flanking markers resulted in the identification of BAC supercontigs that cover 19.2 Mb of the *YrH52* gene region. Further work is underway to refine the physical map and identify candidate gene(s) for *YrH52*. A similar strategy is employed for positional cloning of *Yr15* and *YrG303*, also derived from *T. turgidum* subsp. *dicoccoides*. Collaboration with other groups was established to promote the positional cloning of other wheat genes that reside on 1BS. These results demonstrate the importance of the genomic resources developed by TriticeaeGenome consortium for accelerating positional cloning of target genes in the complex genome of wheat.

High-resolution mapping of areas of low recombination and polymorphism containing the hexaploid wheat loci Pis1 and C.

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Gene mapping and map-based cloning studies in wheat are often complicated by lack of marker polymorphism and/or recombination. Radiation hybrid mapping can address both problems as it relies on radiation-induced breaks to order markers. Due to the nature of RH panels markers are scored as presence/absence, eliminating the need for polymorphism. We utilized this approach to physically map genes based on multiple overlapping deletions induced by γ irradiation. *Pis1* is a wheat floral mutant producing three fully functional pistils per floret instead of the usual single pistil. Compactum (*C*) is responsible for club head phenotype and maps to the low-recombination, pericentromeric region of 2D. The location of *C* with respect to the centromere is not well established. *Pis1* has proven difficult to map in an F_2 population due to lack of marker polymorphism. In this study, independent RH mapping panels were assembled for both genes (282 RH lines for each of *Pist1* and *Compactum*). For each gene, a set of 94 lines were selected and characterized with ESTs and SSRs, specific to the targeted regions. We mapped *Pist1* gene on chromosome 2D (deletion bin 2DL-9) using 14 SSRs and 27 ESTs. Total map distance was 145.0 cR1500 covering ~98 Mb. Even in this region of a recombination hot spot, a cM/cR1500 ratio was found as 1:8; with a mapping resolution of ~750 kb. The closest ESTs flanking *Pist1* are co-segregating and spanned only six rice genes. *Pis1*-linked ESTs were then mapped on a genetic mapping F_2 (Multiovary/Winsome) population. For the *Compactum* locus, 25 ESTs and 16 SSRs were used in mapping. A total map length created was 158.8 cR1500 with average marker retention of 80% and map resolution of ~710 kb. The cM/cR1500 ratio in this region of chromosome was found to be 1:60. Two ESTs flanking *C* locus on this RH map span 15 rice genes. ESTs flanking the *C* locus were mapped on two different bi-parental genetic populations to confirm the outcomes of RH mapping. Putative candidates are being used for developing gene specific markers and work on fine mapping and their eventual cloning is underway.

The rye gene Pm8 conferring resistance to wheat powdery mildew is a homologue of the wheat powdery mildew resistance gene Pm3.

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During wheat breeding, chromosomes of the rye (*Secale cereale* L.) genome have been introgressed into the wheat genome to enhance tolerance to biotic and abiotic stresses. The most widely used wheat–rye translocation nowadays is the 1RS chromosome arm derived from the rye cultivar Petkus carrying three rust resistance genes and the powdery mildew resistance gene *Pm8*. In wheat, *Pm* genes mediate resistance against powdery mildew, a major fungal pathogen. *Pm8* was mapped at the same gene-rich region on the short arm of wheat homoeologous group-1 chromosome as the powdery mildew resistance gene *Pm3* of hexaploid wheat and was, therefore, proposed to be an ortholog of *Pm3*. Southern hybridization analysis showed that there is a sequence in rye and in *Pm8* wheat lines with homology to the *Pm3* promoter region. In a homology-based cloning approach based on primers derived from the cloned wheat powdery mildew resist-

ance gene *Pm3*, we were able to amplify a *Pm3*-homologous gene from the chromosome arm 1RS. By means of transient expression of the *Pm8*-candidate gene in susceptible wheat lines and the generation of stable transgenic lines, we could show that the *Pm8*-candidate gene mediates *Pm8*-specific powdery mildew resistance to *Pm8* avirulent powdery mildew isolates. In two independent mapping populations, we could also confirm that the cloned resistance gene indeed maps to the *Pm8* locus. Furthermore, sequence comparison of *Pm8* with *Pm3* and *Pm3*-like genes revealed a complex mosaic of ancient haplotypes in these resistance genes. Since the *Pm8*-candidate gene is functional and localizes to the previously assigned *Pm8* locus, it is indeed *Pm8* and its high sequence similarity to *Pm3* shows that it is a homologous gene of *Pm3*.

SESSION VII: GENOMICS-ASSISTED BREEDING

Use of genomic selection in 21st century wheat breeding.

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The overall goal of wheat breeding efforts over the past 120 years has limited variability; combine the most positive alleles into one individual plant to maintain the economics and sustainability of wheat production locally and globally. One facet that has changed significantly is the tools at the disposal of current day wheat breeders to implement their breeding goals. The use of molecular markers over the past 25 years has opened new breeding approaches as we are now able to locate QTL and genes of interest, efficiently move them into adapted germplasm, and pyramid them effectively. More recently, the ability to saturate the genome of wheat with single nucleotide polymorphism (SNP) markers and genotyping by sequencing (GBS) has provided the tool of genomic selection. Genomic selection, which is used heavily in animal breeding, is a new tool in wheat breeding for improving quantitative traits in large breeding populations in an attempt to increase the accuracy of the prediction of breeding and genotypic values. By predicting the breeding values of lines in a population through analysis of phenotypes and high-density marker scores, the breeding cycle can accelerate, enhancing gains per unit time. Although most genomic selection models have been through computer simulations, the correlation between true breeding values and the genomic estimated breeding value has been reported to be as high as 0.85. Recently, the wheat breeding programs at Washington State University have begun to evaluate the usefulness of genomic selection in the wheat development effort. Training panels have been established and genotyped, and are in the process of being phenotyped. Perspectives on how this new tool will be used as part of a toolbox will be discussed as breeding programs are developed that more efficiently and effectively release wheat cultivars.

DArT and DArTseq genome profiling with relevant IT support.

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Diversity Arrays Technology (DArT) was developed over a decade ago to enable crop breeding with utilization of the whole-genome profile information. The technology has found numerous genetic and breeding applications in a variety of crops. At the moment, DArT has been developed in over 65 organisms, including all significant ITMI crops and their relatives. In the last two years, we have developed and launched commercially a new service using DArT complexity reduction methods combined with Next Generation Sequencing platforms. This new (DArTseq) platform has been applied to tens of thousands of wheat samples and tested successfully in practically all cultivated Triticeae crops. The technology scans over 100,000 loci in the genome for DNA variation targeting primarily genic regions of the genome. DArTseq integrates DArT markers (presence/absence of restriction fragment in genomic representation) based on SNP and methylation variation with 'traditional' SNP markers on the fragments detected in genomic representations. We will present a number of examples of application of DArT and DArTseq to crop breeding and genetics as well as in product purity and genetic ID testing. Our analytical pipeline for genome profile production and new information technologies for data storage processing will be also presented.