First report of *Phoma herbarum* causing leaf spot on lily in China

Shao-kun Sun¹ · Ting Song¹ · Jun Sun² · Li-jing Chen¹

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Lilies (*Lilium* spp.) are important ornamental flowers globally. In September 2012, the authors found that *Phoma* sp. could colonize leaves of *Lilium* Asiatic hybrid cv. 'Elite'. In Shenyang, China. Early symptoms on the leaves appeared as small, round or irregular water-soaked pale or yellow spots, sometimes with a yellow halo at the edge. Mature spots were brown or gray in the center and dark brown at the edge. Brown pycnidia, 150–220 µm in diameter, developed on symptomatic leaves. Conidia were aseptate, hyaline, ellipsoidal, 4.5–8.5 × 2.3–3.2 µm. These characters are consistent with the generic concept of *Phoma* (Aveskamp et al. 2009). Five symptomatic leaves from different individual plants were excised into small pieces, which were incubated on potato dextrose agar (PDA) medium for 7 days at 28 °C in darkness according to the method described by Chen et al. (2017). Three fungal colonies were isolated and identified as *Phoma* sp. based on their conidial morphology (Boerema et al. 2004). 'Elite' bulbs were planted in a culture bowl containing a basic nutrient substrate. Thirty seedlings were inoculated when their height reached to 15–20 cm by spraying (1 ml/seedling) a spore suspension (10^7 conidia ml⁻¹) of each isolate over both leaf surfaces and incubated under moist conditions for 3 to 4 days at 25 °C. Thirty additional plants were sprayed with water as the control. All leaf spots developed on inoculated leaves were similar in appearance to those observed on diseased leaves in the field. *Phoma* sp. was recovered from the infected tissues, fulfilling Koch's postulates. For molecular identification, ge-

nomic DNA of the isolate Li-BC-02 was extracted and the sequences of rDNA, ITS, LSU, and RPB2 were amplified (Chen et al. 2015). The resulting fragments were sequenced and deposited in GenBank (accession Nos. MK881029, MK888723, MK919487), respectively. BLAST analysis showed that the ITS, LSU and RPB2 sequences shared 100% identity with the corresponding sequences of *Phoma herbarum* isolate CBS 615.75 (FJ427022.1, EU754186 and KP330420). The fungus was identified as *Phoma herbarum* based on phylogenetic analyses using the maximum likelihood method inferred from the combined ITS-LUS-RPB2 sequences. Based on its cultural, morphological and genetic characteristics and phylogenetic relationships, the pathogen was identified as *P. herbarum*. To the best of our knowledge, this is the first confirmed report of leaf spot disease of lily caused by *P. herbarum* in China.

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Shao-kun Sun, Ting Song and Jun Sun contributed equally to this work.

✉ Li-jing Chen
chenlijingsyau@126.com

¹ College of Biosciences and Biotechnology, Shenyang Agricultural University, Shenyang 110866, China

² Cultivation Department, Liaoning Institute of Economic Forestry, Dalian 116031, China