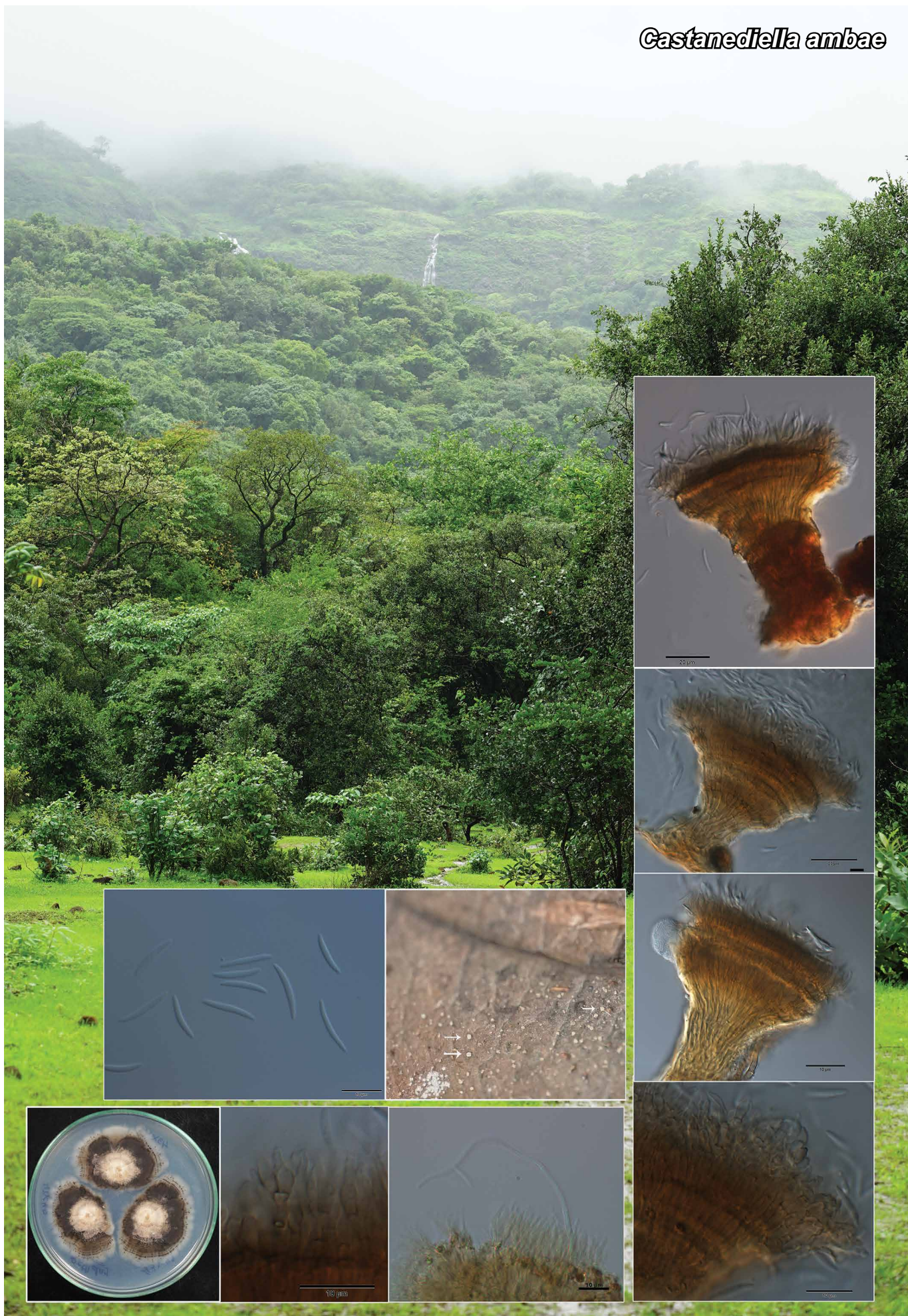


Castanediella ambae



Fungal Planet 1230 – 13 July 2021

Castanediella ambae Rajeshk., Crous, J.Z. Groenew., S. Fatima, S. Lad, *sp. nov.*

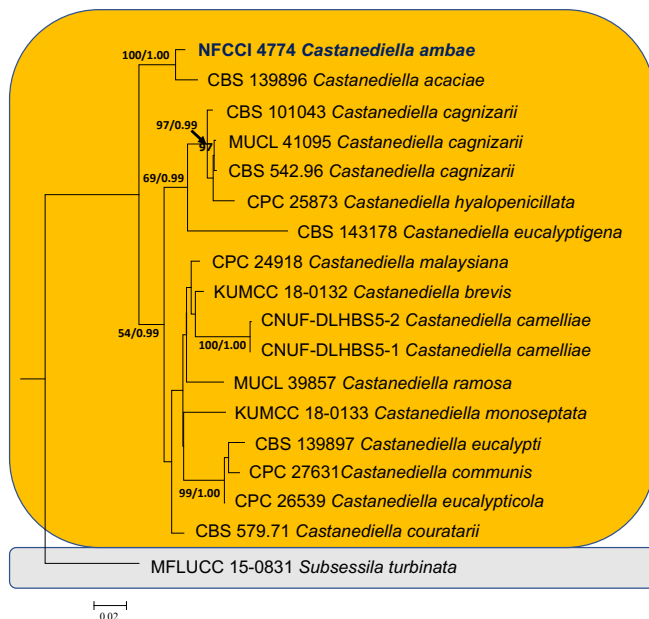
Etymology. Named after 'amba' meaning Mango tree in Marathi language, the host of the fungus.

