PI: Xiwen Cai
PI's E-mail: xiwen.cai@ndsu.nodak.edu

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PROJECT 1 ABSTRACT
(1 Page Limit)

Fusarium head blight (FHB) has been a major threat to the production of wheat and barley in the United States. Limited sources of partial resistance to FHB have been identified in common wheat. A source of effective resistance to FHB has not been found in durum wheat. Screening of wild tetraploid wheat (*Triticum dicoccoides*) accessions for FHB resistance has identified an accession carrying resistance gene(s) to FHB, which holds promise for the development of durum wheat cultivars resistant to FHB. Recombinant inbred chromosome lines (RICLs) are the ideal materials for mapping and cloning of genes. A major quantitative trait locus (QTL) that explains 55% of the genetic variance for FHB resistance, *Qfhs.ndsu-3AS*, was identified using *T. durum* cv. Langdon-*T. dicoccoides* chromosome 3A recombinant inbred chromosome lines. To date, a genetic map of chromosome 3A with 51 molecular markers spanning a map distance of 244.9 cM has been constructed and *Qfhs.ndsu-3AS* has been positioned within a 9.4 cM chromosomal interval. This project will continue generating new markers to saturate this chromosomal region and screening the large F_2 population (>4,000 individuals) to identify more chromosomal recombinants in the QTL region. This will allow for construction of a fine map of this QTL region and placement of the QTL in a smaller chromosomal interval. Comparative analysis of *Qfhs.ndsu-3AS* and the FHB resistance QTL on 3BS *Qfhs.ndsu-3BS* in common wheat indicated that they are not homoeologous loci. Accomplishment of this project will drive us closer to reach the long term goal - cloning of the FHB resistance gene(s). The specific objectives of this project are to:

1. **Assign more markers to the 9.4 cM chromosomal interval spanning *Qfhs.ndsu-3AS*;**
2. **Generate more recombinants within the *Qfhs.ndsu-3AS* region;**
3. **Place *Qfhs.ndsu-3AS* within a smaller chromosomal interval.**

The results obtained from this project will be invaluable in understanding the molecular mechanism of resistance to FHB, and possible isolation of the gene(s) underlying this QTL. Gene(s) that are identified can then be used in collaboration with other researchers to generate transgenic barley and wheat and evaluate its efficacy in conferring resistance to FHB. Additionally, understanding the basic molecular mechanisms involved in resistance to FHB will help devise schemes for developing more resistant lines and cultivars.