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NEW DISEASE REPORT

First report of *Colletotrichum liriopes* on *Liriope muscari* (lily turf) in the United Kingdom

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Lirope muscari is a perennial ornamental plant in the family Liliaceae. In March 2022, reddish-brown necrotic leaf spots (Figures 1–2) were observed on plants of *L. muscari* cv. Big Blue in a UK-grown crop in a garden centre in Kent, UK. Three plants in a batch of ten displayed these symptoms. A diseased plant sample was tested at Fera Science Ltd.

Microscopic visual examination of the sample revealed the presence of setose acervuli on the leaf spots (Figure 2). The acervuli contained aseptate, hyaline, slightly curved conidia. Based on the morphological assessment, the fungus was identified as a *Colletotrichum* species and isolated in pure culture by directly placing some conidia onto potato dextrose agar (PDA) plates. Grey colonies (Figure 3) with numerous setose acervuli containing aseptate, hyaline, slightly curved conidia each measuring 12.5-25 × 2.5-3.75 μm, characteristic of *Colletotrichum*, were obtained (Figure 4).



FIGURE 1 Leaf spots observed on *Liriope muscari* in Kent, UK.

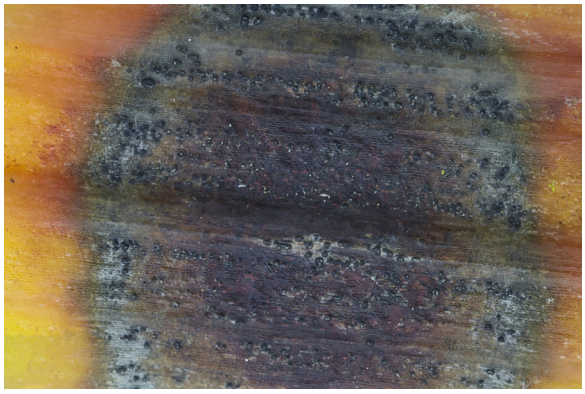

FIGURE 2 Acervuli of *Colletotrichum liriopes* observed on leaf spots on *Liriope muscari*.

Following isolation on PDA, genomic DNA was extracted using a NucleoSpin Plant II mini kit (Macherey-Nagel, Germany) following the manufacturer's instructions. The 5.8S nrRNA gene with the two flanking internal transcribed spacer (ITS) region was amplified with primers ITS5/ITS4 (White et al., 1990). The partial actin gene (ACT) was amplified using ACT-512F/ACT-783R (Carbone & Kohn, 1999). The

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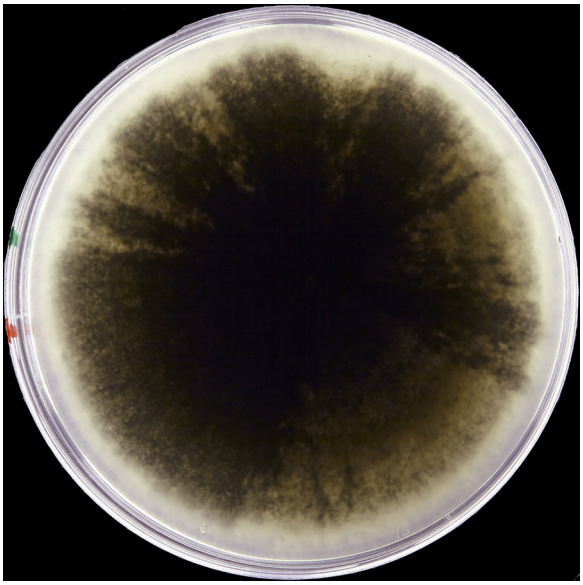

FIGURE 3 *Colletotrichum liriopes* culture on a potato dextrose agar plate after 11 days incubation.

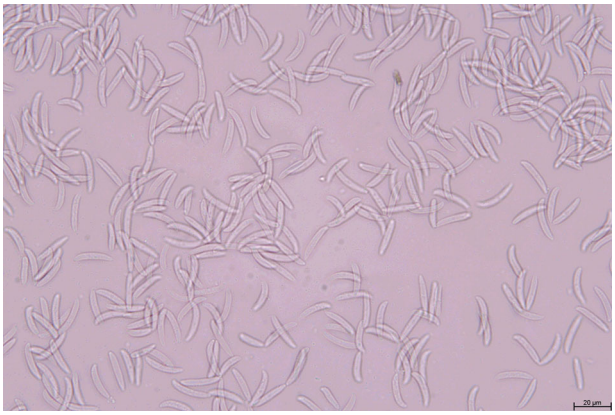

FIGURE 4 *Colletotrichum liriopes* spores at ×400 magnification.

partial beta-tubulin gene (Tub2) was amplified using TUB2Fd/TUB4Rd (Woudenberg et al., 2009). The obtained sequences were deposited in GenBank: ITS (Accession Nos OQ266298-99), ACT (OQ283548-49), and Tub2 (OQ283546-47). These sequences were used in a BLASTn search and sequences with high identities were retrieved and aligned using Geneious (Geneious Prime 2019.2.1, https://www.geneious.com). For phylogenetic analyses, the neighbour-joining method in Geneious was employed. The resulting phylogenetic analysis indicated that these sequences were identical with those of *Colletotrichum liriopes*. The morphological features of the isolates conformed to the description of *C. liriopes* which has been reported to cause anthracnose in *L. muscari* (Oo & Oh, 2017).

In October 2022, *C. liriopes* was detected in another *Liriope* sample in the UK; this time the sample was of *L. muscari* cv. Monroe White from a garden centre in West Sussex, UK. The stock had recently been supplied by a UK nursery but an import connection cannot be excluded for this second finding.

The pathogen has so far been found in Mexico, Korea (Oo & Oh, 2017), USA (Trigiano et al., 2018) and China (Yang et al., 2020). To our knowledge, this is the first report of *C. liriopes* in the UK and in Europe.

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