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**Project Title: Fine Mapping of QTL for FHB Resistance in PI 277012 and Introgression of the Resistance into Adapted Spring Wheat Varieties.**

### PROJECT 3 ABSTRACT

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To diversify the resistance sources and further improve wheat for resistance to the Fusarium head blight (FHB) disease, novel and effective sources of resistance to FHB are desperately needed for wheat breeding programs. In a large-scale evaluation of wheat germplasm for reactions to FHB, Dr. Steven Xu at the USDA-ARS, Fargo, identified a hexaploid wheat accession (PI 277012) that consistently showed a high level of resistance across all environments in both greenhouse and field experiments. To characterize the FHB resistance in this accession, a doubled haploid (DH) mapping population consisting of 130 lines was developed from the cross between PI 277012 and the hard red spring wheat cultivar ‘Grandin’ (susceptible to FHB). The DH population was then evaluated for reaction to FHB under three greenhouse seasons and two field environments. At the same time, a whole genome linkage map was developed, which consisted of 350 SSR markers spanning 2,703 cM of genetic distance. QTL analysis based on FHB disease severity data identified two novel major FHB resistance QTLs located on chromosome arms 5AS and 5AL. The 5AS QTL peaked at marker *Xbarc40* between *Xcfa2104* and *Xgwm617*, and explained up to 20% of the phenotypic variation. The 5AL QTL explained up to 32% of the trait variation and peaked at *Xcfd39* between markers *Xwmc470* and *Xbarc48* (Chu et al. 2011). To make the best use of this novel source of FHB resistance, we propose to fine map the QTL, develop user-friendly DNA markers for their easy identification and transfer, and introgress the FHB resistance into adapted spring wheat varieties for better use in breeding programs. Therefore, the specific objectives of this project are to:

- 1) Conduct saturation mapping of the two PI 277012-derived FHB resistance QTLs in the double haploid (DH) population (Grandin × PI 277012) using various molecular marker techniques, including SSR, STS, and SNP.
- 2) Generate a large population of F<sub>2</sub> progeny from the cross between PI 277012 (resistance to FHB) and the hard red spring wheat cultivar ‘Grandin’ (susceptible to FHB) and conduct fine mapping of the QTL in PI 277012 using the recombinant lines.
- 3) Develop user-friendly DNA markers for marker assisted selection of the QTLs in breeding programs.
- 4) Introgress the FHB resistance from PI 277012 into adapted spring wheat varieties by crosses and backcrosses in combination with marker assisted selection and FHB evaluation.

Identification of new resistance alleles and DNA markers associated with them are essential for accelerating the development of FHB resistant wheat varieties by marker assisted selection and gene pyramiding. The improved FHB resistant lines from the crosses and backcrosses will be used as resistant sources for the spring wheat breeding programs in the region.