

NEW DISEASE REPORT **OPEN ACCESS**

First Report of *Lasiodiplodia brasiliensis* Causing Dieback on *Gmelina arborea* in Mexico

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In April 2024, dieback was observed in 13- to 15-year-old *Gmelina arborea* (melina) trees in Las Choapas, Veracruz, Mexico. Symptoms included progressive drying of shoot tips and young lateral branches, followed by colonisation of the main

branches, leading to generalized foliar chlorosis, progressive decline, defoliation and eventually tree death (Figure 1). Disease incidence ranged from 30% to 60%, affecting a total area of 61 ha.



FIGURE 1 | Melina trees exhibiting dieback symptoms from which *Lasiodiplodia brasiliensis* was isolated.

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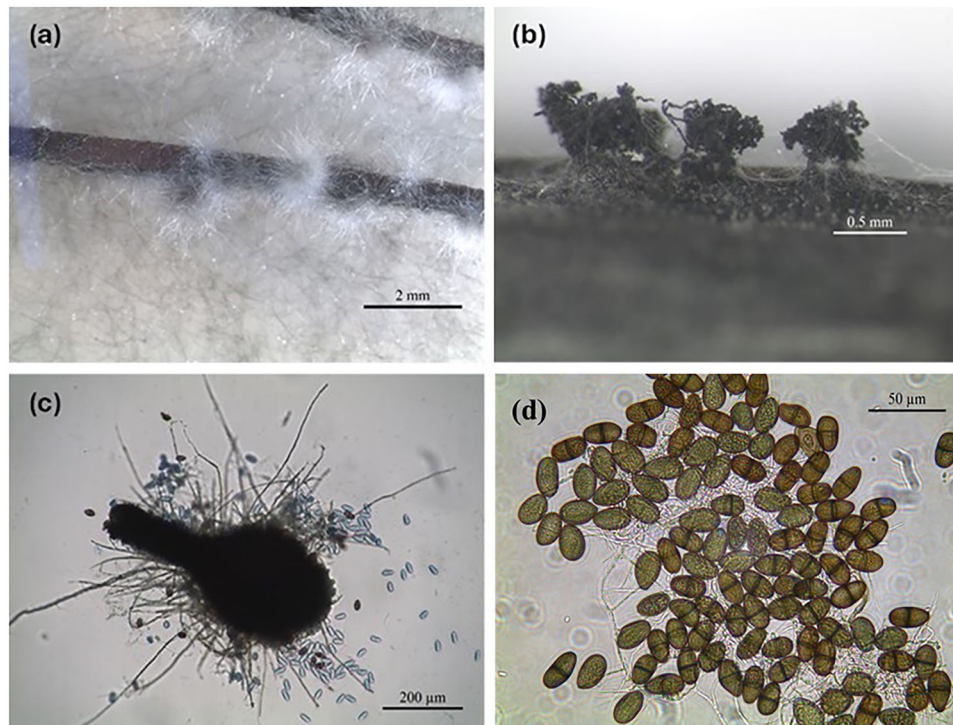


FIGURE 2 | Morphological characteristics of *Lasiodiplodia brasiliensis*: (a) pycnidia on pine needles on water agar; (b) conidial mass released from the pycnidia; (c) black pycnidium; and (d) mature conidia with longitudinal striations.

Diseased bark sections (5 mm²) were surface disinfected, placed on potato dextrose agar (PDA), and incubated at 25°C ± 1°C under a 12-h photoperiod. After 8 days, a representative fungal isolate (ChoVe) was purified through single-spore culture on PDA. The mycelium was compact, initially greyish white becoming black with age, with moderate aerial mycelium development. Pycnidia developed on sterile pine needles on water agar after 4 weeks (Figure 2a). They were globose, ostiolate and black, covered with light brown mycelium (Figure 2b–c). Immature conidia were hyaline, aseptate, granular and ovoid to ellipsoid; mature conidia were olive-brown to dark brown, uniseptate and measured $28.22 \pm 1.55 \times 14.91 \pm 0.86 \mu\text{m}$ ($n = 50$), with longitudinal striations (Figure 2d), consistent with characteristics of the genus *Lasiodiplodia* (Phillips et al. 2013; Netto et al. 2014).

Total DNA was extracted from isolate ChoVe. The ITS region and partial regions of the translation elongation factor 1- α (TEF1) and β -tubulin (TUB2) genes were PCR-amplified and sequenced using the ITS1/ITS4, EF1-728F/EF1-986R and Bt2a/Bt2b primer pairs, respectively (Alves et al. 2023). The sequences were deposited in GenBank (ITS: PX700021.1; TEF1: PX854293.1; and TUB2: PX854294.1). Species identity was resolved through multilocus phylogenetic analysis using the maximum-likelihood method. Isolate ChoVe clustered within the *Lasiodiplodia brasiliensis* clade (Figure 3), showing high affinity with other Mexican isolates.

To evaluate pathogenicity, ten 3-months-old melina saplings were inoculated. A 5-mm deep vertical incision was made at the apex of the main stem, previously disinfected with 70% alcohol. An 8-days-old mycelial plug (5 mm diameter) was placed into the wound, covered with sterile moist cotton, and wrapped with plastic film. Three control plants were inoculated with sterile PDA plugs. After 9 months, the inoculated plants developed symptoms identical to those observed in the field and subsequently died (Figure 4a,b); pycnidia were also observed on the stem apex (Figure 4c). Control plants remained healthy (Figure 4d). The pathogen was re-isolated from inoculated plants, fulfilling Koch's postulates.

