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PROJECT 1 ABSTRACT
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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. The poor DNA marker density necessitates the efforts of saturation mapping of this major QTL.

The objectives of this proposal are to:

1) increase marker density near *Qfhs.ndsu-3BS* using wheat ESTs
2) select recombinants in the *Xgwm533 – Xgwm493* interval from a fine mapping population of 3000 F_2 plants from a cross between two near isogenic lines (NILs) for *Qfhs.ndsu-3BS*
3) Collect FHB phenotype data on selected recombinants to further narrow the location of *Qfhs.ndsu-3BS* Wheat ESTs that have similarity with the sequences of rice PAC/BAC clones located on the distal region of chromosome 1S will be identified with BLASTN search.

Wheat ESTs located on chromosome bin 3BS 0.78-1.00 will also be retrieved from the deletion mapping results of the NSF-funded U.S. wheat EST project. STS (sequence tagged site) primers will be designed from the sequences of non-redundant wheat ESTs. CAP (cleaved amplified polymorphism) markers or SNP (single nucleotide polymorphism) markers will be exploited as needed to convert monomorphic STS markers to polymorphic markers.

One pair of NILs (near isogenic lines) for *Qfhs.ndsu-3BS*, derived from heterozygous plants of advanced breeding lines, will be crossed to generate a fine mapping population. We plan to genotype the F_2 population of 3,000 with markers *Xgwm533* and *Xgwm493*. The recombinants will be screened with additional polymorphic markers located on the deletion bin 3BS 0.78-0.87 to develop a high resolution map. The seeds of recombinants will be increased and homozygous recombinants with crossovers near the major QTL will be selected as needed. A subset of 20 recombinants will be tested for FHB reaction in greenhouse tests to narrow the location of this QTL.

The DNA markers that will be developed in this project will provide wheat breeders with more options for marker-assisted selection and thus expedite the process of developing varieties with FHB resistance. Moreover, the recombinants that will be identified in this project can be used to precisely locate this major QTL, and the saturation mapping will lead to eventual map-based cloning of this major QTL. . Therefore, the objectives of this proposal relate directly to the U.S. Wheat and Barley Scab Initiative's overall goal of minimizing the threat of FHB.