Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Chaetomium globosum* Causing Leaf Blight on *Brassica oleracea* in China

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Funding: This work was supported by the National Key Research and Development Program of China (2017YFD0101804). Plant Dis. 105:1204, 2021; published online as <https://doi.org/10.1094/PDIS-07-20-1540-PDN>. Accepted for publication 1 December 2020.

Cabbage (*Brassica oleracea* var. *capitata* L.) is widely cultivated in China and be of important economic value. In October 2019, all the plants of cabbage inbred line ‘2358’ cultivated in greenhouses of the Chinese Academy of Agricultural Sciences (Beijing) were showing symptoms of leaf wilt. It usually took 2 weeks for the leaves to become completely wilted, and the plants gradually died. Approximately 550 plants were affected, and 30 plants were collected and processed as samples. Symptomatic leaves were cut into small pieces (5 × 5 mm), surface sterilized with 75% ethanol for 30 s, sterilized with 8% NaClO for 3 mins, rinsed three times in sterile distilled water, plated on complete medium (CM: 3 g of casein enzymatic hydrolysate + 3 g of casein acid hydrolysate + 6 g of yeast extract + 10 g of sucrose + 15 g of agar + 1 liter of dH₂O) and incubated at 27°C for 6 days. Subsequently, the purified culture was obtained by tissue isolation and single-spored on CM. The colony on CM was up to about 50 and 70 mm in diameter after 4 and 7 days, respectively. At the same time, the edge of the colony gradually turned brown. Microscopic observation found that the diameter of the mycelium was about 5 µm. The conidia were transparent white and ovoid-shaped, about 0.3 to 0.5 µm in diameter. Fungus in liquid CM was spherical with surface hairs, which was consistent with the morphological characteristics of *Chaetomium globosum*. The rDNA internal transcribed spacer of isolate

ZM2019 was amplified using primers ITS1 (5'-TCCGTAGGT-GAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') (Hong et al. 2013). The amplified product was sequenced and deposited in GenBank. The 573-bp amplicon (GenBank accession no. MN833403) showed 100% homology to *C. globosum* isolate CES5 (MN173145). According to the morphological and molecular characterization, the fungus causing leaf blight on 2358 was identified as *C. globosum*. In order to further distinguish the pathogen species, the β -tubulin (*tub2*) gene region was amplified using primers T-F (5'-CCCCTGAACCTACCCACC-3') and T-R (5'-TATTTGACCCGACTGACC-3') and sequenced. Finally, we further identified this pathogen as *C. globosum* CBS 148.51 (Wang et al. 2016), according to the BLAST result of the sequence (GenBank accession no. MW252170) in National Center for Biotechnology Information. To confirm the pathogenicity of this fungus, the leaves of 12 healthy seedlings of 2358 were inoculated by spraying 10⁶ conidia/ml suspension, and 12 seedlings inoculated with sterile water served as controls. All plants were incubated in a growth chamber maintained at 27°C. Ten days after inoculation, the leaves of all plants became wilted, which was consistent with the symptom in the natural state, whereas the control plants remained disease-free. Subsequently, *C. globosum* was isolated from the inoculated seedlings again. The entire process from isolation to inoculation was repeated again, and the same results were obtained. Reisolation of *C. globosum* and inoculation of the host fulfilled Koch's postulates. *C. globosum* has been reported previously to occur on many horticultural plants such as *Punica granatum* (Guo et al. 2015) and *Cannabis sativa* (Chaffin et al. 2020), but no brassica species has been reported so far as susceptible to *C. globosum*. In this sense, this is the first report of leaf blight caused by *C. globosum* on cabbage in China, under greenhouse conditions.

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The author(s) declare no conflict of interest.

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Keywords: fungi, vegetables, pathogen detection

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