Journal of Phytopathology

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Journal of Phytopathology

SHORT COMMUNICATION OPEN ACCESS

First Report of *Diaporthe arecae* Causing Dieback in *Mangifera indica* in Brazil

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Received: 9 June 2025 | **Revised:** 18 August 2025 | **Accepted:** 26 August 2025

Keywords: mango | phylogeny | Tommy Atkins

ABSTRACT

In 2024, dieback was detected on mango trees in Pernambuco, Brazil, with 40% disease incidence in all areas visited. Three isolates (MP22, MP27 and MP29) were obtained. Based on morphology, cultural and molecular analysis, the causal agent was identified as *Diaporthe arecae*. Koch's postulates were fulfilled by pathogenicity tests carried out on mango tree branches (cv. Tommy Atkins). To our knowledge, this is the first report of *D. arecae* causing dieback in mango (cv. Tommy Atkins) in Brazil.

Mango (*Mangifera indica*) plays a significant role in Brazil's agricultural economy. The country is among the world's leading producers, with the state of Pernambuco standing out as the main contributor to national exports. In January 2024, commercial and domestic cultivated mango trees were observed in Pernambuco State (in the municipalities of Recife, Itapissuma and Petrolina) showing symptoms of dark-coloured cankers, branch dieback and plant decline. Dieback incidence was approximately 40% in all areas. Symptomatic plant tissue fragments were plated onto potato dextrose agar (PDA) and incubated at 26°C for 7 days under continuous light. Three '*Diaporthe*' like isolates (MP22, MP27 and MP29), were obtained and deposited in the 'Coleção de Laboratório de Micologia' at Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brazil. Isolates presented sparse white mycelium with abundant black pycnidia. Alpha-conidia ($n = 30$) were hyaline, guttulate, aseptate and fusiform with slightly pointed ends (4.20–5.10 × 1.0–2.50 μm) consistent with *Diaporthe arecae* (Gomes et al. 2013) (Figure 1). DNA analysis of the nuclear rDNA internal transcribed spacers (nrITS), calmodulin (CAL), histone (HIS3) and translation elongation factor 1-alpha (EF-1α) were performed (GenBank accession numbers: PV090749, PV090750 and PV090751 [ITS]; PV099015, PV099016 and PV099017 [CAL]; PV099022, PV099021 and PV099023 [HIS-3]; and PV099018, PV099019 and PV099020 [EF-1α]). BLASTn searches showed 97% to 99% identities with *D. arecae* CBS16164. Maximum likelihood multi-locus analysis placed the isolates within the *D. arecae* clade (99% bootstrap support) (Figure 1). Pathogenicity tests were conducted on mango tree branches in the greenhouse (cv. Tommy Atkins) with 5 × 5 mm incisions to expose the tissue under the bark. PDA with fungal mycelia plugs (5 mm in diameter) from seven-day-old *D. arecae* isolates were placed in the lesion. PDA plugs without fungal mycelia were used as control. After 3 months, post-inoculation symptoms were similar to the original lesions (Figure 1). Pathogen was reisolated from inoculated branches and confirmed its identity fulfilling Koch's postulates. *Diaporthe arecae* has been reported exhibiting diverse ecological behaviours, acting as an endophyte, plant pathogen and human pathogen. In agriculture, it has been associated with crops diseases of high economic importance, such as *Citrus* spp., *Vitis vinifera* and *Prunus persica* (Guarnaccia and Crous 2017; Manawasinghe et al. 2019). *Diaporthe arecae* (syn. *D. pseudomangiferae*) was previously reported as the causal agent of mango dieback (cv. Haden) in China (Serrato-Diaz et al. 2014).

