

## Project Abstract

<b>Project Title:</b>	Coordinating HWW Genomic Assisted Breeding to Develop FHB Resistant Varieties	
<b>USWBSI Project ID:</b>	FY24-HW-005	
<b>Principal Investigator:</b>	Esten Mason	Colorado State University

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### Project Summary

The priorities of the United States Wheat and Barley Scab Initiative (USWBSI) for Variety Development and Host Resistance (VDHR) in the Hard Winter Wheat Coordinated Project (HWW-CP) addressed by this proposed research are: 1) increase and document the number of varieties with FHB resistance and high productivity, that are tested in state variety trials and available to farmers, to reduce DON in the U.S. grain supplies, 2) increase the efficiency of germplasm selection and cultivar development, and 3) Evaluate and implement new breeding technologies to further enhance short-term and long-term improvement of FHB resistance.

This project will leverage genomic prediction and quantitative trait locus (QTL) haplotyping to improve selection for FHB resistance and agronomic performance. By pooling historical genotypic and phenotypic information, the project aims to generate genomic predictions, QTL haplotypes, and crossing recommendations to enhance performance across programs. To achieve these goals, this proposal suggests a project led by Colorado State University (CSU) which coordinates genotyping and predictive modeling among public HWW breeding institutions in the Great Plains region.

The specific objectives of this collaboration among universities would be to: 1) curate historical genotypic (genome-wide marker data and haplotypes) and phenotypic data for agronomic and disease traits (FHB resistance, grain yield, test weight, heading date, stripe rust resistance, Hessian fly resistance) from the Southern Regional Performance Nursery (SRPN), Regional Germplasm Observation (RGON), and HWW scab nursery for use in predictive modeling, 2) develop predictive model pipelines for genomic estimated breeding values (GEBVs) for FHB resistance traits and other agronomically relevant criteria for successful variety development, 3) develop predictive model pipelines for quantitative trait locus (QTL) haplotype information for FHB resistance traits and other agronomically relevant criteria, 4) develop predictive crossing analytics to support breeders in selection of parents for crossing to increase FHB resistance and agronomically relevant traits, 4) execute exploratory analysis of existing and novel data for marker trait associations via mapping (genome wide association studies (GWAS) or QTL mapping), and 5) publish on findings to enhance knowledge of FHB resistant cultivar development techniques among cultivar development programs.

This research will mutually benefit both breeding programs and growers by 1) giving participating universities additional resources for genotyping in their own programs, 2) providing program specific predictive analytics to all programs involved, and 3) improving selection for resistance to FHB as well as improving agronomic performance to provide growers with better FHB resistance.

