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Transcription factors leading the pathway to survival
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Asian Soybean Rust, a foliar disease, is caused by the fungal pathogen *Phakospora pachyrhizi,* which threatens soybean (*Glycine max*) production in many countries. In the absence of fungicide treatment, yield losses from ASR can be up to 80%. The use of fungicides significantly drives up production costs for farmers. Four resistant genes, Rpp_{1-4}, have been identified for ASR but none of these provide sustained, field resistance due to adaptation by the pathogen. Soybean cultivar Williams 82 is susceptible to ASR, while cultivar DT2000 exhibits significant levels of tolerance to the pathogen. We utilized these two cultivars to examine the differential response in the expression of various transcription factor genes to ASR inoculation. Our goal is to identify transcription factors that contribute to soybean resistance to ASR and to identify the corresponding genes and pathways responsible for resistance. Due to the relatively low abundance of TF gene mRNA, we utilized the qRT-PCR technique to accurately assay gene expression. We also examined the progress of ASR infection by staining infected leaves at different time points after inoculation. In this way, we hope to correlate the expression of specific genes with the stage of infection. After some trial and error, we were able to easily visualize ASR infection in soybean leaves by staining with Calcofluor White. This staining method allowed us to track ASR infection and document the various stages of fungal development. Our initial screens for TF gene expression identified a few TF genes that are clearly differentially expressed between the susceptible and resistance soybean cultivars. We hope in further experiments to understand the function of these TF genes in soybean resistance to ASR and, ultimately, contribute to the development of soybean cultivars that will benefit soybean farmers.