PI: **Carl Griffy** **PI's E-mail:** **cgriffey@vt.edu**

Project ID: **FY10-SW-005** **FY10 ARS Agreement #:** **59-0206-9-084**

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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.**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.

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, 500 to 600 selected lines will be evaluated in observation, preliminary, advance or state yield trials at two to seven locations and in the scab nursery. Approximately 140 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. 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. In 2011, two male sterile recurrent selection populations, developed at Ohio State University to enhance FHB resistance in SRW wheat, will be evaluated for FHB resistance. FHB resistant male sterile plants open-pollinated by a mixture of SRW wheat cultivars and elite lines will be selected, harvested and evaluated in 2012 to identify desirable male fertile FHB resistant genotypes. FHB resistance in the SRW wheat cultivars Roane and Jamestown will be characterized using bi-parental and/or association mapping. In 2011 FHB phenotypic data will be collected on RILs derived from Jamestown/LA97113UC-124 and FG95195/ Jamestown by cooperators in AR (Milus), GA (Johnson), LA (Harrison), and VA (Griffey). FHB phenotypic data also will be collected on RILs derived from crosses between Roane with three KY wheat lines and from the cross Pioneer 25R47/Jamestown by cooperators in MD (Costa), NC (Cowger and Murphy), and VA (Griffey). The Roane derived populations also will be evaluated for FHB in KY (Van Sanford) and MO (McKendry). Phenotypic data collected in field and greenhouse experiments indicate that the SRW wheat cultivar Tribute 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 NCSU and will be used by Virginia Tech and other collaborators 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.