Effects of rhizobacteria association and viral infection on soybean gene expression

Abstract

The proposed project will characterize the transcriptome of soybean plants (*Glycine max*) inoculated with a major viral pathogen, *Bean pod mottle virus* (BPMV), in the presence or absence of two species of beneficial rhizobacteria, *Bradyrhizobium japonicum* and *Delftia acidovorans*, previously implicated in the modification of plant defenses. RNA-Sequencing will be used to obtain the transcripts of the host-pathogen system and results from this work will be integrated with measurements of plant secondary metabolites obtained via gas chromatography and mass spectrometry. I aim to explore whether (*i*) different species of beneficial rhizobacteria result in a distinct transcriptional signature (relative to controls) when the plants are infected with BPMV, and (*ii*) whether virus-induced changes in gene-expression levels correlate with downstream changes in plant secondary metabolites. Results from this proposal will help us to gain a deeper understanding of how soybean responds to BPMV, a disease that causes yield losses up to 52% per year in the U.S, and how beneficial rhizobacteria inoculations can modify soybean resistance.