

**Poster 17. Two homoeologous wheat genes confer sensitivity to a single, host-selective toxin and susceptibility to *Stagonospora nodorum* blotch.**

**Zengcui Zhang**<sup>1</sup>, Timothy L. Friesen<sup>2</sup>, Steven S. Xu<sup>2</sup>, Gongjun Shi<sup>1</sup>, Jack B. Rasmussen<sup>1</sup>, and Justin D. Faris<sup>2</sup>.

<sup>1</sup> Department of Plant Pathology, North Dakota State University, Fargo, ND 58105, USA and <sup>2</sup> USDA-ARS Cereal Crops Research Unit, Northern Crop Science Laboratory, Fargo, ND 58105, USA.

The pathogen *Stagonospora nodorum* produces multiple host-selective toxins that interact with corresponding wheat sensitivity genes in an inverse gene-for-gene manner to cause the disease *Stagonospora nodorum* blotch (SNB) in wheat. We screened accessions of *Aegilops tauschii*, the D-genome donor of common hexaploid wheat (*Triticum aestivum*), with culture filtrate derived from isolate Sn4. One sensitive (TA2377) and one insensitive (AL8/78) accession were selected to develop an F<sub>2</sub> population. Bulk-segregant analysis and molecular mapping indicated that the new toxin sensitivity gene, temporarily designated *Snn5DS*, mapped to chromosome arm 5DS. Inoculation of the population with spores from Sn4 indicated that a compatible host-toxin interaction explained 100% of the variation in SNB development. In related research, *SnTox3*, which interacts with the *Snn3* gene on wheat chromosome arm 5BS, was isolated. Further evaluation of the F<sub>2</sub> population indicated that the toxin interacting with *Snn5DS* was SnTox3. Comparative mapping revealed that *Snn3* and *Snn5DS* are homoeologous and, thus, derived from a common ancestor. Further characterization indicated that, as opposed to most host-toxin interactions in the wheat-*S. nodorum* pathosystem, the *Snn3/Snn5DS*-SnTox3 interaction is not dependent on light, which suggests that a different host metabolic pathway is exploited to cause disease. Saturation and high-resolution mapping delineated the *Snn5DS* locus to a 1.4-cM interval, and analysis of colinearity indicated the *Snn5DS* region is well conserved between wheat, rice and *Brachypodium*, which will aid in the map-based cloning of *Snn5DS*.