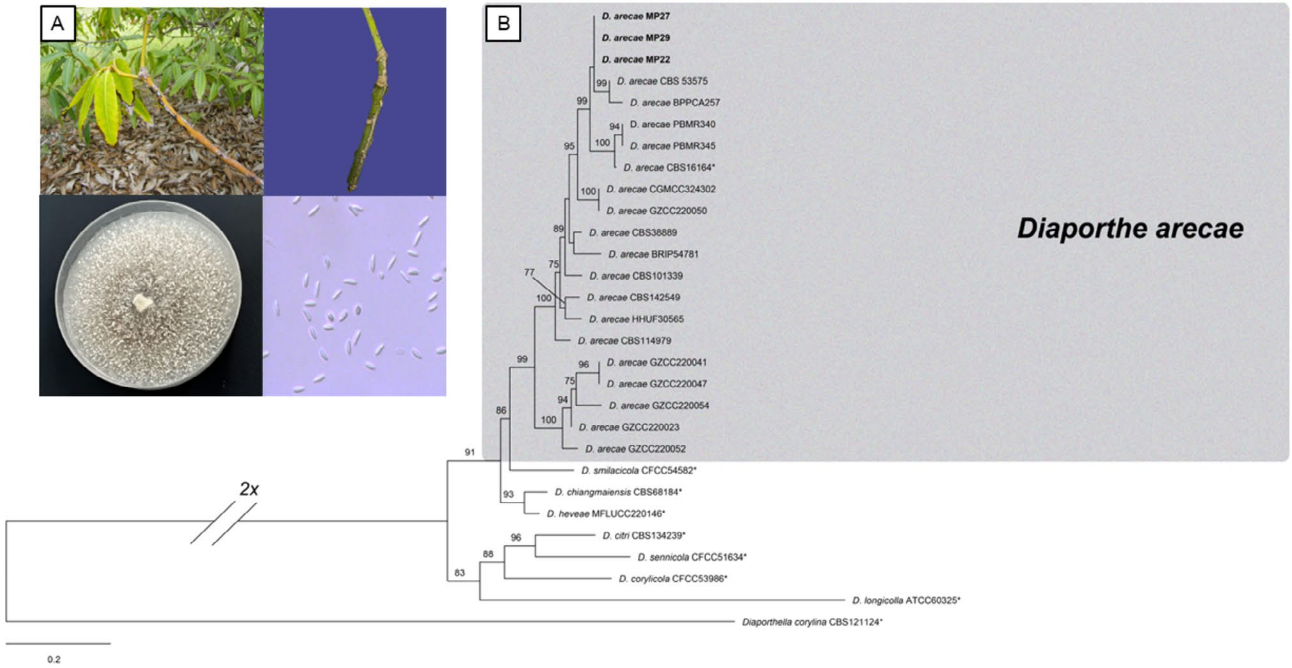

FIGURE 1 | (A) Dieback mango in field. Pathogenicity tests on mango branches. Colony. Alpha conidia morphology of *Diaporthe arecae*. (B) Maximum likelihood tree of the *Diaporthe* inferred on IQ-TREE from a concatenated alignment of ITS, CAL, HIS3 and EF-1. Significant supports for ML (SH-alrt bootstrap ≥ 70) is shown above the nodes. The tree was rooted *Diaporthella corylina*. Ex-type isolates are indicated with '*' in the end of the taxa labels. Isolates from mango are highlighted in bold. The scale bar indicates the average number of substitutions per site.

In Brazil, mango dieback was long attributed to *Botryosphaeria* species; however, our findings demonstrate *Diaporthe areace* might play a significant role in this disease. *Diaporthe arecae* has been reported on a wide range of hosts, emphasising the need for precise species identification to prevent misdiagnosis (Pereira et al. 2023). Recognising Diaporthe *arecae* as a causal agent demands adjustments in diagnostic approaches and control measures, directly influencing integrated disease management programs. To our knowledge, this is the first report of *D. arecae* causing dieback in mango (cv. Tommy Atkins) in Brazil.

Acknowledgements

The Article Processing Charge for the publication of this research was funded by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) (ROR identifier: 00x0ma614).

Ethics Statement

The authors have nothing to report.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Peer Review

The peer review history for this article is available at https://www.webofscience.com/api/gateway/wos/peer-review/10.1111/jph.70163.

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