Genome-Wide Association Studies in *Coffea arabica* for resistance to *Meloidogyne incognita*

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PONCE, Talita P., ARIYOSHI, Caroline, MACHADO, Andressa C. Z., FELICIO, Mariane, SHIGUEOKA, Luciana H., SERA, Gustavo H., PEREIRA, Luiz F.P.

Introduction

The nematode *Meloidogyne incognita* is harmful to coffee production. Controlling it with chemicals or field practices is expensive. Using resistant cultivars is the best option. Most *Coffea arabica* types are susceptible, but Ethiopian genotypes show high resistance. In this work we performed a Genome Wide Association Studies (GWAS) to identify genes and SNPs linked to *M. incognita* resistance in a diverse range of *Coffea arabica* genotypes.

Materials/Methods

Genotyping by Sequencing (GBS) of a collection of 159 *C, arabica* plants, mostly from FAO collection (FAO 1964) was used. Alignment was performed to the reference genome of *C. arabica* Et039 (SALOJÄRVI, 2021), to identify the SNPs. Phenotyping was performed in plants growing at greenhouse conditions inoculated with eggs and J1 stage of *M. incognita.* For each genotype, 8 a 12 plants were evaluated using reproduction factor, nematodes per gram of root, host susceptibility index, and Oostenbrink index. The association between the genotypic and phenotypic data was conducted using multilocus models using the mrMLM.GUI package (WANG et al., 2016) and GAPIT3 (WANG et al., 2021) in the R software.

References:

Salojärvi, J., Arabica Coffee Genome Consortium. (2021). 28th International ASIC, Montpellier, France S1-PO-19.

Wang, S.-B. et al. Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. Scientific Reports/Nature, v. 6, n. 1, p. 19444, 2016

Wang, J. & Zhang, Z. GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. Genomics. Proteomics Bioinformatics 19, 1–12, 2021.

Results

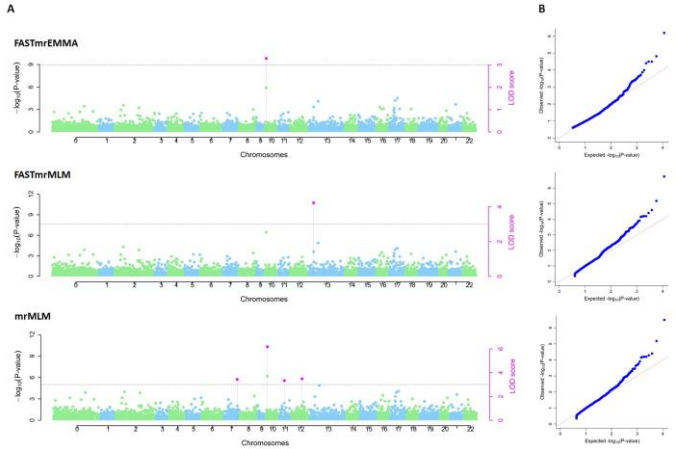

Figure 1: A - Manhattan plots of the reproduction factor related to the multilocus models FASTmrEMMA, FASTmrMLM, and mrMLM. B - Q-Q plots adjusted by Principal Component Analysis (PCA).

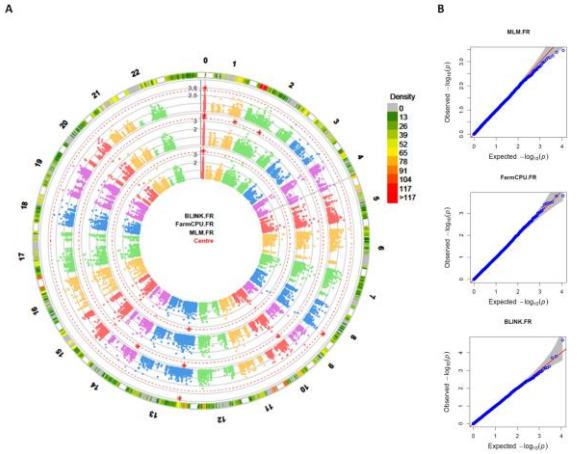

Figure 2: A - The circular Manhattan plot of the reproduction factor related to the single-locus models (MLM) and the multi-locus models FarmCPU and BLINK. B - Q-Q plots adjusted by Principal Component Analysis (PCA).

Phenotyping identified 89 resistant and 31 susceptible plants by reproduction factor. GWAS was perfomed with 11.411 SNPs and 120 plants phenotyped, and 19 SNPs were associated with resistance to *M. incognita*. Five SNPs with the highest association values were selected. In linkage disequilibrium with these SNPs, 3 genes encoded an LRR receptor-like serine/threonine-protein kinase, 1 gene encoded a WRKY transcription factor, and 1 gene encoded a Pathogenesis-related protein.

Conclusion/Perspectives

In this study, the identification of loci related to resistance to *M. incognita* was performed. This characterization can be useful in guiding the breeding process and also as a target for genetic editing. SNPs will be validated using the Taqman® method for marker-assisted selection. Staining root techniques will investigate gene response during plant-pathogen interaction and nematode development providing insights into coffee's resistance to *M. incognita* nematode.