



First report of *Colletogloeum* sp. as the causal agent of marginal leaf blight on *Heliconia rostrata* in India

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Heliconia rostrata (false bird of paradise, Heliconiaceae) is native to South America but is an important herbaceous perennial ornamental plant in India and globally. In December 2016, a foliar blight was observed on six ten-month-old *H. rostrata* plants growing outdoors in Kolkata, West Bengal. Symptoms included a marginal blight, light brown to ash in colour, with a yellow halo (Fig. 1), and disease incidence ranged from 20-50%.

Blighted areas of the leaves were viewed under a microscope (×200) and acervuli were found in a concentric orientation around the diseased tissue. Conidiophores from the acervuli were pale brown, smooth, branched and simple, up to 13 µm long and 4 µm wide, with 1-2 percurrent proliferations. Conidia (n=30) were straight, irregular, sigmoid, tapered markedly to the apex, smooth, thick walled, 5-8 euseptate and 38 × 5 µm in size. Affected parts of ten diseased leaves were kept in a plastic box with wet filter paper and absorbent cotton to induce conidiation. Conidial masses were suspended in 250 µl sterilised distilled water on sterile glass slides and dropped onto 2% (w/v) water agar containing 0.5 mg/l of chloramphenicol. After 24 hours incubation at 25°C, individual germinating conidia were selected and transferred directly to potato dextrose agar and subcultured on peptone salt agar (10 g peptone, 5 g sodium chloride, 0.1 g calcium chloride, 20 g agar per litre). In both media, conidia and conidiophore sizes were similar to those observed on infected leaf tissues. Based on these morphological features the fungus was identified initially as a member of the genus *Colletogloeum* (Sutton & Mehrotra, 1982).

Genomic DNA was extracted from mycelia of the isolated fungus using the CTAB method (Doyle & Doyle, 1990) and the internal transcribed spacer (ITS) region and LSU ribosomal genes of rDNA were amplified using ITS1-F/ ITS4 (White *et al.*, 1990) and LR1/ LR4 (Vilgalys *et al.*, 1994) primers and sequenced (GenBank Accession Nos. MN644508 and MN644486 for ITS and LSU, respectively). BLAST analyses revealed that sequences from the present study had 99-100% identity with the type species of *Colletogloeum* sp. FG2.2 (FJ425194 and FJ031987). Based on the morphological characteristics and the molecular data, the causal agent was identified as *Colletogloeum* sp. (Hemnani *et al.*, 2008).

The pathogenicity of the fungus was tested on six leaves (disinfected by spraying 90% ethanol followed by three rinses with sterile distilled water) from a single five-month-old *H. rostrata* plant grown in the greenhouse at 25°C with a 12/12-hr photoperiod and 100% relative humidity. Ten

millilitres of a 3 × 10⁶ conidial suspension per ml was applied to each leaf. Another set of six leaves were sprayed with sterile distilled water as non-inoculated controls. After seven days, only the inoculated leaves showed leaf blight symptoms resembling those observed on naturally infected *H. rostrata* leaves. The pathogen was consistently re-isolated from the infected leaves thereby completing Koch's postulates.

To our knowledge, this is the first report of *Colletogloeum* sp. causing *H. rostrata* leaf blight in India and worldwide (Farr & Rossman 2019). The pathogen may pose a threat to *H. rostrata* production. These findings will be useful for the development of effective control strategies and further research.

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Figure 1

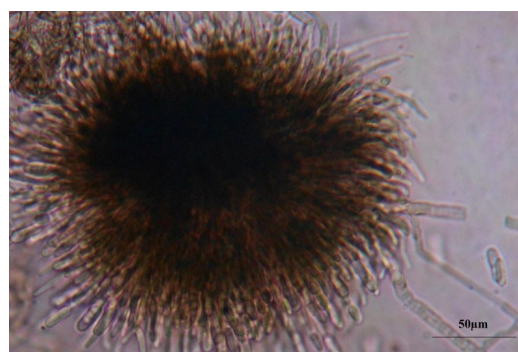


Figure 2

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