Transcriptome analysis of *Arachis stenosperma* for identification of resistance genes to *Meloidogyne arenaria*

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Root-knot nematodes are a group of endoparasites with a large range of host plants. Juveniles penetrate root tip epidermis and form feeding structures called giant cells. The infection leads to a transcriptional reprogramming, resulting in the formation of galls. *Arachis hypogaea* is parasitized by *Meloidogyne* species that cause significant yield losses. Resistance to *M. arenaria* was indentified in *A. stenosperma* as a hypersensitive-like response that prevents giant cell formation. Aiming to understand the early molecular response of *A. stenosperma* to *M. arenaria* and identify genes involved in its resistance, massal transcriptome analysis of infected roots was performed. The bioassay was carried with plants inoculated with juveniles of *M. arenaria*. Root samples were collected at time points: 0, 3, 6 and 9 days after inoculation. The sequence assay was performed in a HiSeq2000 Illumina System. cDNAs libraries, consisting of two biological replicates, were constructed for each time point including adaptors for the multiplex sequencing. It was produced 114,979,230 reads, showing an equal distribution between libraries. The error rates, measure by PhiX reference genome, were below 2% (1.31 and 1.47%), numbers in accordance to Illumina specifications for 100 bp reads. The percentages of reads having a base quality greater or equal than Q30 were 82.7 and 81.7%, higher than 70%, the recommendation for reads longer than 75 bases. This EST databank will allow a better evaluation of the gene expression involved in *Arachis* resistance to *M. arenaria* and can be used as a basic resource for molecular marker development and gene discovery.

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