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