First Report of *Botryosphaeria dothidea* Causing Canker on *Cotinus coggygria* in China

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The smoke-tree (*Cotinus coggygria*) is one of the most important ornamental tree species used in ecological and landscape plantings in China. In summer of 2018, cankers and dieback were observed on *C. coggygria* grown in several forest parks located in Shandong Province, east-central China. More than 50 trees were observed with the disease. Cankers were located on the trunk, and as disease developed, trees showed a progressive dieback. Tissues below the infected bark revealed dark-brown lesions. To identify the causal pathogen, the phloem and xylem sectors of 10 diseased *C. coggygria* trees were collected from three locations in Shandong. Pieces of tissue from the border between necrotic and healthy tissues were surface disinfected by immersing in 75% ethanol for 30 s and rinsing three times with sterilized double distilled water, and then the samples were cultured on potato dextrose agar (PDA) and incubated at 25°C for 5 to 7 days. More than 30 isolates were obtained. Developing fungal colonies produced copious, white, aerial mycelium that became dark green with age. Pycnidia developed after about 20 days. Conidia were hyaline, aseptate, fusiform to ellipsoid, and measured a mean dimension of 22 ± 7 × 6 ± 2 µm (n = 20). Fungal identity was confirmed based on comparisons of DNA sequences of the rDNA internal transcribed spacer region (ITS), partial translation elongation factor 1-alpha (*tef1*) and β-tubulin (*tub*), which were amplified using the primers ITS1/ITS4 (White et al. 1990), EF1-728F/EF1-986R (Carbone et al. 1999), and BT-2a/BT-2b (Glass et al. 1995), respectively. Six isolates selected for sequence analysis showed 100% identity with each other; hence, only one isolate was deposited in GenBank (ITS, MK168571; *tef1*, MK722179; and *tub*, MK720626) and used to perform Koch's postulates. All sequences blasted against the GenBank database showed 98 to 100% identity to records of *B. dothidea* (accession nos. MF409167, KU306118.1, and MG878299.1). Fifteen 1-year-old uninfected *C. coggygria* seedlings used in the pathogenicity experiment were wounded using sterile blades. Mycelial plugs (3 to 4 mm in diameter) of *B. dothidea* from actively growing colonies were incubated to same-size bark wounds at the central region of stems and wrapped with Parafilm. Sterile PDA plugs were used for control seedlings. Inoculated and control seedlings were inoculated in greenhouse conditions of 15 h light/9 h dark at 25°C with 60% relative humidity and watered as needed. After 2 weeks, all *C. coggygria* seedlings developed canker lesions on inoculated stems, and no symptoms manifested on the noninoculated controls. The average lesion size caused by fungal inoculations in stems was 9.5 ± 2 cm (n = 10). *B. dothidea* was recovered from each lesion but not from negative controls, confirming completion of Koch's postulates. *B. dothidea* has been reported to cause canker on *Aucuba japonica* (Zheng et al. 2019) and *Carya cathayensis* (Zhang et al. 2011) in China. Although *B. dothidea* has been reported from herbarium specimens as a colonist of *C. coggygria* in east-central China (Li et al. 2007), to our knowledge this the first report of *B. dothidea* causing stem canker on *C. coggygria* in China.

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Keywords: *Cotinus coggygria*, canker, *Botryosphaeria dothidea*, China

First Report of Stem Rot Caused by *Fusarium oxysporum* f. sp. *opuntiarum* on *Sulcorebutia heliosa* in Italy

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Sulcorebutia heliosa, Cactaceae family, is a succulent plant used as ornamental. During June 2018, several 2-year-old plants of *S. heliosa*, grown in a nursery located in Ventimiglia (43°47′48.648″N, 7°35′34.616″E, Imperia province, northern Italy), showed symptoms of a stem rot. Stems wilted and collapsed. Internal tissues rotted, and eventually affected plants dried and died. About 10% of 1,000 plants were affected. Small fragments (3 mm) were taken from the margins of affected collar and stem tissues and plated onto potato dextrose agar. Colonies of a fungus were isolated that produced whitish to pale purple colonies and pale purple pigments in the medium. On carnation leaf agar medium, colonies produced unicellular, oval to elliptical microconidia supported by short monophialides. Conidia measured 4.3 to 8.2 × 1.7 to 3.4 µm (average, 5.9 × 2.6 µm) (n = 50). On the same medium, colonies produced slightly falcate macroconidia, not formed in sporodochia. Macroconidia were slightly falcate, with a foot-shaped basal cell, a short apical cell, and three (sometimes four) septa. They measured 22.6 to 41.6 × 3.4 to 4.5 µm (average, 31.0 × 3.8 µm) (n = 50). Chlamydospores were smooth walled, terminal or intercalary, in singles or in pairs, and measured 4.8 to 8.6 µm (average, 6.9 µm) in diameter (n = 50). These morphological characteristics are typical of *Fusarium oxysporum* (Leslie and Summerell 2006). A pure culture of the isolate DB18GIU36 was used to extract DNA, using the E.Z.N.A. Fungal DNA Mini Kit (Omega Bio-Tek, Darmstadt, Germany). The elongation factor 1α gene (EF1α) was amplified using primers EF1/EF2 (O'Donnell et al. 1998) and sequenced (GenBank accession no. MK050503). BLASTn analysis of the 677-bp segment showed a 99% similarity with the sequence KY379852 of *F. oxysporum*. Successively, the intergenic spacer (IGS) was amplified using primers CNS1/CNL12 (Appel and Gordon 1995) and sequenced (GenBank accession no. MK050504). BLASTn analysis of the 1,202-bp segment showed 100% similarity with the sequence FJ985530 of *F. oxysporum* f. sp. *opuntiarum*. Pathogenicity of one isolate was tested on three 12-month-old healthy plants of *S. heliosa* by dipping roots in a 4.3 × 10^7 CFU/ml conidial suspension, grown on potato dextrose broth. The roots of three control plants were dipped in sterile water. Successively, all plants were transplanted into pots filled with steamed substrate and maintained at 25 to 35°C. After about 30 days, the first wilt symptoms appeared on inoculated plants, from which *F. oxysporum* f. sp. *opuntiarum* was reisolated (78% reisolation) and identified by the amplification of the EF1α and IGS gene portions (GenBank accession nos. MK910767 and MK910768, respectively). As the disease progressed, stems rotted and plants died. Controls remained symptomless, and attempts to reisolate the pathogen from these failed. This is the first report of *F. oxysporum* f. sp. *opuntiarum* on *S. heliosa* in Italy, as well as worldwide. Although in Italy the production of *S. heliosa* is still limited, many other succulent plants belonging to Cactaceae, hosting *F. oxysporum* f. sp. *opuntiarum*, such as *Schlumbergera truncata* (Lops et al. 2013), are extensively grown, with a risk of severe losses.

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Keywords: *Fusarium*, ornamentals, epidemiology

First Report of Fusarium Wilt by *Fusarium oxysporum* in *Physalis peruviana* in Ecuador

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Physalis peruviana, known locally as uvilla but internationally as goldenberry or Cape gooseberry, is the fourth most important exotic fruit for export in Ecuador, after *Mangifera* spp. (mango), *Cereus* spp. (pitahaya), and *Passiflora* spp. (maracuya and granadilla). Ecuador is the second world exporter of this solanaceous fruit after Colombia. This crop is produced in four provinces located in the center and north of the Andean