Notes

Identification of candidate genes in *Arachis stenosperma* involved in the interaction with root-knot nematode (*Meloidogyne arenaria*)

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Root-knot nematode (*Meloidogyne arenaria*) infection represents a limiting factor for peanut (*Arachis hypogaea*) production. The cultivated peanut species has a narrow genetic base and some wild *Arachis* species could be an alternative source of nematode resistance, showing hypersensitive-like defense response and resistance to root-knot nematode. In the present study, *A. stenosperma* (accession V10309) roots challenged by *M. arenaria* are used to identify candidates genes involved in its resistant interaction. Bioassay was carried out with roots inoculated with juveniles of *M. arenaria* and samples were collected at time points: 0, 3, 6 and 9 days after inoculation (approx. 10 plants per point). Total RNA from roots was extracted using Trizol Reagente® and two pools (5 plants per pool) were formed for each collecting point. cDNA was synthesized from each pool and samples treated with DNAse. Leg 066 primers were used to check DNA contamination by RT-PCR. Primers were then designed from eight host candidate genes, previously identified by our group as involved in the resistant responses of peanut to nematode challenge. RT-qPCR was performed with those primers to determine their efficiency. Two genes (Auxin Repressed Protein and Cytokinin Oxidase) were further selected for validation through RT-qPCR and their relative RNA expression patterns analyzed. Both genes showed distinct expression profiles in *A. stenosperma* roots during its resistance response to *M. arenaria*. The study of the expression profile of host genes is an important step to understanding the mechanisms involved in peanut-nematode interaction.

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