Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Ceratocystis changhui* Causing Postharvest Fruit Rot of Peach in Kunming, China

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The peach (*Prunus persica* [L.] Batsch) is a predominant commercially grown stone fruit in China (Lee and Taylor 1990). *Ceratocystis changhui* is an aggressive pathogen causing typical black rot symptoms on corms of taro (*Colocasia esculenta*) (Liu et al. 2018), and it has not been reported on other hosts. During the summer and autumn of 2013, a postharvest fruit rot disease was observed on several peaches at a farmer's market (N 25°02'; E 102°42') in Kunming City, Yunnan Province, China. The incidence of the disease varied from 5 to 20%. Necrotic spots were first observed on the infected peach fruit (*P. persica* cv. Shuimitao). The spots enlarged gradually and developed into a brown, water-soaked and rotted lesion. Eventually, the whole fruit became soft, rotted, and covered with a gray-brown mycelium. The isolates were obtained from the symptomatic tissues incubated on slices of fresh carrot root (Moller et al. 1968). After 5 to 10 days of incubation, perithecia and mycelium were observed growing on carrot slices. Spore masses were removed from the apices of perithecia, transferred to PDA, and incubated at 25°C for 5 to 10 days, followed by single-spore isolation. All eight single-spore isolates from peach fruits obtained in this study were deposited in the State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, China. In culture, mycelium was initially white, and it gradually turned to greyish-green or brown. Measurements were made 7 days after the formation of perithecia. Perithecia were black, globose, 185.71 to 305.56 × 142.86 to 264.29 µm, and showed a long black neck, 600 to 957.14 µm. Ascospores were helmet-hat shaped and 2.86 to

6.67 × 3.81 to 4.76 µm. Cylindrical conidia 6.67 to 38.95 × 2.86 to 7.62 µm were observed. Chlamydospores, 8.57 to 13.33 × 5.71 to 9.52 µm, were ovoid or obpyriform, smooth. To further verify pathogen identity the internal transcribed spacer (ITS) region of rDNA was amplified using primers ITS1F and ITS4 (Thorpe et al. 2005), and the total genomic DNA from the mycelia of five isolates was extracted using a CTAB method (Lee and Taylor 1990). The nucleotide sequences have been blasted and deposited in the GenBank database. Analysis of the ITS sequences from the isolates T1-1yp, T1-2yp, and T2-1yp (GenBank nos. KY580895 to KY580897) showed 99 to 100% similarity with isolates *C. changhui* CMW43272 (KY643886), CMW43281 (KY643884), CMW46112 (KY643891), and CMW46113 (KY643892) from taro in China. Phylogenetic trees based on the maximum-likelihood (ML) method were constructed using MEGA 7. ITS sequences of other *Ceratocystis* spp. were obtained from NCBI for comparative analysis (Liu et al. 2018), and *Davidsoniella virescens* (CMW11164) served as outgroup. The robustness of the ML tree was evaluated with 1,000 bootstrap values. The pathogen was identified as *C. changhui* based on the phylogenetic analysis. Three isolates (T1-1yp, T1-2yp, and T2-1yp) were used for pathogenicity. Nine *P. persica* cv. Yingzuitao fruits at early maturity (8 points out of 10) were wound inoculated with 200 µl of conidia suspension of the fungus ($\sim 2.0 \times 10^6$ conidia/ml). Degreasing cotton dipped in sterile water was used to raise the humidity in preservation boxes. Boxes were incubated for 10 days at 25°C. Three peaches as controls were treated only with sterile distilled water in the same way. Symptoms of sunken lesions and fruit rot were observed 2 days after inoculation and measured at 1.8 to 3.2 cm from the inoculation point within 5 days. The same pathogen was reisolated from them, confirming Koch's postulates. Control peaches remained symptomless. This fungus was morphologically and phylogenetically identified as *C. changhui*. To our knowledge, this is the first report of *C. changhui* on postharvest peach in Yunnan, China. The disease will affect quality and taste of peach, so it is critical to deploy appropriate management strategies to limit the fungus spread.

References:

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