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Project Title: Identify and Map Novel QTL for FHB Resistance Introduced into Durum Wheat.

PROJECT 1 ABSTRACT

(1 Page Limit)

Deployment of FHB resistance is a major strategy for reducing the impact of FHB on durum wheat and hexaploid common wheat. However, lack of useful and effective sources of FHB resistance in durum wheat varieties remains to be a problem for developing durum varieties with a high level of resistance to FHB. In the past years, great efforts have been devoted to introgress FHB resistance from tetraploid and hexaploid wheat accessions into adapted durum wheat cultivars. However, most of the QTL for FHB resistance existing in the introgression lines are not well characterized or validated. In this proposal, we plan to identify and map QTLs for FHB resistance in two durum wheat genotypes 10Ae564 and Joppa, which carry known and unknown sources of FHB resistance. 10Ae564 is a BC1F8 durum wheat line, derived from cross and backcross of the durum wheat cultivar Lebsock to PI 277012, a hexaploid wheat line with major FHB resistance QTL on 5A. Joppa is a newly released durum wheat cultivar with the least susceptibility to FHB and lowest DON accumulation in grains among durum wheat cultivars currently grown in ND. However, the QTL for FHB resistance in Joppa have not been identified and mapped because the pedigree of Joppa does not involve any known sources of FHB resistance. Our overall goal is to identify effective FHB resistance QTL and associated DNA markers, and eventually introgress them into the cultivated durum varieties as germplasm for breeding FHB resistant durum varieties. A mapping population consisting of 241 recombinant inbred lines (RILs) derived from the cross between Joppa and 10Ae564 is being developed. Therefore, the specific objectives of this proposal are to:

- *Develop a genetic linkage map using a mapping population derived from the cross between Joppa and 10Ae564;*
- *Phenotype FHB resistance and morphological traits of the mapping population from the Joppa/10Ae564 cross;*
- *Identify DNA markers linked to QTL for FHB resistance in Joppa and 10Ae564.*

The RILs and their parents will be genotyped using the wheat 9K-SNP arrays and polymorphic SNP markers will be identified and used for genetic map construction. FHB evaluations will be conducted in greenhouse and field FHB nurseries in multiple seasons and locations. The marker data and genetic map along with the FHB phenotype data will be used for QTL analysis. Composite interval mapping (CIM) will be performed using the software Windows QTL Cartographer Version 2.5 (Wang et al. 2012; http://statgen.ncsu.edu/qtlcart/WQTLCart.htm) to determine the genomic regions (marker intervals) associated with FHB resistance. Identification of DNA markers associated with the FHB resistance QTL will accelerate the development of FHB resistant wheat varieties by marker assisted selection and gene pyramiding. Durum wheat germplasm with improved FHB resistance will be generated through the introgression process and provided to breeders (Dr. Elias and others) for developing FHB resistant varieties or germplasm.