

Project Abstract

Project Title:	Contribution of <i>Fusarium</i> diversity to variability of FHB resistance in barley	
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This project's goal is to determine the effect of *Fusarium* diversity on variability of disease and mycotoxin severity observed in barley genotype screening nurseries. Facilitate incorporation of pathogen genotype data in variety screening programs to enhance resilience of FHB resistance.

Objective 1: Characterize genomic differences in FHB isolates within and among barley screening programs. Outcome will be a publicly available repository of *Fusarium* isolates used in FHB resistance screening studies and associated isolate genome sequence data that can be used by other scientists to replicate experimental procedures and further collect “omics” resources to enhance research efforts. Isolates used by disease phenotype screening programs will be collected and curated in the ARS Culture Collection. Isolates from the same and different screening programs will be compared with respect to species identity, genetic diversity, and mycotoxin profile.

Objective 2: Determine if standard susceptible and resistant barley cultivars exhibit the same level of disease and mycotoxin contamination in response to FHB isolates from different screening programs under controlled conditions. This will reveal the effect of pathogen genetic diversity on variability in disease severity and mycotoxin contamination on standard barley cultivars. A subset of isolates from each breeding program will be used in disease assays. Isolates from the same and different screening programs will be compared with respect to their effects on head weight, pathogen biomass, and mycotoxin contamination.

Objective 3: Determine if barley cultivars exhibit a differential metabolic response to genetically diverse FHB isolates. Non-targeted metabolomic profiles will be determined on day 3 and 7 post inoculation and control barley heads using nuclear magnetic resonance (NMR) and liquid chromatography coupled to mass spectrometry (LC-MS). Metabolic profiles will then be compared using metabolomic software tools to elucidate differential production of barley metabolites upon challenge with selected *Fusarium* isolates used in FHB resistance breeding programs.