Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Seedling Rot of Castor (*Ricinus communis*) Caused by *Choanephora cucurbitarum* in China

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Funding: This study was supported by Guangdong Provincial Science and Technology Projects (2016a 020208015) and by Guangdong Ocean University Innovation and Entrepreneurship Training Program for College Students (CXXL2022347). Plant Dis. 106:2521, 2022; published online as <https://doi.org/10.1094/PDIS-01-22-0111-PDN>. Accepted for publication 1 March 2022.

Castor (*Ricinus communis* L.) oil is used in the manufacture of cosmetics, lubricants, plastics, pharmaceuticals, and soaps and is grown in more than 40 countries with India and China leading in oil production (Tunaru et al. 2012). In June 2021, a seedling rot disease was observed on castor cv. Zibi-5 in a plant nursery in Zhanjiang (21°17' N, 110°18' E), China. Initial symptoms on leaves and stems were water-soaked, dark green lesions that resulted in rapid rotting. Disease incidence was 25% and resulted in seedling death. White fungal mycelia developed on the rotting plant tissues. Leaves and stems were collected from 10 diseased plants and surface disinfected in 0.5% sodium hypochlorite and 75% ethyl alcohol, and tissue pieces were placed in plates of potato dextrose agar (PDA) maintained at 28°C. Hyphal tips from fungal mycelia that developed in the PDA plates were selected to establish pure cultures, and three representative fungal isolates, designated RCC-1, RCC-2, and RCC-3, were selected for further study. The fungal isolates produced sporangiophores that were smooth, hyaline, aseptate, and apically swollen. Sporangiophores bore monosporous sporangia that were broadly ellipsoidal, longitudinally coarsely striate, brown to dark brown, and measured 6.2 to 14.8 × 10.5 to 26.5 μm (*n* = 30). Sporangia contained few to many spores that were spherical, brown, and measured 59 to 150 μm in diameter (*n* = 20). Sporangiospores were ellipsoid, striate, and brown with multiple hyaline polar appendages and measured 6.6 to 12.3 × 10.6 to 25.5 μm (*n* = 30). Based on these morphological characteristics, the fungus was

identified as *Choanephora cucurbitarum* (Berk. & Ravenel) Thaxt. (Kirk 1984). Molecular identification was done using the colony PCR method with MightyAmp DNA Polymerase (Takara-Bio, Dalian, China) (Lu et al. 2012) used to amplify the internal transcribed spacer (ITS) region and large subunit (LSU) with ITS1/ITS4 and NL1/LR3 (Walther et al. 2013). The amplicons were sequenced and the sequences were deposited in GenBank (accession numbers: ITS, OL376748 to OL376750; and LSU, OL763430 to OL763432). BLAST analysis of these sequences revealed 99 to 100% identity with the sequences (ITS, MG650194; 573/573, 573/573, and 573/573; LSU, AF157181; 673/676, 673/676, and 673/676) of *C. cucurbitarum* in GenBank. Pathogenicity tests to fulfill Koch's postulates were performed in a greenhouse with a temperature range of 24°C to 30°C and 80% relative humidity. Thirty-day-old cv. Zibi-5 castor plants were grown in pots and used for inoculation tests. Ten plants were inoculated by placing agar plugs with mycelia of fungal isolate RCC-1 on leaves or stems. Ten control plants were inoculated with agar plugs only and the test was repeated three times in total. Five days after inoculation, all plants, with either leaf or stem inoculations, became infected and began rotting. Symptom progression was consistent with that observed in the nursery and all control plants remained healthy. *C. cucurbitarum* was successfully reisolated from all inoculated plants and identified by morphological characteristics and sequence analysis. This fungus is known to cause serious damage on a wide range of hosts (Liu et al. 2019) and previously was reported on castor in India (Shaw 1984) and Papua New Guinea (Peregrine and Ahmad 1982). We observed that the pathogen grows very rapidly and causes serious damage to castor seedlings, warranting further investigation on the epidemiology and control of this disease.

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The author(s) declare no conflict of interest.

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Keywords: castor seedling rot, *Choanephora cucurbitarum*, *Ricinus communis*

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