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A source of effective resistance to FHB has not been found in durum wheat. Introgression of FHB resistance from common wheat to durum has not been successful. Screening of wild tetraploid wheat (*Triticum dicoccoides*) accessions for FHB resistance identified an accession carrying resistance gene(s) to FHB, which may hold 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 the economically important 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 total of 10 molecular marker loci have been detected in the chromosomal interval harboring *Qfhs.ndsu-3AS*. Assignment of two new EST-derived STS markers (*Xwgc500* and *Xwgc501*) to this QTL region extended map distance of this chromosomal region to 10.3 cM. This project will continue making efforts to saturate this chromosomal region, screening the large F₂ population (>1,000 individuals) to identify more recombinants near the QTL, and developing user-friendly molecular markers for marker-assisted selection (MAS) in breeding. This will further increase the resolution of the QTL map and position the QTL in a smaller chromosomal interval. Comparative analysis of *Qfhs.ndsu-3AS* and *Fhb1* on 3BS in common wheat indicated that they are not homoeologous loci. Construction of a fine map of *Qfhs.ndsu-3AS* will facilitate cloning of this QTL and development of effective molecular markers for MAS in breeding. The specific objectives of this project during this funding period are to:

- 1. Detect more molecular marker loci closely linked to *Qfhs.ndsu-3AS*;**
- 2. Generate more recombinants within the chromosomal region harboring *Qfhs.ndsu-3AS* and position the QTL to a smaller chromosomal interval;**
- 3. Develop more user-friendly markers for MAS in breeding.**

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 facilitate utilization of the resistance source in variety development.