. Only the segregation distortion was found to be lower in the pollen population than in DH plants.

In many cereal crops, meiotic crossovers predominantly occur toward the ends of chromosomes and 30 to 50% of genes rarely recombine. This limits the exploitation of genetic variation by plant breeding. Previous reports demonstrate that chiasma frequency can be manipulated in plants by depletion of the synaptonemal complex protein ZIPPER1 (ZYP1) but conflict as to the direction of change, with fewer chiasmata reported in Arabidopsis thaliana and more crossovers reported for rice. Barakate *et al.* (2014) used RNA interference (RNAi) to reduce the amount of ZYP1 in barley to only 2 to 17% of normal zygotene levels. In the ZYP1(RNAi) lines, fewer than half of the chromosome pairs formed bivalents at metaphase and many univalents were observed, leading to chromosome nondisjunction and semi-sterility. The number of chiasmata per cell was reduced from 14 in control plants to three to four in the ZYP1-depleted lines, although the localization of residual chiasmata was not affected. DNA double-strand break formation appeared normal, but the recombination pathway was defective at later stages. A meiotic time course revealed a 12-h delay in prophase I progression to the first labeled tetrads. Barley ZYP1 appears to function similarly to ZIP1/ZYP1 in yeast and Arabidopsis, with an opposite effect on crossover number to ZEP1 in rice, another member of the Poaceae.

The process of meiosis results in the formation of haploid daughter cells, each of which inherit a half of the diploid parental cells' genetic material. The ordered association of homologues (identical chromosomes) is a critical prerequisite for a successful outcome of meiosis. Homologue recognition and pairing are initiated at the chromosome ends, which comprise the telomere dominated by generic repetitive sequences, and the adjacent subtelomeric region, which harbours chromosome-specific sequences. In many organisms telomeres are responsible for bringing the ends of the chromosomes close together during early meiosis, but little is known regarding the role of the subtelomeric region sequence during meiosis. Calderon Medel *et al.* (2014) report the

observation of homologue pairing between a pair of *Hordeum chilense* chromosomes lacking the subtelomeric region on one chromosome arm indicates that the subtelomeric region is important for the process of homologous chromosome recognition and pairing.

Phillips *et al.* (2015) work examines whether crossovers can be shifted to more proximal regions simply by elevating growth temperature. We utilised a genome-wide marker set for linkage analysis combined with cytological mapping of crossover events to examine the recombination landscape of plants grown at different temperatures. We found that barley shows heterochiasmy, that is, differences between female and male recombination frequencies. In addition, we found that elevated temperature significantly changes patterns of recombination in male meiosis only, with a repositioning of Class I crossovers determined by cytological mapping of HvMLH3 foci. We show that the length of synaptonemal complexes in male meiocytes increases in response to temperature. The results demonstrate that the distribution of crossover events are malleable and can be shifted to proximal regions by altering the growth temperature. The shift in recombination is the result of altering the distribution of Class I crossovers, but the higher recombination at elevated temperatures is potentially not the result of an increase in Class I events (Phillips *et al* 2015).

References:

Barakate A, J.D. Higgins, S. Vivera, J. Stephens, R.M. Perry, L. Ramsay, I. Colas, H. Oakey, R. Waugh, F. C.Franklin, S.J. Armstrong, and C. Halpin. **2014**. The synaptonemal complex protein ZYP1 is required for imposition of meiotic crossovers in barley. Plant Cell 26 (2):729-740. doi:10.1105/tpc.113.121269.

Calderon Mdel C, M. D. Rey, A. Cabrera, and P. Prieto. 2014. The subtelomeric region is important for chromosome recognition and pairing during meiosis. Scientific reports 4:6488. doi:10.1038/srep06488.

Dreissig S, J. Fuchs, P. Capal, N. Kettles, E. Byrne, and A. Houben. 2015. Measuring Meiotic Crossovers via Multi-Locus Genotyping of Single Pollen Grains in Barley. Plos One 10 (9). doi:ARTN e0137677.

Phillips D, G. Jenkins, M. Macaulay, C. Nibau, J. Wnetrzak, D. Fallding, I. Colas, H. Oakey, R. Waugh, and L. Ramsay. 2015. The effect of temperature on the male and female recombination landscape of barley. New Phytol 208 (2):421-429. doi:10.1111/nph.13548.

Coordinator's report: *Eceriferum* genes

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Presence of wax coating and its composition is an important feature of the barley plant. It reduces evaporation of water from the plant and helps protect it against pathogens. The waxless *Eceriferum* and glossy mutants affect the presence and type of epicuticular waxes on the different organs. Many different surface wax mutants have been isolated as induced or spontaneous mutants and much research has been done during the last century both genetically and biochemically. All 79 defined loci are published as descriptions in Barley Genetics Newsletter (BGN) 42, later issues and some of them also updated in this volume. All descriptions are valid and up-to-date.

One allele of all the 79 gene loci have been backcrossed to a common genetic background the cultivar 'Bowman' by J.D. Franckowiak, USA. They are available as Near Isogenic Lines (NIL) at the Nordic Genetic Resource Centre (NordGen), Sweden, www.nordgen.org and at the Small Grain Germplasm Research Facility (USDA–ARS), Aberdeen, ID 83210, USA, nsgchb@ars-grin.gov. But be aware of that many of the lines are a more advanced backcross derived line incorporated at NordGen than those at the Small Grain Research Facility in Aberdeen. The material in Sweden is well phenotyped and gets regenerated continuously.

Since the 1970s three with the highest numbers of alleles in the *Eceriferum* genes, *cer-c*, *cer-q* and *cer-u* with 215, 167 and 160 alleles, respectively, located in chromosome 2HS, very tightly linked, are discussed intensively. These genes affect the epicuticular wax coating on the spike and leaf sheath. They have been of large interest all the time. Intensive discussions were going on if it is one cluster gene, *cer-cqu*, or three different ones. Among all allele tested mutants in this region 13 were found to be multiple ones, among them 7 triple mutants. Mutations reverting in one step to wax formation have also occurred.

