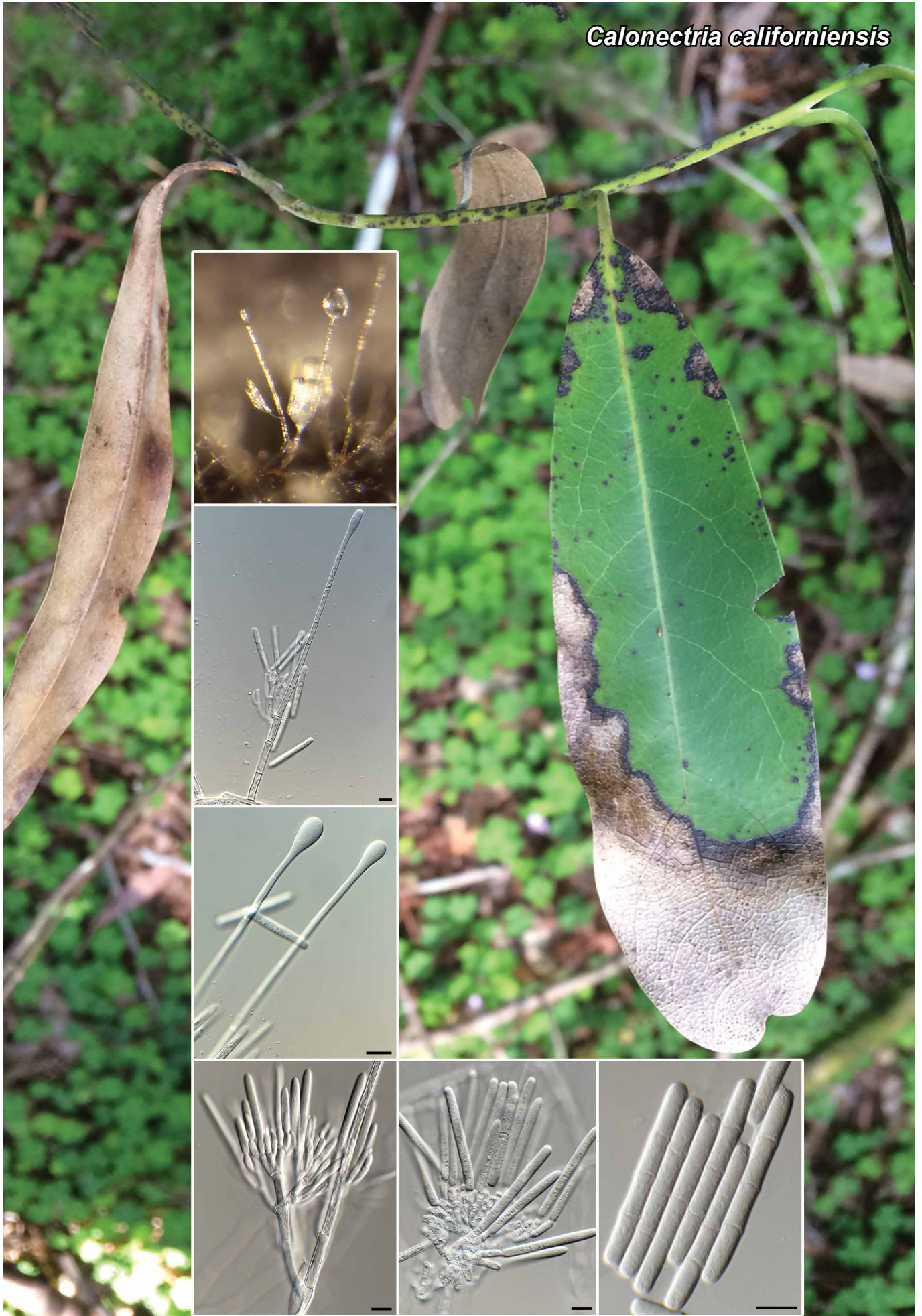


*Calonectria californiensis*



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***Calonectria californiensis* Crous & Roon.-Lath., sp. nov.**

*Etymology.* Name refers to the state of California, USA, where this fungus was collected.

*Classification* — *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

*Macroconidiophores* comprised of a stipe, a penicillate arrangement of fertile branches, a stipe extension, and a terminal vesicle. *Stipe* septate, hyaline at base, smooth, 40–100 × 6–7 µm. *Conidiogenous apparatus* with primary branches aseptate or 1-septate, 15–50 × 4–5 µm; secondary branches aseptate, 8–14 × 3.5–4 µm, each terminal branch producing 2–4 phialides; phialides doliform to reniform, hyaline, aseptate, 8–10 × 3–4 µm, apex with minute periclinal thickening and inconspicuous collarette; stipe extensions septate, straight to flexuous, 100–190 µm long, 3–4 µm wide at apical septum, terminating in ellipsoid to obpyriform to pyriform vesicle, (7–)8–9(–10) µm diam. *Conidia* cylindrical, rounded at both ends, straight, (41–)47–52(–58) × (4.5–)5–5.5(–6) µm, (1–)3-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Chlamydospores* dark brown, thickened, globose, 10–12 µm diam, formed in sparse chains throughout the medium.

*Culture characteristics* — Colonies flat, spreading, with sparse to moderate aerial mycelium and lobate, smooth margin, reaching 30 mm diam after 7 d at 25 °C. On MEA and PDA surface sienna to umber, reverse umber in centre, sienna in outer region. On OA sienna on surface.

