Project Abstract

Project Title:	Genome-enabled selection for FHB resistance in eastern winter feed and malt barley	
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We aim to evaluate and implement whole genome-enabled prediction, selection and mating (GS) to improve FHB resistance in an eastern winter barley breeding program. 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. Special attention will be paid to relationships between FHB resistance and malting quality traits to develop sustainable selection methods for quantitative resistance to FHB without sacrificing malting quality.

Our primary objectives are to 1) evaluate predictive ability of FHB traits, including visual scores, *Fusarium*-damaged kernels (FDK) and DON within the Virginia barley germplasm; 2) determine genetic relationships (i.e. genetic correlations) 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 and malting quality; 3) use genomic information to estimate breeding values for advancement and mating decisions to improve FHB resistance, agronomic performance and malting quality, and 4) evaluate response to selection and impacts on malting quality.

To facilitate decision making on whole-genome genetic values, our program began genotyping all malt barley 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 ~100 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, agronomic performance and malting quality measures. A crossing schedule will be designed based on GEBVs for FHB, yield and malt quality 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.