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IN SILICO ANALYSIS OF PTI (PAMP-TRIGGERED IMMUNITY) SIGNALING COMPONENTS IN THE GENOME OF *Coffea* spp. IN RESPONSE TO PHYTONEMATODES

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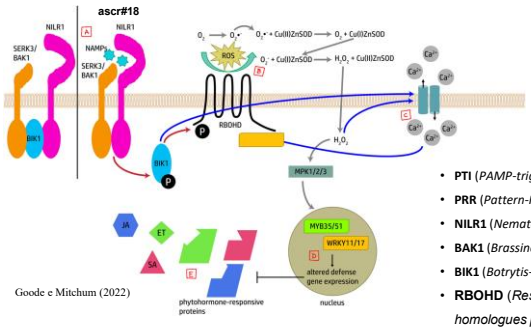
INTRODUCTION

The most widely cultivated coffee species is *Coffea arabica* (allotetraploid), which originated from the hybridization of two diploid species, *C. canephora* and *C. eugenioides*. Nematodes severely impact coffee production, and one way to mitigate this issue is by enhancing the plant's ability to recognize pathogens.

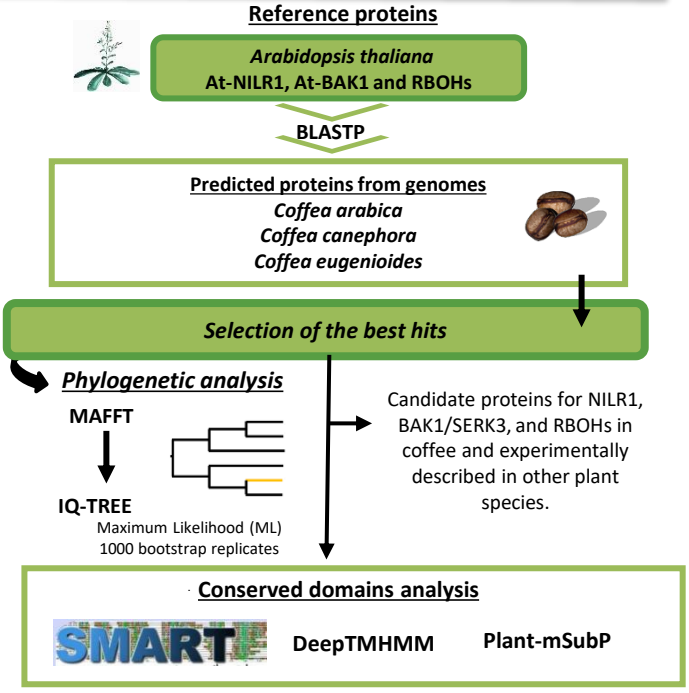


- **PTI** (*PAMP-triggered immunity*)
- **PRR** (*Pattern-Recognition Receptors)*
- **NILR1** (*Nematode-Induced LRR-RLK*)
- **BAK1** (*Brassinosteroid- associated kinase 1*)
- **BIK1** (*Botrytis-induced kinase 1*)
- **RBOHD** (*Respiratory burst oxidase homologues protein D*)