This study represents the first report of *L. brasiliensis* affecting *G. arborea* in Mexico, expanding the known host range for this pathogen. Within the country, it had been previously documented on *Citrus latifolia* (Bautista-Cruz et al. 2019) and *Vitis vinifera* (Rangel-Montoya et al. 2021). Globally, this fungus has also been reported on grapevine (United States) and baobab (Madagascar). In Brazil, it is associated with a wide variety of hosts, including banana, cashew, coconut, jackfruit, maize, mango, melon, papaya, sugar-apple, watermelon and wild tamarind (Netto et al. 2014; Bautista-Cruz et al. 2019; Alves et al. 2023; da Mata et al. 2025; França et al. 2025). Given its history of damaging both commercial and wild hosts, our findings serve as a crucial foundation for establishing biosecurity measures and disease management strategies.

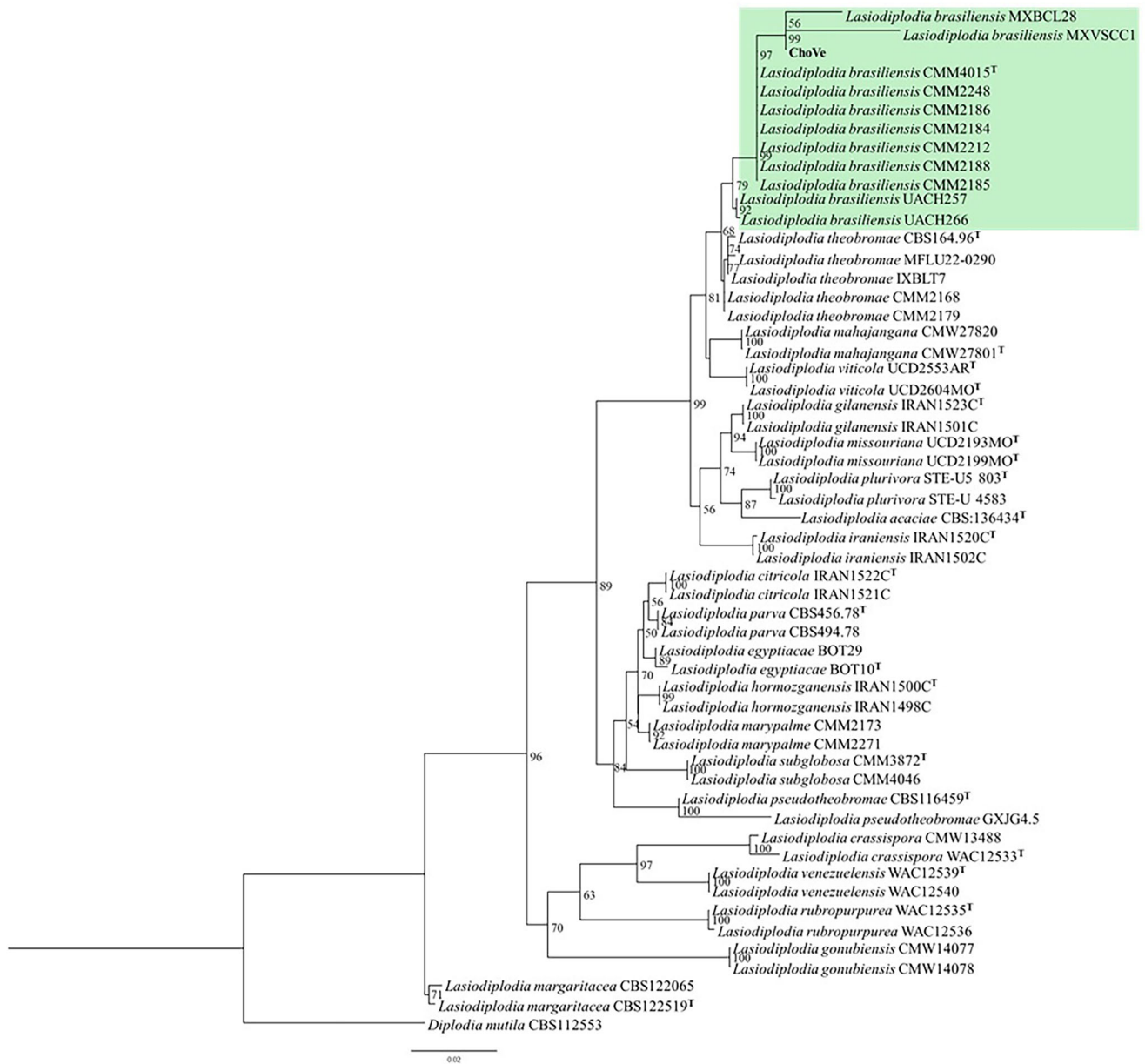


FIGURE 3 | Phylogenetic tree of *Lasiodiplodia* generated using the maximum likelihood method based on concatenated ITS, TEF1- α and TUB2 sequences, constructed with IQ-TREE. Bootstrap values $\geq 50\%$ are indicated at the nodes. The Mexican isolate ChoVe grouped within the *L. brasiliensis* clade with 79% bootstrap support. *Diplodia mutila* (CBS 112553) was used as the outgroup. Type strains are highlighted with a (T).



FIGURE 4 | Melina plants growing under greenhouse conditions: (a and b) exhibiting shoot tip death and leaf necrosis, and (c) pycnidia on the stem, 9 months after inoculation with *Lasiodiplodia brasiliensis* strain ChoVe; and (d) without symptoms in control plants.

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