Poster 49. QTL mapping of adult-plant resistance to Stagonospora nodorum leaf blotch in bread wheat line 'Shanghai-3/Catbird'.

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Leaf blotch, caused by *Stagonospora nodorum* (teleomorph: *Phaeosphaeria nodorum*), is a severe disease on wheat in Norway and other wheat-producing areas with a temperate and rainy climate. Insufficient resistance in the currently grown cultivars causes severe grain shriveling and reduced yield in years with favorable conditions for the disease. As an alternative to fungicide applications there is a need to improve the levels of resistance. The bread wheat line 'Shanghai-3/Catbird', from the wheat breeding program at CIMMYT, which is currently utilized as a source of non-Sumai 3 resistance to Fusarium head blight, was identified in our field nurseries to exhibit high levels of resistance to *Stagonospora nodorum* leaf blotch. The objective of the present study was to identify the main genetic factors behind the resistance in 'Shanghai-3/Catbird'.

A population of 168 recombinant inbred lines (RILs) from the cross of 'Shanghai-3/Catbird' with the susceptible spring wheat cultivar Naxos was tested in hillplot trials naturally infected with *S. nodorum* across two locations in southeastern Norway during the 2009, 2010, and 2011 growing seasons. Leaf blotch severity was scored as percentage of diseased leaf area based on the whole canopy. To avoid confounding effects of earliness, the severity data was regressed against days to maturity and the resulting maturity-corrected leaf blotch severities were used for the QTL analysis. Preliminary QTL mapping results indicate that 'Shanghai-3/Catbird' carries major disease-reducing alleles on chromosomes 2DL and 7DS, and Naxos contributes resistance alleles on 3BL and 5BL. Work is currently under-way to saturate the linkage map with markers surrounding the known toxin-sensitivity loci *Tsn1*, *Snn1*, *Snn2*, *Snn3*, and *Snn4*, in order to determine their potential involvement in the leaf blotch resistance segregating in this population.

Poster 50. Identification and genomic mapping of three new Stagonospora nodorum blotch susceptibility genes in wheat.

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Stagonospora nodorum is a necrotrophic fungal pathogen of wheat that causes the disease Stagonospora nodorum blotch (SNB). The wheat–*S. nodorum* pathosystem involves pathogen-produced necrotrophic effectors (NEs) (formerly known as host-selective toxins) that are recognized by corresponding host genes to confer disease susceptibility. To date, five host gene–NE interactions have been reported in the wheat–*S. nodorum* system, all of which play significant roles in the development of SNB. Here, we present the identification and mapping of three additional wheat genes that confer sensitivity to different NEs produced by *S. nodorum*. One NE sensitivity gene (temporarily designated *Snn4B*) was identified in the durum wheat variety Lebsock and mapped to the long arm of chromosome 4B in a population of doubled haploids. Evaluation of SNB in this population indicated that the *Snn4B* locus explained as much as 53% of the variation demonstrating that *Snn4B* is a major SNB susceptibility gene. The second NE sensitivity gene (*Snn6A*) was identified in the hexaploid variety Opata 85 and mapped to the long arm of chromosome 6A in the ITMI population. This gene accounted for 20% of the variation in SNB development. Finally, a third NE sensitivity gene (*Snn5D*) was discovered in the hexaploid landrace Chinese Spring and mapped to the long arm of chromosome 5D using chromosome deletion lines. Further characterization, analysis, and marker development for these susceptibility genes is underway. This research broadens our knowledge of the wheat–*S. nodorum* pathosystem and will lead to the efficient development of SNB resistant wheat varieties.