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**Project Title: Identification and Validation of FHB Resistance QTLs in Synthetic Wheat Lines.**

## **PROJECT 2 ABSTRACT**

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The synthetic hexaploid wheat (SHW) lines derived from crosses between tetraploid wheat (AABB genome) and *Aegilops tauschii* (D genome) possesses resistance to various diseases including Fusarium head blight (FHB). However, the genetics of FHB resistance in these synthetic lines is poorly understood. In the past two years, we identified three QTLs (on 5A, 5B and 7D, respectively) in the double haploid (DH) mapping population derived from the cross between the synthetic hexaploid wheat (SHW) line TA4152-60 (Scoop1/*Ae. tauschii* [358]) and a spring wheat line ND495 (susceptible to FHB). The QTLs were identified based on two seasons of greenhouse phenotyping and one season of field experiment. In this study, we will confirm the putative QTLs by conducting one more greenhouse experiment and one more field experiments. In addition, we will collect preliminary data on another mapping population derived from a cross between “Largo” (Langdon/*Ae. tauschii* PI 268210, developed by Dr. L. R. Joppa at USDA-ARS, Fargo) and ND495. “Largo” is a synthetic wheat line with a high level of FHB resistance based on several seasons of evaluation in the greenhouse. This synthetic wheat line is different from TA4152-60 by possessing resistance to tan spot (caused by *Pyrenophora tritici-repentis*), Stagonospora nodorum blotch (caused by *Phaeosphaeria nodorum*) in addition to FHB. The mapping population consists of 215 recombinant inbred lines (F<sub>7</sub> generation) from the cross between “Largo” and ND 495. We will evaluate the mapping populations along with their parents, resistant and susceptible checks for Type II resistance to fungal spread in the greenhouse in the spring and fall of 2010. Field data will be collected from two inoculated, misted nurseries in the summer of 2010. The resistant DH lines and RI lines will be used as resistant sources for the spring wheat breeding programs in the region. 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.