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PROJECT 1 ABSTRACT

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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. Analysis of North Dakota hard red spring (HRS) wheat lines carrying Sumai3 derived FHB resistance, their susceptible parental and sister lines indicated the presence of a QTL region significantly associated with resistance on 3BS. Even though, this study only confirmed previous results it proved that association mapping methodologies can be developed and adapted to plant populations for a relatively quick and statistically robust study. Populations of 388 F₆ derived lines from crosses of Wangshuibai to ND674 (adapted HRS line) and reciprocal cross have been developed. Quantitative trait locus analysis indicates a significant effect on 3BS at 14 and 21 days post inoculation. However, secondary loci with major epistatic interactions with the 3BS QTL have been identified that in some cases explain close to 67% of the phenotypic variance. We have also developed lines from various sources that show significant reduction in FHB infection (in certain cases they are almost tolerant). Thus, the specific objectives of this project are:

- 1. identify important epistatic interactions among FHB resistance QTL regions derived from Wangshuibai for efficient pyramiding into wheat cultivars;**
- 2. analyze early generation lines derived from cltr9445, a Chinese source of resistance, for the presence of important FHB QTL regions; and**
- 3. identify chromosomal regions introgressed into HRS wheat associated with FHB resistance derived from two *Triticum dicoccoides* accessions (PI478472 and PI48121)**

Specifically, we would like to perform a more detailed analysis of Wangshuibai recombinant inbred line population for epistatic interactions for they are important for efficient and effective pyramiding of resistance loci in a single cultivar. The accession Cltr9445 is possibly one of the most Type II FHB resistant lines identified to date (score of 5% or less). Crosses with this line are in early generation. Therefore, we would like to perform Transmission Disequilibrium Test to identify the resistance QTL contributed by this accession. This type of analysis will allow us to determine the utility of such an approach (extensively used in human genetics) in plant populations for quick determination and identification of important regions. We also have developed introgression lines from *T. dicoccoides* which show promising levels of resistance. Marker analysis is necessary to determine the important regions for efficient marker assisted selection project and reduction of donor parent background.