Schneider *et al*. (2016) report that recently developed genomic resources and mapping populations in barley defined the cluster gene *cer-cqu* to a small region on chromosome arm 2HS. Sequencing more than 50 independent mutants for each gene confirmed their identification. *Cer-c* is a chalcone synthase-like polyketide synthase, designated diketone synthase. *Cer-q* is a chalcone/carboxyl transferase and *Cer-u* is a P450 enzyme. A physical map revealed the order *Cer-c*, *Cer-u* and *Cer-q* with the flanking genes 101kb apart, confirming that they are a gene cluster, *Cer-cqu*. Homology-based modeling suggests that many of the mutant alleles affect overall protein structure or specific active site residues. By constructing several F2 mapping populations between the Near Isogenic Lines (NIL) BW 409 (*gsh6.s* allele, a mutation in the *cer-c* gene), BW 404 (*gsh1.a*, an allele in the *cer-q* gene) and BW 411 (*gsh8.ag*, an allele in the *cer-u* gene) and several cultivars defined in this SNP marker analyses the location of *Cer-c, Cer-q* and *Cer-u* to an interval flanked by distal marker 1_0718 and proximal marker 1_1059. After selecting candidate genes all results provide strong evidence that

MLOC_59804, *MLOC_13397* and *AK373499* encode *CER-C, -Q* and *U*, respectively. Thus the *cer-c* mutants that are caused by mutations in the CHS-like synthase encoded *MLOC_59804*, analysis of the mutants across the *MLOC_13397* model supports that *cer-q* encodes a lipase, and finally analysis supports the conclusion that *AK373499* (*Cer-u*) encodes a cytochrome *P450*. Finally the conclusion stated that *cer-c, cer-q* and *cer-u* are three different independent gene loci but very closely linked.

Li, Chao et al. (2015) reported on the characterization of epicuticular wax coating and genetic mapping of the *eceriferum-ym* (*cer-ym*) locus. The *cer-ym* mutant showed abnormally strong glossy spikes, sheaths and leaf blades. The mutant leaves showed a substantial reduction in the amounts of the major cutin monomers and a high increase in the main wax component. It is a semi-dwarf phenotype, a cutin defective mutant and is similar to the phenotype of Bowman-Near Isogenic line carrying the *cer-zv.268* allele, known as a cuticular recessive mutant. Analysis of Bowman-Near isogenic line BW 144 (*cer-ym.753*) compared with its wild barley accession 'OUH602' mapped the gene to chromosome 4H, co-segregated with AK364461 which is a marker that co-segregates with *cer-zv* in the pericentromeric region. *Cer-ym* was mapped within a 0.8 cm interval between EST marker AK370363 and AK251484. In conclusion *cer-ym* is located on chromosome 4H in the pericentromeric region which is very important for cuticle development.

Li, C. *et al*. (2012) reports on cuticle-associated genes that are protected by a cuticle against abiotic and biotic stresses. A better understanding of the determination of cuticle formation and function has the potential to contribute to the breeding of more drought tolerant and disease resistant crop cultivars. It was suggested by microarray analysis that some barley homologs have expression in epidermis of elongation zone of leaves where wax synthesis happens. The research demonstrates to facilitate the cloning of such genes. They found a case of complete linkage between an *eceriferum* (*cer*) locus and a known cuticle-associated gene: *HvCER6* of *Arabidopsis thaliana* and *eceriferum-zg* (*cer-zg*). This gene is affecting the epiticular wax coating on the leaf blades but reduced and only on the three upper leaves. It is located on chromosome 4H. *CER6* encodes an elongase condensing enzyme involved in the synthesis of very long chain fatty acid precursors. The data show therefore suggestive that *CER-ZG* might be the homolog of *AtCER6*. The phenotypes of *atcer6* and *cer-zg* mutants were similar to one another, therefore they suggest that *HvCER6* is the candidate gene of *CER-ZG*.

References:

Li, C., X. Ma, A. Wang, E. Nevo, and G. Chen. 2012. Genetic Mapping of Cuticle-associated Genes in Barley. Cereal Research Communications. DOI: 10.1556/CRC.2012.0020.

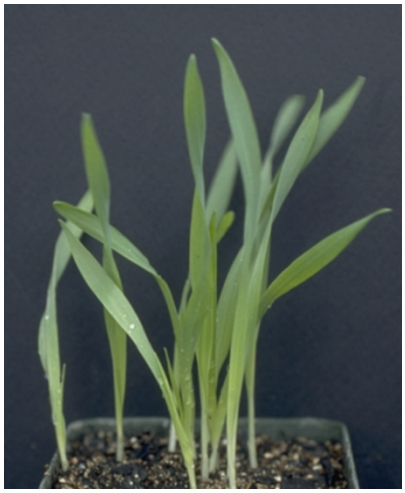
Li, Chao, Ch. Liu, X. Ma, A. Wang, R. Duan, Ch. Nawrath, T. Komatsuda, and G. Chen. 2015. Characterization and genetic mapping of *eceriferum-ym (cer-ym)*, a cutin deficient barley mutant with impaired leaf water retention capacity. Breeding Science 65:327-332.

Schneider, L M., N. M. Adamski, C.E. Christensen, D. B. Stuart, S. Vautrin, M. Hansson, C. Uauy, and P. von Wettstein-Knowles. 2016. The Cer-cqu gene cluster determines three players in a β-diketone synthase polyketyde pathway synthesizing aliphatics in epicuticular waxes. Journal of Experimental Botany Advance Access. Doi:10.1093/jxb/erw105.

