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Prospecting wild *Arachis* spp. genes involved in resistance to the nematode Meloidogyne arenaria through massal transcriptome analysis

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Root-knot nematodes (*Meloidogyne* spp.) are a group of obligate endoparasites with a large range of host plants, including important tropical and temperate crops. The juveniles penetrate the root tip epidermis and move through the intracellular space to form specialized feeding structures, the giant cells. The infection leads to transcriptional reprogramming of surrounding cells, causing hyperplasia and hypertrophy of pericycle and cortical cells, which result in the formation of root knots or galls. It impacts plant yield and enhances its susceptibility to other pathogens. Chemical methods of nematode control tend to be abolished due to environmental concerns, and the development of resistant cultivars and transgenic plants appears as a promising alternative. Peanut, *Arachis hypogaea*, is parasitized by Meloidogyne species that cause significant yield losses. Resistance to M. arenaria race 1 was indentified in two wild *Arachis* species, *A. stenosperma* and *A. cardenasii*. In the former, the resistance mechanism was characterized as a hypersensitive-like response that prevents giant cell and gall formation. Aiming to understanding the early molecular response of *A. stenosperma* to *M. arenaria* and identifying genes involved in resistance to the nematode, massal transcriptome analysis of infected roots was performed. The bioassay was carried out in a greenhouse with one-month-old A. stenosperma plants, inoculated with 22,000 second-stage juveniles of *M. arenaria* race 1. Root samples were collected at four time points: 0, 3, 6 and 9 days after inoculation. RNA was extracted with lithium chloride and treated with DNase. The sequence assay (mRNA-Seq) was performed in a HiSeq2000 Illumina System. cDNAs libraries consisting of two biological replicates per time point, were constructed for each time point including adaptors for the multiplex sequencing in four channels. Approximately 15 billion bases were sequenced distributed in 11 billion reads. The individual percentage of reads attributed to each library ranged from 10.6 to 16.5% of the total of reads, showing that sequences were well distributed among the eight libraries. The quality of the reads was satisfactory, with a mean error rate of 1.39%. This EST databank will allow a better evaluation of the complexities of gene expression involved in *Arachis* resistance to *M. arenaria*, and can be used as a basic resource for molecular marker development and gene discovery, representing an important tool for peanut and other important crop breeding.

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