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Project Title: Double Haploids to Expedite Development of FHB Resistant Soft Winter Wheat Varieties

PROJECT 2 ABSTRACT

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In 2003 and 2009 and more recently in 2014 and 2015, scab epidemics devastated much of the wheat crop in the southeastern U.S., resulting in significant losses in yield and quality. In the Southern Soft Wheat Variety Development and Host Resistance Cooperative Project, information provided from extensive and collaborative phenotypic and genotypic characterization of both exotic and native FHB resistance in breeding lines, commercial cultivars, and mapping populations is now being deployed through marker-assisted (MAS) and genomic (GS) selection, resulting in the pyramiding of complementary FHB resistance genes. Despite these collaborative efforts, the long life cycle (8-12 months) of winter wheat compared to spring wheat (3-4 months) and other crops is still a constraint to breeders. The process of inbred line development can be expedited through the use of doubled haploid technology, where inbred lines can be produced in 12-18 months and will reduce the variety development time to 4-5 years.

Each year the southern VDHR breeding programs make multiple single and three way crosses to pyramid validated FHB QTL and other traits of interest. For this proposal, each program (AR, VA, LA, GA, and SC) will use one or more of these crosses to develop 350+ double haploid lines per year. These lines will be genotyped in collaboration with the Eastern Regional Genotyping Center and collaboratively phenotyped through exchange after initial selection for basic adaptation.

The proportion of DH lines derived from sources of FHB resistance within the Southern VDHR CP is increasing each year, with 368 DH lines in advanced testing, 736 DH lines in observation level testing and ~6500 DH lines in the head-row stage (Table 1). Many of these have resulted from DH exchange between programs. Many of these lines contain a pyramid of multiple genes, such as FHB1, 2DL, 3BS and 5AS of Ning 7840 (Sumai 3 derivative), 2B, 3BSc, 4B and 5A of Ernie, Neuse_1A, Neuse_4A, Bess_2B, Bess_3B and JT_1B, combined with other favorable agronomic traits.