Project Abstract

Project Title:	Genome-enabled selection for FHB resistance in winter wheat	
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We aim to evaluate and implement whole genome-enabled prediction, selection and mating (GS) to improve FHB resistance in a large soft red winter wheat breeding program. These efforts will be compared to ongoing efforts for Marker-Assisted Selection (MAS) for known QTL (FY22 multi-PI proposal: "A Double Haploid Initiative to Speed Development of FHB Resistant Soft Winter Wheat."). We hope to gain insight into whole-genome relationships between morphology, phenology and agronomic traits and FHB traits, while optimizing whole-genome selection for elite materials with improved FHB resistance and lower DON accumulation.

Our primary objectives are to 1) evaluate available adapted wheat germplasm for FHB resistance and determine the predictive ability of FHB traits, including visual scores, FDK and DON within the Virginia germplasm; 2) determine the linear (and potentially non-linear) genetic relationships (i.e. genetic correlation) between morphology (e.g. height), phenology (e.g. heading date, flowering time), and FHB traits (FHB index, FDK, DON), and their impact on agronomic performance; 3) use genomic information to estimate genetic and breeding values for advancement and mating decisions, respectively, to improve FHB resistance and agronomic performance, and 4) evaluate
response to selection and any unexpected consequences thereof.

To facilitate decision making on whole-genome genetic values, our program began genotyping all soft wheat lines that enter into first year yield trials with genome-wide markers in 2021. Currently, all breeding materials at year 2 (Y2; preliminary) yield trials and beyond are observed in our scab nursery. To facilitate genomic prediction of year 1 (Y1; observation) materials for FHB traits, a subset of ~200 lines representing all Y1 families will be phenotyped in the scab nursery for visual scores, FDK and DON. Selection of Y1 materials will be based on predicted FHB and agronomic performance. A crossing schedule will be designed based on GEBVs for FHB and agronomic traits using a Smith-Hazel selection index. Genotypic and phenotypic data collected will be made publicly available through upload to T3, facilitated by the program adopting its own private T3 database. All developed
lines will be made available upon request to public breeding programs for use as parents and checks.