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PROJECT 2 ABSTRACT

(1 Page Limit)

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. We have developed lines from various sources (Cltr9445 a Chinese accession, PI478472 and PI48121 *T. dicoccoides* accessions) that show significant reduction in FHB infection (in certain cases they are almost tolerant). Thus, the specific objectives of this project are:

- 1. complete analysis of early generation lines derived from Cltr 9445 for the presence of important FHB QTL regions;**
- 2. identify chromosomal regions introgressed into HRS wheat associated with FHB resistance derived from two *Triticum dicoccoides* accessions (PI478472 and PI48121); and**
- 3. develop the populations for early generation analysis of lines derived from five different sources (PI 192863, PI 349478, PI 382154, PI 382161, PI 382167) of FHB resistance.**

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 (i.e. association mapping) 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.