

# Disease Note

## Diseases Caused by Fungi and Fungus-Like Organisms

### First Report of *Stemphylium vesicarium* Causing Onion Stemphylium Leaf Blight in Mauritius

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In August 2021, severe leaf blight symptoms were observed on onion (*Allium cepa* L. cvs. Francia and Askari F1 hybrid) in commercial fields located in Mauritius, namely, La Forêt (20°19'56.1"S, 57°30'04.9"E), St. Aubin (20°29'47.0"S, 57°32'29.4"E), and Chapiron (20°20'46.8"S, 57°29'12.8"E). Infected leaves displayed small circular to oblong, yellow to pale-brown, spindle-shaped lesions, which later coalesced and formed necrotic areas with black sporulation. Three fields were selected from each region, and along a W pattern across the fields, a disease incidence ranging 53 to 93% and a severity of 9 to 28% were recorded. Ten symptomatic leaves were collected from each region, and small pieces of infected tissues were surface disinfected using 1% NaOCl for 2 min, rinsed with sterile distilled water, air-dried, transferred to potato dextrose agar (PDA), and incubated for 7 days at 20°C under a 12-h/12-h light/dark cycle. Fungal cultures with uniform appearance forming multiseptate conidia typical of the genus *Stemphylium* (Simmons 1969) were consistently isolated. Monosporic colony of the isolates SVCWLF24/3, SVSSA23/1, and SVCWLMC26/1 developed similar olivaceous green to light and dark gray mycelium with an average daily growth rate of 6.5 mm at 25°C in the dark. Conidiophores were straight and light brown with a distinct swollen apex on which olive

brown to dark brown, oblong to ovoid, septate conidia formed with the dimensions 16.2 to 44.7 × 8.0 to 22.9 μm (average 29.5 × 14.7 μm; *n* = 50) typical of *Stemphylium vesicarium* (Wallr) E.G. (Simmons 1969; Woudenberg et al. 2017). Genomic DNA of the three isolates was extracted from fungal mycelium (Ranghoo and Hyde 2000). The internal transcribed spacer (ITS), calmodulin (*cmdA*), and glyceraldehydes-3-phosphate dehydrogenase (*gapdh*) genes of the isolates were amplified with the primers ITS4/ITS5 (White et al. 1990), CALDF1/CALDR1 (Lawrence et al. 2013), and Gpd1/Gpd2 (Berbee et al. 1999) and sequenced. Sequences were submitted to GenBank under accession numbers OR131271, ON620213, and OR188702 for ITS; OR350623, OR350622, and OR166368 for *cmdA*; and OR684516, OR684517, and OR684518 for *gapdh*. The BLAST search of the sequences showed 100% similarity with the *S. vesicarium* strain CBS 155.24 under accession numbers KU850555 (ITS), KU850702 (*gapdh*), and KU850845 (*cmdA*) (Woudenberg et al. 2017). Phylogenetic trees inferred from the ITS, *cmdA*, and *gapdh* concatenated datasets with the maximum-likelihood algorithm allowed clustering of the isolates within the *S. vesicarium* clade, confirming the morphological identification. Pathogenicity tests were performed using all the three isolates cultured on PDA at 25°C in a 12-h/12-h dark/light cycle. Ten 60-day-old onion plants (cv. Francia) were spray inoculated each with 10 ml of conidial suspension ( $1 \times 10^4$ /ml) of each isolate, while 10 healthy plants sprayed with sterile distilled water served as controls. They were incubated in a greenhouse at 25°C with a 12-h photoperiod and >80% humidity. Necrotic circular lesions appeared on leaves after 7 to 10 days, whereas the control plants remained symptomless. Reisolations made from symptomatic leaf tissues on PDA consistently yielded cultures with similar morphology as the original isolates, thus fulfilling Koch's postulates. This is the first report of *S. vesicarium* as the causal agent of leaf blight of onion in Mauritius. It is a reemerging fungal disease (Hay et al. 2021) with a wide host range, threatening local onion production. This finding will contribute to early detection of leaf blight, implementation of surveillance, and integrated disease management in affected regions.

#### References:

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The author(s) declare no conflict of interest.

#### e-Xtra

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