



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

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The goal of this project is to provide a unique “reverse genetics” platform for the soybean research community. Thousands of new soybean mutant lines adapted to the North Central region will be made available. The lines exhibit a wide range of traits including: yield, seed composition, disease, nematode and insect resistance; and response to water, nutrients, climate, soil and environmental conditions.

The lines will be available for researchers interested in identifying genes underlying these traits and breeders interested in using the novel alleles derived from these populations. A searchable database is being created where researchers can identify lines that are carrying mutations for any given gene of interest. This would be an unprecedented resource for the soybean research community.

Project Objectives

1. Generate greater numbers of unique mutant lines. Our goal is to have a minimum of 1,500 independent mutant lines by the Spring of 2019.
2. Perform genome and exome resequencing on a collection of M2-derived soybean ENU mutants.
3. Create a searchable public database that hosts all of the sequence polymorphism information for the resequenced mutant plants.
4. Store M3 seeds for the collection. Distribute seed to users in the research community based on their specific needs and requests.

Progress Overview

Objective 1: Generate greater numbers of unique mutant lines.

To increase the size of the population, we planted and harvested a second batch of mutagenized M1 materials in the greenhouse in the summer of 2018. The M2 seeds were harvested and will be planted in the field in 2019.

Objective 2: Perform genome and gene space resequencing on a collection of M2-derived soybean ENU/EMS mutants.

As described in previous reports, the first batch of 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 seeds and planted them in the 2018 field. We took preliminary field notes on the individuals and identified some mutated phenotypes.

A set of fifty-two mutant plants, some with interesting characteristics important to agronomic traits, were selected for whole genome resequencing to discover novel mutations. Two parent plants of the MN1806CN mutant population were also sequenced to verify that mutations discovered are in fact novel and not present in the parent line. This set of fifty-four plants were aligned to the reference genome Williams82 version 2 assembly (Wm82.a2) to verify locations of mutations. All possible sequence variants have been called on this set, and filtering of a high confidence variant dataset, which can be used by soybean researchers, has been initiated.

Objective 3: Create a searchable public database that hosts all of the sequence polymorphism information for the resequenced mutant plants.

The resequencing data will need to be fully analyzed before we can meet this objective.

Objective 4: Store M3 seeds for the collection. Distribute seed to users in the research community based on their specific needs and requests.

M3 seed has been successfully harvested and stored from approximately 1150 M2 plants grown during the 2018 field season. Five plants each of an additional 900 M2 families will be grown in the field this year to increase the population size. Numerous mutants from 2018 displayed phenotypes with delayed maturity or reduced fertility, which in turn reduced the total number of seeds harvested.

To ensure that these genotypes will be available to the scientific community, M3 plants will be grown in rows and bulk harvested to produce M4 seed. Roughly 250 M3 lines belonging to 100 M2 families will also be grown in the field this year for additional phenotyping. These lines/families display novel segregation for important traits (plant height, fertility, canopy architecture, etc.) and may be useful for cloning genes of interest.