BW404 (*gsh1.a*) mutant to the left compared with cultivar Bowman

BW409 (*gsh6.s*) to the left compared with cultivar Bowman

Eceriferum-zg (*cer-zg*) leaf blade to the left compared with cultivar Bowman



BW 144 (*cer-ym.753*) mutant to the left compared with cultivar Bowman, showing water drops on seedlings

Coordinator´s Report: Disease and Pest resistance genes

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In the table below you will find papers published in 2015 extending last year´s list of information available on molecular markers for major resistance genes in barley published in Barley Genetics Newsletter 44.

List of papers published on mapped major resistance genes in barley updated until December 21, 2015

Resistance gene	Chromsomal location	Reference(s)
Puccinia graminis		
Rpg5	5H	Dracatos et al. 2015b, Mamo et al. 2015
rpg4	5H	Mamo et al. 2015
Puccinia hordei		
Rph3	7H	Gutiérrez et al. 2015
Rph20	5H	Dracatos et al. 2015a
Rph22	2H	Johnston et al. 2015
Rph23	7H	Singh et al. 2015, Dracatos et al. 2015a
Rynchosporium commune		
Rrs1	3H	Looseley et al. 2015
Pyrenophora teres		
Rpt4	7H	Tamang et al. 2015
Rpt6	5H	Tamang et al. 2015
Rpt7		Tamang et al. 2015
Ustilago nuda		
Un8	1H	Zang et al. 2015
Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV)		
Rym16^{Hb}	2H	Johnston et al. 2015

References:

Dracatos, P., D. Singh, U. Bansal, and R.F. Park, 2015a. Identification of new sources of adult plant resistance to *Puccinia hordei* in international barley (*Hordeum vulgare* L.) germplasm. Eur J Plant Pathol 141: 463-476.

Dracatos, P., D. Singh, T. Fetch, and R. Park, 2015b. Resistance to *Puccinia graminis f.sp avenae* in barley is associated with the Rpg5 Locus. Phytopathology105: 490-494.

Gutiérrez, L., S. Germán, P.M. Hayes, C.A. Pérez, F. Capettini, A. Locatelli, N.A. Berberian, E.E. Falconi, R. Estrada, D. Fros, V. Gonza, H. Altamirano, J. Huerto-Espino, E. Neyra, G. Orjeda, S. Sandoval-Islas, R. Singh, K. Turkington, and A.J. Castro, 2015. Multi-environment multi-QTL association mapping identifies disease resistance QTL in barley germplasm from Latin America. Theor. Appl Genet 128: 501-516.

Johnston, P.A., V. Meiyalaghan, M.E. Forbes, A. Habekuss, R.C. Butler, and R. Pickering, 2015. Marker assisted separation of resistance genes *Rph22* and *Rym16^{Hb}* from an associated yield penalty in a barley: *Hordeum bulbosum* introgression line. Theor Appl Genet 128: 1137-1149.

Looseley, M.E., R. Keith, D. Guy, G. Barral-Baron, A. Thirugnanasabandam, D. Harrap, P. Werner, and A.C. Newton, 2015. Genetic mapping of resistance to Rhynchosporium commune and characterization of early infection in a winter barley mapping population. Euphytica 203: 337-347.

Mamo, B.E., K.E. Smith, R.S. Brueggeman, and B.J. Steffenson, 2015. Genetic characterization of resistance to wheat stemm rust race TTKSK in landrace and wild barley accessions identifies the rpg4/Rpg5 locus. Phytopathology 105: 99-109.

Singh, D., P. Dracatos, L. Derevnina, M. Zhou, and R.F. Park, 2015. *Rph23*: A new designated additive adult plant resistance gene to leaf rust in barley on chromosome 7H. Plant Breeding 134: 62-69.

Tamang, P., A. Neupane, S. Mamidi, T. Friesen, and R. Brueggeman, 2015. Association mapping of seedling resistance to spot form net blotch in a world wide collection of barley. Phytopathology 105: 500-508.

Zang, W., P.E. Eckstein, M. Colin, D. Voth, A. Himmelbach, S. Beier, N. Stein, G.J. Scoles, and A.D. Beattie, 2015. Fine mapping and identification of a candidate gene for the barley Un8 true loose smut resistance gene. Theor Appl Genet 128: 1343-1357.

Coordinator's report: Nuclear genes affecting the chloroplast

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Barley chlorophyll mutants have been named *albina*, *xantha*, *viridis*, *chlorina*, *tigrina* and *striata* depending on their colour and colour pattern. In the *albina* mutants the leaves are completely white due to lack of both chlorophyll and carotene pigments. The *xantha* mutants are yellow and produce carotene, but no chlorophyll. The *chlorina* and *viridis* mutants are both pale green, but differ in *chlorina* being viable. The *tigrina* and *striata* mutants are stripped transverse and along the leaves, respectively.

The fifth ring of the chlorophyll molecule is formed by the cyclase, which is the least known enzyme in the chlorophyll biosynthetic pathway. So far, only one subunit has been identified, encoded by *Xantha-l* in barley. Staccanella et al. (2015) used Arabidopsis mutants as well as the barley mutants *viridis-k.23*, *viridis-k.170*, *viridis-zb.63* and *xantha-l.35* to suggest that plastoquinol might function as an electron donor for the cyclase reaction.

Barley mutant *chlorina-f.104* was explored in a study concerning a chloroplastic protein with an NmrA domain, cpNrp (Brestic *et al*. 2015). The NmrA domain serves as a receptor for oxidized NAD^+/$NADP^+$ and the ability to discriminate between their oxidized and reduced forms may be linked to a possible role in redox sensing. The mutant *chlorina-f.104* shows a modified structure of the light-harvesting antennae and offered a useful system to examine the factors that determine the photosynthetic performance in leaves (Brestic *et al*. 2015). It was suggested that cpNrp is a member of a new protein family and can serve as a chloroplastic redox receptor.

