



First report of *Diaphorthe masirevicii* causing leaf blight of *Gloriosa superba* in India

J. Naveen¹, H.M. Navya¹, G. Hithamani², S.R. Niranjana¹ and P. Hariprasad^{3*}

¹ Department of Studies in Biotechnology, University of Mysore, Manasagangotri, Mysore 570 006, Karnataka, India; ² CSIR-Central Food Technological Research Institute, Mysore 570020; ³ Centre for Rural Development and Technology, Indian Institute of Technology, Delhi, Hauz Khas, New Delhi 110016

*E-mail: phari@iitd.ac.in

Received: 29 Sep 2017. Published: 02 Mar 2018.

Gloriosa superba (Glory lily, Colchicaceae) is an endangered perennial climbing herb, grown in Africa and Asia for its medicinal properties (Jain & Suryavanshi, 2010). A leaf blight disease (Fig. 1) was observed during surveys performed in the region of Mysore, India. The first symptoms of infection were small (2-5 mm diameter), circular to oval, light brownish spots, surrounded by a yellow halo. Leaf spots occurred on the leaf tips, margins and midribs of the leaves, enlarging to form spots with concentric rings. Embedded in the necrotic tissues were black fruiting bodies of a fungus. These symptoms also appeared later on the stem.

Infected leaves were surface sterilised with 70% ethanol followed by three washes with sterile distilled water and incubated for seven days on moist blotter discs. After incubation, colony development was examined and the fungus isolated and maintained on potato dextrose agar (PDA). The fungus was identified based on its colony type, morphology and production of pycnidial ooze (Fig. 2). Pycnidiospores were produced in slimy masses and were of two types, alpha and beta. Alpha conidia were fusoid to ellipsoidal and biguttulate, while beta conidia were filiform, slightly curved and rarely straight (Fig. 3). The morphological characters of the fungus were compared with the description of Thompson *et al.* (2015) and identified as *Diaphorthe* sp. Fungal DNA was extracted from mycelium following standard procedures (Saitho *et al.*, 2006). The fungus was identified by amplifying and sequencing the internal transcribed spacer (ITS), β -tubulin and transition elongation factor (TEF) regions using specific primers (Table 1). BLAST analysis revealed identities of 99% for ITS, 99% for β -tubulin and 100% for TEF to *D. masirevicii* isolate 054 (GenBank Accession No. KR024727), *D. masirevicii* isolate BRIP 57892a (KJ197257) and *D. masirevicii* isolate BRIP 54120a (KJ197243), respectively. These sequences were submitted to GenBank (ITS: MF682435, β -tubulin: MF668289 and TEF: MF668290).

Pathogenicity tests were conducted using a detached leaf assay (n=25) and

whole plant assay (n=10), under greenhouse conditions (22-28°C and under natural light). A suspension of alpha conidia was prepared by flooding 18 to 21-day-old PDA cultures with sterile distilled water and adjusting the spore concentration to 1×10^6 conidia/ml. Detached healthy and surface-sterilised leaves were wounded by pricking with a sterile needle, and 10 μ l of conidial suspension placed onto the wound site. Wounded control leaves received only distilled water. The leaves were incubated in a moist chamber at $28 \pm 2^\circ\text{C}$ for three-seven days. The appearance of water-soaked lesions and brown spots on inoculated leaves confirmed pathogenicity (Fig. 4). The whole plant assay was conducted using three-month-old plants. Plants were spray inoculated with either a suspension of 1×10^6 conidia/ml, or water as a control and observed for symptoms for the next thirty days. The pathogen was reisolated from infected leaves showing typical symptoms, thus fulfilling Koch postulates.

As per our knowledge and from a literature survey, this is the first report of *Diaphorthe masirevicii* causing leaf blight of *Gloriosa superba* in India.

References

- Jain AP, Suryavanshi S, 2010. *Gloriosa superba* Linn. - A pharmacological review. *International Journal of Pharma Research and Development* **2**, 24-26.
- Saitoh K-I, Togashi K, Arie T, Teraoka T, 2006. A simple method for a mini-preparation of fungal DNA. *Journal of General Plant Pathology* **72**, 348-350. <http://dx.doi.org/10.1007/s10327-006-0300-1>
- Thompson SM, Tan YP, Shivas RG, Neate SM, Morin L, Bissett A, Aitken EAB, 2015. Green and brown bridges between weeds and crops reveal novel *Diaporthe* species in Australia. *Persoonia: Molecular Phylogeny and Evolution of Fungi* **35**, 39-49. <http://dx.doi.org/10.3767/003158515X687506>

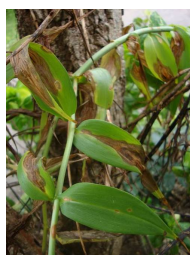


Figure 1



Figure 2

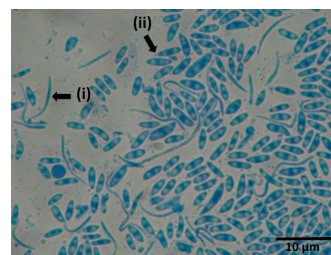


Figure 3



Figure 4

Table 1. Primers designed to detect the internal transcribed spacer, β -tubulin and transition elongation factor regions.

Region	Primer name	Sequence (5'-3')
Internal transcribed spacer	ITS1	TCCGTAGGTGAACCTCGGG
	ITS4	TCCTCCGCTTATGATATGC
β -tubulin	Bt2a	GGTAACCAATCGGTGCTTTC
	Bt2b	ACCCTCAGTGTGACCTTGGC
Transition elongation factor	EF1-728F	CATCGAGAAGTTCGAGAAG
	EF1-986R	TACTTGAAGGAACCTTACC

Figure 5

To cite this report: Naveen J, Navya HM, Hithamani G, Niranjana SR, Hariprasad P, 2018. First report of *Diaphorthe masirevicii* causing leaf blight of *Gloriosa superba* in India. *New Disease Reports* **37**, 13. <http://dx.doi.org/10.5197/j.2044-0588.2018.037.013>
 ©2018 The Authors This report was published on-line at www.ndrs.org.uk where high quality versions of the figures can be found.