Poster 23. SNP mapping in a doubled haploid, hexaploid wheat population.

Adrian L. Cabral [1], Mark Jordan [1], Curt McCartney [1], Curtis Pozniak [2], and Gavin Humphreys [1].

[1] Cereal Research Centre, Agriculture and Agri-Food Canada, Winnipeg, MB R3T 2M9, Canada, and [2] Crop Development Centre, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada.

A total of 294 SNP (single nucleotide polymorphisms) markers were developed via a KASP assay (KBioscience®) on a DH hexaploid population comprising 182 individuals generated from a cross between parental cultivars 'RL 4452/AC Domain'. Of these 294 SNP markers, 225 were polymorphic between both parents, and the remaining 69 were either monomorphic or found unsuitable for mapping. These 225 SNP markers were meant to be integrated into an existing 'RL 4452/AC Domain' map comprising 652 SSR, DArT, and EST markers. The 225 polymorphic SNPs were mapped on 163 of the 182 DH progeny using MapDisto, resulting in the final assignment of 211 SNP markers to 18 of the 21 chromosomes. The majority of markers (55%) mapped to B-genome chromosomes, and the remaining 94 markers were assigned to chromosomes belonging to the A (27%) and D (18%) genomes. On a per chromosome basis, 5B had the most SNPs (15%), followed by 1B (12%) and 1D (9%). None of the SNP markers mapped to chromosomes 3D, 4D, and 7D. The integration of SNP markers into existing 'RL 4452/AC Domain' maps resulted in an overall reduction in the map sizes of 13 of the 18 chromosomes, with reduced map lengths varying between 0.5 cM and up to12.3 cM. No correlation could be established between reduced map size and number of SNP markers per chromosome. Most of the SNP markers either flanked or co-segregated with existing SSRs/QTL for several important genes/traits, making them useful for further fine mapping studies.

Poster 24. Study of pre-anthesis development in barley (Hordeum vulgare L.).

Ahmad M. Alqudah [1], Benjamin Kilian [2], and Thorsten Schnurbusch [1]. [1] Plant Architecture Group and [2] Genome Diversity Group, Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Genebank Department, Corrensstr. 3, D-06466 Gatersleben, Germany.

Optimal anthesis time is one of the important strategies used in breeding programs to acclimatize crops to environment and subsequently achieving high yield potential. The pre-anthesis phase is one of the most important phases and has direct impact on yield potential and final grain yield. Maximum number of spikelet primordia per spike (maximum yield potential) and its survival are the major events during this phase. The pre-anthesis phase can be divided into three sub-phases: 1) leaf initiation, 2) spike initiation, and 3) spike growth phases. The lengths of these phases are affected by environmental conditions such as photoperiod and vernalization as well as genotypes. Such factors directly contribute to reach the final time of anthesis and yield potential. Hence, genetic analysis of pre-anthesis phases in cereals is necessary at this time point to a better understand the role of these phases in increasing yield. We are interested to use molecular-genetic approaches to explain the role of pre-anthesis development in barley for yield potential and final grain yield. The present study of pre-anthesis development using molecular markers and genetic associations may identify QTL for growth and developmental traits. Through synteny between barley and other grass species (rice, Sorghum, and Brachypodium), we aim to deduce candidate genes underlying QTL for growth and developmental traits by mapping and sequencing.

Poster 25. Sequencing of vrs1 and int-c loci shows that labile barleys (Hordeum vulgare convar. labile) have a six-rowed genetic background.

Helmy M. Youssef, Ravi Koppolu, and Thorsten Schnurbusch. Genebank Department, Plant Architecture Group, Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, D-06466 Gatersleben, Germany.