Classification — *Castanediellaceae*, *Xylariales*, *Sordariomycetes*.

On decaying leaves of *Mangifera indica*: Mycelium pale to dark brown, immersed, septate, hyphae 2–3.5 µm diam. *Conidiomata* sporodochial, scattered, erumpent, starting as a penicillate tuft of conidiophores with central attachment point, expanding lateral and apical, becoming densely branched, but with central attachment, stipitate, 20–80 µm diam, 35–120 µm high. *Setae* rare, hyaline, flexuous or undulate with obtuse tips, attached to the base of the sporodochia, up to 87 µm long and 2–2.5 µm wide. *Conidiophores* subcylindrical, densely branched, multi-septate, medium to dark brown, smooth. *Conidiogenous cells* terminal and intercalary, ampulliform, pale brown, smooth, apex truncate, polyblastic, phialidic?, 7–10.5 × 2–2.8 µm. *Conidia* solitary, hyaline, smooth, falcate with subobtuse or acute ends, 0–2-guttulate, (8–)9.5–15.5(–19) × 1.5–1.8(–2) µm.

Culture characteristics — (on malt extract agar at 25 ± 2 °C after 1 mo): Colonies floccose or umbonate at centre, grey (5E1) to brownish orange (5C4) (Kornerup & Wanscher 1978), velutinous or immersed, dark brownish grey (5F2) to dark grey (5F1); reverse dark brownish grey (5F2) to dark grey (5F1), colonies reaching 40–50 mm diam.

Typus. INDIA, Tamhini Ghats, Tamhini village, on leaves of *Mangifera indica* (*Anacardiaceae*), 23 July 2018, K.C. Rajeshkumar (holotype AMH 10211, cultures ex-type NFCCI Raj18 = NFCCI 4774, ITS and LSU sequences GenBank MN660236 and MN660235, MycoBank MB 833316).



Colour illustrations. Habitat forest area near Tamhini village. Sporodochia (right column); conidia; conidiomata on *Mangifera indica* (upper row); colonies on MEA; conidiogenous cells; hyaline seta (lower row). Scale bars = 10 µm.

Notes — Morphologically, *C. ambae* resembles *C. acaciae* (Crous et al. 2015a), having sporodochial conidiomata compared to all other species of *Castanediella*. However, the sporodochia in *C. ambae* are smaller in width and slightly longer than those of the type species *C. acaciae*. The presence of hyaline, flexuous setae with obtuse tips arising from the base of the sporodochia, is another unique feature of *C. ambae*. Furthermore, conidia are marginally longer in *C. ambae* in comparison to those of *C. acaciae*. Phylogenetic analyses based on combined ITS and LSU sequence data resulted in a unique clade for the sporodochial *Castanediella* species, *C. acaciae* and *C. ambae* from other taxa in *Castanediella*. The new species form a fully supported (100 % bootstrap support, posterior probability = 1.00) clade with *C. acaciae*. Based on a megablast (type BLASTn) search of NCBI's GenBank nucleotide database, the closest hits using the **LSU** sequence are *C. acaciae* (GenBank KR476763; Identities = 844/848 (99 %), no gaps), *C. cagnizarii* (GenBank MH874222; Identities = 837/848 (99 %), no gaps) and *C. eucalypti* (GenBank KR476758; Identities = 837/851 (98 %), three gaps (0 %)). Closest hits using the **ITS** sequence had highest similarity to *C. acaciae* (GenBank NR_137985; Identities = 506/526 (96 %), five gaps (0 %)), *C. tereticornis* (GenBank NR_161116; Identities = 487/532 (92 %), eight gaps (1 %)) and *C. cagnizarii* (GenBank MH862597; Identities = 481/530 (91 %), ten gaps (1 %)).

Phylogram generated from a maximum likelihood (ML) analysis based on LSU and ITS sequence data representing the genus *Castanediella* in RAxML v. 8.2.12 (Stamatakis 2014). Related sequences are taken from Lin et al. (2019). Eighteen strains are included in the combined analyses which comprise 1363 characters and 530 characters for LSU and ITS, respectively, after alignment. *Subsessilia turbinata* (KX762288, KX762289) was used as the outgroup taxon. Single-gene analyses were also performed to compare the topology and clade stability with combined gene analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis performed in siMBa (Mishra & Thines 2014). The best scoring RAxML tree with a final likelihood value of -3866.720205 is presented. The matrix had 256 distinct alignment patterns, with 7.71 % undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.253765, C = 0.209910, G = 0.261361, T = 0.274964; substitution rates AC = 1.675661, AG = 3.141033, AT = 2.412224, CG = 0.281419, CT = 6.326033, GT = 1.000000; gamma distribution shape parameter α = 1.214174. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 50 % and Bayesian posterior probability clade credibility values greater than 0.95 (BPP); the rounding of values to 2 decimal proportions) from Bayesian-inference analysis (siMBa) labelled on the nodes (MLBS/BPP). The newly generated sequence is indicated in **bold**.

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