0203-KA-058 Saturation Mapping and Contig Development for Qfhs.ndsu-3AS, a Major FHB Locus in Durum Wheat.

PI: Kalavacharla, Venugopal S.; E-mail: venu.kalavacharla@ndsu.nodak.edu
North Dakota State University, Department of Plant Sciences, Fargo, ND 58105
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PROJECT ABSTRACT
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Fusarium head blight (FHB) is 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 substitution lines (RICLs) allows 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 aritificial 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 for development of molecular markers and to conduct saturation mapping of the region around *Qfhs.ndsu-3AS.* In addition to these resources cytogenetic deletion stocks of group 3A of *T. aestivum* cultivar Chinese Spring are available that will help assign newly generated molecular markers, and BAC clones and subclones from the *T. monococcum* BAC library onto the wheat physical map. We propose to use these valuable tools to generate a saturated map around this major FHB QTL. The specific objectives of this project are to:

1) **Develop a highly saturated linkage map for the region surrounding *Qfhs.ndsu-3AS* (short term objective);**
2) **Develop a BAC contig containing the *Qfhs.ndsu-3AS* (medium term objective);**

The results obtained from this research will be invaluable in helping understand the molecular mechanisms 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 lines.