PI: Carl Griffey	**PI's E-mail:** cgriffey@vt.edu
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Project Title: Improving FHB Resistance in Winter Wheat via Traditional, GS, MAS and DH Methods.

PROJECT 3 ABSTRACT

(1 Page Limit)

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. Scab epidemics in Virginia also were significant in 2013 and 2017. Currently, production of cultivars having moderate resistance to scab (Fusarium Head Blight) 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. Enhanced efforts are needed to develop cultivars and superior parental lines having gene *Fhb1* combined with other validated genes and quantitative trait loci (QTL) derived from both exotic and native sources. Lack of elite and locally adapted FHB resistant germplasm and diagnostic DNA markers for use in gene introgression and pyramiding have greatly hindered efforts to develop competitive cultivars having enhanced levels of FHB resistance. Simultaneous use of both marker assisted selection (MAS) and Doubled Haploid (DH) breeding methods offers great potential to accelerate the development of cultivars having FHB resistance superior to that conferred solely by gene *Fhb1* or QTL from native sources.

Research will continue to 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 are assessed and utilized to enhance breeding efficiency. Markers linked to 15 scab resistance genes located on wheat chromosomes 2D, 3B (Fhb1), and 5A of Ning 7840, 1B and 6A of Jamestown, 1A and 2A of Tribute, 3B and 4B of Ernie, 2B and 3B of Bess, 3B of Massey, and 1A, 4A, and 6A of Neuse are being used to screen, characterize and select parents and their progeny for FHB resistance genes. Plants from top cross populations developed in 2015 (13), 2016 (13), and 2017 (15) comprised of parents having FHB resistance QTL derived from Ning 7840 and other native sources have been enriched via MAS for FHB resistance and will be advanced using either the DH and/or pedigree method to derived pure lines.

Research will also focus on Genomic Selection to provide information on genomic estimated breeding values (GEBV) to aid in selection of superior elite lines, parents and crosses. Parental lines will be selected and crosses made on the basis of phenotypic and genotypic data, and GEBV derived from GS models including both agronomic and disease data. A training population of ~ 200 lines consisting of elite wheat lines derived from our program and other programs evaluated in regional or uniform yield nurseries, and three FHB nurseries will be further evaluated for FHB resistance in a scab nursery at Mt. Holly, VA. Genotypic data is routinely generated and available for wheat entries in regional, uniform, and scab nurseries by the USDA-ARS Genotyping Center in Raleigh, NC. New elite lines derived from the GS project will be genotyped and evaluated in observation yield tests at two locations and in the scab nursery at Mt. Holly. MAS breeding efforts and GS in conjunction with doubled haploid (DH) technology will aid in increasing breeding efficiency and development of FHB resistant varieties.