PI: James Anderson **PI's E-mail: ander319@umn.edu**

Project ID: 0405-AN-075 **FY03 ARS Agreement #: 59-0790-9-025**

Research Area: **BIO** **Duration of Award: 1 Year**

Project Title: High Resolution Mapping of a Fusarium Head Blight Resistance QTL in Wheat.

PROJECT 1 ABSTRACT
(1 Page Limit)

A major QTL (*Qfhs.ndsu-3BS*) for FHB (Fusarium head blight) resistance, derived from 'Sumai 3', has been identified and verified by several research groups via molecular marker analysis. Further research of this major QTL is justified by the significant and consistent effect of this QTL. We have developed a strategy to quickly add additional DNA markers to this QTL region and have developed a high resolution map based on 1,600 F_2's developed from F_7-derived NILs.

The objectives of this proposal are to:
1) Develop and map more DNA markers in the fine map region containing *Qfhs.ndsu-3BS*.
2) Select more recombinants in the *Xgwm533 – Xgwm493* interval from another 1600 F_2 plants, and further narrow down the genomic region containing *Qfhs.ndsu-3BS*.
3) Screen a BAC library and construct a BAC contig spanning the *Qfhs.ndsu-3BS* region.

After we place *Qfhs.ndsu-3BS* on the current high resolution map (Fall 2003 and Spring 2004), we will continue to exploit the rice or barley sequences of the orthologous region and all wheat ESTs in GenBank to develop DNA markers close to *Qfhs.ndsu-3BS*. To increase the likelihood of identifying polymorphisms of these markers on the fine mapping population we will design primers based on the 3' UTR region, develop CAP or SNP markers. To find additional recombinants in the *Qfhs.ndsu-3BS* region, another 1600 F_2 plants from the same NIL population will be screened with markers already mapped on the fine mapping population and additional markers to construct a new high resolution map of the region. FHB data of the homozygous recombinants will be used to further narrow down the genomic region containing *Qfhs.ndsu-3BS*. Homozygous recombinants will be screened by point inoculation at the University of Minnesota and North Dakota State University. Forty to fifty spikes of genotype will be assessed in each test. On the basis of results from objective 2) above, the DNA marker closest to *Qfhs.ndsu-3BS* will be used to screen a wheat chromosome 3B BAC library. Positive BAC clones will be fingerprinted to begin making a BAC contig of the region, and eventual cloning of *Qfhs.ndsu-3BS*.