

## Project Abstract

<b>Project Title:</b>	<b>Metagenomics Informed Trait Development for Breeders</b>	
<b>Principal Investigator:</b>	<b>Barney Geddes</b>	<b>North Dakota State University</b>
<b>Co-Investigator:</b>	<b>Thomas Baldwin</b>	<b>North Dakota State University</b>
<b>Co-Investigator:</b>	<b>Briana Whitaker</b>	<b>USDA-ARS, Peoria IL</b>

Fusarium head blight (FHB) is a devastating disease of wheat and barley that affects both small grain yield and contamination with mycotoxins, including deoxynivalenol (DON). Breeding for FHB resistance in barley has made little progress in overcoming disease. On the other hand, microbial inoculants as biocontrols have proven difficult to translate, due to an inability of introduced microbes to compete for residence in the microbiome in the complex environment of the field. To overcome this limitation, we are working to identify biocontrol taxa that are recruited from the environment under FHB biotic stress and also responsive to plant genotype (Year 1 TRSC “Breeding potential for microbiome protection against Fusarium head blight”). Here we propose to expand this work with the overall project goal of developing an assay for disease-recruited and genotype-responsive microbial biocontrols that can be directly translated into trait screening pipelines for barley.

Objective 1) Identify FHB recruited and genotype-responsive microbes, under non-drought conditions

Objective 2) Metagenome analysis of barley genotypes with identified FHB recruited and genotype responsive microbes

In Objective 1 we will support promising data for FHB-recruited and genotype-responsive microbial taxa from FY21 TRSC by repeating microbiome sampling and analysis from diseased and non-diseased barley heads across 10 different genotypes at Fargo, ND and Ithaca, NY, Kimberly, ID and St. Paul, MN. By comparing the microbial community composition of diseased and healthy plants, we will identify groups of closely related microbes that are enriched in the diseased condition. The abundance of taxa will be compared in pairwise categories with plant genotype, and taxa that show significantly altered abundance between plant genotypes in the same field site will be considered genotype-responsive. Microbial taxa that are identified as both FHB-recruited and genotype-responsive will be considered as candidates for selective breeding..

In Objective 2 we will utilize metagenomics to refine our understanding of microbial species and functional genes recruited by barley genotypes during FHB infection. Select barley lines from Objective 1 will be used for metagenomics to refine our resolution to specific DNA signatures (biomarkers) from recruited microbes identified in Year 1. The expected outcome from Objective 2 is a set of unique biomarkers associated with FHB antagonistic microbiome recruitment that could be used in a deployable assay to measure FHB antagonistic taxa recruitment to enable trait selection in breeding pipelines.

Breeding research will be enhanced by the ability to screen elite germplasm for microbial signatures of FHB resistance, with our research being the first approach of its kind targeted to a barley breeding population. Tools developed from this program could be utilized by stakeholders and farmers to map the susceptibility to FHB in their fields based on microbiome health. Lastly, the proposed research would also serve as a starting point for investigating further FHB-microbiome interactions in the field and during the malting process.