Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Geotrichum candidum* Causing Sour Rot of Peach in China

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Peach (*Prunus persica* L. Batsch) is one of the most important fruit crops in China (Wang et al. 2011). Yangshan Town of Jiangsu Province is one of the four major peach-producing areas in China, with a growing area of 2,000 ha (Tian et al. 2018). During June 2020, a postharvest disease presenting with brown necrosis and rot occurred on peaches in Yangshan Town. The estimated damage was more than 10% of the total harvest. The symptoms included soft rot, and the lesion appeared sunken, accompanied with a sour odor and white mycelia. Twelve peaches with representative symptoms were sampled for pathogen isolation. Pieces (about 5 × 5 mm) from the lesion edge of symptomatic fruits were dissected and surface disinfected (3% NaClO for 10 s and 75% ethanol for 30 s) and then rinsed three times with distilled water, dried on sterile filter paper, and transferred to potato dextrose agar medium plates supplemented with 150 ng/ml of streptomycin sulfate. The plates were incubated at 28°C for 3 days. Forty-eight isolations were obtained from the plates, and isolates were single-spored. All isolates presented white, flat, milky, yeast-like colonies with radial mycelia. Hyphae under microscope were septate, branched, and disarticulating into arthroconidia measuring 3.39 to 9.27 × 2.05 to 7.71 µm. The morphological characteristics are consistent with *Geotrichum candidum* (De Hoog et al. 1986). The internal transcribed spacer (ITS) and 18S nuclear ribosomal small subunit (SSU) of the 48 isolates were amplified and

sequenced using the primers ITS5/ITS4 and NS1/NS4 for molecular identification (Schoch et al. 2012). The resulting sequences showed no difference among all the isolates. Alignment by BLASTn showed the sequence of ITS and SSU were 100% (accession no. GQ376093) and 99.7% identical (accession no. KY977411.1) to *G. candidum*, respectively. The sequences of ITS (accession no. MW493646) and SSU (accession no. MW493648) were submitted to the GenBank. Commercial ripe peaches with the size of about 15 × 15 × 10 cm were used for the pathogenicity test. Peaches were surface disinfected with 75% ethanol, and then a wound 4 mm in diameter and 5 mm in depth was made on the surface of each fruit. Ten peaches were inoculated with 10 µl (1 × 10⁵ spores/ml) of the isolate suspension. Another 10 peaches were inoculated with 10 µl of sterile water as the control. Peaches were incubated individually at 28°C and a relative humidity of about 85%. After 3 days, large scale of pits and necrosis appeared on every peach inoculated, and the symptoms were consistent with the diseased peaches in Yangshan Town, whereas no symptoms on the noninoculated control peaches were observed. The pathogen was reisolated from the diseased fruit and was identified again by sequencing of ITS and SSU. All the tests were conducted three times. Taken together, the pathogen was identified as *G. candidum*. *G. candidum* causing sour rot was reported in kiwifruit, strawberry, melon, and other fruits (Alonzo et al. 2021; Cheng et al. 2021; Halfeld-Vieira et al. 2020). To our knowledge, this is the first report of *G. candidum* causing sour rot of peach in China, which may cause a great loss to the peach industry of China.

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