



North Central Soybean Research Program

Increasing the Rate of Genetic Gain for Yield in Soybean Breeding Programs

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Focus of the research

The focus of this project is to increase the rate of genetic gain for yield in soybean breeding programs by increasing genetic variance, decreasing non-genetic sources of variability, and decreasing the length of the breeding cycle. This will be accomplished through coordinated activities to be carried out across twelve breeding programs in the north-central region.

Increases in soybean yield through breeding have been slower than growers expect, with the rate of yield increases for soybean substantially less than that for corn. Reports of genetic gain in corn generally range from 1.0 to 1.2 bu/ac/yr, whereas a collaborative study led by Brian Diers of a historic set of MG II-IV soybean varieties released from 1923 to 2008 revealed a recent rate of genetic gain of 0.43 bu/ac/yr

Project objectives

- Increase selection intensity and decrease non-genetic sources of variability through improved progeny row testing.
- Increase selection coefficient and decrease length of breeding cycle through genomic selection.
- Increase additive genetic variance. One of the key issues in the slow rate of soybean yield increase is the lack of genetic diversity in the commercial soybean gene pool.
- Develop a metric to estimate genetic gains on an annual basis

Here are some of the results

1. We evaluated the selections from progeny row testing made in year 1 as well as carrying out a second year of the methods of progeny row testing from year 1. Results are pending.
2. The genomic selection study from the SoyNAM population has been completed. Databasing and genotyping from the Uniform Regional Trials is continuing on an ongoing basis as yearly entries are submitted and yield data is collected.
3. Preliminary tests of predictive ability using the Uniform Regional Trial training set has been exploring using cross validation on adjusted means of Uniform Regional Trial lines.

Further refinement of the analysis indicates respectable prediction accuracies ranging from 0.50 to 0.68 across maturity groups.

4. A cost-effective genotyping strategy has been developed.
5. We conducted the first year of our 2-year evaluations of the 250 PI (Plant Introduction) accession selected for the validation set from across the distribution of predictions for yield of ~9,700 untested PI accessions.
6. As this is likely the only time that such a collection of PIs will be evaluated in replicated trials across many environments, we are taking the opportunity to collect as much phenotypic data as reasonable.
7. We have successfully taken several approaches to identify potential yield loci through QTL analysis, GWAS, as well identification of signatures of selection through population diversity statistics.
8. An introductory video about genetic gain has been developed and is posted on the [Soybean Research & Information Initiative website \(YouTube Channel\)](#).

Why is this important?

- Soybean breeders will be able to take advantage of the improved breeding methods that can be implemented in essentially any soybean breeding program.
- Diverse germplasm will be made available through selection methods. As a result, farmers will reap the benefits of higher yields from new cultivars.
- Improved breeding methods as well as the development and release of community genotypic and yield data and models to soybean breeders will directly translate to greater yield gains in soybean breeding, and, ultimately, to higher yielding soybean varieties. In addition, the development of extension materials aimed at explaining genetic gains to non-experts, will be useful for education.