Poster 51. Genomic analysis and fine-mapping of two homoeologous wheat genes conferring susceptibility to Stagonospora nodorum blotch.

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The necrotrophic fungal pathogen *Stagonospora nodorum* produces multiple necrotrophic effectors (NEs), also known as host-selective toxins, which interact with corresponding wheat genes in an inverse gene-for-gene manner to cause the disease *Stagonospora nodorum* blotch (SNB). In previous research, we showed that the homoeologous wheat genes *Snn3-B1* and *Snn3-D1*, located on wheat chromosome arms 5BS and 5DS, respectively, both recognize the NE SnTox3 to confer effector-triggered susceptibility. Here, we describe genome analysis and mapping results from ongoing efforts to clone the two *Snn3* genes. Saturation mapping of the genes in relatively small F_2 populations using SSRs and EST-derived markers followed by comparative analysis with the rice and *Brachypodium* genomes revealed that both the *Snn3-B1* and *Snn3-D1* regions were highly conserved with regions of rice chromosome 12 and *Brachypodium* chromosome 4. This colinearity allowed us to develop numerous additional markers to further saturate the *Snn3-B1* and *Snn3-D1* regions. Subsequent fine-mapping of both genes in large F_2 populations resolved some co-segregating markers and delineated the genes to small intervals. BAC contigs identified with flanking markers were anchored to the *Snn3-D1* genetic map. The ratio of physical to genetic distance in the *Snn3-D1* region was estimated to be 500–800 kb/cM. Because these two NE sensitivity genes are homoeologous, we can work towards cloning them in parallel and, once cloned, we can study their evolutionary history and investigate their functional roles in mediating recognition of SnTox3.

Poster 52. Characterization of natural variation in the Tsn1 gene in Aegilops speltoides.

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The *Tsn1* gene confers sensitivity to the necrotrophic effector (NE) ToxA, which is produced by the pathogens that cause tan spot and *Stagonospora nodorum* blotch on wheat. Although *Tsn1* is a susceptibility gene, it contains resistance gene-like features such as protein kinase, nucleotide binding (NB), and leucine-rich repeat (LRR) domains. Previous research indicated that *Tsn1* arose in the diploid B-genome progenitor of polyploid wheat. However, nucleotide variation in *Tsn1* is nearly nonexistent among polyploids. Here, accessions of *Aegilops speltoides* (SS genome), a close relative of the B-genome progenitor, were studied to further characterize the structure, function, evolution, and diversity of *Tsn1*. Multiple plants from each of 123 accessions were evaluated for reaction to ToxA and genotyped for presence of *Tsn1*. A total of 95 accessions were insensitive to ToxA and null for *Tsn1*, whereas the remaining 28 harbored *Tsn1* alleles and were either sensitive or insensitive to ToxA. Comparative sequence analysis of the 4,473-bp coding region from 15 sensitive *Ae. speltoides* plants revealed numerous single nucleotide polymorphisms (SNPs) compared to the *Tsn1* allele in the durum wheat variety Langdon. Among *Ae. speltoides* accessions, there were approximately the same number of nonsynonymous and synonymous mutations, but none of the nonsynonymous changes occurred within the protein kinase, NB, or LRR domains indicating the importance of these domains for *Tsn1* function. The diversity in *Ae. speltoides* allowed us to gain a better understanding of the evolution of *Tsn1*, and further studies will enhance our understanding of *Tsn1*-ToxA interactions.