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Project Title: Fine Mapping and Utilization of FHB Resistance QTL Derived from PI 277012 in Spring Wheat.

PROJECT 2 ABSTRACT

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Previous studies indicated that the wheat line PI 277012 consistently showed a high level of resistance similar to Sumai 3 across all environments in both greenhouse and field experiments. Using a mapping population consisting of 130 doubled haploid (DH) lines from the cross between PI 277012 (resistant to FHB) and the hard red spring wheat cultivar 'Grandin' (susceptible to FHB), two major FHB resistance QTLs were mapped on chromosome arms 5AS and 5AL of PI 277012, respectively (Chu et al. 2011). The 5AS QTL peaked at the marker interval between *Xbarc180* and *Xgwm186*, and explained up to 20% of the phenotypic variation, while the 5AL QTL peaked at the interval between markers *Xwmc470* and *Xgwm595*, and explained up to 32% of the trait variation (Chu et al. 2011). More recently, we have genotyped the DH population using the wheat 9K-single nucleotide polymorphism (SNP) arrays and identified 4,317 polymorphic SNP markers that segregated in the population. Among these SNP markers, 25 and 13 SNP markers were positioned between *Xbarc180* and *Xgwm186*, and *Xwmc470* and *Xgwm595*, where the two major QTL are located, respectively. In this proposal, we plan to further fine map the FHB resistance QTL loci using a larger population of recombinant inbred lines (RILs) and to validate the FHB resistance introgressed into adapted spring wheat varieties. Therefore, the specific objectives of this project are to:

1) Genotype 1052 recombinant inbreed lines (RILs) from the cross between PI 277012 (resistance to FHB) and the hard red spring wheat cultivar 'Grandin' (susceptible to FHB) with targeted SNP markers.
2) Fine map QTL for FHB resistance in PI 277012 using the recombinant inbred lines from the cross between PI 277012 and Grandin.
3) Develop user-friendly DNA markers for marker assisted selection of the QTLs in breeding programs.
4) Evaluate and validate the FHB resistance QTL of advanced wheat lines derived from the crosses and backcrosses of PI 277012 to adapted spring wheat varieties.

The SNP markers identified by the 9k chips will be used to genotype the RILs as well as F2 population from the PI 277012/Grandin cross. Additional SNP markers will be developed using the chromosome 5A-specific sequencing data generated by the International Wheat Genome Sequencing Consortium (http://www.wheatgenome.org/) and used to genotype the recombinant populations. We will also phenotype the recombinants for reactions to FHB in greenhouse and field. Eventually, DNA markers that are most closely linked to the QTLs will be developed for marker assisted selection. In the meantime, introgression lines derived from crosses and backcrosses of PI 277012 to ND spring wheat varieties will also be characterized. Identification of DNA markers associated with the novel QTL will accelerate the development of FHB resistant wheat varieties by marker assisted selection and gene pyramiding. Improved germplasm with the novel FHB resistance QTL will be provided to the wheat breeders for developing FHB resistant varieties.