

Prospection of Resistance Genes to *Meloidogyne mayaguensis* in Peanut Plants
(*Arachis hypogaea*)

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In several areas of Brazil, including the Sao Francisco River Valley, *Meloidogyne mayaguensis* has been the main responsible for guava trees death, resulting in significant losses in the production of this fruit crop. Up to now, chemical products experimentally tested have not been efficient and there are no nematicides registered in the Ministry of Agriculture, Livestock and Food Supply for use in guava. Based on the difficulties, search for resistance factors against this nematode in immune plants, like peanuts, would be of great importance to the biotechnology area, seeking for immunity in susceptible plants. Among plant defense mechanisms against pathogen infection, those mediated by *R* genes are the best characterized so far. Most of the proteins expressed by these genes have a central domain composed of a nucleotide binding site (NBS), followed by a terminal leucine rich region (LRR) on the C-terminal region. In this context, the objective of the present study was to look for genes related to resistance to *M. mayaguensis* in peanut plants. For this purpose, peanut genomic DNA was extracted and a PCR reaction was performed using specific primers for the NBS (Nucleotide Binding Site) region of the *R* genes. A positive amplification of a 500 bp DNA fragment was achieved by using such strategy. The fragment was then automatically sequenced and the resulting data was compared with other *R* genes sequences available within the GenBank database.

Key words: *R* genes, root-knot nematodes, *Meloidogyne mayaguensis*, peanut.