A SURVEY OF GENES POTENTIALLY INVOLVED IN *ARACHIS STENOSPERMA* RESISTANCE TO *MELOIDOGYNE ARENARIA* RACE 1

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Root-knot nematodes (*Meloidogyne* spp.) are the most frequently endoparasite in crops, with a broad host range. The most used control strategy is the use of nematicides, which are toxic to the environment and human health. Therefore, the use of resistant cultivars is a promising approach to reduce crop damage caused nematodes. Host resistance to *Meloidogyne* species has been identified in many plants, including peanut, *Arachis hypogaea*, and its wild relatives. In *A. stenosperma*, the induction of feeding sites by *M. arenaria* race 1 was associated with an early hypersensitive response and tissue necrosis, thereby hindering nematode development. The understanding of the molecular mechanisms of host-pathogen interactions provides additional resources for developing new forms of durable plant defenses. In this study, the expression profile of 18 genes was analyzed, during the early phases of *A. stenosperma-M. arenaria* interaction, aiming to identify those with potential for increasing resistance to root-knot nematode. Four-week plants of *A. stenosperma*, the resistant species, and *A. hypogaea* cv Florunner, the susceptible cultivar, were inoculated with 22,400 *M. arenaria* race 1 juveniles J2 each. Control plants received a mock inoculum. Plants were arranged randomly on a bench in a greenhouse and collected at 0, 3, 6, and 9 days after inoculation (DAI). Total RNA was extracted from roots of *A. stenosperma*, pooled from three plants, forming two biological replicates, treated with DNase, and reverse transcribed using a oligo$(dT)_{20}$ primer. Candidate genes were selected for analysis from our wild *Arachis* transcripts database and also from literature. For qRT-PCR (reverse transcription real-time quantitative PCR), a SYBR Green based kit was used in three technical replicates. Glyceraldehyde 3-phosphate dehydrogenase and ribosomal 60S genes were used as reference for gene expression normalization. Primer efficiency and optimal cycle of quantification values (Cq) were determined using the PCR Miner software and expression ratios were statistically tested using REST software. The genes analyzed comprise those coding pathogen stress response proteins (resistance protein MG13, patatin, catalase, resveratrol synthase, calmodulin, phosphate-induced protein 1, and a U-box protein), membrane and cell wall components (lipocalin, integrin, tetraspanin, expansin, xyloglucan endotransglycosylase, and endomembrane protein 70), transcription factors (basic helix–loop–helix, nuclear factor Y, and DC1 domain protein), and two genes with unknown function. Among the 18 genes analyzed, 15 were found to be differentially expressed in *A. stenosperma* infected roots, when compared to non-infected controls, seven genes being differentially expressed in all three time points analyzed. All genes, with one exception, were differentially expressed at 3 DAI, suggesting an extensive transcriptional regulation in the first stages of nematode infection. This study provides new insights for the understanding of *Arachis* resistance to *Meloidogyne* species and its use in plant breeding and in transgenic approaches.

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