Received: 15 November 2023 | Accepted: 19 December 2023

DOI: 10.1002/ndr2.12241

New Disease Reports Open Access BSPP WILEY

NEW DISEASE REPORT

First report of papaya anthracnose caused by *Colletotrichum salsolae* in Mauritius

M. Romjon[1] | **A. Gungoosingh-Bunwaree**[2] | **V. M. Ranghoo-Sanmukhiya**[1]

[1]Department of Agricultural and Food Science, Faculty of Agriculture, University of Mauritius, Reduit, Mauritius

[2]Plant Pathology Division, Food and Agricultural Research and Extension Institute, Reduit, Mauritius

Email: m.sanmukhiya@uom.ac.mu

Funding information
European Union, Grant/Award Number: FOOD 2019/406 182

KEYWORDS
Carica papaya, fungal plant disease

Anthracnose is an important fungal disease of papaya (*Carica papaya*) and is caused by *Colletotrichum* species (Nascimento *et al*., 2010). Papaya is an economically important crop which is cultivated primarily in tropical and sub-tropical countries (Saini *et al*., 2017). In February 2022, papaya fruits displaying anthracnose symptoms were collected from Flacq, Mauritius (-20°11'22.99" S, 57°42'51.98" E). Large, circular brown to black spots, surrounded by a pink-coloured edge, containing black fruiting bodies or salmon conidial masses were observed on affected fruit (Fig. 1). Small pieces of tissue were excised from the diseased fruit using a flame-sterilised scalpel. The pieces were surface disinfected using 1% sodium hypochlorite for three minutes followed by two rinses in sterilised distilled water. The diseased tissues were transferred onto potato dextrose agar and incubated at 25°C for seven days. Pure cultures were obtained by single hyphal tip isolation and two different types of colonies were recovered. The first fungal colony type (PapF) was greyish coloured with white aerial mycelium and light brown with brown concentric rings of growth on the underside (Fig. 2a-b). The second type (PapF2) was white and light brown to olive-coloured on the reverse side (Fig. 2c-d). The conidia (n = 30) were unicellular, straight, aseptate, with a rounded apex and acute base (Fig. 3). The mean length and width of the conidia were 11.0 ±1.1 μm × 3.0 ±0.4 μm and 12.2 ±2.2 μm × 3.4 ±0.4 μm for PapF and PapF2, respectively. 4

Fungal DNA was extracted using a CTAB-based DNA isolation method (Ranghoo & Hyde, 2000). Four genomic loci, the ITS region, GADPH, TUB2 and CHS-1 genes, were PCR-amplified and sequenced using primer pairs ITS4/ITS5 (White *et al*., 1990), GDF/GDR, T1/Bt2b and CHS-79F/CHS-345R (Gan *et al*., 2016), respectively. ITS sequences confirmed that the isolates were *Colletotrichum* with 100% identity to the *C. gloeosporioides* species complex (Accession Nos. KU534982.1 and KU534983.1). BLASTn search results showed that the GADPH and TUB2 sequences had 100% identity with KY401637.1 and JX009916.1, and MN746330.1 and CHS-1 JX009791.1, respectively, confirming that the species was *C. salsolae*. All sequences were deposited in Genbank under Accession Nos. OR739404-OR739405 (ITS), OR757306-OR757307 (GAPDH), OR757302-OR757303 (TUB2) and OR757304-OR757305 (CHS-1).

To prove the pathogenicity of *C. salsolae*, four fruits of papaya cv. Solo were surface disinfected using 1% NaOCl and rinsed twice with sterile distilled water. An aliquot of a conidial suspension (50 μL, 10^6 conidia/mL) from each of the isolate types was separately deposited on three sites of each fruit. A control papaya fruit was inoculated with sterile distilled water and all fruits were held at room temperature. Five days after inoculation the inoculated fruits developed typical anthracnose symptoms (Figure 4) while the control fruits showed no disease symptoms. The original isolate was recovered from the inoculated fruits, thus fulfilling Koch's postulates. The experiment was repeated three times and similar observations were made on each occasion.

