First report of *Chaetomella raphigera* causing brown spot on *Eucalyptus urophylla* × *E. grandis* in China

Xiu-Xiu Cao¹ · Ji-Guang Wei¹ · Jian-Gan Hou¹ · Chun-Li Fan¹ · Ji Luo² · Yao-Jun Wu² · Xiu-Hao Yang² · Ji-Tong Luo³ · Xiao-Bing Yang⁴

Received: 29 July 2020 / Accepted: 29 December 2020 / Published online: 18 January 2021
© Società Italiana di Patologia Vegetale (S.I.Pa.V.) 2021

Keywords Brown spot · *Chaetomella raphigera* · *Eucalyptus urophylla* × *E. grandis*

Eucalyptus urophylla × *E. grandis* has strong adaptability. Symptoms of brown necrotic lesions on leaves of *E. urophylla* × *E. grandis* were observed in 16 counties of Guangxi, China, with a disease incidence ranging from 1% to 30%. Diseased leaves were surface disinfected in 75% ethanol for 10 s, then 5% sodium hypochlorite solution for 2 min, and finally rinsed with sterilized distilled water. The leaves were cut into segments and plated onto potato dextrose agar (PDA), cultured at 27 °C in the dark. Colonies (reference isolate MAO) were pale brown with rare aerial mycelium and abundant pycnidia production. Pycnidia were pale to dark brown, globose or oblate (245.98–491.33 × 123.14–274.11 μm), covered with setae. Setae were pale to dark brown, 0–4 septates, 42–125 μm, straight with rounded end, clavate to curved at apex. Conidia were hyaline, oval or boat-shaped (5.19–6.52 × 1.87–2.66 μm). Some conidia had two oil globules. Those morphological characteristics were matched with *Chaetomella raphigera* Swift (Swift 1930). The nuclear rDNA was amplified using primers ITS1/ITS4 and sequenced (GenBank accession No. MN700624). The DNA sequence was 99% identical to *C. raphigera* in GenBank (KF193633). Sixteen healthy leaves of *E. urophylla* × *E. grandis* were inoculated with plugs colonized by the mycelium of isolate MAO.

Sixteen control leaves were treated with plugs of PDA. After keeping moist at 27 °C for 7 days, brown necrotic lesions were observed on inoculated leaves, while control leaves were symptomless. The reisolated fungus had the same morphological characters of MAO reference isolate. *Chaetomella raphigera* has been reported as a pathogen on *Punica granatum* L. in India (Gajbhiye et al. 2016). To our knowledge, this is the first report of *C. raphigera* causing leaf spot on *E. urophylla* × *E. grandis* in China and worldwide (Farr and Rossman 2020).

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s42161-020-00737-6>.

Acknowledgements This work was financed by the Guangxi Special Projects for Innovation Drive (Grant/Award Number: AA17204087-10 and AA17204058-9).

References

- Farr DF, Rossman AY (2020) Fungal databases, U.S. National Fungus Collections, ARS, USDA. December 9, 2020, from <https://nt.ars-grin.gov/fungal-databases/>
- Gajbhiye M, Sathe S, Shinde V, Kapadnis B (2016) Morphological and molecular characterization of pomegranate fruit rot pathogen, *Chaetomella raphigera*, and its virulence factors. Indian J Microbiol 56(1):99–102
- Swift ME (1930) A new species of *Chaetomella* on rose. Mycologia 22: 165–168

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

✉ Ji-Guang Wei
jiguangwei@gxu.edu.cn

¹ College of Agriculture, Guangxi University, Nanning 530004, Guangxi, China

² Guangxi Academy of Forestry Sciences, Nanning 530002, Guangxi, China

³ Guangxi Forest Pest Management Station, Nanning 530028, Guangxi, China

⁴ Iowa State University, Ames, IA 50011, USA