Diseases Caused by Fungi and Fungus-Like Organisms

Leaf Spot Caused by *Boeremia linicola* on Siberian Ginseng in China

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Siberian ginseng (*Eleutherococcus sessiliflorus* [Rupr. & Maxim.] S.Y. Hu, Araliaceae) is a perennial medicinal plant that is widely cultivated in China. Leaf spot was observed in 2- and 3-year-old Siberian ginseng in Zuoqia County (126°05'23.2"E, 44°03'09.5"N), northeast China, in August 2019. Polygonal or irregular black spots ranging from 2 to 9 mm in diameter were found on infected leaves, and each leaf had dozens of spots. The green color around the lesions gradually faded. As the disease progressed, the spots withered and multiple lesions merged into large disease spots, causing leaf wilting. More than 38% of plants in one 25-ha field were infected in 2019. Fifteen diseased leaves were collected from those plants and cut into 5-mm pieces. The pieces were surface disinfected by immersion in 1% NaOCl for 2 min and then rinsing twice with sterile distilled water. The leaf pieces were placed on acidified potato dextrose agar (PDA, pH 4.7) in Petri plates and incubated in the dark at 25°C. Nineteen isolates were obtained, and all were purified from a single spore in water agar. Isolate CWJ7 was randomly selected for identification and pathogenicity testing. The colonies on PDA were olivaceous gray to olivaceous black, velvety, with dense hyphae and a scalloped or irregular margin. The reverse side was gray-black and surrounded by tawny halos. The conidia were aseptate and variable in shape and dimension: piriform, columnar, drop-shaped, dumbbell-shaped, or oval, measuring 4.90 (7.03) 9.50 × 2.10 (2.78) 3.40 µm ($n = 100$), and chlamydospores were absent. Black pycnidia (132.2 to 241.5 µm in diameter) appeared after 7

days. The pathogen was initially identified as *Phoma* or *Phoma*-like (Boerema et al. 2004). Further confirmation was also determined by sequencing the nuclear ribosomal internal transcribed spacer region (GenBank accession no. MT912950), 28S ribosomal RNA gene (MT912968), and genes encoding β -tubulin (MT920618), the second largest subunit of RNA polymerase II (MT920619), and translation elongation factor (MT946526) (de Hoog and Gerrits van den Ende 1998; Liu et al. 1999; Rehner and Samuels 1994; Vilgalys and Hester 1990), and BLAST searches showed 90 to 100% homology with GU237754, GU237938, KT389780, KT389575, and KY484705, respectively. In a phylogenetic analysis combining all loci, CWJ7 and the type strains of *Boeremia linicola* clustered in one group. Based on its morphological characteristics and phylogenetic analysis, isolate CWJ7 was identified as *B. linicola* as revised in 2019 (Jayawardena et al. 2019). Healthy 2-year-old plants were used for pathogenicity testing. The leaves of nine potted plants (one plant per pot, three plants per replicate) were spray inoculated with a suspension of conidia (1×10^5 spores/ml) from colonies on PDA for 7 days and cultured for 48 h under continuous black light. Nine plants were sprayed with sterile water as the control. This experiment was repeated twice. All plants were cultured in a greenhouse (25°C, 12-h photoperiod, 78% relative humidity). Clear plastic bags were used to maintain high humidity. After 7 days, the inoculated plants showed lesions on the leaves, similar to those observed in the field. The control plants remained symptomless. The pathogen was reisolated and identified by sequencing. This is the first report of *B. linicola* causing Siberian ginseng leaf spot, and a new record of this species in China. This disease poses a threat to production, and management strategies should be developed.

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