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

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 500 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 for reaction to other diseases at a second location, and lines in the southern and northern tests 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. Each year 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. Progeny selected from two male sterile recurrent selection populations, initially developed at Ohio State University and subsequently advanced at Virginia Tech to enhance FHB resistance in SRW wheat will be evaluated in observation yield tests and subsequently in replicated yield tests. Additional genotyping and final mapping of FHB resistance QTL in the SRW wheat cultivars Roane and Jamestown will be completed and the results made publicly available and submitted for publication in 2014. Phenotypic data on a Tribute / Pioneer 26R46 mapping population comprised of 109 doubled haploid (DH) lines developed at NCSU was collected by the southern winter wheat cooperators in 2013 for FHB resistance, DON, and *Fusarium* damaged kernels (FDK). Initial genotyping using SSR markers has been conducted in our lab, and the mapping population has recently been submitted for genotypic analysis using a 90K SNP platform. A second year of phenotypic data will be collected in 2014. Linkage maps will be developed using MapManager/JoinMap 4.0/Multi-point and QTL will be identified by QTL Cartographer/MapQTL 5.0. MapChart 2.2 will be used for the construction of the linkage maps, QTL intervals, and LOD graphs. Preliminary data and results will be presented at the 2014 FHB Forum and final results will be made publicly available and submitted for publication in 2015.