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

Project Title: Improving FHB Resistance in SRW Wheat via Integrated Mapping, Phenotypic and MAS.

PROJECT 2 ABSTRACT

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Objectives: 1) Increase acreage planted to FHB and DON resistant cultivars via generation and dissemination of competitive cultivars having effective and enhanced levels of resistance, and implement grower adoption of best management strategies including use of resistant cultivars, disease forecasting, and fungicides; 2) Increase efficiency of CP breeding programs to develop and release FHB resistant cultivars via collaborative efforts to accelerate and improve phenotypic characterization of commercial cultivars, elite breeding lines, mapping and breeding populations to enhance FHB resistance via gene introgression and pyramiding and; 3) Develop new breeding technologies and germplasm to enhance improvement of FHB resistance via mapping and development and application of diagnostic markers for target FHB resistance QTL present in native and exotic sources of FHB resistance.

Problems and rational of the projects: Scab epidemics were widespread in Virginia in 1998 and resulted in significant losses in yield and quality. In 2003 and 2009 scab epidemics devastated much of the wheat crop in Virginia and the southeastern U.S. Currently, production of cultivars having moderate FHB resistance derived predominantly from native sources, and fungicide applications offer the primary means of disease control. However, neither control strategy provides optimal protection in years of severe epidemics. Extensive and collaborative phenotypic and genotypic characterization of FHB resistance in elite breeding lines, commercial cultivars, and mapping populations is needed to generate reliable information on the type, effectiveness and diversity of FHB resistance, and to facilitate MAS and pyramiding of complementary FHB resistance genes. Enhanced efforts are needed to develop cultivars and readily available superior parental lines having gene *Fhb1* derived from Chinese germplasm and for thorough characterization, mapping, and marker development of resistance in native sources. Lack of elite and locally adapted FHB resistant germplasm and diagnostic markers for use in gene introgression and pyramiding greatly hinder efforts to develop competitive cultivars having enhanced levels of FHB resistance.

Project approaches: Each year approximately 300 new crosses will be made, 300 to 500 breeding populations will be evaluated and advanced in an inoculated, mist irrigated scab nursery, pure lines will be selected among 5000 to 8000 headrows, 600 to 700 selected lines will be evaluated in observation, preliminary, advance or state yield trials at two to seven locations and in the scab nursery. Approximately 150 elite lines in the GAWN and Mason Dixon regional nursery will be evaluated in replicated yield trials and in the scab nursery. Entries (~180) in the southern, northern, and preliminary northern uniform winter wheat scab nurseries will be evaluated in the scab nursery and for reaction to other diseases at a second location, and lines in the southern test also will be harvested for grain quality analyses and evaluated for type II resistance in greenhouse tests. Research will focus on enhanced MAS breeding efforts in selection of parents, designing crosses, gene introgression and pyramiding, population enrichment, and selection of pure lines. Marker haplotypes of parents for validated FHB resistance QTL and other traits of importance such as dwarfing genes, disease and insect resistance, rye translocations, and quality will be assessed and utilized to enhance breeding efficiency. We will continue to collaborate with the University of Kentucky, University of Maryland, North Carolina State University, and USDA-ARS Genotyping Center on introgression of gene *Fhb1* and other QTL derived from Asian, South American, native, and wild relative sources into the SRW wheat cultivars. About 200 F_5 headrows from a top cross population having FHB resistance derived from Tribute, Futai8994, and Ernie will be evaluated and selections made via MAS and phenotypic selection. Populations being advanced and enrichment for FHB resistance, derived from Ernie and Sumai 3, and other important traits include 17 F_3, six F_2, and eight F_1 three-way populations.

We will continue fine mapping of the FHB resistance QTL in Massey (154 Becker/Massey F_{13} RILs) as two major QTL are associated with dwarfing genes *Rht1* and *Rht2*. Two minor QTL are also associated with *Rht8* and *Ppd1* genes. Available markers will be tested in our VA00W-38/Pioneer26R46 population (200 F_8 RILs) to gain a better understanding of scab resistance QTL in native sources. We will validate the major scab resistance QTL for each resistance source and diagnostic markers will be developed and tested in collaboration with the genotyping center. Phenotypic data collected in field and greenhouse experiments indicate that Tribute likely possesses resistance to both FHB and DON, and haplotyping results indicate that Tribute does not have common target alleles for QTL of Sumai3 and Ernie. A DH mapping population (Tribute/Pioneer 26R46) is currently being developed at CIMMYT to characterize FHB resistance in Tribute. We will initiate cooperative genetic mapping with the genotyping center and regional phenotyping of the population once seeds are available.