


Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose Caused by *Colletotrichum nymphaeae* on Strawberry Fruits in Central Argentina

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Strawberry (*Fragaria × ananassa*) production in Argentina extends to around 1,700 ha. Coronda City, located in Santa Fe Province, is an important strawberry producer because of ideal agroecological conditions for culture and a high specialization for production. In November 2021, anthracnose symptoms were observed on strawberries (cvs. San Andreas and Splendor) in Coronda (31°58'S, 60°55'W), central Argentina. During these years, the incidence of the disease reached 40% of the production. Symptoms included 2- to 3-mm circular to irregular dark brown spots, which enlarged rapidly and became sunken. Under high-humidity conditions, concentric rings of pinhead-sized salmon-colored acervuli developed on the lesions. The causal agent was isolated by touching acervuli with a sterile needle, and monospore cultures were obtained on potato dextrose agar after 10 days at 25°C, with a 12-h light period. Colonies were white to gray on the top and orange on the underside, where concentric rings of salmon-colored acervuli were clearly distinguished. The width and length of 100 conidia were examined in three isolates (CF1, CF2, and CF3), ranging from 3.27 to 5.53 µm (average = 4.3 µm) and from 10.37 to 19.52 µm (average = 14.27 µm), respectively. The conidia were hyaline, smooth walled, aseptate, and cylindrical to clavate, with one end round and the other acute. These morphological characteristics corresponded to species belonging to the *Colletotrichum acutatum* species

complex (Damm et al. 2012; Liu et al. 2022). To accurately identify the species, DNA was extracted from the isolates and β-tubulin (*TUB2*), glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), and histone (*HIS3*) genes were partially amplified and sequenced (Vieira et al. 2020). *TUB2*, *GAPDH*, and *HIS3* sequences showed a 100% identity with *Colletotrichum nymphaeae*. The nucleotide sequences were deposited in GenBank (*TUB2*, OR271556 to OR271558; *GAPDH*, OR271559 to OR271561; *HIS3*, OR271562 to OR271564). Multilocus phylogenetic analyses performed with reference sequences (Damm et al. 2012) showed that the three isolates clustered with *C. nymphaeae* in accordance with BLAST results. To confirm pathogenicity, each isolate was inoculated in eight detached fruits of the cultivar from which it was originally obtained. Two drops of 10 µl of conidial suspension (1×10^5 conidia/ml) were deposited in nonwounded areas on fruits previously disinfected with 1% sodium hypochlorite solution for 1 min and rinsed two times with sterile distilled water. Eight fruits treated with drops of sterile water served as controls. Pathogenicity tests were repeated two times. Fruits were kept in a moist chamber (80 ± 5% relative humidity) at 25°C for 10 days. First symptoms appeared 4 days after inoculation. After that, all of the isolates produced symptoms identical to those previously described, whereas the controls remained symptomless. The pathogen was reisolated from lesions and identified as *C. nymphaeae* by morphological characteristics and based on the *TUB2* sequences, as previously described. Strawberry anthracnose in Argentina was previously associated with *C. acutatum*, *C. gloeosporioides*, and *C. fragariae* based on morphological characteristics (Mónaco et al. 2000; Ramallo et al. 2000), but molecular identification has not been performed to date. To our knowledge, this is the first report of *C. nymphaeae* causing anthracnose on strawberry in Argentina. This accurate identification will help develop more efficient management strategies.

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