Labile-barleys (*Hordeum vulgare* L. convar. *labile* (Schiem.) Mansf.) are found in the highlands of Ethiopia, Eretria, and north India–Pakistan districts. They represent a distinct spike form showing row-type alterations even within individual spikes of the same genotypes. Variation at the *six-rowed spike 1* (*vrs1*) locus is sufficient to control barley lateral spikelet fertility, which is also modified by alleles at the *intermedium-c* (*int-c*) locus. This study aimed at resequencing these two loci in 221 supposedly *labile*-barley accessions from Ethiopia to investigate whether these *labile*-barley accessions have a two-rowed genetic background, resulting in increased lateral spikelet fertility, or show reduced lateral fertility if they

possess a six-rowed genetic background. The resequencing results of *Vrs1* revealed 13 accessions with two novel *vrs1.a1* haplotypes. Following the current nomenclature of *vrs1* haplotypes, the new haplotypes were named as haplotypes 66 and 67. Resequencing at the *int-c* locus showed that 118 of the *labile*-barleys possessed the previously described *Int-c.a* allele, but only one accession was found having a novel *Int-c.a* haplotype in the homozygous state (termed *Int-c.a haplotype1*; *Hap_1*). Interestingly, 101 *labile*-barleys carried the *Int-c.a* allele and *Int-c.a haplotype1* simultaneously, suggesting maintained heterozygosity or recent gene duplication at this locus. Only one accession had a two-rowed haplotype (*Vrs1.b3*, *int-c.b1*), and one accession possessed the *Vrs1.t* (*deficiens*) and *Int-c.a* alleles (six-rowed). These two accessions were considered as misclassified *labile* genotypes and not included in further analysis. On the other hand, the phenotypic data obtained from the *labile* accessions and their comparison to the observed allele/haplotypes combinations showed that, in spite of the presence of *vrs1.a* and *Int-c.a* (genotypically six-rowed alleles) in the large majority of the analyzed accessions, the observed phenotypic data did not support the expected six-rowed phenotype in *labile*. The *labile*-barley spike phenotype displays a variable number of fertile lateral spikelets (from 0 to 2) at each rachis node. Thus, our analysis demonstrated that all of the 219 *labile* accessions studied in this work showed six-rowed alleles at *vrs1* and *int-c* but reduced lateral spikelet fertility. This reduction is most likely caused by the recessive *labile* (*lab*) locus which we are in the process to characterize further.

Poster 26. A large-scale, mutant panel of einkorn wheat developed by heavy-ion beam mutagenesis and its application for flowering-time mutant screening.

Aiko Nishiura [1], Yusuke Kazama [2], Tomoko Abe [2], Miyuki Nitta [3], Shuhei Nasuda [3], and Koji Murai [1].

[1] Department of Bioscience, Fukui Prefectural University, Eiheiji-cho, Fukui 910-1195, Japan; [2] RIKEN, Nishina Center, Wako, Saitama 351-0198, Japan; and [3] Graduate School of Agriculture, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan.

Mutation analysis is a powerful tool for investigation of gene function. Heavy-ion beam mutagenesis has been recognized to be an effective method of producing mutations because of its high linear energy transfer (LET). High-LET radiation effectively induces DNA double-strand breaks than other mutagenic methods. We have been constructing a large-scale, mutant panel of diploid einkorn wheat (*Triticum monococcum*) using heavy-ion beam mutagenesis for 12 years. Seeds of the einkorn wheat strain KU104-1, KU104-2, or DV92 were treated with 50–58 Gy of N or C ion beam with LET of 30 ke/Vμm and then sown in the field. The spikes of M_1 plants were bagged and the harvested selfed seeds of each spike were used to produce the M_2 lines. Every year, we obtained about 1,000 M_2 lines, eventually developing a mutant panel with a sum of 10,000 M_2 lines. We are using this mutant panel for screening mutation of reproductive growth, especially for flowering-time mutants. We have identified several flowering-time mutants of great interest; nonflowering mutants (maintained vegetative phase), late-flowering mutants, and early-flowering mutants. In the late-flowering mutants, for example, we identified a mutation that had an abnormally large number of nodes; we termed this mutation *fushi-darake* (*fdk*), which means too many nodes in Japanese. The *fdk* mutant plants have increased numbers of nodes and leaves. WT plants show spiral phyllotaxy; however, *fdk* mutants have 1/2 alternate phyllotaxy with a shortened plastochron. Each tiller in the *fdk* plants branches at the upper part of the culm. A small spike sometime appears from the tip of culm in main tiller. The SEM analysis of developing SAMs indicated that transformation of spikelet meristems into vegetative shoot meristems in the *fdk* plants. Based on the phenotype, we concluded that the *fdk* mutant has a heterochronic nature, i.e., both reproductive and vegetative programs are simultaneously in operation during the reproductive phase, resulting in a shortened plastochron and transformation of reproductive spikelets into vegetative shoots.