

Mitochondrial coding genome analysis of tropical root-knot nematodes

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The polyphagous parthenogenetic root-knot nematodes of the genus *Meloidogyne* are considered to be the most significant nematode pest in sub-tropical and tropical agriculture. Despite the crucial need for correct diagnosis, identification of these pathogens remains problematic. Scientists of Ghent University (Belgium), the National Plant Protection Organization (the Netherlands) en het International Institute of Tropical Agriculture (Nigeria) refined the identification of the nematodes.

The traditionally used diagnostic strategies, including morphometrics, host-range tests, biochemical and molecular techniques, now appear to be unreliable due to the recently-suggested hybrid origin of root-knot nematodes. In order to determine a suitable barcode region for these pathogens nine quickly-evolving mitochondrial coding genes were screened. Resulting haplotype networks revealed closely related [lineages](#) indicating a recent speciation, an anthropogenic-aided distribution through agricultural practices, and evidence for reticulate evolution within *M. arenaria*. Nonetheless, nucleotide polymorphisms harbor enough variation to distinguish these closely-related lineages.

Furthermore, completeness of lineage sorting was verified by screening 80 populations from widespread geographical origins and variable hosts. Importantly, our results indicate that mitochondrial haplotypes are strongly linked and consistent with traditional esterase isozyme patterns, suggesting that different parthenogenetic lineages can be reliably identified using mitochondrial haplotypes. The study indicates that the barcode region Nad5 can reliably identify the major lineages of tropical

root-knot nematodes.

More information: Toon Janssen et al. Mitochondrial coding genome analysis of tropical root-knot nematodes (Meloidogyne) supports haplotype based diagnostics and reveals evidence of recent reticulate evolution, *Scientific Reports* (2016). [DOI: 10.1038/srep22591](https://doi.org/10.1038/srep22591)

Provided by Ghent University

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