

Gene expression revealed during the interaction of resistant *Arachis stenosperma* and *Meloidogyne arenaria*

S-PAD04

Guimarães PM^{1,*}, Morgante CV², Roberts PA³, Silva -Jr OB¹, Arrais L¹, Leal-Bertioli SC¹, Araujo ACG¹, Moretzsohn MC¹, Bertioli D⁴, Brasileiro ACM¹

¹EMBRAPA Genetic Resources and Biotechnology Brasilia, Brazil

²EMBRAPA Semi -Arid, Petrolina, Brazil

³University of California Riverside, CA 92521, California-USA

⁴University of Brasilia, Brasilia, Brazil

*E-mail: patricia.guimaraes@embrapa.br

Abstract

The plant-parasitic root-knot nematodes have evolved sophisticated strategies for exploiting plants with high impacts in agriculture worldwide. The wild species *Arachis stenosperma* shows high levels of resistance to *M. arenaria* and other parasites. A genome-wide overview of differential gene expression during this plant–nematode interaction at different time points (3, 6 and 9 DAI) and healthy roots was conducted using *Illumina Hi-Seq 2000*. Eight cDNA libraries produced a total of 38'241'633 reads with an average sequence size of 200 bp and were assembled into 44,133 contigs. These unique sequences were grouped into eight clusters corresponding to their expression profile estimated by RPKM values. We found that a comparable number of genes were up- and down-regulated during the resistance response and genes belonging to the same family were often differentially regulated. Defence-related genes (calmodulin, patatin, DC1, RGAs and PR), transcription factors and components of hormonal signaling pathways (ARP, CKX) were further characterized using qRT-PCR for validation of their expression profile. This study aimed to characterize genes regulated during early response of resistant *Arachis* to *M. arenaria*, which in association with gene-expression analysis at the cellular level, *in planta* gene function validation and biochemical data, will provide a set of candidate genes for plant transformation aiming nematode resistance in peanut.