North Central Soybean Research Program

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. We propose to make available thousands of new soybean mutant lines adapted to the north-central region that exhibit a wide range of traits, including yield, seed composition, disease resistance/susceptibility, nematode resistance/susceptibility, insect pest resistance/susceptibility, response to water, nutrients, climate, soil and environmental conditions.

These 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.

We will also provide an internet-searchable database wherein 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.

Research Objectives

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

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.

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

Progress report April 2018

Overall, the project addresses the RFP's stated goal of "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 chemically-treated seed was directly planted in the field in Saint Paul in May of 2017, and the resulting M1 mutant generation germinated well. However, the chemically-treated M1 seedlings were particularly sensitive to abiotic stresses. Following several hard rains and a hail storm, the mutant seedlings were essentially destroyed and the field population was abandoned. We repeated the mutagenesis treatment a second time in the fall and germinated the seeds in a greenhouse. Under greenhouse conditions, a larger proportion of the seedlings survived. They plants were grown in small flats with short daylengths to accelerate maturity; we will harvest the seed by the end of March, 2018. The M2 seeds will then be planted in the 2018 field (these should be field-hearty, as they will not be chemically treated). We expect to extract DNA from ~400 independent plants, and fifty will be resequenced measure the rate of mutagenesis in the population.

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.

No progress 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.

The current plan is to harvest the first round of M3 seeds following a field grow-out of the population in 2018.