



ISBN 978-85-66836-16-5

PHYLOGENETIC ANALYSIS OF *Bursaphelenchus cocophilus* POPULATIONS / Análise filogenética de populações de *Bursaphelenchus cocophilus*. A.P. Silva¹; V.P. Campos¹; S.S. Costa¹; E.S. Freire⁴; C.S.L. Vicente³; L.G. Ferreira²; R.M. Souza²; M. Mota³. ¹Department of Phytopathology/UFLA, 37200 000, Brazil / ²Laboratory of Nematology/UENF, 28013 602, Brazil / ³NemaLab/ICAAM – Department of Biology, Évora University, 7002 554, Portugal / ⁴University of Rio Verde, 75909 477, Brazil. E-mail: esfreire@unirv.edu.br.

Molecular characterization of *Bursaphelenchus cocophilus*, causal agent of 'red ring disease' (RRD), is imperative for efficient identification procedures in Brazil and Colombia, since quarantine species such as *B. xylophilus* and *B. mucronatus* are already listed in both countries. The main purpose of this study was to explore intraspecific phylogenetic relationships of RRD populations through the molecular characterization of the 28S rDNA of the plant-parasitic nematode *B. cocophilus* from different geographic. D2-D3 segments of 28S rDNA were used to characterize 13 isolates of *B. cocophilus* obtained from coconut (*Cocos nucifera* L.) plantations in Brazil and Colombia. The phylogenetic analysis of 28S region of different species of *Bursaphelenchus* genera confirms that all isolates analyzed in this study are *B. cocophilus*. The D2-D3 segments showed that all isolates formed a single monophyletic group with high Bayesian posterior probability (100%). Multiple sequence alignment of 28S region reveals the presence of T nucleotides insertion only in the Columbian populations. The low genetic diversity among Brazilian and Colombian populations of *B. cocophilus* may suggest a single introduction of the pest in these countries.

Keywords: *Bursaphelenchus cocophilus*; 28S; Red ring disease.

Acknowledgements : This work was supported by CAPESPDSE (Proc. 9999.012780/2013-08), FAPEMIG (PhD fellowship to the first author), CNPq and ICAAM – Universidade de Évora.