Project Abstract

Project Title:	Implementing Genomic Selection in the NWW-CP	
Principal Investigator:	Clay Sneller	The Ohio State University

Our overall objective is to improve the efficiency of developing high yielding, FHB resistant cultivars for the upper Midwest. This will be achieved utilizing genomic selection within the Norgrains breeding consortium which is composed of breeding programs from IL, IN, KY, OH, MI and NY. Our specific objectives are

1. Pool samples for genotyping to obtain low cost genotyping using a common genotyping platform and bioinformatics pipeline. *Outcome: This reduces the genotyping cost per sample and ensure data compatibility across programs.*
2. Genotype all new breeding lines from each program and add that information to the existing genotype data set. *Outcome: Each year the genotype data base will increase by ~5,000 lines such that we will have ~38,000 lines genotyped by the end of year 4.*
3. Enter all phenotypic data from all breeders and all trials into Breedbase, including the P+NUWWSN and the 5 State Nurseries. *Outcome: We will compile phenotypic on more than 30,000 lines by the end of the project. The data will be used to advance selections, release new cultivars, and make predictions*
4. Use data to predict the local and broad adaptation of all lines from all breeders: *Outcome: all breeders will be able to predict the value of all lines from all breeders phenotyping those lines in their environments. This will greatly increase the effective size of their programs without out significant increase costs.*
5. Conduct simulations to improve the efficiency of the uniform scab nurseries: P+NUWWSN. *Outcome: We will develop a more efficient use of the resources allocated to the P+NUWWSN trials and allow testing of more lines.*
6. Conduct simulations to evaluate the best way to integrate GS into each breeding program. *Outcome: We will assess the best application of GS to each program. This will allow each program to become more efficient*.

We genotype all new breeding lines from all programs each year. We will compile all phenotypic data from all trials from all breeders into breed base. This data will be used in various GS predictions within programs and across programs. Various GS models will be used including incorporating marker x environment interactions. The compiled data will also be used to model various modifications of breeding schemes and use of GS to derive efficient breeding schemes and allocation of testing resources for the P+NUWWSN.