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Research Category: **VDHR-SPR** **Duration of Award: 1 Year**

Project Title: Mapping of an Inhibitor of Fhb1, the Major QTL for FHB Resistance in Wheat.

PROJECT 2 ABSTRACT

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The literature contains many reports of QTLs for FHB resistance being derived from the "susceptible" parent in biparental crosses. While investigating *Fhb1* candidate genes as part of our ongoing efforts to clone this gene, we discovered that the recipient genotype, 'Bobwhite' inhibited the effect of *Fhb1*. A mapping population fixed for the Sumai 3 *Fhb1* allele is being developed from the cross 260-2/Bobwhite. This population will be at the F_6 generation in Fall 2010 when we plan to conduct point inoculations in the greenhouse to map genetic factor(s) that affect *Fhb1* penetrance. The major outcome of this research will be the knowledge of the location of gene(s) inhibiting the affect of *Fhb1*. This could be important for breeders as this knowledge may help explain why *Fhb1* (and possibly other FHB QTLs) show little or no affect in some genetic backgrounds. Breeders may avoid using parents shown to have inhibitory effects in their crossing program or use the marker(s) we intend to develop to eliminate this gene from progeny lines.

The objectives of this project are to:

1) Map an inhibitor of *Fhb1*
2) Develop diagnostic DNA markers for this inhibitor.
3) Haplotype spring wheat germplasm for presence of the *Fhb1* inhibitor.

A population of 600 lines at the F_3 generation was produced in summer 2009. This population will be advanced by single seed descent to the F_5 generation. After attrition and selecting only lines homozygous for *Fhb1* (using marker UMN10), we expect to have a population of 150-200 RILs. Seeds from single F_5 plants will be bulked and used to grow $F_{5:6}$ families for point inoculation screening (Type II, resistance to fungal spread) in the greenhouse in the fall 2010 and spring 2011. Because we have evidence that a single gene is responsible for the inhibitory effects on *Fhb1*, we will use Bulked Segregant Analysis (BSA) to identify the genomic region containing the inhibitor. Bulks of DNA will be formed using 20 resistant and 20 susceptible individuals from the population. The two BSA samples and parental DNA will be sent for DArT mapping. SSR markers near the region indicated by the DArT markers will be targeted for polymorphism screen and subsequent mapping in the entire population.

During year two of this project we expect to map at least one diagnostic marker that is within 1cM of the inhibitor. Additional marker resources available at the time (2010-2011) will be exploited to identify more closely linked, diagnostic markers. These are likely to include ESTs and SNPs.

The diagnostic marker(s) developed will be used to screen the 2008, 2009, 2010, and 2011 hard red spring regional yield and FHB nurseries. This is the most heavily used parental germplasm in the region and will provide an indication of how widespread this gene may be in the spring wheat germplasm. In addition, all U of MN lines in 2011 yield trials (approximately 700 total lines) will be screened for presence of the inhibitor.