Based on the morphological, molecular and pathogenicity analyses, the fungal isolates were identified as *C. salsolae*. *Colletotrichum salso-*

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.
© 2024 The Authors. *New Disease Reports* published by John Wiley & Sons Ltd on behalf of British Society for Plant Pathology.



FIGURE 1 Anthracnose symptoms observed on papaya from which isolates PapF (left) and PapF2 (right) were recovered.

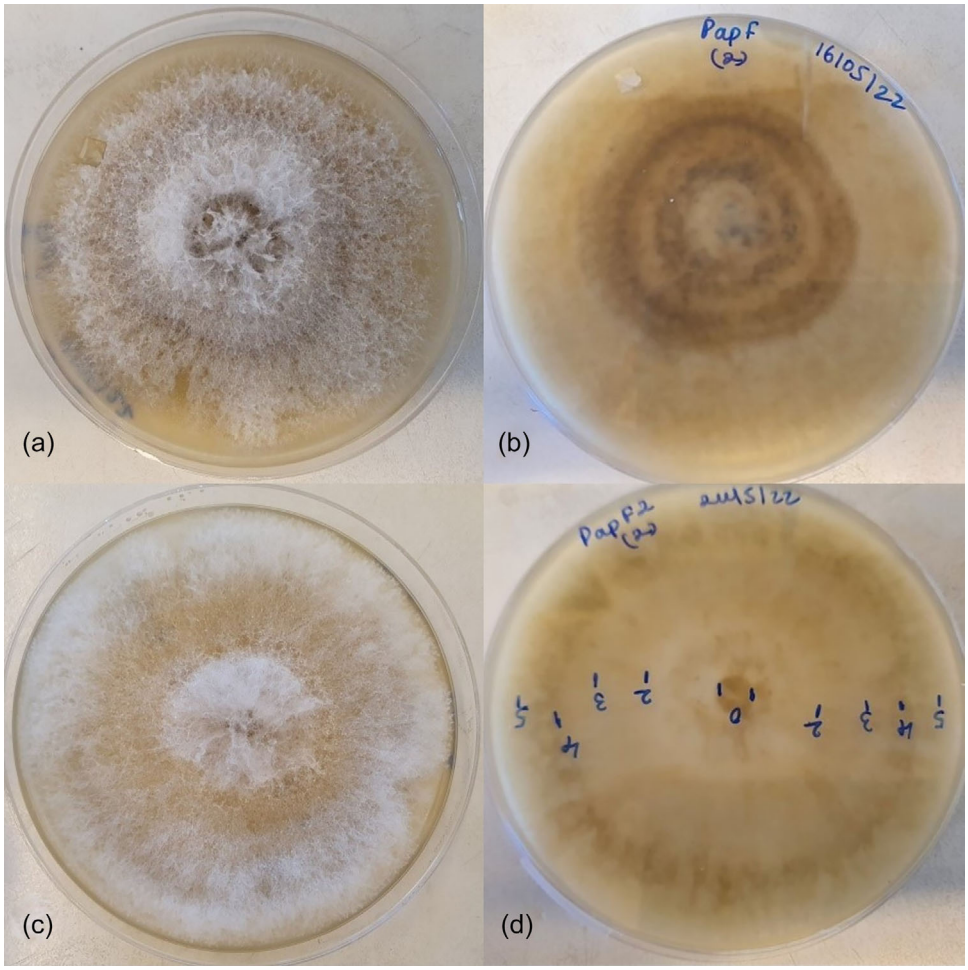


FIGURE 2 Appearance of colonies of isolates PapF (a & b) and PapF2 (c & d); A & C: top view, and B & D: reverse view.

lae was first reported from *Salsola kali* subsp. *tragus* in Hungary and then reported on *Carica papaya* in India (Weir *et al*., 2012; Saini *et al*., 2017). To our knowledge, this is the first report of *C. salsolae* causing anthracnose of papaya in Mauritius. Dissemination of these findings will create awareness among farmers about this disease-causing agent and emerging threat to papaya production in Mauritius.

