

# Discovering underlying gene functions in soybean traits

Funding: \$100,000

#### **Principal Investigator**

Robert Stupar, University of Minnesota

### **Co-Principal Investigators**

Gary Muehlbauer, University of Minnesota Amy Skog, University of Minnesota

### Overview of project objectives

The goal of this project is to provide a unique "reverse genetics" platform for the soybean research community. The researchers intend 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, nematode and insect resistance; and 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. A searchable database will be 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.

# **Key results**

A novel chemical mutant population was developed in the soybean genotype 'MN1806CN' using a combination of ENU and EMS mutagenesis. This population demonstrated a range of unique traits in the M2 generation, indicating successful mutagenesis. The researchers are currently sequencing the whole genomes of 50 mutant plants from this population to identify which genes and regulatory regions have mutations. Also, they are using MIPs sequencing to gather mutation information specifically on smaller gene regions for a larger set of mutants (371 plants). This sequencing data will be shared on a public database, allowing researchers to identify mutations in genes of interest and order these lines from our population. This will allow for more efficient breeding with novel traits and discovery of gene functions.

## **Benefit to farmers**

This project aims to build a better community resource for soybean mutants of the North Central region, thereby enabling both publicand private-sector researchers to directly investigate the function(s) for any gene of their choosing. While most projects have the capacity to add knowledge to a specific trait or process, this project has the capacity to accelerate numerous other projects and enable researchers working on virtually any trait or process controlled by genetics. Farmers will benefit from this project long-term as it helps researchers develop a higher quality soybean product in the future.

#### Links

<u>Discovering and finally understanding the functions of genes that underlie major agricultural traits in soybean</u>

USB National Soybean Checkoff Research Database