

Genetic diversity of *Pratylenchus brachyurus* populations present in coffee plants

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Introduction

Pratylenchus brachyurus
(root lesion nematode)

Presents **intraspecific variability**

Causes damage to **coffee production**

This research investigated genetic variability in three coffee-associated populations of *P. brachyurus* (PbDR, PbFR and PbGA) and one from cotton (PbSD).

Material and Methods

Morphometric analyses



Glass slides with females from all populations were analyzed;
Analysis: measurement of morphometric variables; De Man indices; principal component analysis (PCA); discriminant analysis of principal components (DAPC).

Molecular analyses

Sequencing of ITS-1 region of rDNA



Results and Discussion

Morphometric analyses

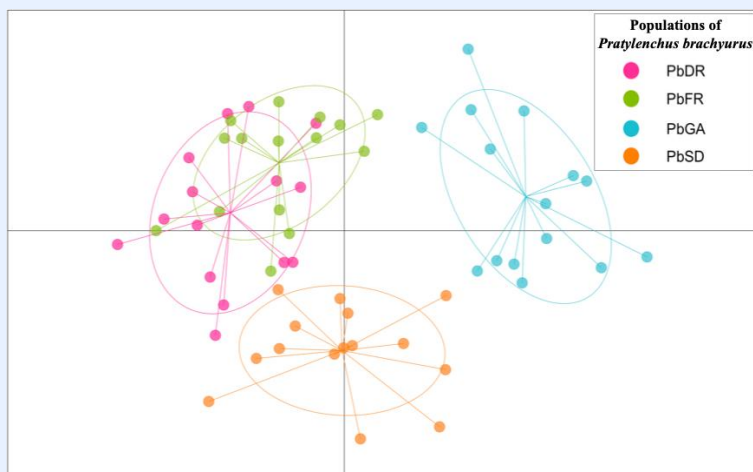


Figure 1: Analysis discriminant of principal component (ADCP) of the PbDR, PbFR, PbGA and PbSD populations of *Pratylenchus brachyurus*

PbDR, **PbFR**, and **PbSD** were morphometrically similar to each other and **PbGA** was the most distinct population. Molecular data showed diversity within and between populations.

Molecular analyses

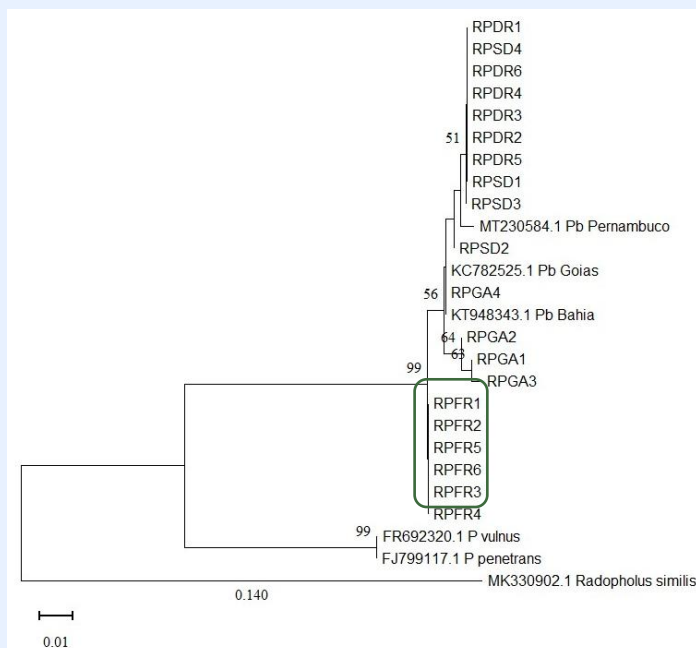


Figure 2: Phylogenetic tree demonstrating the relationships between populations of *Pratylenchus* and *Radopholus similis* (outgroup) based on sequences of the ITS-1 region of rDNA. Numbers indicate bootstrap values greater than 50.

Conclusion and Perspectives

The intraspecific variation in *P. brachyurus* has been demonstrated. This is useful in genetic improvement programs that target resistance to this pathogen.