The stock list of barley mutants defective in chlorophyll biosynthesis and chloroplast development is found in Barley Genetics Newsletter issue 37 (2007): 37-43. Seeds of most mutants listed can be obtained from Mats Hansson (http://www.biology.lu.se/mats-hansson).

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Coordinator's report: Early maturity and Praematurum genes

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The demand for early maturity in barley has become an important goal for plant breeding during the last century. Time of flowering has an important impact on yield and has been a key trait in the domestication of crop plants worldwide. Early maturity material has been collected in different geographic regions and climate conditions, today a critical issue in times of global warming. Many different *early maturity* and *Praematurum* mutants are isolated in many different cultivars, and they are stored in Gene banks in several parts of the world. Only in Scandinavia about 1250 different mutants have been isolated, their phenotypes described, analysed genetically and used in plant breeding worldwide. The *Praematurum* mutants are grouped into three categories according to their heading and maturity time with a variation between one and ten days: (1) drastically altered earliness; (2) medium increase of earliness; (3) slightly modified earliness. Long term studies made it possible to identify 10 early maturity (*eam*) and 9 *Praematurum* (*mat*) loci, among them also day-length neutral ones. All identified gene loci are incorporated into a common background, the barley cultivar 'Bowman' by J.D. Franckowiak, USA, and he established Bowman backcross derived lines (Near Isogenic Lines, 'NIL'). All these early maturity lines are well phenotyped, documentated and long-time stored in NordGen, Alnarp, Sweden. They are very important and useful for intensive molecular studies, cloning genes and understanding the barley genome.

Cultivated barley (*Hordeum vulgare L. subsp. vulgare*), like most temperate cereal crops, is a long day plant with two growth types, spring and winter. The growth habit is determined by the interaction of two genes; *Vrn-H2*, a strong inhibitor of flowering under long day conditions and *Vrn-H1* (also known as *HvVRN1*). Phytochromes play an important role in light signalling and photoperiodic control of flowering time in plants. Pankin *et al.* (2014) reported mapping and sequencing a candidate gene for the *Early maturity 5* (*Eam5*) locus. The Bowman Near-Isogenic Line having the *Eam5* allele is early flowering under both short and long day conditions, and the genetic interaction with the major barley photoperiod response gene *Ppd-H1* were analysed. The *Eam5* gene was originally located on chromosome 5H and originated from an ICARDA/CYMMIT selection. They suggested that the red/far-red light photoreceptor HvPhytochrome C (*HvPHYC*) is a candidate underlying the *early maturity 5* locus. They fine mapped the gene using a mapping-by-sequencing approach applied on the whole-exome capture data from bulked early flowering segregates derived from the backcrossed-derived Bowman line. They show that the *Eam5* gene disrupts circadian expression of clock genes, it also interacts with the major photoperiod response gene *Ppd-H1* to accelerate flowering under non-inductive short days. They suggest that *HvPHYC* participates in transmission of light signals to the circadian clock and thus modulates light-dependent processes such as photoperiodic regulation of flowering.. It also showed that *HvPHYC* carried a nonsynonymous mutation in the NIL Bowman line for *Eam5* which causes the missense substitution that leads to a change of the hydrophobic phenylalanine to the hydrophilic serine (mutation F380S).

Therefore they proposed that *HvPHYC* as the candidate gene for *Eam5*. They also found according to their segregation analysis that both *Vrn-H1* and *HvPHYC* were tightly linked to the early flowering phenotype.

Nishida *et al.* (2013) reported on different flowering time genes. The spring-type near isogenic line (NIL) of the winter-type barley (*Hordeum vulgare ssp. vulgare*) var. Hayakiso 2 (HK2) was developed by introducing *VERNALIZATION-H1 (Vrn-H1*) for spring growth habit from a spring-type var. Indo Omugi. Contrary to expectations, the spring-type NIL line flowered later than winter-type HK2. They stated that this phenotype difference was controlled by a single gene, which co-segregated only with *phytochromeC (HvPhyC*) which is one of the candidates around the *Vrn-H1* region (*Vrn-H1, HvPhycC and CASEIN KINASE IIα*). That indicated that *HvPhyC* was the most likely candidate gene for flowering time. Compared with the late flowering allele *HvPhyC-l* from NIL, the early-flowering allele *HvPhyC-e* from HK2 had a single nucleotide polymorphism T1139C in exon 1, which caused a nonsynonymous amino acid substitution of phenylalanine at position 380 by serine in the functionally essential GAF domain. Functional assay using a rice (*Oryza sativa*) *PhyA phyC* double mutant line showed that both of the *HvPhyC* alleles are functional, but *HvPhyC-e* have a hyperfunction. Expression analyses using NILs carrying *HvPhyC-e* and *HvPhyC-l*, respectively, showed that *HvPhyC-e* up-regulated only the flowering promoter *FLOWERING LOCUS T1* by bypassing the circadian clock genes and flowering integrator *CONSTANS1* under a long photoperiod. There were no apparent differences in *HvPhyC* expression between NIL (*HvPhyC-e*) and NIL (*HvPhyC-l*), despite their allelic differences. In both of the NILs, *HvPHyC* was expressed all day and seemed to show diurnal fluctuation under both long and short photoperiod conditions with the trend that it was up-regulated around dusk and down-regulated during the day. They also stressed in addition to the above mentioned genes, novel gene resources for early flowering will be important to elucidate the genetic mechanism of the flowering time and future breeding programs. Recent comparative studies in genetic pathways for flowering revealed that temperate grass species share a similar gene set with dicot species *Arabidopsis*, especially for photoperiodic pathways.

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Coordinator's report: ear morphology genes

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Barley today ranks fourth behind wheat, rice and maize among the world's cereals for the importance of its contribution, whether direct or indirect, to the production of food. The global production is estimated in 2015 in 135 millions of metric tons (Mt) in a harvested area of 50 millions of hectares with an average grain yield of 2.7 t/ha.

