58. Molecular characterization of resistance responses of *Coffea canephora* 'clone 14' upon infection with *Meloidogyne paranaensis*.

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Coffee is one of the major commodities in the world and an important source of income for producing countries. However, biotic and abiotic stresses are great limiting factors to coffee yield. In Brazil, root-knot nematodes cause considerable yield reduction and the use of resistant plants is the most promising method to control *Meloidogyne* spp. The aim of this work was to characterize the molecular mechanisms underlining the previously identified resistance to *M. paranaensis* in *C. canephora* 'Clone 14', by means of RNAseq experiments. Differential expression was tested using RNA extracted from roots of plants from clones 14 and 22 of *C. canephora*, previously identified as resistant and susceptible to *M. paranaensis*, respectively; and grown in sand before being inoculated with the nematodes. Root samples were collected at different time points post inoculation as well as roots from an uninfected plant (negative control). The RNA was treated with DNAse and subsequently, a portion of the sample was lyophilized for RNAseq experiments and another portion kept for validation by qPCR experiments. After sequencing and chromosome data analysis, it was observed that, genes related with resistance mechanisms were greatly expressed during the last phases of nematode infection in roots of clone 14. However, the expression of genes coding for proteins directly associated to the resistance process, such as the NBS-LRR Resistance Protein or the Disease Resistance Protein (RPP1), appeared mainly expressed during the first days after infection until the 20th. A set of candidate genes for resistance to *M. paranaensis* was selected and are currently under validation by qPCR experiments.

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