Gene Expression in Giant Cells Induced in Host Plant Roots by Meloidogyne Javanica

Wang Z.H. and Jones M.G.K.
Plant Biotechnology Research Group, WA State Agricultural Biotechnology Centre, Murdoch University, Perth WA 6150.

Plant parasitic nematodes are major pathogens of a wide range of crops. Giant cells induced by root-knot nematodes are highly specialised cells which function as transfer cells and provide nutrients to support the growth and reproduction of the nematode. Using a differential display approach, 81 differential displayed bands were detected between the cytoplasm of giant cells induced in tomato roots by Meloidogyne javanica and control tissues. Of these, 73 were up-regulated and 8 were down-regulated. Sixteen were further analysed by real-time quantitative RT-PCR. The most highly up-regulated transcript increased 56 fold in giant cells, and the greatest down-regulation was 11 fold. A time course of expression of selected transcripts using RT-PCR from giant cell enriched tissue showed similar changes. Sequenced transcripts showed significant homology to mitogen-activated protein kinase, S-adenosylmethionine decarboxylase, cysteine synthase, cytochrome c reductase subunit, and ribosomal proteins. The expression analysed reflects the high metabolic rate in mature giant cells rather than processes of giant cell induction. This work has been extended to microarray analysis using Affymetrix GeneChip microarrays. A comparison of transcripts between giant cell enriched and control root tissues of Arabidopsis revealed a total of 2,448 genes with more than 2-fold changes in expression (about 10% of the 24,000 genes on the chips). Of these genes, 744 were up-regulated in nematode feeding cells and 1,704 were down-regulated. These genes have been classified into functional groups, and the results show substantial changes in gene expression in giant cells that is consist with the function of giant cells in supporting the development of the nematode parasites.