Barley spike is one of the important source of food for humans and it has been estimated that barley production needs to increase to meet demand of increasing population. This means that the grain number of the barley spike must be improved in the near future, together with the biomass increase. As reported in previous Barley Genetic Newsletter (BGN) reports, grain number enhancement can be theoretically obtained through modifications of the spike fertility and morphology. Due to the implications in grain production and yield, the genetic dissection of the developmental plan of this storage sink is therefore of outstanding relevance to design the barley for the future in which innovative traits can be implemented through pre-breeding strategies.

Barley developmental mutants can be a Mendelian solution to identify genes controlling key steps in the establishment of the spike morphology. Large collections of natural and induced mutants have been developed since the 1920s, with the aim of understanding developmental and physiological processes and exploiting mutation breeding in crop improvement. The collections are comprehensive not only of single Mendelian spike mutants, but even of double and triple mutants obtained by intercrossing simple mutants. In recent years the integration of the most advanced omic technologies with the historical mutation-genetics research helped in the isolation and validation of some of the genes involved in spike development. Interestingly, some genes known from long time to be responsible for mutant phenotype have been recently cloned and functionally characters. Several of these genes are involved in mutations that, selected by ancient farmers, transformed wild plants in domesticated ones, giving a major contribution to the development of early agrarian societies. The most important trait selected by humans during the barley domestication process and related to the evolution of barley spike is the transformation of brittle into non-brittle spike. Loss of the natural mode of grain dispersal was perhaps the most important single event in this process. At maturity, the spike in wild (i.e. ancestral) barley forms ‘‘constriction grooves’’ and disarticulates at each rachis node, allowing mature grain to disperse freely. This phenotype is referred to as ‘‘brittle rachis.’’ Classical genetic studies have established that a mutation in either of two complementary and tightly linked genes on barley chromosome 3HS, Non-brittle rachis 1 (*btr1*) or Non-brittle rachis 2 *(btr2*), converts the brittle rachis into a non-brittle type. Pourkheirandish *et al*. (2015) identify *Btr1 and Btr2* genes and elucidate the mechanism underlying disarticulation of the wild-type barley spike. Independent recessive mutations in each of these genes caused cell wall thickening in a highly specific grain ‘disarticulation zone’, converting the brittle floral axis (the rachis) of the wild-type into a tough, non-brittle form that promoted grain retention.

The authors hypothize that anthropogenic selection operated in favor of mutations in two adjacent complementary dominant genes, the products of which are suggestive of a signal transducing receptor and its protein ligand. The two genes products, BRT1 and BRT2, act together to control the cell wall thickening in the disarticulation zone of the rachis node through a molecular mechanism using comparative DNA sequence information and archaeo botanical data. The authors demonstrated independent origin of barley domestication. Two ‘‘transition zones’’ were found, where major frequency changes between *btr1*- and *btr2*-types occur: the region between Iran and Afghanistan and the Levant and the southern part of the Mediterranean Sea. Besides these two transition zones, *btr1*-types were found to predominate in India and Ethiopia. While possible that *btr1*- and *btr2*-type barleys may be better adapted to different eco-climatic zones, an alternative scenario is that their current distribution is a direct result of human migration.

Figure 1 Spike of a barley plant derived from the small caryopsis “seeded in hood”. It is evident the large size of the hood in which fertile organs are well developed.

Figure 2 Reproductive organs in the Hood and developing grain "Seeded in Hood"

***Laxatum* (*lax*) and *Cleistogami* (*cly1*).**

Reduction or increase of the rachis internode length results in different spike density. Classical genetic studies have identified several loci involved in modulation of spike density, such as dense spike, zeocriton and laxatum. Spike density in barley is under the control of several major genes, as documented previously by genetic analysis of a number of morphological mutants.
The recessive mutation laxatum-a (*lax-a*) in barley, which causes pleiotropic changes in spike development resulting in:
(i) extended rachis internodes conferring a more relaxed (lax) inflorescence.
(ii) broadened base of the lemma awns.
(iii) thinner grains that are largely exposed due to reduced marginal-growth of the palea and lemma.
(iv) and homeotic conversion of lodicules into two stamenoid structures.

Map-based-cloning enforced by mapping-by-sequencing of the mutant *lax-a* locus enabled the identification of a homolog of BLADE-ON-PETIOLE1 and 2 (BOP1 and 2) as the causal gene. Cloning of the *laxatum*-a gene might open future perspectives in plant breeding, provide that adverse phenotypic effects can be moderated or eliminated. *Laxatum* florets can open without impetus force of lodicules, which were previously reported to be essential for open flowering in barley. Since the wild-type structure of lemma and palea help keeping barley flowers closed during anthesis, the open flowering *laxatum-a* phenotype may help to achieve open flowering independent of lodicules to facilitate hybrid breeding in barley. Furthermore and similarly to the effect of the *nud* gene, the mostly hulless *lax-a* seeds should be preferred for human food supply. The relaxed spike architecture should be beneficial in humid growing conditions to unfavor fungal growth and to achieve robust dry seeds for mechanical harvest. (Jost *et al*. 2016).

