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(142) Comparative analysis of MspI satellite repeats of the pinewood nematode, *Bursaphelenchus xylophilus*, at different geographic scales

Vieira P, Castagnone C, Mallez S, Espada M, Navas A, Mota M and Castagnone-Sereno P

NemaLab/ICAAM, Instituto de Ciências Agrárias e Ambientais Mediterrânicas, Universidade de Évora, Núcleo da Mitra, Ap. 94, 7002-554 Évora, Portugal

Email: pvieira@uevora.pt

The MspI satellite DNA (satDNA) family of the pinewood nematode *Bursaphelenchus xylophilus* is herein analyzed in an attempt to understand the intraspecific variability at different geographic scales. A total of 425 MspI monomer units, either PCR-amplified from isolates of local (Peninsula of Setúbal, Portugal) or worldwide origin, or retrieved from the *B. xylophilus* genome sequence, were characterized and compared. Whatever their origin, sliding window analysis of sequence variability patterns among monomers revealed low, moderate and highly variant domains, indicating that variable levels of evolutionary constraint may act upon the entire monomers. The phylogenetic inference based on the different sets of MspI satDNA family for this species shows a broad polymorphism of the individual monomers, which were distributed into four main clusters. However, such clustering appeared independent from the geographic origin of the nematodes, and could not discriminate isolates or groups of geographically close isolates. Rather, the formation of different phylogenetic groups within this satDNA family suggests an a priori embodying of a set of diverging repeats from a common ancestor satDNA library, which have been differently amplified along the evolutionary pathway of this species. The present work improves knowledge on the evolutionary dynamics of satDNA at the intraspecific level, and provides new information on satDNA sequence variability among natural populations sampled at a local geographic scale.