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DISEASE NOTES



First Report of Anthracnose of Olive Fruit Caused by Colletotrichum theobromicola in Argentina

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The olive (Olea europaea L.), family Oleaceae, is an important crop in Argentina, mainly in the production of olive oils and table olives. In the country, that economic loss to the olive industry caused by anthracnose is estimated to be over \$9 million dollars a year. During the harvest of 2018 to 2019, severe symptoms of anthracnose were observed with an incidence of 73% on 483 olive tree (cv. Manzanilla) in a commercial orchard located in Capital, La Rioja, Argentina. Lesions Article History on olive fruits were irregular, becoming dark brown and depressed, with mature fruit mummification, being typical lesions of anthracnose. For fungal isolation, conidia were collected Published: 19 Nov 2019 from orange masses of spores, in acervuli, from 20 infected fruits of 10 olive tree, and were placed in Petri plates containing potato dextrose agar (PDA). Plates were incubated at 25°C in the dark for 6 days, and colonies that were morphologically similar to species of Colletotrichum were transferred to PDA. Three isolates were obtained and then single-spore purified. The isolates (IPAVE 071, IPAVE 072, and IPAVE 076) were preserved and deposited in the Culture Collection of Instituto de Patología Vegetal (IPAVE) at the Instituto Nacional de Tecnología Agropecuaria (INTA) (Córdoba, Argentina). Colonies presented mycelium that were flat with a white margin, and gray aerial mycelium. Conidia were hyaline, aseptate, straight, subcylindrical and clavate, (12.3 to) 13.9 to 19.1 (to 20.57) × (3.5 to) 4.1 to 5.61 (to 6.1) μ m, mean \pm SD = 14.8 \pm $0.2 \times 4.8 \pm 0.1$ µm, length/width ratio = 3.1 (n = 50). Morphological characterization was



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Symptom of maize ear rot caused by Fusarium sporotrichioides (B, B, Wang et al.), Photo credit: C, X, Duan. Systemic symptoms of alfalfa mosaic virus (AMV) isolate CaM on leaves of potato (X. Z. Nie et al.). Photo credit: X. Z. Nie.

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Information

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consistent with the description of Colletotrichum theobromicola (Rojas et al. 2010). For molecular identification, gene sequences were obtained from the partial glyceraldehyde-3-phosphate dehydrogenase (GAPDH), actin (ACT), and β-tubulin 2 (TUB2) regions, which were amplified by PCR (Weir et al. 2012) and sequenced. Sequences obtained in this study were deposited in GenBank for isolates IPAVE 071, 072, and 076, respectively (accessions nos.: GAPDH, MN027902, MN027903, MN027904; ACT, MN027899, MN027900, MN027901; and TUB2, MN027905, MN027906, MN027907). A phylogenetic analysis based on Bayesian inference was performed, which shows that the isolated fungi belong to the C. theobromicola clade. Pathogenicity tests were conducted on 10 olive fruits (cv. Manzanilla). Fruits were surface disinfested by immersing them in a 1% sodium hypochlorite solution for 1 min, washed three times with sterile distilled water, and dried on sterilized filter paper. The fruits were wounded at the center by inserting a sterile needle (to a depth of 2 mm) and inoculated with 6 μ l of conidial suspension (1 × 10⁶ conidia/ml). Control fruits were inoculated with sterilized water. Fruits were incubated at $25 \pm 1^{\circ}$ C for 48 h in semihermetic plastic containers to ensure a high relative humidity (>90%). The fruits were maintained at 25 ± 1 °C (12 h light/12 h dark). Typical anthracnose symptoms were observed after 10 days. C. theobromicola was successfully reisolated from symptomatic olive fruits to fulfill Koch's postulates. C. theobromicola was previously reported on olive causing anthracnose in Australia (Schena et al. 2014). This is the first occurrence of C. theobromicola in Argentina and the first report causing anthracnose of olive fruit (O. europaea).

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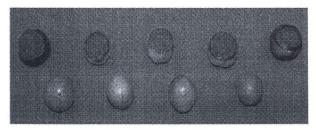


Figure \$1. Symptoms of anthracnose on inoculated olive fruits caused by Colletotrichum theobromicola, and control fruits inoculated whit sterilized water.

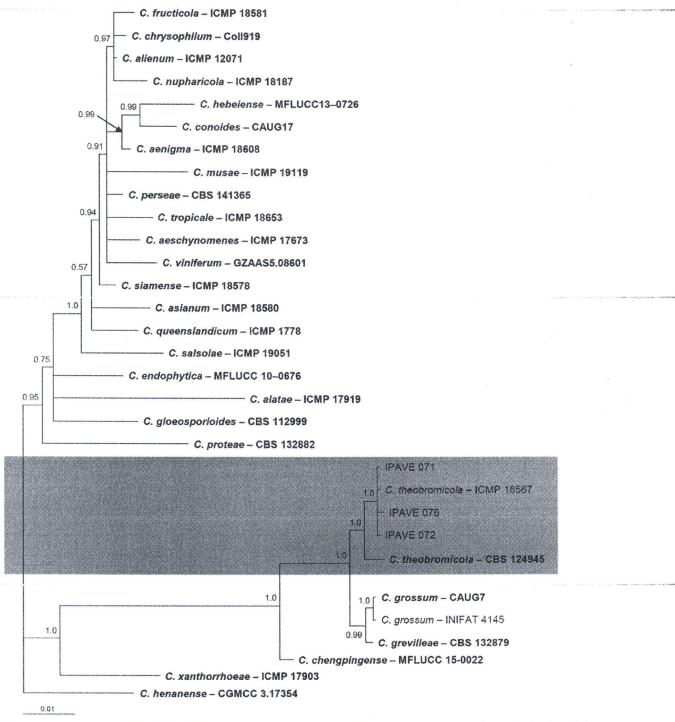


Figure S2. Bayesian tree obtained from the GAPDH, ACT and TUB2 gene sequences alignment of the partial Colletotrichum gloeosporioides species complex. Bayesian posterior probability values above 0.50 are shown at the nodes. Colletotrichum henanense is used as outgroup. Numbers of ex-holotype and ex-epitype isolates are emphasized in bold. The scale bar indicates the number of expected changes per site.