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PROJECT 1 ABSTRACT

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Durum lines that are genetically resistant to FHB are critical to continued production of this important crop in the US. Despite concerted effort of DUR-CP researchers and advances in recent years, there is a need to develop even more resistant durum cultivars. Our association analysis, based on lines derived from crossing of five Tunisian tetraploid sources of resistance with durum cultivars 'Ben', 'Maier', 'Lebsock' and 'Mountrail', has proven powerful. Several significant QTL regions for FHB resistance as well as DON accumulation and FDK were identified. A possibility of having susceptibility or suppressor of resistance gene(s) on durum wheat chromosome 2A was further confirmed in this material explaining the problem in developing resistant genotypes without counter selection against this region. The outcomes of these projects were germplasm that can be easily incorporated into the breeding programs to derive more resistant cultivars. We plan to take the most significant of these QTL regions to pyramid in selected durum cultivars.

Additionally, past attempts at transfer of resistance genes/QTLs from hexaploid sources into durum wheat have met with limited success. Various studies, including several by our groups, suggest that either the cultivated durum genome carries a suppressor of FHB resistance or is missing enhancers of resistance on D-genome chromosomes. To test these hypotheses, we treated six advanced durum breeding lines with 5-Methyl-azacytedine that removes CG methylation. The resulting lines were advanced to the M_4 generation and tested for FHB resistance under both the greenhouse and field conditions with 24 lines identified that show great promise having less than 20% infection as compared with 80-100% value for parental lines and checks, a highly significant difference. We plan to further advance these lines and cross them with the parental cultivars to test the stability and inheritance of resistance. Additionally, we plan to analyze the changes in DNA methylation and transcription levels. In a similar project we plant to initiate the development of deletions for portions of chromosome 2A. The immediate objectives are:

1. continue with pyramiding of the FHB resistance regions on chromosomes 5AL, 5BL and 2BL identified in Tunisian derived lines into durum cultivars;
2. develop diagnostic markers for routine and effective screening of breeding populations;
3. characterize the epigenetic changes of FHB resistant durum cultivars produced by altering the DNA methylation pattern, and
4. characterize durum cultivars missing portions of chromosome 2A region that may contain a FHB suppressor locus.

The ultimate objectives of this project are to incorporate the QTL regions identified in Tunisian derived germplasm into advanced durum breeding lines, and to enhance the resistance in durum cultivars by removal of a persistent suppression mechanism.