

SOYGEN 2: Increasing Genetic Gain for Yield and Seed Composition Developing Tools, Know-How and Community among Public Breeders

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Principal Investigators

Leah McHale, Ohio State University, lead; Asheesh Singh, Iowa State University; William Schapaugh, Kansas State University; Dechun Wang, Michigan State University; Katy M Rainey, Purdue University; Brian Diers, Matthew Hudson and Nicolas Frederico Martin, University of Illinois; Aaron Lorenz, University of Minnesota; Pengyin Chen and Andrew Scaboo, University of Missouri; and George Graef and David Hyten, University of Nebraska

Overview of project objectives

The research community has partnered for some time using critical public resources for soybean breeding work, including collaborative yield trials like the Northern Uniform Soybean Trials (NUST) and soybean checkoff-funded genotypic data and genotyping platforms. Now, researchers are using these tools to further gains for yield and seed composition. SOYGEN (Science Optimized Yield Gains across Environments) is a project that leverages and advances ongoing and previously funded work with the goal of increasing soybean genetic gain for yield and enhanced seed composition through tools, know-how and community among public breeders. Four objectives of the work are:

- Elevation of standardized collaborative field trials
- Development of a genomic breeding facilitation suite
- Evaluation of soybean breeding methods that increase yield gain while ensuring high levels of high-quality soy seed protein
- Characterization and use of the USDA Soybean Germplasm Collection as a foundation for future success

Key results

During the last year, researchers began developing a breeding database to be housed within the community-supported USDA-ARS repository for soybean genetics and genomic data. In addition, researchers were able to begin adding environmental data to the NUST and genotypic data to both the NUST and soybean cyst nematode regional trials to facilitate breeding objectives for stability of increased yield and seed composition. Work continues on developing a genomic breeding facilitation suite to feature genotyping breeding lines and genomic analyses. A database and workflow of software tools will allow breeders to interact and collaborate.

Progress on evaluating soybean breeding methods that will increase yield and composition gain moved forward during the 2021 season. For example, soybean crosses with model-predicted parents and breeder-selected parents were carried out for eight breeding programs. In some instances, crosses were sent to Puerto Rico for the winter growing season to advance results more quickly.

With regard to the USDA Soybean Germplasm Collection, a genome-wide association analysis for each seed composition trait was completed using the multi-year, multi-location phenotype data collected, along with existing genotype data from the collection.

Benefit to farmers

This multi-year project will ultimately result in greater genetic gains for higher soybean yield, as well as any other trait targeted by the industry. Farmers will have access to improved cultivars that can achieve higher yields and higher quality.

USB National Soybean Checkoff Research Database link

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