The closed floret habit (cleistogamy) is under the control of *cly1*, a gene that operates by inhibiting the development of the lodicule. In non-cleistogamous cultivars, *cly1* mRNA is degraded by miR172-directed cleavage, allowing the lodicules to swell; however, in cultivars carrying the recessive allele *cly1.b*, a single-nucleotide substitution destroys the miR172 target site preventing mRNA cleavage. Barley cv. SV235 is cleistogamous; its *cly1* coding sequence is identical to that of *cly1.b*, but its lodicules develop, although insufficiently to produce a non-cleistogamous flower. In this cultivar, the downregulation of *cly1* is unrelated to miR172-directed mRNA degradation, but rather caused by an epiallele that represses transcription. Allelic relationships between known *cly1* alleles were explored by the quantification of lodicule vascularization and an assessment of the response of the spike to the supply of exogenous auxin. The SV235 phenotype can be manipulated by a pre-anthesis application of 2,4-D, a feature that could be of interest in the context of hybrid barley grain production based on cleistogamy. The application of 2,4-D to spikes of *cly1.b2* carriers induced floret gaping and anther extrusion, thereby offering the possibility of manipulating flower type by the simple expedient of spraying with 2,4-D. In the context of F_1-hybrid grain production, fully open flowering is necessary for both pollen dispersal and cross-pollination. The *cly1.b2* allele offers a practical means of controlling flowering type in F_1-hybrids involving two carriers of *cly1.b2*. A 2,4-D application supplied prior to anthesis should encourage the non-cleistogamy needed for F_1-hybrid grain production, while the F_1-hybrid plants themselves are cultivated normally and so remain cleistogamous. Closed flowering is advantageous as it limits the entry of certain pathogens (in particular Fusarium head blight fungus) and inhibits pollen-derived gene flow (important in the context of genetically modified varieties). (Wang e*t al*.2015).

Florigen is a systematic signal that is produced in leaves in response to the stimulus of inductive day length and is transported to the shoot apex to induce flowering. Li *et al*. (2015) have studied the FLOWERING LOCUS T (FT) protein as central component of a mobile flowering signal (florigen) that is transported from leaves to the shoot apical meristem (SAM). Two FT monomers and two DNA-binding bZIP transcription factors interact with a dimeric 14-3-3 protein bridge to form a hexameric protein complex. This complex, designated as the 'florigen activation complex' (FAC), plays a critical role in flowering. The wheat homologue of FT, designated FT1 (= VRN3), activates expression of *VRN1* in the leaves and the SAM, promoting flowering under inductive long days. The authors show that FT1, other FT-like proteins, and different FD-like proteins, can interact with multiple wheat and barley 14-3-3 proteins, and they also identify the critical amino acid residues in FT1 and FD-like proteins required for their interactions, and demonstrate that 14-3-3 proteins are necessary bridges to mediate the FT1–TaFDL2 interaction. Using *in vivo* bimolecular fluorescent complementation (BiFC) assays, it has been demonstrated that the interaction between FT1 and 14-3-3 occurs in the cytoplasm, and that this complex is then translocated to the nucleus, where it interacts with TaFDL2 to form a FAC. In addition the authors demonstrate that a FAC including FT1, TaFDL2 and Ta14-3-3C can bind to the *VRN1* promoter *in vitro* and finally, they show that relative transcript levels of *FD-like* and *14-3-3* genes vary among tissues and developmental stages. Since FD-like proteins determine the DNA specificity of the FACs, variation in *FD-like* gene expression can result in spatial and temporal modulation of the effects of mobile FT-like signals.

Compositum Barley

Canonical barley spike has a branchless shape. However, mutants characterized by branched spikes have been described as naturally occurring since ancient times. Poly-row-and-branched spike (*prbs*) mutation has been described as involved in the inflorescence differentiation from a panicle into a spike. This mutation in fact can alter the inflorescence morphology in two ways: a) determining the conversion of the rudimentary lateral spikelets specific of two-rowed genotypes into fertile spikelets, b) determining the development of additional spikelets in the middle of the spike, resulting in a branched spike. In mutant *prbs*, new meristems initiated at the flanks of lateral spikelets and middle spikelet meristems were converted to branch meristems, developing branched spike. *Prbs* gene has been mapped on chromosome 3H and demonstrated that this gene is not allelic to *Vrs4*. *Vrs4* has been found involved even in another mutant phenotype derived from a particular development of the node.

'Compositum-Barley' and tetraploid 'Miracle-Wheat' (*T. Turgidum* convar. *compositum* (L.f.) Filat.) display non-canonical spike-branching in which spikelets are replaced by lateral branch-like structures resembling small-sized secondary spikes. As a result of this branch formation 'Miracle-Wheat' produces significantly more grains per spike, leading to higher spike yield. Poursarebani *et al*. (2015) investigated the genetic and molecular basis of "true spike-branching" in 'Compositum-Barley' and tetraploid 'Miracle-Wheat'

The gene *com2* was positional cloned on barley chromosome 2HS, and found that it is orthologous to *bht* that regulates spike-branching in 'Miracle-Wheat'. Both genes possess orthologs with similar functions in maize *BRANCHED SILKLESS 1* [(*BD1*); rice *FRIZZY PANICLE/BRANCHED FLORETLESS 1* [(*FZP/BFL1*); and *Brachypodium distachyon MORE SPIKELETS 1* (*MOS1*)]. This candidate gene represents a putative transcription factor consisting of a single exon, encoding a protein of 307 amino acids containing an ethylene-responsive element DNA binding factor (i.e. AP2/ERF). mRNA *in situ* hybridization, microarray experiments, and independent qRT-PCR validation analyses revealed that the branch repression pathway in barley is governed through the spike architecture gene *Six-rowed spike 4* regulating *COM2* expression, while *HvIDS1* (barley ortholog of maize *INDETERMINATE SPIKELET 1*) is a putative down-stream target of *COM2*. These findings provide new insights into the genetic basis of spike architecture in *Triticeae*, and have disclosed new targets for genetic manipulations aiming at boosting yield potential.

