

Metabolomics analysis of interaction of *Coffea arabica* resistant and susceptible to *Meloidogyne paranaensis*

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Introduction

Meloidogyne paranaensis is a threat coffee growing in Brazil and Latin America. Little is known about resistance mechanisms involved. A histopathological study indicate impairment of giant cells development in resistant coffee plants derived from germplasm Amphillo at 14 days after inoculation (DAI) (Alves et al. (2019). The present work aimed to identify resistance-related metabolites of the *Coffea arabica* genotype 16-6-I, derived from the germplasm Amphillo, to *M. paranaensis*.

Materials/Methods

The genotype 16-6-I resistant to *M. paranaensis* (R) and cultivar Catuaí Vermelho IAC 144, susceptible (S) were evaluated in this study. Plants were inoculated with 2500 J₂ de *M. paranaensis*. Leaves samples were collected of three plants at 2, 4, 8, 14, 22, e 32 DAI. Leaf extracts were obtained according to Kim et al. (2010) and were analysed by ¹H NMR.

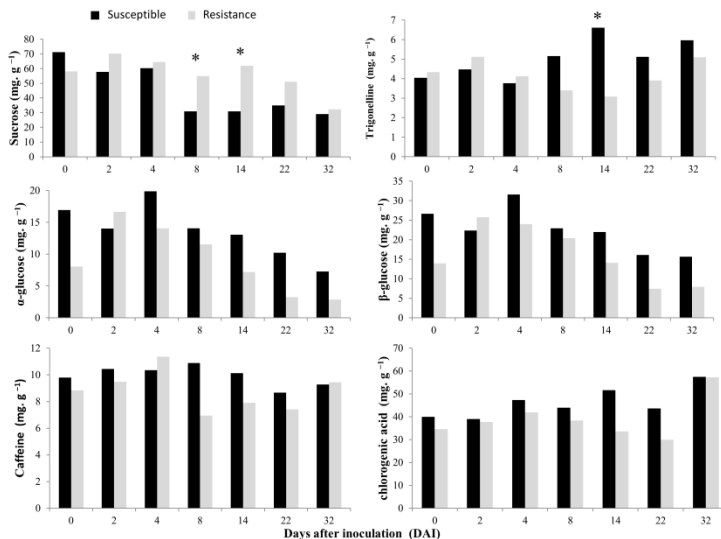


Figure 1: Metabolites identified and quantified by ¹H NMR in leaves of the genotypes R and S to *Meloidogyne paranaensis*.

Results/Discussion

The most significant change observed was the increase of trigonellin concentration at 14 DAI in susceptible plants, probably a late response of resistance (Figure 1). Higher sucrose concentrations were observed from 8 to 22 DAI in resistant plants, possibly blocking the action of cytokines, indispensable for the formation and maintenance of feeding sites. At 14 DAI, slight differences were also observed in caffeine, chlorogenic acid, α-glucose, β-glucose concentration between resistant and susceptible plants, and generally maintained until 22 DAI.

Conclusion/Perspectives

Considering the concentrations of trigonellin and sucrose: Suscetible plants show late resistance response to nematodes. In R plants, the establishment and formation of the feeding sites seems to occur after 8 DAI. These results complement the study of Alves et al. (2019) highlighting that resistance responses are full active at 8 DAI. Future works in gene expression and physiology must be conducted in order better understand this pathosystem.

References:

Alves et al. 2019. Nematology. DOI: 10.1163/15685411-00003254