

## Colletotrichum species complex affecting avocado fruit

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## Abstract

Mexico is the largest avocado (Persea americana) producer and an important exporter in the world. For export, the fruits must be of a high commercial quality. The quality is affected by several fungal diseases as anthracnose. Until recently, one fungus responsible for this outbreak: Colletotrichum gloeosporioides, has been thought to be the unique causal agent of anthracnose in most avocado regions (1). However, in 2007, C. acutatum was reported as a causal agent in Mexico (2). In a recent report, C. boninense has been identified by molecular approaches as another causal agent of anthracnose in the same country (3). This study was conducted to determine the Colletotrichum species complex involved as causal agents of avocado anthracnose in the main avocado producer state in Mexico. During 2004 to 2010, avocado fruits from 10 counties of Michoacan state, Mexico exhibiting brown-black and reddish spots on the pericarp and soft rot in the mesocarp, were studied. Fungal isolates were cultured on PDA. Thirty five isolates were selected for molecular, morphological and pathogenicity analyses. The molecular approaches employed sequence typing of the internal transcribed spacer region and of the partial nuclear large ribosomal subunit. Primers ITS5 and NL4 were used to amplify a fragment measuring approximately 1100 bp. Each sequence was compared with sequences deposited in the GenBank database by BLAST. The species were identified as C. gloeosporioides (71%), C. acutatum (16%), C. boninense (13%) and a fourth Colletotrichum sp (6%). Morphological features such as the size and shape of conidia were different for each species, as well as the conidial mass color. Pathogenicity tests were conducted by inoculating healthy fruits. All isolates developed symptoms within 3 days after inoculation. This last species encountered did not match to the previous species by BLAST. It seems that a new species is affecting the avocado fruit and a new different pair of primers will be necessary to identify correctly the new pathogen. The sequences of these three species were deposited in the GenBank under the accession nos.: EU294268, EF221829 for C. gloeosporioides; EF175780, EF221831 for C. acutatum, and EU294267, JN215365 for C. boninense.

(1)Prusky, D. 1996. Annu. Rev. Phytopathol. 34:413. (2) Avila-Quezada et al. 2007. Plant Dis. 91:1200. (3)Silva-Rojas H., Avila-Quezada G, 2011. Plant Pathology 60:899-908.