Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Leaf Blight Caused by *Alternaria alternata* on *Platanus acerifolia* in China

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Platanus acerifolia Willd. is widely planted in cities in China due to its strong adaptability to different environmental conditions. In August 2021, light brown, oval to circular, sunken spots were observed on leaves of *P. acerifolia* trees with 8 to 35% incidence, leading to severe necrosis and abscission of leaves on a street in Haidian district of Beijing (39.9593°N, 116.2984°E). Small pieces (5 × 5 mm) were taken from the margin of diseased tissues, disinfected with 0.3% sodium hypochlorite for 2 min and 70% ethanol for 40 s, rinsed with sterile water, plated on potato dextrose agar (PDA), and incubated at 28°C. After 4 days, representative isolates were transferred to new PDA plates. Four isolates with similar morphological characteristics were obtained and deposited in the culture collection (DAA3, DAA5, DAA6, and DAA7) of our laboratory. Colonies on PDA were dense, fluffy, and light to dark gray, with a prominent white margin. Conidia formed in chains on the branched conidiophores and were obpyriform to ellipsoid, 19.5 to 32.3 × 5.5 to 10.2 µm (average = 26.4 × 7.1 µm, n = 30) in size, with three to five transversal and one to three longitudinal septa. These morphological characteristics matched those of *Alternaria* spp. (Simmons 2007). Genomic DNA was extracted with a modified cetyltrimethylammonium bromide method, and the internal transcribed spacer (ITS) region, translation elongation factor 1-α (*EF1-α*), RNA polymerase II largest subunit (*RPB2*), glyceraldehyde-3-phosphate dehydrogenase (GPD), endopolygalacturonase (*EndoPG*), and *Alternaria* major allergen (*Alt a1*) genes were amplified with primer pairs ITS1/ITS4 (White et al. 1990), EF1-728F/EF1-986R (Carbone and Kohn 1999), RPB2-5F/RPB2-7cR (Liu et al. 1999), gpd1/gpd2 (Berbee et al. 1999), PG3/PG2b (Andrew et al. 2009), and Alt-for/Alt-rev (Hong et al. 2005), respectively. The obtained sequences were deposited in GenBank (accession nos. OM228653 to OM228656, OM221523 to OM221542). In a BLAST search, the sequences were 100% identical to corresponding sequences of *Alternaria alternata*. Phylogenetic analysis based on combined sequences using the maximum parsimony method showed that the four isolates clustered together with the type strain CBS 916.96 of *A. alternata*. For pathogenicity testing, three healthy leaves of three 1-year-old *P. acerifolia* plants were wounded with a sterile needle and inoculated with 20 µl of spore suspension (10^6 conidia/ml). Plants inoculated with sterile water were treated as a control. The pathogenicity test was also conducted on unwounded leaves. After 8 days of inoculation at 25°C and 90% relative humidity with a 12-h photoperiod, the symptoms on spore suspension-inoculated leaves were similar to those observed on trees in the street, whereas the control leaves remained symptomless. Lesions on wounded leaves were larger than those on unwounded leaves. The assay was repeated twice with consistent results. The pathogen was reisolated from symptomatic leaf tissues and identified based on morphological and rDNA-ITS sequencing, thus fulfilling Koch's postulates. Examples of other tree species for which *A. alternata* has been reported to cause leaf blight were *Ophiopogon japonicas* in China (Wang et al. 2021) and *Pistacia terebinthus* in Spain (López-Moral et al. 2018). To our knowledge, this is the first report of *A. alternata* causing leaf blight on *P. acerifolia* in China. The identification could provide information for developing effective disease management strategies.

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