GENE RESPONSES OF COTTON ROOTS TO RENIFORM NEMATODE INFECTION

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Abstract

The reniform nematode (RN) *Rotylenchulus reniformis* is one of the major problems of cotton production in Louisiana, Mississippi, Alabama, and parts of Arkansas and Texas. In the absence of resistant cultivars, efforts are being made to transfer resistance from diploid cotton relatives (*Gossypium arboreum*, *G. herbaceum*, and *G. longicalyx*) to upland cotton *G. hirsutum*. But, little is know about the cotton root responses either in compatible and incompatible interactions with the RN. In *G. arboreum* the RN is able to penetrate the roots of both resistant and susceptible accessions, but in the resistant ones, reproduction is very low or does not occur. It is hypothesized that gene expression at the feeding site determines if the plant is resistant or susceptible to the RN. The objective of this study is to characterize the cotton root responses at the transcriptome level to RN infection. Oligonucleotide Microarray chips developed by the Wendel group at Iowa State University were utilized to describe the gene response of cotton roots at 16 days post inoculation. Resistant (A2-194) and susceptible (A2-128) plants of *G. arboreum* were either inoculated with 37,000 nematodes (R-I, S-I) or mock inoculated with water (R-NI, S-NI) to obtain the four treatments evaluated in this study. As expected, cell wall modification genes putatively involved in syncytia formation appeared to be equally up-regulated in resistant and susceptible *G. arboreum*, allowing the nematode to establish the feeding site in both accessions. The hypersensitive reaction observed in A2-194 may be led by up-regulation of senescence associated genes such as Leaf Senescence and the MYB transcription factor; and by the cell accumulation of hydrogen peroxide due to the down-regulation of peroxidase, an enzyme that detoxifies it.