markers to deletion bins within the D genome of reference polyploid wheat (Chinese Spring) will allow for the construction of a physical marker scaffold that will aid in genome sequence completion and future mapping and cloning studies. To design an optimal marker array, we tested hybridization temperature, oligo length, and different statistical analysis methods. After determining appropriate marker design and experimental conditions we screened a pool of 206,486 repeat junction markers as well as 26,800 gene markers representing 6,700 genes. Screening results provided 46,224 markers in total that were selected for design of a final mapping array. These 46,224 markers are comprised of 30,900 repeat junction markers and 15,324 gene markers representing 6,330 genes. This final mapping array is being used to construct a high-resolution, physical map using D-genome deletion lines and radiation hybrid panels. Here we present our methods for design and analysis of the NimbleGen comparative genomic hybridization arrays constructed from *Ae. tauschii* repeat junction markers, the construction of a NimbleGen repeat junction array using selected markers, and its use in the development of a physical map for the D genome of hexaploid wheat.

Poster 10. Genome-wide characterization of transposable element repeat junctions in barley and their application in marker development for chromosome 3H.

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Transposable elements (TEs) account for about 70% of the barley (*Hordeum vulgare* L.) genome. TEs move in the genome by inserting to new regions through copy-and-paste or cut-and-paste mechanisms. Insertion of TEs in DNA regions generates unique junctions between the TEs and the sequences in which they land. We investigated the uniqueness of these junctions throughout the barley genome and their potential application for marker development. The 10-Gb survey sequencing data of the seven barley chromosomes was searched with the 'RJPrimers' pipeline to estimate the frequency of repeat junctions (RJs). We found 988,750 RJs distributed evenly among the chromosomes with an average of 1 RJ per 10 Kb. Repeat junction markers (RJMs) for each chromosome were designed based on detected repeat junctions. Each RJM consists of one primer that spans unique insertion site of TE, whereas the second primer is designed from any region within 1 Kb of the junction. We randomly chose 36 RJMs from chromosome 3H to amplify five barley cultivars (Betzes, Golden Promise, Bowman, and Haruna Mugi) and two wild barley (*H. bulbosum* L.) accessions. Out of 36 RJMs, 28 (68%) amplified a single band and 21 (58%) were polymorphic. Based on scoring data of 21 RJMs, we were able to separate all tested barley accessions and cluster them into two main groups. The abundance of RJMs makes them an ideal marker for genome saturation. Further, the high level of polymorphism makes them ideal for molecular breeding applications.

Poster 11. Best practices for RNA-Seq differential expression analysis in barley.

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Barley (*Hordeum vulgare*) being a member of the grass family is one of the most important large-genome cereals and a close relative of wheat. It has a complex diploid genome of 5.1 Gb and is being extensively used for genetic studies. As a part of the Barley Genome Sequencing Project, RNA-Seq experiments were performed using eight different tissues representing different developmental stages, including 4-day embryos, roots, and shoots from seedlings, young developing inflorescences (5-mm and 10–15 mm stages), at the six-leaf stage, and from the developing grain (5 and 15 days post anthesis). These datasets have been used to improve the barley gene model predictions and to detect differentially expressed transcripts. Here we discuss the results of the expression analysis that we implemented using different available