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Project Title: Innovated Selection Plan to Improve the FHB Resistance of Hard Winter Wheat	

PROJECT 2 ABSTRACT
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The project addresses CP objective 3: Evaluate and implement new breeding technologies and germplasm to further enhance short term and long-term improvement of FHB resistance and to efficiently introgress effective resistance genes into breeding germplasm.

Improving FHB of wheat requires reliable and accurate phenotyping. Phenotyping can be supplemented with genotyping to build prediction models based on the solid phenotypic data. Despite increasing incidence of FHB in the Great Plains, breeders in the Great Plains struggle to produce the reliable phenotypic data needed for any selection scheme due to high temperatures, low humidity, and high winds at flowering/infection time. It is likely that phenotyping hard winter wheat (HWW) in the humid and cooler Eastern USA, would produce better results than screening in the Great Plains. Once reliable phenotypic data is obtained on a large set of HWW then a genomic selection (GS) model could be built upon that data and used to predict the FHB resistance of other HWW lines that were not phenotyped. Our Objectives are:

1) Phenotype 400 HWW lines in NE, SD, and Ohio
2) Build GS models and use the models to predict the FHB resistance of HWW that were not phenotyped
3) Use the predicted values to select HWW lines and then validate their resistance by phenotyping them in NE, SD, and OH.

The OSU FHB nursery routinely produces high levels of FHB infection and excellent separation of the checks. The OSU nursery has included HWW lines from Nebraska and produces good data for those lines as their flowering date is similar to the SRWW that OSU routinely screens. We propose to phenotype a total of 400 HWW lines from NE and SD (200 each) in a three replicated test in a misted, inoculated FHB nursery per year (2020-2021 and 2021-2022 season). OSU will collect Index data and grain samples from each entry. The grain samples will be assessed for FDK and DON. All 400 $F_{3:6}$ lines would be genotyped using GBS. An additional 3,000 HWW $F_{3:5}$ lines related to the 400 lines would be genotyped. The phenotypic data from the 400 phenotyped lines would be used to build the GS model that would then be used to predict the FHB resistance of the other 3,000 lines. The best/worst of the 3,000 lines will be selected based on the GEBVs and phenotyped in OH in 2021-22 season as part of the 400 entries.