

## Project Abstract

<b>Project Title:</b>	Development of a Multi-parent Population to Enhance FHB Resistance in Barley	
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Our overall goal is to reduce the losses caused by Fusarium head blight (FHB) especially quality discounts due to the accumulation of mycotoxins such as deoxynivalenol (DON). This can be best achieved by identifying and incorporating into barley cultivars genes that confer a high level of resistance to the disease and mycotoxin accumulation. Our project objectives, within a four-year timeframe, are to: 1) develop a Multi-parent Advanced Generation Intercrosses (MAGIC) population using the most resistant barley accessions possessing unique haplotypes at characterized FHB/DON loci; 2) phenotype the MAGIC population for resistance to FHB and DON accumulation in multiple environments; 3) genotype the MAGIC population with single nucleotide polymorphism (SNP) markers and perform quantitative trait locus (QTL) analyses to identify and map alleles conferring resistance to FHB and DON accumulation; and 4) identify progeny with enhanced resistance and distribute them to barley breeders. Within the Barley Coordinated Project, our proposal aligns closely with Objective 3 under the Research Area of Variety Development and Host Resistance (VDHR), but is also an important step in advancing Objective 2 within VDHR.

We will develop the MAGIC population by intercrossing eight founder accessions possessing unique alleles conferring the highest level of resistance to FHB and DON accumulation. Two of the eight founder parents selected for the population are agronomically advanced (an advanced breeding line and a cultivar) and will therefore increase the chances of identifying agronomically advanced progeny with low FHB severity and DON levels. Through additional intercrosses and selfing generations, we expect to generate 800-1000 recombinant inbred lines (RILs) that will be phenotyped for disease reaction, mycotoxin concentration, and relevant agro-morphological traits in multiple environments. The MAGIC population will also be genotyped with SNP markers to identify and map loci contributing to FHB resistance and low DON accumulation through QTL analyses. The MAGIC population crossing scheme promotes the pyramiding of favorable alleles underlying complex traits; thus, we anticipate identifying several agronomically acceptable progeny with enhanced resistance to FHB and DON accumulation.

We will work closely with breeders to ensure that materials developed in this project are immediately available as parents in their respective barley improvement programs. The knowledge and germplasm generated from this study will lead to the development of barley cultivars with FHB resistance and low DON accumulation, thereby minimizing this disease threat for producers, processors, and consumers.