

DISEASE NOTE

**FIRST REPORT OF *PYTHIUM*
ARRHENOMANES ASSOCIATED WITH
ROOT ROT OF MAIZE (*ZEA MAYS*) IN OMAN**

**M.S. Al-Ansari^{1,2,3}, M.R. Finckh¹, M. Deadman³
and A.M. Al-Sadi³**

¹Ecological Plant Protection, University of Kassel, Germany,

²Royal Court Affairs, P.O. Box 17, Muscat 111, Oman

³Department of Crop Sciences, College of Agricultural
and Marine Sciences, Sultan Qaboos University, Oman

Maize is an important fodder crop in Oman. During November 2013, maize plants grown at the Sultan Qaboos University, Alkhoud (Oman), exhibited root rot symptoms, associated with weakened plants and the disease was observed as patches in the field. After isolating from symptomatic plants onto PDA, representative isolates were transferred to V8 agar where smooth, globose, light brown oogonia (31 to 33 mm in diameter) were produced. Identification of the pathogen was morphologically based on Plaats-Niterink (1981) and was confirmed by sequencing the ITS region (primers ITS1/ITS4) for two isolates. A BLAST search showed that the two isolates from Oman share 99% nucleotide identity with the ex-type of *Pythium arrhenomanes* (CBS 324.62, GenBank accession No. AY598628.1) (Levesque and DeCock, 2004). *Pythium arrhenomanes* was first described by Drechsler in 1928 causing root rot of corn in Wisconsin and Illinois (Elliott, 1942). Pathogenicity tests of *P. arrhenomanes* were conducted by inoculating maize seeds with suspensions of the pathogen in pots containing autoclaved soil. In order to fulfill Koch's postulates, re-isolations were performed from the plants that had survived and identity of the pathogen was confirmed molecularly. *P. arrhenomanes* induced root rot symptoms on the inoculated seedlings as observed in the field and fresh weight was significantly reduced ($P < 0.05$). The two *P. arrhenomanes* isolates were deposited at Sultan Qaboos University Culture Collection under the accession number (Msa.Pa01 and Msa.Pa02). To our knowledge, this is the first report of *P. arrhenomanes* in Oman and also as a root pathogen of maize in the country.

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Corresponding author: M.S AL-Ansari
E-mail: ansari.mahmoud@gmail.com

Received June 21, 2017
Accepted July 4, 2017

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**FIRST REPORT OF ANTHRACNOSE
ON CHERIMOYA CAUSED BY
COLLETOTRICHUM TROPICALE IN CUBA**

L. García and A.M. Manzano

*Instituto de Investigaciones en Fruticultura Tropical, Ave. 7ma No.
3005 e/ 30 y 32, Miramar, Playa, La Habana, Cuba*

Cherimoya (*Annona cherimola* Mill.) fruits with preharvest anthracnose symptoms were collected in Province Artemisa, Cuba, in April 2015. Necrotic, sunken lesions with orange spore masses were observed on 71% of the fruits. Single spore isolations on potato dextrose agar (PDA) were initially white and became light gray with scant aerial mycelium and abundant orange conidiomata in concentric rings. Conidia were $12.5\text{-}17.5 \times 5\text{-}6.5 \mu\text{m}$, subcylindrical with rounded ends, aseptate and hyaline, morphological characters consistent with *Colletotrichum tropicale* (Rojas *et al.*, 2010). To confirm pathogen identity, the ITS region, the Apn2-Mat1-2 intergenic spacer and partial mating type (Mat1-2) gene (ApMat) and a partial sequence of the glutamine synthetase gene (GS) were amplified and sequenced (European Nucleotide Archive Accession Nos. LT853592, LT853593 and LT853594, respectively). A phylogenetic analysis using Bayesian inference with published ApMat, GS, and ITS data for *Colletotrichum* species in the *C. gloeosporioides* complex (Jayawardena *et al.*, 2016) placed our isolate INI-FAT 4144 in the *C. tropicale* clade. For assessing pathogenicity, five detached cherimoya fruits were inoculated with a suspension of 10^5 spores/ml by depositing 30 μl droplets of the suspension on the surfaces of non-wounded and wounded fruits with a sterile needle. Control fruits received sterile water. Typical anthracnose symptoms were observed in all inoculated fruits after 3 to 5 days. Control fruits presented no symptoms. The pathogen was consistently re-isolated from the infected fruits. To our knowledge, this is the first report of *C. tropicale* in Cuba and the first report on *A. cherimola*.

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Corresponding author: A.M. Manzano
E-mail: fitopatologia17@iift.cu

Received July 4, 2017
Accepted August 28, 2017