Project Abstract

Project Title:	**A Low-Cost Genotyping Platform to Develop FHB-Resistant Barley**	
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Barley (*Hordeum vulgare*) is a global crop that is vulnerable to Fusarium head blight (FHB). Genomic selection (GS) is a promising molecular breeding method to accelerate the development of FHB resistant barley cultivars that also meet quality requirements of the maltsters and brewers.

The overall goal of the project is to develop an inexpensive Illumina multi-species genotyping array to enable GS more widely.

Specific project goals are to:

1) Characterize population sub-structure and diversity of US breeding germplasm.Identify a set of evenly spaced markers for a low-cost assay.

3) Evaluate dual-hybridization mode of the Infinium multi-species array.

Expected outcomes of these objectives are:

1) Sub-structure designations and genetic relationships among US breeding germplasm to facilitate sharing decisions and to set up molecular marker sub-setting.

2) A set of approximately 3,000 molecular markers that flag all useful linkage blocks in as many breeding programs as possible.

3) A protocol for dual hybridizing samples to decrease per-sample cost of the new genotyping platform.

The approaches we will use to accomplish these goals are to first analyze diversity and sub-population structure of US breeding germplasm genotyped with the Illumina 50K array. Segregation within each sub-population will be used as a metric to rank the 50K markers within genetic bins along the chromosome. Then the best-performing markers will be selected for addition to a multi-species Illumina array. To further decrease the cost per sample, dual hybridization will be evaluated in the 2nd year by checking concordance of genotyping calls arising from the standard protocol and one where barley DNA is mixed with oat or wheat DNA.

The output of this project will be the development of a low-cost assay that will be available to researchers and breeders and enable wide implementation of GS to improve quantitative traits like FHB and yield. This array will also be useful to researchers for applications that only require a small set of molecular markers, such as diversity analysis and fingerprinting. An additional output of this project is the integration of genome-wide genotypes of barley lines from breeding programs throughout the United States. As more information is gathered with a common platform every year, the data set will be useful for global analyses. These will assist in identifying relationships among programs that can be leveraged for better coordination or germplasm sharing and will enable meta-QTL analysis and bulk genomic selection modeling.