0203-AN-066 Mapping of FHB Resistance Genes in the Wheat Lines Wuhan 3 and Fujian 5114.

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PROJECT ABSTRACT
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Wheat breeders throughout the U.S. are interested in methods to more efficiently select for FHB resistance among their breeding materials. DNA markers for FHB resistance genes can reduce the screening workload by identifying those lines that contain resistance genes. We have discovered a major QTL for FHB resistance derived from Sumai 3 and are currently testing the feasibility and effectiveness of using it in a marker-assisted selection scheme. To protect against heavy inoculum levels and environmental condition particularly conducive to Fusarium infection and spread and to lessen the reliance on a single resistance source, it is wise to pursue other resistance sources. We propose to map FHB resistance genes in two Chinese resistance sources that putatively have high levels of resistance but likely differ from Sumai 3 for one or more genes. Having DNA markers for the genes from different resistance sources can be used to help combine the genes into a single source.

Our objectives are:
1) Identify DNA markers for new FHB resistance genes from Wuhan 3.
2) Identify DNA markers for new FHB resistance genes from Fujian 5114.
3) Confirm the presence of QTLs identified in Objectives 1) and 2) in Sumai 3/Wuhan 3 and Fujian 5114/Sumai 3 populations, respectively.

Two segregating recombinant inbred spring wheat populations will be screened for FHB resistance and molecularly mapped to identify QTL. The first population is 110 F6-derived lines from the cross Wuhan 3/Norm. The second population is 78 F6-derived lines from the cross Fujian 5114/Norm. Both populations have been evaluated in greenhouse (2X) and field (3 or 4 environments) FHB nurseries. We will first map at least one marker per QTL region identified in Sumai 3 and other resistance sources. We expect that several of these QTL will be important in the two populations being investigated in this research. To identify new QTL, we will systematically test at least two SSR per chromosome arm and will fill in gaps in the maps with ESTs. Our goal for each of these populations is to explain at least 60% of the phenotypic variation in FHB resistance with the DNA markers. Two additional populations, Sumai 3/Wuhan 3 and Fujian 5114/Sumai 3 will be evaluated for FHB reaction in additional greenhouse screening and used to verify the presence of QTL discovered in the above two populations.