

Early Expressed Genes in the Coffee Resistance Response to Root-Knot Nematodes (*Meloidogyne* sp.) Infection

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SUMMARY

To understand physiological and molecular mechanisms underlying the resistance response of coffee to the root-knot nematode *M. exigua*, we undertook a genomic approach based on the construction of subtractive (SSH) cDNA libraries enriched in genes induced during the early stages of HR. Two different libraries were generated from root tips of resistant vs. susceptible and resistant vs. control coffee varieties 2-4 days (pooled time-points) after inoculation with *M. exigua*. A total of 1180 non-redundant ESTs were obtained and these sequences appeared to be specific of each library since only 41 (4%) were common to both. Functional annotation of the unigene set showed that 30% of the ESTs encoded putative homologues of known defence-related proteins involved in disease resistance (resistance gene analogs, NPR1, HIN1), programmed cell death (cathepsin, cysteine proteinase, 26S proteasome, Bax inhibitor), cell wall strengthening (peroxidase, HRGP, xyloglucan transglycosylase), signalling (ABC transporters, calcium dependent-kinase, WRKY and AP2 transcription factors), antimicrobial activity (PR10, beta-1,3-glucanase) and the production of anti-microbial compounds (phytoalexin precursors, snakine, cytochrome P450). In addition, 14% of the annotated ESTs encoded proteins of unknown function and 35% shared no significant similarity to plant protein database entries. Ongoing studies focus on differential screening of the cDNA libraries and on expression analyses of genes during an infection time-course of resistant and susceptible coffee varieties with *M. exigua* using real-time quantitative RT-PCR in order to identify candidate genes activated in HR exhibiting plants.