Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on Peach Fruit Caused by *Colletotrichum siamense* in Uruguay

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Peach (*Prunus persica* L.) is an economically important deciduous fruit crop in Uruguay. Anthracnose caused by species of the genus *Colletotrichum* is one of the major diseases in peach production, causing significant yield losses in the United States (Hu et al. 2015), China (Du et al. 2017), Korea (Lee et al. 2018), and Brazil (Moreira et al. 2020). In February 2017, mature peach fruits cv. Pavia Canario with symptoms resembling anthracnose disease were collected from a commercial orchard located in Rincon del Colorado, Canelones, in the southern region of Uruguay. Symptoms on the peach fruit surface were characterized as circular, sunken, brown to dark brown lesions ranging from 1 to 5 cm in diameter. Lesions were firm to the touch with wrinkled concentric rings. All lesions progressed to the fruit core in a V-shaped pattern. The centers of the lesions were covered by orange conidial masses. Monosporic isolates obtained from the advancing margin of anthracnose lesions were grown on PDA at 25°C and a 12-h photoperiod under fluorescent light. The representative isolates DzC1, DzC2, and DzC6 were morphologically and molecularly characterized. Upper surfaces of colonies varied from white or pale-gray to gray, and on the reverse, dark gray with white to pale gray margins. Conidia were cylindrical, with both ends predominantly rounded or one slightly acute, hyaline and aseptate. The length and width of conidia ranged from 9.5 to 18.9 µm ($\bar{x}$ = 14.1) and from 3.8 to 5.8 µm ($\bar{x}$ = 4.6), respectively. The ACT, βTUB2, GAPDH, APN2, APN2/MAT-IGS, and GAP2-IGS gene regions were amplified and sequenced with primers ACT-512F/ACT-783R (Carbone and Kohn 1999), BT2Fd/BT4R (Woudenberg et al. 2009), GDF1/GDR1 (Guerber et al. 2003), CgDLR1/ColDLF3, CgDLF6/CgMAT1F2 (Rojas et al. 2010), and GAP1041/GAP-IGS2044 (Vieira et al. 2017),

respectively, and deposited in the GenBank database (MZ097888 to MZ097905). Multilocus phylogenetic analysis revealed that Uruguayan isolates clustered in a separate and well supported clade with sequences of the ex-type (isolate ICMP 18578) and other *Colletotrichum siamense* strains (isolates Coll6, 1092, LF139, and CMM 4248). To confirm pathogenicity, mature and apparently healthy peach fruit cv. Pavia Canario were inoculated with the three representative isolates of *C. siamense* (six fruit per isolate). Fruit were surface disinfested with 70% ethanol and wounded with a sterile needle at two equidistant points (1 mm diameter × 1 mm deep). Then, fruit were inoculated with 5 µl of a spore suspension (1×10^6 conidia ml⁻¹) with four inoculation points per fruit (two wounded and two unwounded). Six fruit mock-inoculated with 5 µl sterile water were used as controls. Inoculated fruit were placed in a moist chamber and incubated at 25°C for 10 days. Anthracnose lesions appeared at 2 and 4 days after inoculation in wounded and unwounded points, respectively. After 7 days, disease incidence was 100% and 67% for wounded and unwounded fruit, respectively. The control fruit remained symptomless. The pathogens were reisolated from all lesions and reidentified as *C. siamense*. *C. siamense* was previously reported in South Carolina causing anthracnose on peach (Hu et al. 2015). To our knowledge, this is the first report of anthracnose disease on peach caused by *C. siamense* in Uruguay. Effective management strategies should be implemented to control anthracnose and prevent the spread of this disease to other commercial peach orchards.

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