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Characterization of soybean genes involved in soybean cyst nematode (SCN) resistance

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The expansion of the soybean cyst nematode (SCN; Heterodera glycines) across soybean producing regions of the United States shows no signs of slowing. Resistant soybean germplasm has been used as the primary strategy to manage this pest. However, soybean resistance against SCN is derived from a narrow genetic base and repeated plantings have selected for populations of SCN that can break the resistance. Therefore, understanding the molecular mechanisms of soybean resistance is critical for designing novel strategies to improve crop plant resistance to SCN. To identify genes potentially involved in SCN resistance, we previously coupled laser capture microdissection with microarray profiling to compare gene expression profiles of nematode feeding cells induced in resistant and susceptible near-isogenic lines (NILs) of soybean. We identified 390 soybean genes that were differentially expressed between the resistant and susceptible NILs. Bacterial artificial chromosome (BAC) pools of soybean DNA were then screened for the presence of a subset of these genes. Three genes, believed to be involved in soybean stress and defense responses, were selected for further functional studies. Full length gene and cDNA sequences are being isolated using genome walking and RACE PCR approaches. RNAi and overexpression studies will be used to test the function of these genes in resistance to SCN.

This project was completed to fulfill a Capstone requirement.