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.