

Title: Broadening resistance of soybean to the soybean cyst nematode using biotechnology

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Abstract:

Nematodes are major pests of plants causing billions of dollars in losses each year. Soybean cyst nematode (SCN; *Heterodera glycines*) is the major pathogen of soybean (*Glycine max*) and causes an estimated \$0.8 billion in losses per annum in the U.S. We identified changes in gene expression in soybean roots during resistant and a susceptible reactions and changes in gene expression in the nematode before and during infection using microarrays containing 37,500 soybean and 7,500 SCN gene probes. We used laser capture microdissection (LCM) to isolate syncytia from roots to study gene expression specifically at the feeding site. Gene expression analysis was overlaid on KEGG biochemical pathways for easier visualization of changes in genes encoding enzymes. These and other analyses provided a group of candidate genes that may increase soybean resistance to SCN. A subgroup of nematode genes were also selected as candidate target genes by comparing the SCN EST (expressed sequence tag) database with genes from *Caenorhabditis elegans*. Genes were identified that would cause *C. elegans* death if mutated or silenced. To test constructs of some of these candidate genes, we developed a system to rapidly transform soybean roots with DNA constructs to determine their effect on SCN survival. We transformed soybean roots with a series of vector constructs and challenged the transformed soybean roots with SCN or root knot nematodes to determine if there was a change in resistance compared to control roots. Several constructs reduce the number of females achieving maturity at 30 days as indicated by Female Index comparisons. This approach may be useful for controlling these and other plant nematodes.