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Project Title: Mapping QTLs for Resistance to Fusarium Head Blight in a Synthetic Hexaploid Wheat Line TA4152-60.

PROJECT 1 ABSTRACT

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The synthetic hexaploid wheat (SHW) line TA4152-60 (Scoop1/*Ae.tauschii* [358]) developed by CYMMIT exhibited a high level of Type II resistance to FHB during two seasons of evaluation in the greenhouse and one season of test in the field. An average of 13% disease severity was recorded for TA4152-60, which is slightly higher than that (10%) in the resistant check Sumai 3 but much lower compared to the 60% severity in the susceptible checks. Based on the pedigree and the fact that the durum wheat parent is highly susceptible to FHB, the resistance alleles in this SHW line could be different from other QTLs that have been mapped in hexaploid wheat. A mapping population was generated, consists of 210 double haploid (DH) lines from the cross between a hard spring wheat line ND 495 (highly susceptible to FHB) and TA4152-60. A genetic map was also developed from the cross using 643 DNA markers. Our overall goal is to identify QTLs for the FHB resistance and identify DNA markers associated with the QTLs in TA4152-60. Therefore, the specific objectives of this project are:

1) Obtain phenotype data of the DH population derived from TA4152-60/ ND 495;
2) Understand the inheritance and action mode of the FHB resistance in TA4152-60;
3) Identify QTLs for the FHB resistance based on the genetic map developed.

We will evaluate the mapping population in greenhouse and field trials for FHB incidence, FHB severity, and DON content. The phenotype data will be used to analyze the inheritance and action mode of the FHB resistance in TA4152-60 and identify the genomic regions with QTL for FHB resistance using the genetic linkage map developed from the same population. The FHB resistance-associated DNA markers identified will facilitate the transfer of the resistance loci into spring wheat varieties. The proposed research addresses the following research priorities in the Action Plan: increase efficiency of individual breeding programs to develop FHB resistant varieties, efficiently introgress effective resistance genes into breeding germplasm, and develop and map diagnostic markers for effective sources of FHB resistance.