

PI: Cai, Xiwen**Project ID: 0304-CA-103****Research Area: BIO****Project Title: Saturation and Physical mapping of *Qfhs.ndsu-3AS* in durum wheat.****PI's E-mail: xiwen.cai@ndsu.nodak.edu****ARS Agreement #: NEW****Duration of Award: 1 Year**

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. The identification of *Triticum dicoccoides* accessions that are resistant to FHB holds promise for the development of durum that is resistant to FHB. The development of Langdon-dicoccoides recombinant inbred chromosome lines (RICLs) allows for the rapid assignment of molecular markers to the region of *T. dicoccoides* chromosome 3A substituted in Langdon durum. We have identified *Qfhs.ndsu-3AS*, a major quantitative trait locus (QTL) that explains 55% of the genetic variance for FHB resistance. A DNA-based probe, NDSU.fhb3A derived from a microsatellite marker that is tightly linked to this locus has been placed in the chromosomal bin location 3AS4-0.45-1.00 of the wheat physical map. A *T. monococcum* bacterial artificial chromosome (BAC) high-density filter set was screened with this probe and identified fifteen BAC clones. Sequence information from wheat expressed sequence tags (ESTs) is available and has been used to develop molecular markers for saturation of *Qfhs.ndsu-3AS* region. In addition to these resources cytogenetic deletion stocks of group 3A of *T. aestivum* cv. 'Chinese Spring' are available that will help assign newly generated markers, and BAC clones and subclones onto the wheat physical map. We propose to use these valuable tools to generate a saturated map around this major FHB QTL and estimate the genetic to physical distance within this region. The specific objectives of this project are to:

- 1. Screen a population of over 4000 individuals for recombination within *Qfhs.ndsu-3AS* segment using flanking molecular markers**
- 2. Develop a saturated map of *Qfhs.ndsu-3AS* region**
- 3. Determine the physical to genetic distance ratio within the *Qfhs.ndsu-3AS* region**

The results obtained from this project will be invaluable in helping understand 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 researchers generating transgenic barley and wheat to 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 line and cultivars.