Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum siamense* Causing Anthracnose on *Zinnia elegans* in China

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Zinnia elegans Jacq. (syn. *Zinnia violacea*), known as common zinnia, is one of the most spectacular ornamental plants in the family Asteraceae. Zinnia plants are widely cultivated in China for their impressive range in flower colors and profuse bloom over a long period. In April 2019, zinnia plants grown in Ningbo Botanical Garden (29°56'57"N, 121°36'20"E), Zhejiang Province, were found to have many circular necrotic lesions. In the early infection stage, the lesions appeared as small circular specks, which developed later into large spots (15 to 32 mm diameter) with brown centers and chlorotic edges. Disease incidence reached approximately 80% of plants in the affected field. Moreover, zinnia plants that are infected with this disease showed early flowering time and small flowers. To identify the causative pathogen associated with the disease, 10 symptomatic leaves were collected from 10 different zinnia plants. Leaf tissues were cut from the lesion margins, surface sterilized with 75% ethanol for 30 s, and rinsed three times in sterile distilled water. The leaf tissues were then dipped into 10% sodium hypochlorite for 2 to 3 min, washed three times in distilled water, and dried on sterile filter paper. After drying, the surface-sterilized leaf discs were transferred to potato dextrose agar (PDA) plates and incubated at 28°C for 2 to 3 days under a 12-h photoperiod. A total of 10 pure fungal isolates were obtained, and all the isolates displayed the same colony characteristics. Afterward, three pure strains were randomly selected (F1, F3, and F5) for further study. The fungal colonies showed gray to brownish aerial mycelia with pink-colored masses of conidia. Conidia were one-celled, hyaline, cylindrical to subcylindrical, spindle-shaped with

obtuse ends, measuring from 15.6 to 17.3 × 4.6 to 5.1 μm (average 15.9 × 4.8 μm, $n = 50$) with both ends rounded. These morphological characteristics were consistent with the description of *Colletotrichum gloeosporioides* complex (Weir et al. 2012). The identity of a representative isolate, F3, was confirmed by a multilocus approach. DNA of isolate F3 was extracted, and partial sequences of actin (ACT), chitin synthase (CHS), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), ribosomal internal transcribed spacer (ITS), manganese-superoxide dismutase (SOD2), glutamine synthetase (GS), beta-tubulin (TUB2), and calmodulin (CAL) were amplified and sequenced as previously described (Weir et al. 2012). These nucleotide sequences were deposited in GenBank (accession nos. MN972436 to MN972440, and MT266559 to MT266561; all sequences in FASTA format are shown. SOD, TUB2, and CAL sequences showed similarity to *Colletotrichum siamense* with 100, 100, and 100% identity, respectively. The phylogenetic trees were constructed by the maximum likelihood method using JTT model implemented in the MEGA 7. Results inferred from the concatenated sequences (ACT, CHS, GAPDH, ITS, SOD, GS, TUB2, and CAL) placed the isolate F3 within the *C. siamense* cluster. To confirm pathogenicity of the fungus, Koch's postulates were conducted by spraying 20 zinnia plants (60 days old) with a 1×10^6 conidia/ml suspension. Conidial suspension was obtained from PDA plates after 5 days of incubation in the biochemical incubator at 28°C, and concentration was counted in a hemacytometer. Plants were maintained in the growth chamber at 25°C and 85% relative humidity under a 12-h photoperiod. After 10 to 15 days, symptoms were observed on all inoculated leaves and resembled those observed in the field, whereas the control plants remained asymptomatic. Here, *C. siamense* was isolated only from the infected *Zinnia* leaves and identified by morphological and phylogenetic analyses. *C. siamense* has been reported in many crops in China (Chen et al. 2019; Wang et al. 2019; Yang et al. 2019). However, to our knowledge, this is the first report of anthracnose caused by *C. siamense* on *Z. elegans* in China.

References:

- Chen, X., et al. 2019. Plant Dis. 103:1423.
- Wang, Y., et al. 2019. Plant Dis. 103:372.
- Weir, B. S., et al. 2012. Stud. Mycol. 73:115.
- Yang, S., et al. 2019. Plant Dis. 103:2127.

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