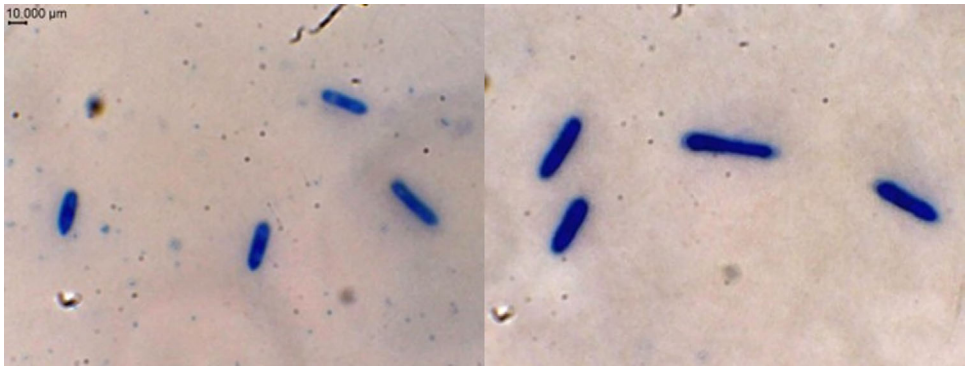


FIGURE 3 Conidial shape of isolate PapF (left) and PapF2 (right).



FIGURE 4 Symptoms on papaya five days after inoculation with Colletotrichum salsolae.

ACKNOWLEDGEMENTS

This study was funded by the University of Mauritius and the European Union under the project "Enhancing climate resilience in agriculture for improved food and nutrition security through research, innovation and training in the Republic of Mauritius" under the contract number (FOOD 2019/406 182).

ORCID

V. M. Ranghoo-Sanmukhiya https://orcid.org/0000-0001-7767-276X

REFERENCES

Gan, P., Nakata, N., Suzuki, T., & Shirasu, K. (2016) Markers to differentiate species of anthracnose fungi identify *Colletotrichum fructicola* as the predominant virulent species in strawberry plants in Chiba Prefecture of Japan. *Journal of General Plant Pathology*, 83, 14–22. https://doi.org/10.1007/s10327-016-0689-0

Nascimento, R.J., Mizubuti, E.S.G., Câmara, M.P.S., Ferreira, M.F., Maymon, M., Freeman, S. *et al.* (2010) First report of papaya fruit rot caused by *Colletotrichum magna* in Brazil. *Plant Disease*, 94, 1506. https://doi.org/10.1094/PDIS-08-10-0555

Ranghoo, V.M., & Hyde, K.D., 2000. *Ascominuta lignicola*, a new loculoascomycete from submerged wood in Hong Kong. *Mycoscience*, 41, 1–5. https://doi.org/10.1007/BF02464379

Saini, T.J., Gupta, S.G., & Anandalakshmi, R. (2017) First report of papaya anthracnose caused by *Colletotrichum salsolae* in India. *New Disease Reports*, 35, 27. https://doi.org/10.5197/j.2044-0588.2017.035.027

Weir, B.S., Johnston, P.R., & Damm, U. (2012) The *Colletotrichum gloeosporioides* species complex. *Studies in Mycology*, 73, 115–180. https://doi.org/10.3114/sim0011

White, T.J., Bruns, T.D., Lee, S., & Taylor, S. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis, M.A., Gelfand, D.H., Sninsky, J.J. and White, T.J. (Eds.) *PCR Protocols - A Guide to Methods and Applications*, Amsterdam, Netherlands: Elsevier, pp. 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

How to cite this article: Romjon, M., Gungoosingh-Bunwaree, A., & Ranghoo-Sanmukhiya, V.M. (2024) First report of papaya anthracnose caused by *Colletotrichum salsolae* in Mauritius. *New Disease Reports*, 49, e12241. https://doi.org/10.1002/ndr2.12241