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Project Title: Improving FHB Resistance in SRW Wheat via MAS and Mapping in Native Sources.

PROJECT 2 ABSTRACT

(1 Page Limit)

Scab epidemics were widespread in Virginia and parts of the eastern U.S. in 1998, 2003, and 2009 and devastated much of the wheat crop. 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. Each year more than 500 new crosses, including at least one FHB resistant parent, will be made, and approximately 300 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 a scab nursery. 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 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. Each year approximately 10 MAS populations (three way crosses) will be developed and F_1 plants will be haplotyped and selected for validated FHB resistance QTL and other traits of importance such as dwarfing genes, disease and insect resistance, rye translocations, and quality. Two male sterile recurrent selection populations, developed at Ohio State University to enhance FHB resistance in SRW wheat, and initially evaluated and allowed to cross pollinate with the best regionally adapted SRW cultivars and elite breeding lines in 2011 will be handled similarly in a second cycle of selection and advanced via the pedigree method. Male sterile heads will be tagged and those lacking FHB will be planted and evaluated in 2013 for FHB resistance. In both years heads will also be selected from desirable FHB resistant male fertile plants. 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 were 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 were collected on $F_{4:6}$ 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 were also evaluated for FHB in KY (Van Sanford) and MO (McKendry). The populations were also phenotyped for type II resistance in the greenhouse in 2011. FDK and DON data for 2011 are currently being collected. In 2012, all of the populations will be phenotyped a second time for type II resistance and by soft wheat CP collaborators for FHB resistance, DON, and FDK. Doubled haploid (DH) lines for a mapping population Tribute / Pioneer 26R46 developed at NCSU in 2011 will be planted in headrows at Warsaw, VA or in the greenhouse during fall 2011 to increase seed stocks. The population will be phenotyped for FHB resistance, DON, and FDK by southern CP collaborators during 2013 and 2014. During the next two years, genotypic data (SSR, SNP, and/or DArT markers) will be obtained in house, through private service labs, and/or in collaboration with the USDA-ARS genotyping center.