M-156

Using high throughput molecular data combined with phenotypic evaluation to identify genetic basis for partial resistance to white mold in soybean

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Soybean [*Glycine max* (L.) Merr.] crop is frequently exposed to field pathogens including *Sclerotinia sclerotiorum* the causal agent of white mold (WM). Soybean growing regions of northern United States and Canada being cool and moist have favorable environmental conditions for the development of WM, which can cause significant damage to yield and grain quality in some years. In soybean, there is no evidence of complete resistance against this pathogen, however, partial resistance has been reported in a number of independent studies, which have rarely been validated. Genomics tools such as QTL analysis and RNA-Seq offer an opportunity to dissect the complex nature of underlying genetics for partial resistance to WM in soybean across different plant populations. The objective of this study was to use QTL mapping, RNA–*Seq* combined with GBS and phenotyping to elucidate genomic regions controlling partial resistance to WM in different genotypes. Fourteen plant introductions (PI) and 20 Canadian cultivars with known partial resistance and susceptible phenotypes were genotyped to obtain haplotypes and phenotyped using a reproducible inoculation method to determine their reaction to the pathogen. Resistance was assessed by measuring the length of the lesion on the main stem after seven days post-inoculation, which ranged between 0.9 and 19.1 cm across the genotypes. Haplotypes will be compared against the phenotype for reported QTL alleles and candidate genes variation as determined by RNA-Seq.