Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Collar Rot in Purple Passion Fruit (*Passiflora edulis*) Caused by *Neocosmospora solani* in Yunnan Province, China

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Purple passion fruit (*Passiflora edulis* Sims) is a perennial climbing vine native to South America that is grown worldwide as an edible tropical fruit with excellent nutritional value and high economic value (Zibadi et al. 2007). With the increasing expansion of the plantation area in China, considerable economic loss caused by collar rot has attracted wide attention. From 2018–2020, collar rot resulted in the death of many plants of *P. edulis* ‘Mantianxing,’ a commercial cultivar in China, in southwest China’s Yunnan Province. The disease spread quickly, and field incidence reached more than 50%. Stem rot symptoms were observed at the base of the stem, about 5 to 10 cm from the ground, resulting in wilting, defoliation, and death of plants. Representative symptomatic samples were collected from the base of five plants, surface disinfested for 30 s with 75% ethanol and 15 min with 10% hypochlorite, washed three times with sterile distilled water, then transferred to potato dextrose agar (PDA) dishes. After 2 days in the dark at 28°C, emerging fungal colonies were purified on new PDA dishes cultured at 28°C for 7 days. The mycelia were flocculent. The color of the surface and the reverse colony was white and cream, respectively. On synthetic nutrient agar (SNA), microconidia were oval, ellipsoidal or reniform, 0- or 1-septate, and 6.7 to 23.1 µm long ($n > 30$); macroconidia were straight to slightly curved, 3- or 5-septate, and 30.8 to 53.9 µm long ($n > 30$). Genomic DNA, extracted

from six isolates, was amplified with three pairs of primers, ITS1 and ITS4 (White et al. 1990), EF1-728F and EF1-986R (Carbone and Kohn 1999), and rRPB2-5F and rRPB2-7cR (Liu et al. 1999). The amplicons from all six isolates were sequenced and identical sequences obtained. The sequence of one representative isolate was uploaded to the National Center for Biotechnology Information (NCBI) and analyzed with BLASTn in the *Fusarium* MLST database (<https://fusarium.mycobank.org>). The sequence of the internal transcribed spacer 1 (ITS1) region (GenBank MN944550) showed 99.1% (449/453 bp) identity to *Fusarium solani* strain NRRL 53667 (syn: *Neocosmospora solani*, GenBank MH582405). The sequence of the translation elongation factor-1 (EF-1) gene (GenBank MN938933) showed 97.8% identity (263/269 bp) to *F. solani* strain NRRL 32828 (GenBank DQ247135). The sequence of the second largest subunit of RNA polymerase II (RPB2) gene (GenBank MW002686) showed 98.7% identity (810/821 bp) to *F. solani* strain NRRL 43441 (GenBank MH582407). Based on a multilocus phylogenetic analysis of the ITS1, EF-1, and RPB2 sequences, coupled with the morphological characteristics, the isolate (designated as NsPed1) was considered to be *N. solani* (syn: *F. solani*) (Crespo et al. 2019). Subsequently, 3-month-old healthy seedlings and 45-day-old cuttings of *P. edulis* ‘Mantianxing’ plants were inoculated with the isolate NsPed1 to test its pathogenicity. Stems were wounded, ~1 to 2 mm deep, in the collar region of plants at 2 cm above the soil. A disk (9 mm in diameter) of NsPed1-colonized PDA was placed on the wound. Sterile PDA served as control. All plants were kept in a growth chamber at 28 to 30°C, 60% relative humidity, and 16/8-h light/dark photoperiod. Fifteen plants were used for each treatment and replicated three times. Two weeks after inoculation, the stems of the inoculated plants turned brown with a lesion, 2 to 5 cm in length, and the leaves wilted. These symptoms were similar to those of the diseased plants in the field. The control plants were asymptomatic. *N. solani* NsPed1 was reisolated from the infected plants, satisfying Koch’s postulates. Taken together, *N. solani* NsPed1 was identified as the causal pathogen of collar rot in *P. edulis* ‘Mantianxing.’ Knowledge of the causal organism of collar rot in purple passion fruit will lead to improved measures to prevent and control the disease in China and other countries.

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