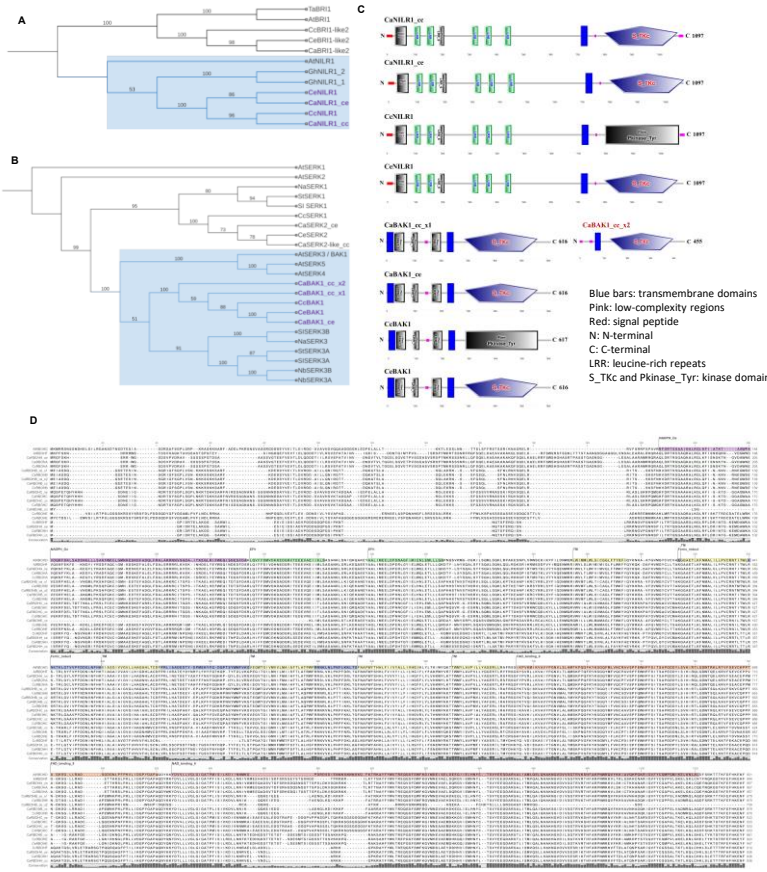
Fig 1. Broad-spectrum interaction between nematodes and hosts. For PTI to be activated, PRRs must recognize NAMPs. NILR1 is required for NAMP perception. BAK1 phosphorylates cytoplasmic BIK1, which then phosphorylates RBOHD to catalyze the formation of reactive oxygen species necessary for the defense response.

Objective: Identify and characterize the PRR NILR1, its co-receptor BAK1, and RBOHs in the genomes of *C. arabica* (Ca), *C. canephora* (Cc) and *C. eugenioides* (Ce).

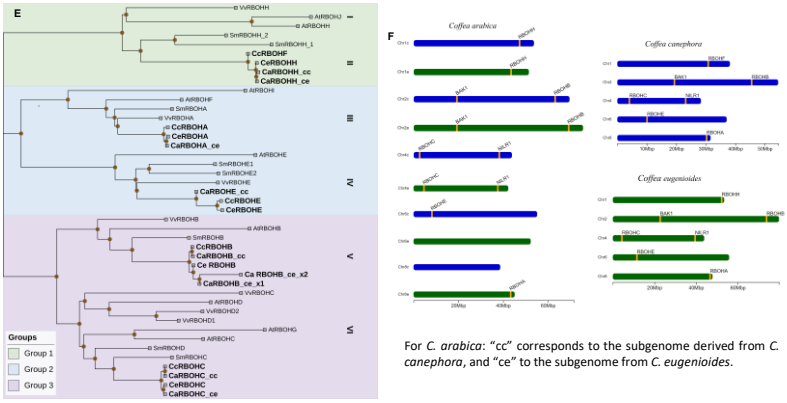
MATERIALS/METHODS



RESULTS



TM: Transmenbrane, EFh: EF-hand.



For *C. arabica*: "cc" corresponds to the subgenome derived from *C. canephora*, and "ce" to the subgenome from *C. eugenioides*.

Fig 2. **(A, B, and E)** Phylogenetic analysis of candidate sequences for NILR1, BAK1, and RBOHs in *C. arabica* (Ca), *C. canephora* (Cc), and *C. eugenioides* (Ce), including orthologs described in other plant species. **(C)** Conserved domains for NILR1 and BAK1. The numbers following each figure represent the protein sizes; the isoform is highlighted in red**. (D)** Alignment of reference RBOHD and RBOHF sequences described in *A. thaliana* and candidate RBOHs for Ca, Cc, and Ce. The transmembrane domains overlap with the Ferric_reduct domain. The numbers at the end of the alignment indicate the protein sizes in number of amino acids. **(F)** Chromosomal distribution of the candidate sequences.

CONCLUSION / PERSPECTIVES

The candidate sequences for NILR1, BAK1, and RBOHs display characteristic domains of reference proteins and were predicted to act in the plasma membrane, indicating that they are likely to perform the same functions. The findings may support biotechnological strategies such as gene expression analysis and gene knockout approaches to better understand the precise function of these genes/proteins in coffee defense against nematodes.

References: 1.GOODE, Kelly; MITCHUM, Melissa G. Physiologia Plantarum, v. 174, n. 2, p. e13680, 2022.

2. MENDY, Badou et al.. PLoS pathogens, v. 13, n. 4, p. e1006284, 2017.

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