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PROJECT 1 ABSTRACT

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We will continue developing new STS and SSR markers near the FHB resistance QTL *Qfhs.ndsu-3AS* and increasing marker density within the chromosomal interval harboring this QTL. We have identified a number of unmapped wheat ESTs and BACs using molecular markers flanking the QTL and comparative analysis of corresponding genomic regions in wheat, rice, and *Brachypodium distachyon*. We will use the ESTs and BAC end sequences to develop more STS and SSR markers closely linked to the QTL. Meanwhile, we will increase the F_2 population size to 2,000 individuals and genotype the large population at 4-6 molecular marker loci flanking the QTL. This allows for the identification of new recombinants within the chromosomal interval containing the QTL. Then we will identify homozygous recombinants among the F_3 progeny derived from recobinant F_2 individuals. These homozygous recombinants will be evaluated for FHB resistance in a replicated trial. Eventually this FHB resistance QTL will be positioned within a smaller chromosomal interval and resolution of this QTL map will be significantly increased. In addition, we will provide more effective molecular markers for MAS and haplotyping of this QTL in breeding and germplasm development. The specific objectives of this project for year 2 are to:

1) Develop new STS and SSR markers to further saturate the chromosomal interval containing *Qfhs.ndsu-3AS*;
2) Increase resolution of the QTL map by genotyping and phenotyping a larger segregating population (2,000 individuals);
3) Provide more user-friendly molecular markers to assist selection and pyramiding of this QTL in breeding and germplasm development.