

## **Pine wilt disease and red ring disease of coconut: opportunities and perspectives in the study of two nematodes *Bursaphelenchus xylophilus* and *B. cocophilus*.**

La enfermedad de marchitamiento de los pinos y el anillo rojo de coqueos: oportunidades y perspectivas en el estudio de dos nematodos, *Bursaphelenchus xylophilus* y *B. cocophilus*.

Manuel Mota<sup>1</sup>, Ricardo Souza<sup>2</sup>, Paulo Vieira<sup>1</sup>, Margarida Espada<sup>1</sup>, Francisco X. Nascimento<sup>1</sup> & Cláudia S. L. Vicente<sup>1</sup>.

<sup>1</sup>NemaLab, Instituto de Ciências Agrárias e Ambientais Mediterrânicas (ICAAM), Universidade de Évora, 7002-554 Évora, Portugal

<sup>2</sup> Grupo de Pesquisa em Nematologia, Universidade Estadual do Norte Fluminense Darcy Ribeiro, CCTA/LEF, 28015-620, Campos dos Goytacazes (RJ), Brasil

Corresponding author: [mmota@uevora.pt](mailto:mmota@uevora.pt)

The xylophagous nematodes *Bursaphelenchus cocophilus* and *B. xylophilus* (Nematoda: Parasitaphelenchidae), are causative agents of two serious diseases, “red ring disease” (RRD) with great importance to coconut and certain oil palm species in Central and South America, and in “pine wilt disease” (PWD), which has wreaked havoc in forest areas in the Far East and now more recently in Europe (Portugal and Spain). PWD has not yet been detected in Brasil or any other country in Central or South America, but there is great risk of introduction due to worldwide movement of wood and wood products through major sea ports. Recently, for example, wood shipments originating from Brasil, infested with *B. xylophilus*, have been intercepted in China. Due to the taxonomical proximity between these two nematodes (the only two plant pathogenic species within the genus *Bursaphelenchus*, containing nearly 100 species), the similarity of life cycles (with the insect vectors *Rhynchophorus palmarum* for *B. cocophilus* and *Monochamus* spp. for *B. xylophilus*) and the likely genomic and proteomic similarities, a comparative study between these two nematodes may provide important insights into understanding RRD, in particular through the genome sequencing of *B. cocophilus*, and comparison with the recently sequenced genome of *B. xylophilus*. Knowledge on specific pathogenicity genes, involved in the RRD process, combined with past and present knowledge, should be helpful in designing new and effective control methods for this major tropical disease of coconut and palm.