

PI: Kianian, Shahryar**PI's E-mail: S.Kianian@ndsu.edu****Project ID: FY06-KI-114****FY05 ARS Agreement #: 59-0790-4-109****Research Area: HGG****Duration of Award: 1 Year****Project Title: Development of Markers Linked to FHB Resistance in Durum Wheat.****PROJECT 1 ABSTRACT**

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North Dakota leads the nation, by far, in total acreage and production of durum wheat. The extensive economic damage caused by *Fusarium* head blight (FHB) or scab to the North Dakota durum and wheat producers is well recognized. The most cost-effective way of reducing losses from this devastating disease is through the development of genetic resistance in the host plant. Once resistance genes are identified, transfer into adapted wheat germplasm remains a lengthy and difficult task because undesirable traits generally accompany the transfer. In durum wheat this process is confounded by the effect of hexaploid to tetraploid crosses and complications that arise due to the aneuploidy of an entire genome (D-genome). Additionally, certain regions prove to be less effective in durum background than bread wheat genetic background. Markers linked to resistance genes can accelerate selection, germplasm development and time to variety release expediting this process and providing diverse germplasm for durum breeding. The specific objectives of this project are to:

- 1) **identify QTL region(s) for FHB resistance in Wangshuibai derived RIL populations of durum wheat;**
- 2) **develop the populations and methodology to quickly screen number of tetraploid FHB resistant sources from Tunisia; and**
- 3) **demonstrate the utility of the work by analysis of populations developed for breeding programs.**

We have developed 274 Wangshuibai derived (a resistant source from China) recombinant inbred lines (RILs) and are in the process of screening this population for molecular markers. Results to date indicate that the 3BS QTL (major QTL from this source in hexaploid wheat crosses) plays a less important role in durum wheat. Additional analysis is continuing to identify other regions and associated markers that are critical to FHB resistance and help selection of backcross derived breeding lines under development from this source. In over 55 replicated FHB trials conducted by the durum wheat breeding program at NDSU, five tetraploid resistant lines from Tunisia were identified. Analysis of these lines using RILs or double haploid (DH) populations is time consuming and slows progress toward development of resistant cultivar. We plan to employ modified association mapping strategies to identify markers linked to resistance regions in early generation breeding lines to aid the selection process and speed time required for variety release. . In this project we will use all marker classes to identify and develop PCR based "breeder friendly" markers to aid the breeding programs as well as combine the resistance QTL from *T. dicoccoides*, Sumai3, Wangshuibai and other new sources of resistance in a single variety.