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Fusarium head blight (FHB) has been a major threat to wheat and barley production 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 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 genetic map of chromosome 3A with 60 molecular markers spanning a map distance of 162.2 cM has been constructed and *Qfhs.ndsu-3AS* has been positioned within a 6.8 cM chromosomal interval. This project will continue making efforts to saturate this chromosomal region and screening the large F₂ population (>4,000 individuals) to identify more chromosomal recombinants in the QTL region. This will allow us to increase the resolution of the QTL map and position the QTL in a smaller chromosomal interval. Comparative analysis of *Qfhs.ndsu-3AS* and the FHB resistance QTL *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 QTL *Qfhs.ndsu-3AS*. The specific objectives of this project are to:

- 1. Assign more markers to the chromosomal region spanning *Qfhs.ndsu-3AS*;**
- 2. Generate more recombinants within the *Qfhs.ndsu-3AS* region and position the QTL within a smaller chromosomal interval;**
- 3. Develop user-friendly markers to assist selection for the QTL 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 involved in resistance to FHB will help devise schemes for developing more resistant lines and cultivars. Generation of user-friendly markers will be helpful in selection of the QTL in breeding and facilitate utilization of the resistance source in variety development.