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**Research Category: VDHR-SWW**

**Duration of Award: 1 Year**

**Project Title: Improving FHB Resistance in SRWW via Breeding, MAS and Mapping in Native Sources.**

## **PROJECT 2 ABSTRACT**

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Scab epidemics were widespread in Virginia in 1998 and 2013, and devastated much of the wheat crop in 2003 and 2009. 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 marker assisted selection (MAS) and pyramiding of complementary FHB resistance genes.

Each year more than 600 new crosses, including at least one FHB resistant parent, will be made, and about 300 breeding populations will be evaluated and advanced in an inoculated, mist irrigated scab nursery. Pure lines will be selected among 5,000 to 10,000 headrows, 500 to 600 selected lines will be evaluated in observation, preliminary, advance, or state yield trials at two to seven locations and in a scab nursery. Data on FHB incidence, severity, and DON will be obtained from the scab nursery. FHB and DON data for entries in the state's official variety trial will be reported along with standard agronomic data in the annual Small Grains Variety Bulletin and posted online to promote selection and production of FHB resistant cultivars. Approximately 140 elite lines in the GAWN and Mason Dixon regional nurseries will be evaluated in replicated yield trials and in a scab nursery. Entries (~180) in the southern, northern, and preliminary northern uniform winter wheat scab nurseries will be evaluated in a mist irrigated scab nursery and in observation yield tests for agronomic performance and reaction to other diseases at a second location; grain samples will be sent to the SWQL for quality analyses.

Research will focus on enhanced MAS breeding and genomic selection (GS) to facilitate selection of parents, designing crosses, gene introgression and pyramiding, population enrichment, and selection of pure lines. Progeny derived from FHB populations (three way crosses) enriched via MAS for validated FHB resistance QTL and other traits of importance such as dwarfing genes, disease and insect resistance, rye translocations, and quality will be evaluated in headrow and yield tests. A training population from Yield Validation Panel and/or Allele Based Breeding Panel for GS was evaluated for FHB at Blacksburg, VA in 2016, and in 2017 will be evaluated in scab nurseries in VA, NC, and KY. The genotypic (GBS data from TCAP database) and phenotypic data on Yield Validation Panel and/or Allele Based Breeding Panel will be used to develop GS model for FHB resistance. Results from the Pioneer 26R46/Tribute DH mapping population indicate that FHB resistance is associated with chromosomes 1AS, 2AL, and 3BS, which differ from those previously identified in Jamestown on chromosomes 1BL and 6AS. Markers associated with these QTL for FHB resistance are being used to haplotype wheat lines and parents in our lab and at the Genotyping Center in Raleigh, NC. They are also being used to pyramid genes and QTL for FHB resistance via marker assisted selection in development of DH lines and population enrichment.