*Typus.* USA, California, Sonoma County, Guerneville, on leaves of *Umbellularia californica* (*Lauraceae*), 5 May 2015, S. Rooney-Latham, CDF A267 (holotype CBS H- 24751, culture ex-type CPC 29621 = CBS 147604, LSU, *actA*, *cmdA*, *his3*, *tef1* (first part) and *tub2* sequences GenBank MZ064514.1, MZ078156.1, MZ078169.1, MZ078182.1, MZ078238.1 and MZ078279.1, MycoBank MB 839545).

*Additional material examined.* USA, California, Sonoma County, Guerneville, on leaves of *U. californica*, 5 May 2015, S. Rooney-Latham, CPC 29619, ITS, LSU, *actA*, *cmdA*, *his3*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064457.1, MZ064515.1, MZ078157.1, MZ078170.1, MZ078183.1, MZ078213.1, MZ078239.1 and MZ078280.1; *ibid.*, CPC 29620, ITS, LSU, *actA*, *cmdA*, *his3*, *tef1* (first part) and *tub2* sequences GenBank MZ064458.1, MZ064516.1, MZ078158.1, MZ078171.1, MZ078184.1, MZ078240.1 and MZ078281.1; *ibid.*, CPC 29622, ITS, LSU, *actA*, *cmdA*, *his3*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064459.1, MZ064517.1, MZ078159.1, MZ078172.1, MZ078185.1, MZ078214.1, MZ078241.1 and MZ078282.1.

*Notes* — Brayford & Chapman (1987) reported a wilting disease of *Laurus nobilis* on the Isles of Scilly, and later on *Arbutus andrachnoides* and *Gaultheria shallon* in West Devon, UK. Lechat et al. (2010) linked this disease to a new species, *Calonectria lauri* (validated by Liu et al. 2020), which was reported from leaves of *Ilex aquifolium* in France and the Netherlands, and roots of *Buxus sempervirens* in Belgium. *Calonectria lauri* is sister to *C. californiensis* described in the present study. Although the two species can be distinguished in that *C. lauri* has conidia that are somewhat larger, (45–)55–68(–73) × (4–)5–6(–7) µm, they are best separated based on their DNA phylogeny.

*Colour illustrations.* Symptomatic leaves of *Umbellularia californica*. Conidiophores with stipe extensions on SNA; vesicles; penicillate conidiogenous apparatus; conidia. Scale bars = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 29619 had highest similarity to *Calonectria lauri* (strain CMW 23682 (R), GenBank MT359736.1; Identities = 534/534 (100 %), no gaps), *Calonectria citri* (strain CMW 23675 (R), GenBank MT359683.1; Identities = 533/534 (99 %), no gaps) and *Calonectria tunisiana* (now synonym of *Calonectria pseudomexicana*; strain CAL-EU2, GenBank MT345681.1; Identities = 531/534 (99 %), no gaps). The ITS sequences of CPC 29619, 29620 and 29622 are identical (533/533 (100 %)). Closest hits using the LSU sequence are *Calonectria lauri* (strain CMW 23682 (R), GenBank MT359496.1; Identities = 821/821 (100 %), no gaps), *Calonectria penicilloides* (strain CMW 23696 (R), GenBank MT359559.1; Identities = 819/821 (99 %), no gaps) and *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT359498.1; Identities = 819/821 (99 %), no gaps). The LSU sequences of CPC 29619, 29620, 29621 and 29622 are identical (781/781 (100 %)). Closest hits using the *actA* sequence of CPC 29619 had highest similarity to *Calonectria lauri* (strain CMW 23682 (R), GenBank MT335043.1; Identities = 221/221 (100 %), no gaps), *Calonectria citri* (strain CMW 23675 (R), GenBank MT334992.1; Identities = 213/222 (96 %), one gap (0 %)) and *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT335045.1; Identities = 214/222 (96 %), one gap (0 %)). The *actA* sequences of CPC 29619, 29620, 29621 and 29622 are identical (559/559 (100 %)). Closest hits using the *cmdA* sequence of CPC 29619 are *Calonectria lauri* (strain CMW 23682 (R), GenBank MT335275.1; Identities = 654/662 (99 %), no gaps), *Calonectria citri* (strain CMW 23675 (R), GenBank MT335222.1; Identities = 627/663 (95 %), two gaps (0 %)) and *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT335277.1; Identities = 618/662 (93 %), no gaps). The *cmdA* sequences of CPC 29619, 29620 and 29622 are identical (662/662 (100 %)). Closest hits using the *his3* sequence of CPC 29619 had highest similarity to *Calonectria lauri* (strain CMW 23682 (R), GenBank MT335515.1; Identities = 399/415 (96 %), no gaps), *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT335517.1; Identities = 387/419 (92 %), ten gaps (2 %)) and *Calonectria citri* (strain CMW 23675 (R), GenBank MT335462.1; Identities = 372/415 (90 %), four gaps (0 %)). The *his3* sequences of CPC 29619, 29620, 29621 and 29622 are identical (412/412 (100 %)).

(text continues on Supplementary material page FP1225)

**Supplementary material**

**FP1225** Consensus phylogram (50 % majority rule) of 9752 trees resulting from a Bayesian analysis of the *Calonectria* multigene (*actA* / *cmdA* / *his3* / ITS / LSU / *rpb2* / *tef1* / *tub2*) sequence alignment (45 sequences including outgroup; 5068 aligned positions; 96 / 310 / 192 / 69 / 59 / 253 / 282 / 308 unique site patterns, respectively; 65000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). The alignment is derived from the dataset of Liu et al. (2020) and methodology used and GenBank accession numbers of the reference sequences can be found in the same reference. Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The tree was rooted to *Curviciadiella cigneae* (culture CBS 109167) and the species described here is highlighted with a coloured block and bold face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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