Project Abstract

Project Title:	**Leveraging the Pangenome to Investigate Genetic Background Effects on the *Fhb1* Locus**	
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Spring wheat is vulnerable to Fusarium head blight (FHB) or scab, and the most efficient way of combating the disease is to grow varieties with genetic resistance. Currently, many of the widely grown cultivars are susceptible or moderately susceptible to FHB. A few major gene regions for disease resistance are available, and marker assisted selection (MAS) has been used extensively to move these genetic intervals (or linkage blocks) into adapted germplasm. However, genetic background effects influence QTL—which leads to unpredictable performance after introgression. Our previous FHB resistance-source pangenome project greatly expanded the genomic resources available to map QTL and identify high quality markers for tracking.

The overall goal of the project is to investigate the genetic background effects on *Fhb1* function.

The specific objectives we will use to achieve this goal are:
1) Isolate Sumai 3 *Fhb1* linkage block in elite germplasm.
2) Develop mapping populations to evaluate specific background effects.
3) Evaluate background gene expression effects on *Fhb1*.

The expected outcomes of these objectives are:
1) Near-isogenic germplasm that carry small Sumai3 *Fhb1* QTL, which can be used to minimize linkage drag, and precisely measure locus effect on disease resistance.
2) Mapping populations to identify QTL that work with *Fhb1* to promote resistance or performance.
3) Gene expression information in breeding germplasm under FHB infection with and without the *Fhb1* locus. This will provide candidate genes that may play a role in altering *Fhb1* function.

The approaches we will use to obtain these objectives will be to use high-density molecular markers for foreground and background selection in a back-crossing scheme to introgress the *Fhb1* gene region into elite germplasm. We will generate biparental mapping populations to identify new QTL and use RNA-Seq to identify differentially expressed genes that may play a role in disease resistance and *Fhb1* expression.