



Discovering and finally understanding the functions of genes that underlie major agricultural traits in soybean

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The project addresses gene discovery and germplasm development for traits critical to soybean growers, namely yield enhancement and seed composition improvement. The heart of the project focuses on developing soybean mutant genetic resources that will increase our understanding of the genes that underlie traits of agronomic importance.

The development of these resources has been designed to overcome factors that have limited similar projects in the past; such factors include issues with seed source, seed purity (minimizing background genetic heterogeneity), mutagenesis source, genotyping, phenotyping, and seed storage.

The new mutant resources will allow researchers to identify mutant stocks for their gene(s) of interest by simply searching a genomic database that will be developed by this project. This will provide an unparalleled public resource in which researchers can quickly identify the mutations, order mutant seeds, and test the agricultural function and importance of the gene(s). Our research objectives and current progress are summarized below.

Objective 1: Perform genome and exome resequencing on a collection of M2-derived soybean ENU mutants.

Seeds were mutagenized using a combination of N-ethyl-N-nitrosourea (ENU) and ethyl methanesulfonate (EMS) chemicals. The plants were grown under greenhouse conditions in small flats with short daylengths to accelerate maturity. We harvested the M2 seed and planted it in the 2018 field. We took preliminary field notes on the individuals and identified some mutated phenotypes. We collected leaf tissue from ~400 independent plants and are in the process of isolating DNA for each individual. We plan on resequencing approximately 50 plants to measure the rate of mutagenesis in the population. Furthermore, to increase the size of the population, we planted another batch of mutagenized M1 materials in the greenhouse this summer. We are hoping to harvest M2 seeds this fall from nearly 1,000 individuals and grow the M2 materials in the field in 2019.

Objective 2: Create a searchable public database that hosts all of the sequence polymorphism information (SNP and small indel mutations) for the subset of sequenced mutant plants.

Progress: None to date, as the resequencing data will need to be accomplished before we can meet this objective.

Objective 3: Store M3 seeds for the collection. Distribute seed to users in the research community based on their specific needs and requests.

Progress: We will soon harvest the first round of M3 seeds from the 2018 field. Harvest will be done on a plant-by-plant basis to ensure purity of each mutant line.