

Project FY22-NW-008: Implementing Genomic Selection in the NWW-CP

1. What are the major goals and objectives of the research project?

1. Genotype breeding lines from six NWW-CP programs in a cost-effective manner.
2. Distribute data to all NWW-CP breeders for their use in genomic selection.
3. Conduct simulations on resource-efficient breeding schemes that employ genomic selection and sparse testing

2. What was accomplished under these goals or objectives? (For each major goal/objective, address these three items below.)

What were the major activities?

1. Compiled samples for genotyping
2. All lines from all programs were genotyped together
3. SNPs were called on all lines and data distributed to breeders
4. Individual breeders used the data in genomic selection
5. Conducted simulations on allocation of resources in sparse testing

What were the significant results?

1. We genotyped 7,200 new samples using genotype-by-sequencing technology
2. The new SNP data was combined with SNP data from past sequencing and was distributed to individual breeding programs.
3. All breeders used the data to predict the value of their lines and used the data in making advancement decisions.
4. The SNP data was also used in 12 graduate student project including four FHB-based
5. The sparse testing study revealed a cost-effective allocation of resources in a genomic selection scheme.

List key outcomes or other achievements.

1. The FHB resistance, yield, and test weight values were predicted on the 7,200 new samples, as well as lines genotyped in previous years.
2. The sparse testing study assessed testing all lines in all of 7 locations, each lines in just one location, and then testing a percentage of lines in 2 to 6 additional locations. Increasing the percentage of lines tested in multiple locations, and the locations used always increased GS accuracy but also always increased the cost, but with diminishing returns. Testing each line in one location, and then about 30% in an additional three location provided the best GS accuracy per dollar.

3. What opportunities for training and professional development has the project provided?

The project directly trained 1 post-doc. The marker data though was fundamental in training 12 graduate students.

4. How have the results been disseminated to communities of interest?

Every breeder uses the data in a unique fashion. The sparse testing work will be published once completed.

5. What do you plan to do during the next reporting period to accomplish the goals and objectives?

The project was not funded for FY24. Every program will need to find their own funds for genotyping. The genotyping effort will not be coordinated. Each program will handle their own samples and payment. This will likely increase the cost of genotyping as each program has few samples. The effort will not be coordinated and marker data storage will not be centralized. Each program will need to call their own SNP if they are using GBS and SNP calling pipelines may not all be the same.