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PROJECT 4 ABSTRACT
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Successful breeding requires evaluating large number of lines in the early stages of testing to identify a line with acceptable trait levels for all traits. It is difficult for individual public breeding programs to assess a large number of lines when using only phenotypes. Genomic selection (GS) provides a way for the NWW-CP breeders to effectively combine their germplasm and data to leverage their resources and effectively enlarge the size of their selection population without expanding their expensive phenotyping programs. As genotyping costs less than phenotyping, the use of GS could allow a breeder to evaluate many times more lines than phenotypic selection for the same amount of money. It also allows a breeder to access, assess, and select among all genotyped lines from all collaborators: each breeder will select among all lines from all breeders. The plan will allow each breeder to assess the values of thousands of more lines than possible by just phenotyping their own lines, resulting in greater selection intensity, gain from selection, and probability of identifying new cultivars. The plan leverages our genetic and financial resources to better serve our clientele by releasing a greater number of superior cultivars.

This use of GS is enabled by new, low cost genotyping technologies. Implementing this form of GS will require 1) genotyping lines from all breeders with the same markers and combining our phenotypic and genotypic data to create an initial training population whose data can be used to predict the value of other lines. In this proposal we are seeking funds for a person to coordinate all aspect of the joint breeding effort, and funds to genotype the germplasm needed to initiate the GS plan. The coordinator will organize samples for genotyping, interact with the genotyping lab, submit orders, organize genotypic and phenotypic data into databases, filter phenotypic and genotypic data, perform analyses to predict the value of lines and crosses over all programs, and assist with within program analyses.

We propose in year 1 to genotype ~5,200 lines from seven programs to form the initial training population. All of these lines will have been phenotyped for yield, FHB resistance, and other traits in replicated, multi-environment trials. In year 2 we will genotype ~5,200 new lines that are in the early stages of testing. The prediction model from the initial training population will be used to predict the yield, FHB resistance, and value for other traits of all ~5,200 newly genotyped lines. Predicted values can be overall environments or a specified subsets of environments. Each breeder will select among the ~5,200 lines for further testing in their program.