

CHARACTERIZATION OF *Phytophthora cinnamomi* Rands ISOLATES FROM THE AVOCADO-PRODUCING AREA OF MICHOACAN, MEXICO

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Michoacan State concentrates the greatest area for avocados in Mexico and worldwide. Nevertheless, one of the main phytosanitary problems on avocado culture is the fungal disease avocado root rot, caused by *Phytophthora cinnamomi* Rands. The genetic diversity of the causing pathogen is unknown; this has limited the generation of effective pathogen control strategies. With the aim of determining the genetic diversity of this phytopathogen, avocado roots affected by *P. cinnamomi* Rands were collected; oomycete isolates were obtained on PDA (Potato-Dextrose-Agar medium) and re-cultured on V8 medium. A total of 60 isolates from the whole avocado-producing area of Michoacan were analyzed. The morphological characterization indicated variations in the colony growth shape of different isolates: cotton-like with sharp tips (20 %), rose-like without sharp tips (15 %), cotton and rose-like without tips (20 %), rose-like (10 %), open camellia-like (5 %), no-camellia formation (5 %), open-camellia forming a flower (10 %) and concentric rose-like (20 %). In order to perform a molecular DNA characterization, a set of oligonucleotides designed for the amplification of the Internal Transcribed Spacer 1 (ITS1) region of the nuclear ribosomal DNA of *Phytophthora* spp. was employed. Products of amplification of approximately 750 pb were obtained. Sequenced amplicons presented a maximum identity of 95 % with *P. cinnamomi* according to a BLAST (Basic Local Alignment Search Tool, NCBI) analysis of the nucleotide sequences.