First report of leaf spot caused by *Phoma matteucciicola* on *Commelina communis* in Liaoning, China

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Commelina communis L. is an important traditional Chinese medicine (Zhang et al. 2018). In July 2018, symptoms of leaf spot were observed on nearly 25% of *C. communis* leaves in a garden in Xingcheng (Liaoning Province). Lesions on leaves, circular to irregular, brown to dark brown. Later, within the spots, scattered, glabrous, dark brown to black, subglobose and ostiolate pycnidia measuring 65 to 160 (124) μm ($n=20$) in diameter were observed on the upper side of leaf lesions. Conidia from the leaf lesions were hyaline, unicellular, biguttulate, and 10.0 to 20.0 (15.85) $\times$ 2.5 to 5.0 (4.57) μm ($n=50$). Symptomatic leaves were collected and cut into small pieces. The fungi were isolated following standard protocols. Fungal colonies on PDA medium were white aerial mycelia and a canary yellow color on the reverse side. Chlamydospores were single or in chains, brown, and 5.0 to 7.5 (6.6) $\times$ 7.5 to 15.0 (10.65) μm ($n=50$). Based on morphological characteristics, the fungi were identified as *Phoma* sp. (Boerema et al. 2004). Two loci including the *ITS* and *TUB* were amplified and sequenced (Zheng et al. 2018). The sequences were deposited in GenBank (accession No. MT860494 for *ITS* and No. MT876429 for *TUB*). Multi-locus phylogenetic analyses confirmed the fungus as *Phoma matteucciicola* with 99% bootstrap support. Pathogenicity was assayed on five healthy plants by spraying spore suspensions (1×10^6 spore/ml) on the leaves. The control

plants were treated with sterile water. All plants were incubated at $20 \sim 29$ °C and 60~90% relative humidity (the field environment). After 15 days, all inoculated plants showed typical leaf spot symptoms as previously described, while the control plants remained healthy. The pathogen *P. matteucciicola* were reisolated from the inoculated leaves. To our knowledge, this is the first report of *P. matteucciicola* causing leaf spot on *C. communis* in Liaoning, China.

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1007/s42161-021-00981-4>.

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