First report of *Neofusicoccum parvum* causing leaf spot of *Camellia drupifera* in China

Fengyu Yu¹ · Xiaoyu Liu¹ · Xiaocheng Jia¹ · Dengqiang Fu¹ · Weiwei Song¹ · Xiaoqing Niu¹

Received: 25 February 2021 / Accepted: 19 October 2021 / Published online: 12 November 2021
© Società Italiana di Patologia Vegetale (S.I.Pa.V.) 2021

Keywords *Neofusicoccum parvum* · Leaf spot disease · *Camellia drupifera*

Oil-tea camellia (*Camellia drupifera*) is an economically important woody plant indigenous to southern China that produces edible oil. In January 2017, leaf spots were observed on about 60% of 3000 3-year-old oil-tea camellia in Hainan Province, China. Infected leaves exhibited gray necrotic lesions surrounded by watery borders. From 45 leaves of 15 diseased plants 27 same fungal colonies were consistently isolated. Colonies were initially pale to white on PDA, with diffuse yellow pigment observed in the agar 5 days later. After 10 days, the aerial mycelium became gray, and the substrate mycelium became black. Conidia were hyaline, nonseptate, and fusiform. They measured $19.9 \pm 2.1 \times 8.0 \pm 0.8 \mu\text{m}$ ($n = 100$). These morphological characteristics are consistent with the genus *Neofusicoccum*. ITS region of rDNA and part of beta-tubulin gene were amplified using ITS1, ITS4 and Bt1a, Bt1b primers (Glass and Donaldson 1995), respectively. The sequence data were deposited in GenBank. BLAST analysis identified the fungus as *Neofusicoccum parvum* (Pennycook & Samuels) Crous, Slippers & A. J. L. Phillips. Based on the ITS sequence, the tested isolate (GenBank Accession No. MH265978) showed 99.63% identity with the isolate P24 (KX648517). Based on the beta-tubulin sequence, the tested isolate (MZ439862) showed 99.51% identity with the isolate p24 (KX648460). Hence, both morphological and molecular characteristics confirmed the fungus as *N. parvum*. The pathogenicity of the fungus was tested by inoculating surface-sterilized leaf wounds of three 13-month-old seedling of *C. drupifera* with a mycelial plug. Sterile PDA plugs were used as control. Plants were moved into a greenhouse at $25 \pm 1^\circ\text{C}$. Three

days after inoculation, symptoms observed on inoculated leaves were similar to those in field, while the control still remained symptomless. *N. parvum* was recovered from the inoculated leaves but not from the control leaves, confirming Koch's postulates. This fungus is the pathogen of many economic crops in China (Li et al. 2020; Yu et al. 2015), but this is the first report of leaf spot on oil-tea camellia caused by *N. parvum* in China.

Acknowledgements The authors would like to thank the Hainan Provincial Natural Science Foundation of China (319MS081), which funded the research.

Declarations

Informed consent This manuscript is new and not being considered elsewhere. All authors have approved the submission of this manuscript.

Research involving human participants and/or animal The authors declare that no humans and animals were involved in this study.

Conflict of interest The authors declare that there are no conflict of interest.

References

- Glass NL, Donaldson GC (1995) Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Appl Environ Microbiol 61(4):1323–1330
- Li ZJ, Li WJ, Mao YY, He LS, Li SJ (2020) Identification and biological characteristics of branch withered disease causing pathogen to *Koeleruteria paniculata* Laxm. Journal of Northwest A & F University (Nat Sci Ed) 48(9):53–63 (in Chinese)
- Yu ZD, Tang GH, Peng SB, Chen H, Zhai MZ (2015) *Neofusicoccum parvum* causing canker of seedlings of *Juglans regia* in China. J for Res 26(4):1019–1024

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

✉ Fengyu Yu
yufengyu17@163.com

¹ Coconut Research Institute, Chinese Academy of Tropical Agricultural Sciences, Hainan Key Laboratory of Tropical Oil Crops Biology, Wenchang, Hainan, China