Marker Development for Maker Assisted Breeding of Resistance to *Phytophthora sojae* in Soybean

Author: Rhianon Schneider
Major: Crop Science
Project Advisor: Leah McHale

One of the most destructive diseases of soybean is Phytophthora root and stem rot, caused by the oomycete pathogen *Phytophthora sojae*, which thrives in wet conditions and poorly drained soils. This disease can cause major damage to soybean yields resulting in economic losses. *P. sojae* has been successfully controlled by genetic resistance in soybean cultivars. Breeding for this resistance is critical to Ohio agriculture and business because of soybean's importance as an export, animal feed, and industrial product. All new cultivars released from the OSU-OARDC soybean breeding program have *P. sojae* resistance, or *Rps* genes. Current methods for breeding for resistance to *P. sojae* involve time-consuming disease assays requiring a relatively large number of seed. Alternatively, molecular markers can be efficiently applied to a single plant from large numbers of breeding lines. In addition, molecular markers can be used for the combination of multiple resistance genes that will provide a full spectrum of resistance.

Currently, I am beginning to analyze the sequences for the 68 NBS-LRR encoding genes and 8 microsattelite markers that co-locate with the *Rps* genes using Sequencher version 4.1 (Gene Codes corporation, Ann Arbor, MI). There were some initial steps in the procedure prior to the sequence analysis. First, genomic DNA was extracted from twelve soybean cultivars that may have none or at least one of the Rps genes present in its' germplasm. Next, I designed primers from the previously sequenced NBS-LRR encoding gene using the Primer3 primer/probe design application (Rozen and Skaletsky, 2000). Afterwards, I ran PCRs using my designed primers and the genomic DNA from the twelve cultivars and sent the PCR products for sequencing. During the sequence analysis, I will be identifying sequence differences associated with each *Rps* gene. This will be used for developing markers in predicting the presence of each *Rps* gene.