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## First Report of Black Sigatoka Disease in Bananas Caused by *Pseudocercospora fijiensis* on Mauritius Island

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# Disease Note

## Diseases Caused by Fungi and Fungus-Like Organisms

### First Report of Black Sigatoka Disease in Bananas Caused by *Pseudocercospora fijiensis* on Mauritius Island

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*Pseudocercospora fijiensis*, the causal agent of black leaf streak disease (BLSD) of bananas (genus *Musa*), is a major threat to banana cultivation (de Bellaire et al. 2010). The disease is distributed throughout humid tropical regions and has been previously reported in the Southwest Indian Ocean (SWIO): in 1993 in Mayotte and Comoros islands (Jones and Mourichon 1993), in 2000 in Madagascar (Jones 2003), and in 2018 in Reunion Island (Rieux et al. 2019). In Mauritius, the presence of *P. fijiensis* was suspected in 1996 (Soomary and Benimadhu 1998) but has never been confirmed, as symptoms could have been confounded with *P. musae* or *P. eumusae*, two causal agents of other leaf spot diseases of banana that were previously described in Mauritius in 1959 (Orieux and Felix 1968) and 2000 (Carlier et al. 2000), respectively. In March 2022, typical BLSD symptoms were observed at relatively low prevalence in a Cavendish crop in the Balance John area (site S1) of Mauritius. Typical early symptoms (stage 2) were 1- to 4-mm long brown streaks on the abaxial leaf surface, and typical older streaks (stages 3 and 4) were also observed. These symptoms were mixed with symptoms of Eumusae leaf spot disease caused by *P. eumusae*. The species cannot be clearly distinguished only on symptoms, so conidial sporulation at stage 2 was checked in the laboratory (Ngando et al. 2015) since *P. eumusae* does not produce conidia at young stages. In April 2022, banana leaves with symptoms of leaf spot diseases were collected at seven sites. All leaf fragments were sent to the CIRAD laboratories for molecular diagnosis following the protocol developed by Arzanlou et al. (2007). In brief, genomic DNA was extracted from ground symptomatic leaf fragments using the DNeasy Plant Mini Kit (Qiagen, Courtaboeuf, France). At each site, six lesions cut from six leaves were pooled. DNA extracts were added

as templates for a real-time PCR assay designed to specifically detect the presence of *P. fijiensis*, *P. musae*, and *P. eumusae* using MFbf/MFbrtaq/MFbp, MEbf/MEbrtaq/FMep, and MMbf/Mmbrtaq/FMep primers and probes, respectively (Arzanlou et al. 2007). Both positive and negative controls were included in the assay and every sample reaction was duplicated. *P. fijiensis* was found at two sites (S2 and S7). *P. eumusae* was found at all sites, and *P. musae* was found at one site (S6). Interestingly, we also found coinfection by *P. fijiensis* and *P. eumusae* and *P. musae* and *P. eumusae* at several sites. The presence of *P. fijiensis* was confirmed by investigations of conidia isolated from S2 samples including (i) morphological observations of conidia displaying the *P. fijiensis* type description (Pérez-Vicente et al. 2021); (ii) DNA sequencing of 16S ribosomal gene with ITS1 and ITS4 primers (GenBank OR515810 to OR515818) with BLAST results displaying identities >99.70% with type strains; and (iii) Koch's postulates were fulfilled by artificial inoculation of detached leaf pieces (Pérez-Vicente et al. 2021). In brief, for artificial inoculation, symptoms obtained after inoculation of both a strain isolated in Mauritius (S2-MAU) and a positive control (T+) were shown to be typical of *P. fijiensis* species for the three replicates. To our knowledge, this is the first official report of *P. fijiensis* and BLSD in Mauritius. This is important for both agriculture and science, shedding light on the potential spread and impact of this pathogen in previously unaffected regions. From a global perspective, this shows the interconnectedness of agricultural ecosystems and the need for care in monitoring and responding to emerging plant diseases in an interconnected world. Future study is required to monitor the spread of BLSD on the island, describe the genetic structure of populations, and identify routes of invasion in the SWIO.

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#### e-Xtra

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