Project Abstract

Project Title:	**Identification, Characterization, and Development of FHB-resistant Germplasm**	
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In recent years FHB and DON contamination of barley and wheat has occurred in the Intermountain West. Useful resistance to DON accumulation has been identified in elite Aberdeen spring barley lines, but the uniqueness of the resistance is not known and efforts to systematically improve Aberdeen, Idaho spring and winter malting barley for FHB resistance are still in their infancy. The overall goals of this project are to characterize the genetic architecture of resistance in order to guide planning for producing new lines with effective combinations of resistance alleles; and to facilitate the release of new cultivars with FHB resistance as necessary to protect growers in the Intermountain West from this disease.

Objectives: 1) Characterize FHB resistance in elite barley germplasm; 2) incorporate a genomic selection approach towards barley improvement involving models of predicting disease severity, fungal biomass and DON levels; and 3) characterize existing spring barley populations for the number, effect sizes and locations of QTL contributing to FHB resistance and lower DON.

Outcomes: 1) Identification of elite germplasm with FHB resistance; 2) approximately 50 hybridizations planned to optimize combinations of genomic regions contributing towards FHB resistance, lower fungal biomass and reduced DON levels; and 3) knowledge of quantitative trait loci that influence barley response to FHB infection, their location and effect sizes.

Approach: Elite breeding lines will be evaluated for FHB resistance in Aberdeen and Kimberly, Idaho (200 spring and 50 winter); at Langdon and Fargo, North Dakota (100 spring); and at St. Paul, Minnesota (100 spring).

A genomic selection training population of 250 lines will be evaluated in Idaho and North Dakota. This data will be used to predict the breeding value of spring barley and to select parents for a crossing block aimed at improving FHB resistance. Approximately 50 crosses will be made based on predicted breeding value. Lines will be advanced by single seed descent.

Bi-parental populations, created by crossing Aberdeen breeding lines 95SR316A and 2Ab08-X5M10-82 with foliar disease resistance donor cultivars ND Genesis and Conlon, will be phenotyped in field nurseries in Idaho and North Dakota using existing funds. DON and fungal biomass data will be obtained for these lines to supplement the field data. Genotypes for these populations are already available. Linkage mapping will be used to identify QTL contributing to FHB response.