



## **North Central Soybean Research Program**

### **Characterization and enhancement of soybean genetic resources for soilborne disease resistance**

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#### **Overview**

Soilborne diseases caused by various oomycete and fungal pathogens have been a major limitation to soybean production. *Phytophthora sojae*, *Pythium ultimum*, *Pythium irregulare*, and *Fusarium graminearum* are the major pathogens in the North Central Regions.

Development and planting disease-resistant soybean cultivars remains the most practical, economical, and environmental-friendly solution for eliminating or reducing soybean yield losses from these pathogens. Due to rapid changes of the pathogen, most known resistance genes have become ineffective or partially effective.

The primary goals of this project are to characterize, identify, and/or isolate novel genes/QTLs conferring resistance or partial resistance to *P. sojae*, *P. ultimum*, *P. irregulare*, and *F. graminearum*, and to deploy the new sources of resistance towards effective disease management in the North Central region.

#### **Project Objectives**

1. Evaluate soybean germplasm for resistance or partial resistance to *P. sojae*, *P. irregulare*, *P. ultimum* and *F. graminearum*).
2. Identify QTLs underlying resistance to *P. sojae*, *P. irregulare*, *P. ultimum* and *F. graminearum* by association mapping.
3. Fine map, isolate and functionally verify two uncharacterized *Rps* genes conferring resistance to *P. sojae*.
4. Develop highly adapted soybean cultivars, or experimental lines, with major resistance QTLs and *Rps* genes by marker-assisted selection.

#### **Benefit to Soybean Farmers**

The goal of this research is to capitalize on molecular methods for identifying novel resistance to seed and seedling rot pathogens. The potential impact of this research would add to the options available to soybean farmers for managing these diseases. The potential benefit for American soybean farmers would be an increase in yield of as much as 10% based on estimates of yield

lost to *P. sojae* and the complex of seedling diseases that include *Fusarium* and *Pythium* species.

The research is necessitated by changing patterns in the occurrence of diseases common in the corn-soybean cropping system. Identification of additional highly effective *Rps* genes is a necessity because of the appearance of new and complex *P. sojae* pathotypes capable of overcoming currently available resistance genes. Resistance to *F. graminearum* is necessitated by the increased prevalence of this fungus as a pathogen of soybeans grown in rotation with corn.

Resistance to *Pythium* species is increasingly important as the prevalence of *Pythium* species that infect both corn and soybean become more common with planting of sequences consisting of only these two crops. Because resistance would be available as a varietal trait, the benefit would be available at the lowest cost. In addition, effective control of seed and seedling rots would protect the value of seed, currently the largest single expense in soybean production. In combination with seed treatment fungicides and management practices, varietal resistance would enhance the ability of these tactics to limit losses caused by seed, seedling, and root rots.

#### **Research Progress October 2017**

**Objective 1:** Evaluate soybean germplasm for resistance or partial resistance to *P. sojae*, *P. irregulare*, *P. ultimum* and *F. graminearum*).

Seed, seedling, and root rot caused by *F. graminearum* and *P. ultimum* var.*ultimum* was evaluated in experiments to complete phenotyping of all 280 ancestral lines for resistance to *P. irregulare* seedling rot (three experiments until the beginning of June).

Plants are now being evaluated and assigned root necrosis scores, and root lengths, and root dry weights are being determined and data recorded. After completing this phenotyping step, three reps of the 280 ancestral lines will be planted and inoculated with *P. irregulare* to phenotype these lines for resistance to seed rot in vitro and seedling, and root rot in growth media.

The third replicate of the *F. graminearum* phenotyping is also being planted upon completion breakdown and evaluation of the *P. ultimum* and *F. graminearum* experiments.

**Objective 2:** Identify QTLs underlying resistance to *P. sojae*, *P. irregulare*, *P. ultimum* and *F. graminearum* by association mapping.

Data from phenotyping for resistance to *Fusarium graminearum*, *P. ultimum*, and *P. irregulare* in the seedling assay is being prepared for association analysis to identify markers associated with QTLs for resistance to the three pathogens.

We have developed a protocol to use soybean hairy root transformation system to validate *RpsUN1* and *RpsUN2* candidate genes that have been pinpointed by a combination of fine-

mapping and candidate gene expression analysis. We are in the process of evaluating resistance of the candidate genes.

**Objective 3:** Fine map, isolate and functionally verify two uncharacterized *Rps* genes conferring resistance to *P. sojae*.

We have continued the backcrossing process assisted with marker assisted selection towards the introgression of RpsUN1 and RpsUN2 into four Purdue elite cultivars. The backcrosses have been done in the field and progeny seeds have just been harvested. These seeds are being planted in greenhouse for one generation of self-pollination. We have also analyzed the haplotypes of the genomic regions harboring the two candidate genes using the SNP genotyping data available for the entire USDA soybean germplasm collection.

**Objective 4:** Develop highly adapted soybean cultivars, or experimental lines, with major resistance QTLs and *Rps* genes by marker-assisted selection.

Progeny seed of crosses of RpsUN1 and RpsUN2 into elite breeding lines has been harvested from crosses in Chilean winter nursery during the winter of 2016 and 2017, was planted in local plots during the summer of 2017, and is now at the F4 plant stage.