PI: Cai, Xiwen	PI's E-mail: xiwen.cai@ndsu.edu
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## **PROJECT 1 ABSTRACT** (1 Page Limit)

A source of effective resistance to FHB has not been found in durum wheat. *Qfhs.ndsu-3AS* is a major FHB resistance QTL derived from wild tetraploid wheat (*Triticum dicoccoides*) and has been mapped to the short arm of chromosome 3A in a population of 83 recombinant inbred chromosome lines (RICLs). It has been used to enhance resistance of durum wheat to FHB. We have saturated the chromosomal region harboring *Qfhs.ndsu-3AS* with newly developed molecular markers (STS and SSR) and identified rice genomic regions collinear with the QTL region through comparative mapping. Meanwhile, we have been increasing resolution of the QTL map using a large  $F_2$  population (>2,000 individuals) segregating only at the loci within the QTL region (10.7 cM). Here we propose to further saturate the chromosomal interval harboring *Qfhs.ndsu-3AS*, to genotype the large  $F_2$  population for identifying more recombinants near the QTL, and to develop user-friendly molecular markers for marker-assisted selection (MAS), haplotyping, and gene pyramiding in breeding and germplasm development. This will further increase resolution of the QTL map and position the QTL in a smaller chromosomal interval. Construction of a fine map of *Qfhs.ndsu-3AS* will facilitate cloning of this QTL and development of effective molecular markers for MAS. The specific objectives of this project during this funding period are to:

- 1. Identify more molecular markers to further saturate the chromosome region harboring *Qfhs.ndsu-3AS*;
- 2. Increase resolution of the QTL map and position the QTL to a smaller chromosomal interval;
- **3.** Develop more user-friendly markers for MAS and haplotyping in breeding and germplasm development.

Results obtained from this project will be invaluable in understanding the molecular mechanism of resistance to FHB, and isolation of the gene(s) underlying this QTL. The gene identified can then be used in collaboration with other researchers to generate transgenic wheat and barley and evaluate its efficacy in conferring resistance to FHB. Additionally, understanding the basic molecular mechanisms of FHB resistance will help devise schemes for developing more resistant germplasm and cultivars. Generation of user-friendly markers will be useful in selection of the QTL in breeding and germplasm development and facilitate utilization of the resistance source in variety development.