Liller *et al*. (2015) recently evidenciated that mutation in barley row type genes have pleiotropic effect on shoot branching. They suggest that the same genes or regulatory modules can regulate both inflorescence branching and tillering, and they studied pleiotropic effects of row type genes on seed size, seed number per spike, thousand grain weight and tillering in barley to better understand the genetic correlations between individual yield components. Allelic mutants of nine different row type loci (36 mutants), in the original spring barley cultivars Barke, Bonus, Foma and introgressed in the spring barley cultivar Bowman, were phenotyped under greenhouse and outdoor conditions. Two main mutant groups were identified and characterized by their relationships between seed and tillering parameters. The first group comprises all mutants with an increased number of seeds and significant change in tiller number at early development (group 1a) or reduced tillering only at full maturity (group 1b). Mutants in the second group are characterized by a reduction in seeds per spike and tiller number, thus exhibiting positive correlations between seed and tiller number. Reduced tillering at full maturity (group 1b) is likely due to resource limitations. In contrast, altered tillering at early development (groups 1a and 2) suggests that the same genes or regulatory modules affect inflorescence and shoot branching. Genes involved in development of the branched inflorescence architecture of the grasses also control seed size and shoot branching. These results indicate that correlations between shoot and spike architecture are due to a) competition between different sink organs for limited assimilates or b) the direct involvement of row type genes in the initiation and growth control of different plant organs, seeds and tillers. The authors thus speculate that the same regulatory genes or modules may control the development of different meristematic structures

andorgans in plants. Understanding how these genes are regulated and in turn control downstream targets in different plant organs is important to improve yield by modifying shoot and spike architecture. Understanding the genetic bases of the trade-offs between these traits is important for the genetic manipulation of individual yield components.

Double Mutants

Double mutants *Hv-Hd/tw*$_2$, formed by hybridization, are characterized by inherited phenotypic instability and by several new features, such as bract/leaf-like structures, long naked gaps in the spike, and a wide spectrum of variations in the basic and ectopic flowers which are absent in single mutants. Several of these features resemble those of mutations in auxin distribution, and thus the aim of this study was to determine whether auxin imbalances are related to phenotypic variations and instability. The effects of auxin inhibitors and 2,4-D (2,4-dichlorophenoxyacetic acid) on variation in basic and ectopic flowers were therefore examined, together with the effects of 2,4-D on spike structure. The occurrences of various malformations of spike structure, including leaf/bract-like structures, also demonstrate the existence of other developmental trends. Consequently, phenotypically unstable barley double mutants are a highly promising genetic system for the investigation of gene expression modules and trend rodersi. (Šiukšta *et al*. 2015)

The *erectoides-m anthocyanin-less 1* (*ert-m ant1*) double mutants are among the very few examples of induced double mutants in barley. From phenotypic observations of mutant plants it is known that the *Ert-m* gene product regulates plant architecture whereas the *Ant1* gene product is involved in anthocyanin biosynthesis. Zakhrabekova *et al*. (2015) used a near-isogenic line of the cultivar Bowman, BW316 (*ert-m.34*), to create four F_2-mapping populations by crosses to the barley cultivars Barke, Morex, Bowman and Quench. They phenotyped and genotyped 460 plants, allowing the *ert-m* mutation to be mapped to an interval of 4.7 cM on the short arm of barley chromosome 7H. Bioinformatic searches identified 21 candidate gene models in the mapped region. One gene was orthologous to a regulator of *Arabidopsis thaliana* plant architecture, *ERECTA,* encoding a leucine-rich repeat receptor-like kinase. Sequencing of *HvERECTA* in barley, *ert-m* mutant accessions identified severe DNA changes in 15 mutants, including full gene deletions in *ert-m.40* and *ert-m.64.* Both deletions, additionally causing anthocyanin deficiency, were found to stretch over a large region including two putative candidate genes for the anthocyanin biosynthesis locus *Ant1*. Analyses of *ert-m* and *ant1* single- and double-deletion mutants suggest *Ant1* as a closely linked gene encoding a R2R3 myeloblastosis transcription factor.

The *mirEX 2.0* portal provides the plant research community with easily accessible data and powerful tools for application in multi-conditioned analyses of miRNA expression from important plant species in different biological and developmental backgrounds. Zielenzinnski *et al*. (2015) demonstrate that the mirEX 2.0 portal is dedicated to researchers working on specific microRNA functions and expression profiles of entire microRNA family members during a particular organ/developmental stage or on microRNA biogenesis and evolution. The mirEX 2.0 web-based portal is a one-stop solution for the exploration of plant microRNA expression data covering mutants and three plant species representing scientifically (*Arabidopsis thaliana*), economically (*Hordeum vulgare*), and evolutionarily (*Pellia endiviifolia*) attractive research models. The provided user-friendly tools allow to explore expression data in any combination of species, tissues and developmental stages, thus leading to the rapid discovery and hypothesis-building of underlying relations and regulatory mechanisms. The developed technology also allows for unlimited further expansion of the data content and provides an environment for the design of novel tools following the needs of the plant community involved in the exploration of microRNA biology.

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Coordinator's report: Semidwarf genes

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Yield losses and quality reductions caused by lodging are a frequent production problem in barley (*Hordeum vulgare* L.) Minimizing such losses has been a goal of barley growers since the crop was domesticated. The strategy most frequently employed to minimize losses is a genetic reduction of plant height. However, lodging is a complex trait in which can be expressed from around heading time until harvest. Lodging about heading is often the most frequent cause of losses, but post-ripe straw breakage or crinkling of straw prior to mechanical harvest causes losses also.

