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Project ID: 0304-KI-110
Research Area: BIO

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ARS Agreement #: 59-0790-9-48
Duration of Award: 1 Year

Project Title: Development of markers linked to FHB resistance in hexaploid wheat.

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. Majority of these lines have now been evaluated for FHB resistance in both greenhouse and field over 6 seasons. The resistant lines from this population are even more resistant than the lines derived from Sumai3. Mapping of these populations and QTL identification is now underway. The need for investigation of FHB resistance in this population as well as identification of different sources of FHB resistance is evident. Thus, the specific objectives of this project are:

- 1. identify QTL region(s) for FHB resistance in ND671/Wangshuibai RIL population**
- 2. analyze early generation lines derived from cltr9445, a Chinese source of resistance, for the presence of important FHB QTL regions**
- 3. develop populations from new sources of FHB resistance for introgression of important regions into hexaploid wheat**

Specifically, we would like to perform a more detailed analysis of Wangshuibai recombinant inbred line population for it holds great promise as a new source of FHB resistance gene(s). 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 plan to initiate crosses involving sources of FHB resistance from differing geographical regions to identify loci valuable for pyramiding in a common background.