NEW DISEASE REPORT



First record of Erysiphe diffusa causing powdery mildew on Bergera koenigii in the USA

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KEYWORDS

Curry leaf tree, Erysiphe diffusa, powdery mildew

Bergera koenigii L., commonly known as the curry tree, belongs to the family Rutaceae (Singh et al., 2014). Its leaves are used as a spice for flavor in Indian cuisine and are a good source of vitamins and antioxidants (Rao et al., 2011). In March 2023, powdery mildew was observed on the young leaves of a potted B. koenigii plant in Raleigh, North Carolina (Fig. 1). The incidence of the disease on the plant was 30–40%; the mycelium mostly present on the adaxial surface. Hyphal appressoria were lobed, the foot cells of the conidiophores ranged from 23 to 60 μ m in length. Hyaline conidia were formed singly, ellipsoid to cylindrical, without fibrosin bodies. The size of the conidia (n = 40) ranged from $14-38 \times 11-18 \mu m$, germ tubes were terminal. Mature chasmothecia were dark brown, globose, 92-100 μ m in diameter, with most appendages unbranched, except one appendage with loosely dichotomously branched apex, tips of the ultimate branchlets straight. Each chasmothecium contained up to six asci that were broad ellipsoid-obovoid, with a short stalk. Each ascus contained four to six ellipsoid to ovoid amber-coloured ascospores (17-23 imes 5-9 μ m) (Fig. 2). Morphological features were consistent with the genus Erysiphe (Braun & Cook 2012). A few infected compound leaves were deposited in the herbarium at North Carolina State University (Catalog No. 000024426).

DNA was extracted from the diseased leaves to determine the powdery mildew species. PCR and sequencing of the ITS region was performed using the Erysiphaceae-specific primers PM ITS1/PM ITS2 (Cunnington et al., 2003) and the sequence was deposited into Gen-

Bank (Accession No. OQ780858). The 720 bp amplicon had 99% identity with E. diffusa MK673961.1. Sequences which were highly similar to the curry leaf tree sample in BLAST analysis and type sequences of E. diffusa were used for phylogenetic analysis. Maximum likelihood analysis was performed using MEGA 11 with Podosphaera cerasi as an outgroup. The sequence from the specimen on curry leaf tree (BKPMNC) clustered with another E. diffusa sequence (LC010060.1) (Fig. 3). The phylogenetic analysis confirms E. fallax (on Carica papaya) and E. vignae (on legumes) as species closely allied to E. diffusa. Braun et al. (2017) reduced Oidium caricae to synonymy with E. diffusa and showed with sequence analyses that C. papaya is also a host of E. diffusa. Both E. diffusa and E. fallax occur on Carica papaya, but the relation between E. fallax and E. vignae remains to be clarified.

This is the first report of a powdery mildew infection on this host in the United States and the world. It is also the first record on a host of the Rutaceae and the second outside of legumes, which are the main hosts of E. diffusa (Braun & Cook 2012). Since curry tree leaves are edible and have commercial value, knowledge about this powdery mildew disease will help take timely management options where this crop is commercially grown.

Acknowledgments

We thank Dr. Matthew Bertone and Mr. Mike Munster for helping with the micrographs.

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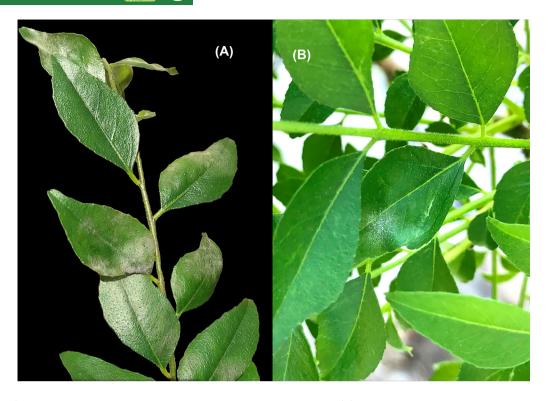


FIGURE 1 A) Compound leaf of *Bergera koenigii* with powdery mildew infection and (B) close-up view of the powdery mildew symptom on the curry leaf

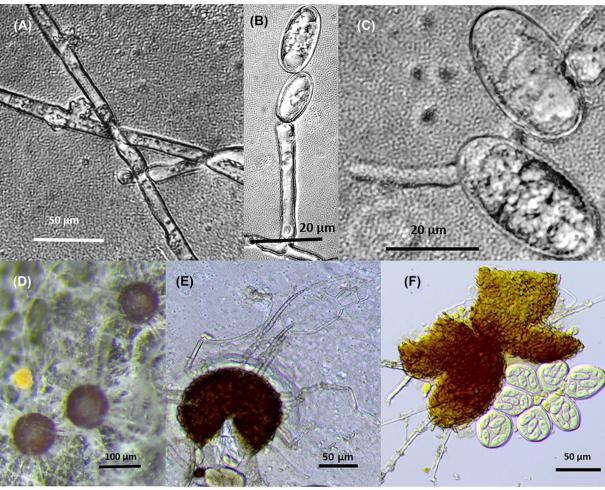


FIGURE 2 A) Lobed appressorium (in the middle), B) conidiophore, C) conidia, D) chasmothecia on the leaf surface, E) chasmothecium with appendages and F) chasmothecia with asci and ascospores.

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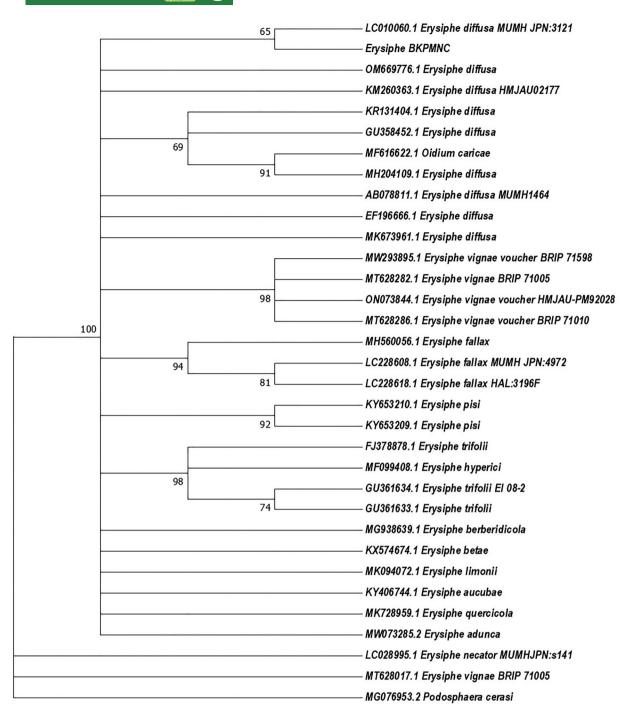


FIGURE 3 Maximum likelihood tree based on ITS region sequences of *Erysiphe diffusa* and closely related taxa. *Podosphaera cerasi* was used as an outgroup. Bootstrap values >65 (1,000 replications) are indicated at nodes. GenBank accession numbers are given for each sequence, except the sequence from the current study which is included as BKPMNC.

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How to cite this article: Moparthi, S.S., Jailani, A.K. & Braun, U. (2023) First record of Erysiphe diffusa causing powdery mildew on Bergera koenigii in the USA. New Disease Reports, 47, e12175. https://doi.org/10.1002/ndr2.12175