Plant height genes - Mutant genes that reduced plant height or elongation of culm internodes are often the focus of breeding efforts. The most commonly used genes for height reduction in barley have involved specific alleles at three loci: the *uzu1.a* allele at the uzu 1 locus, the *sdw1.c* (denso) allele at the semidwarf 1 locus, and *ari-e.GP* (Golden Promise) allele at the breviaristatum-e locus. The *uzu1.a* gene was widely used in winter barleys developed in East Asia (Chono *et al*., 2003; Dockter *et al*., 2014). The *sdw1.c* gene has been widely deployed in Europe and is used in some other barley growing regions of the world (Jia *et al*., 2011; Malosetti *et al*., 2011). The *ari-e.GP* has been used to a limited extent in England and Australia (Ellis *et al*., 2002; Malosetti *et al*., 2011; Walia *et al*., 2007). More recently the *sdw4.ad* allele at the semidwarf 4 locus has found favor in winter grown spring barley cultivars developed for China and Japan (Sameri *et al.,* 2009; Yu *et al*., 2010). Despite their favorable effects on plant height, worldwide deployment of these semi-dwarfing genes in barley improvement is restricted because their origin in genetic background poorly adapted to the target production area and the semidwarf genes have pleiotropic effects on other agronomic characteristics. Most notable are the sensitivity of the *uzu1*.a mutant to high temperatures (Dockter *et al*., 2014) and delayed maturity associated with *sdw1.c* and other mutants at that locus (Jia *et al*., 2011).

Haploblock identification - The characterized semidwarf genes do not explain all the observed variation in plant height (Pasum *et al*., 2012). The advent of relatively dense molecular maps for barley has facilitated further dissection of qualitative trait loci (QTL) associated with specific traits. Using identity by descent and allele associated haplotypes, or preferably a haploblock of adjacent molecular markers, presence or absence of specific height genes can be determined in breeding materials and historic cultivars. Using procedures for DArTseq marker identification (Diversity Arrays Technology, Yarralumla, ACT 2600, Australia; http://www.diversityarrays.com), over 10,000 polymorphic SNP markers with assigned chromosomal positions were characterized for an array of Australian breeding lines, cultivars, and historic accessions (Wang *et al*., 2015). Visual realignment of markers based on breakpoints in a doubled-haploid population (NRB091087/NRB091047) and closely related breeding lines increased the number of positioned markers to

over 17,000. The relative positions of the realigned markers were used to identify haploblocks associated with specific plant height genes (Table 1).

Additional plant height genes – Haploblocks associated with semidwarf genes should be present in short stature breeding lines; however, this association was not observed in all Australian semidwarf cultivars. Likewise in a worldwide collection of barley cultivars, Pasum *et al*. (2012) reported that QTL distributed across the barley genome are associated with variation in plant height. Hence, additional semidwarf loci may exit in cultivated barley. One candidate group is the semidwarf accessions that originated from the International Center for Agricultural Research in the Dry Areas (ICARDA) barley breeding program at the International Maize and Wheat Improvement Center (CIMMYT) in Mexico. Negeri (2009) identified a plant height QTL in the short arm of chromosome 6H in the Chinese cultivar Shenmai 3 (Gobernadora/Humai 10), which was selected at CIMMYT from a cross to Gobernadora (OC640/Mari//Pioneer/3/Maris Concord). A unique haploblock was found in 6HS in Canela (Maris Canon/Laurel//Aleli) and several other ICARDA lines from Mexico (Table 1). This haploblock is near the 6HS position was identified by Pasum *et al*. (2012) as having a large effect on plant height. The recommended locus symbol for this QTL is *sdw5* and the recommended allele symbol is *sdw5.be*. The haploblock associated with the *sdw5.be* allele is present in several Australian cultivars. These include Commander (Keel/Sloop//Galaxy) and Keel (CPI18197/Clipper//WI2645).

The semidwarf genes are considered here because their deployment of various combinations can further reduce plant height and may reduce losses caused by lodging. The presence of various haploblocks associated with plant height genes suggests that several Australian cultivars already have two or more semidwarf genes. Hindmarsh (Chariot/VB9409) has the haploblocks associated with the *ari-e.GP* and *sdw1.c* genes. Commander has the haploblocks associated with *sdw1.c* and *sdw5.be*. Since other relatively short stature cultivars have one or no identified semidwarf gene, additional semidwarf genes in cultivated barley are still to be identified.

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Table 1. A partial list of plant height genes involved in adaptation of barley to specific production areas including origin, chromosomal position, and phenotypic effects.

Locus name	Chromosome position		DArTseq marker / phase	Marker position	Gene or mutant source	Probable trait origin	Notes
Plant height genes							
sdw1.c (denso)	Semidwarf 1	3H bin12	3264976 - 3663177 - 3397429 +	124.00	Abed Denso Triumph	Europe	Reduced height, delayed heading and smaller kernels
sdw4.ba	Semidwarf 4	7H bin11	3661780 - 3265446 + 3396373 -	118.24	Zhenongda 7	China	China / Japan semidwarf, short basal culm internodes
Table 1 continued							
sdw5.be (q6HT4)	Semidwarf 5	6H bin05	3985790 + 4189414 + 3931643 +	35.98	Canela Keel	Mexico Australia	Semidwarf gene in CIMMYT-ICARDA cultivars
ari-e.GP	Breviaristatum-e	5H bin06	4186599 + 3273517 + 3273238 +	50.00	Golden Promise	England	Short awned semidwarf mutant from Maythorpe
uzu1.a (HvBRI1)	Uzu 1	3H bin06	Gene not present		Winter six-rowed	China	Degree of dwarfing is temperature sensitive, short awns

Coordinator's report: Wheat-barley genetic stocks

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It has been possible to produce five disomic addition lines (2H,3H,4H,6H,7H) of six-rowed Ukrainian winter barley cultivar 'Manas' to 'Asakazi' wheat (Marta Molnar- Lang et al 2012). Furthermore, new wheat x barley hybrids (wheat Mr9kr1 x barley Igri; wheat Mr9kr1 x barley Betzes; wheat Asakaze komugi x barley Manas have been produced by (M.Molnar-Lang et al 2000, E.Szakacs et al 2007, I. Molnar et al 2007) Partial sets of addition, substitution and translocation lines were then developed from these hybrids. Tatyana et al (2013) reported the production of ditelosomic 7HL(7D) and monotelosomic 7HL(7A) and 7HL(7B) substitution lines of *Hordeum marinum ssp gassoneanum* to common wheat cv. Saratovskaya.

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