

Clitopilus austroprunulus



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***Clitopilus austroprunulus* Morgado, G.M. Gates & Noordel., sp. nov.**

Etymology. austro (L) = southern, being a southern counterpart of *Clitopilus prunulus*.

Macroscopic description — *Pileus* 40–90 mm diam, convex when young, expanding to concave or infundibuliform, with involute margin, becoming irregularly shaped with age with undulating marginal zone. Not hygrophanous, not translucently striate, uniformly pale grey, sometimes with a slight brown tinge at the centre (10YR 7/3–4), adpressed-tomentose all over. *Lamellae* arcuate-decurrent, grey-pink with entire, concolourous or more or less hyaline edge, crowded. *Stipe* 30–60 × 10–15 mm (apex), usually central, rarely eccentric, tapering towards base, white or with a greyish brown tinge like pileus, tomentose. *Context* white, firm and rather thick in pileus. *Odour* very strongly farinaceous-rancid. *Taste* farinaceous-rancid.

Microscopic description — *Spores* (8–)9–11 × 4.5–6 µm, Q = 1.7–2.1, Qav = 1.9, slender fusiform occasionally amygdaliform, thin-walled, distinctly ribbed lengthwise with 5–8 longitudinal ribs, angular in polar view. *Basidia* 20–30 × 4–8 µm, 4-spored. *Lamella* edge fertile or with scattered subcylindrical cheilocystidia, 20–40 × 4–11 µm. *Pileipellis* a cutis of densely packed, narrow cylindrical, 4–8 µm wide hyphae with dark brown coloured walls, and scattered fine encrustations. Clamp-connections absent.

Habitat — Terrestrial in litter on wet sclerophyll forest of *Eucalyptus regnans* with an understorey of *Acacia*, *Olearia*, *Bedfordia*, *Pomaderris* and *Phebalium*.

Typus. AUSTRALIA, Tasmania, Kermantie Falls, Lower Track, S43°12' E146°52', 24 Mar. 2009, M.E. Noordeloos 2009062 (L); ITS sequence GenBank KC139085, MycoBank MB802264.

Additional collections AUSTRALIA, Tasmania, Kermantie Falls, Lower Track, S43°12' E146°52', 16 Mar. 1999, G. Gates E 226; ibid., 23 May 2000, G. Gates E 936; ibid., 5 Apr. 2001, G. Gates E 1072; ibid., 16 May 2002, G. Gates E 1508; ibid., 10 Apr. 2003, G. Gates E 1694; ibid., Upper Track, 26 Apr. 2001, G. Gates E 1131; Reuben Falls, 15 May 1999, G. Gates E 507; Tahune, hanging bridges walk, S43°06', E146°43', 14 Mar. 2009, M.E. Noordeloos 2009001 (L), ITS sequence GenBank KC139084.

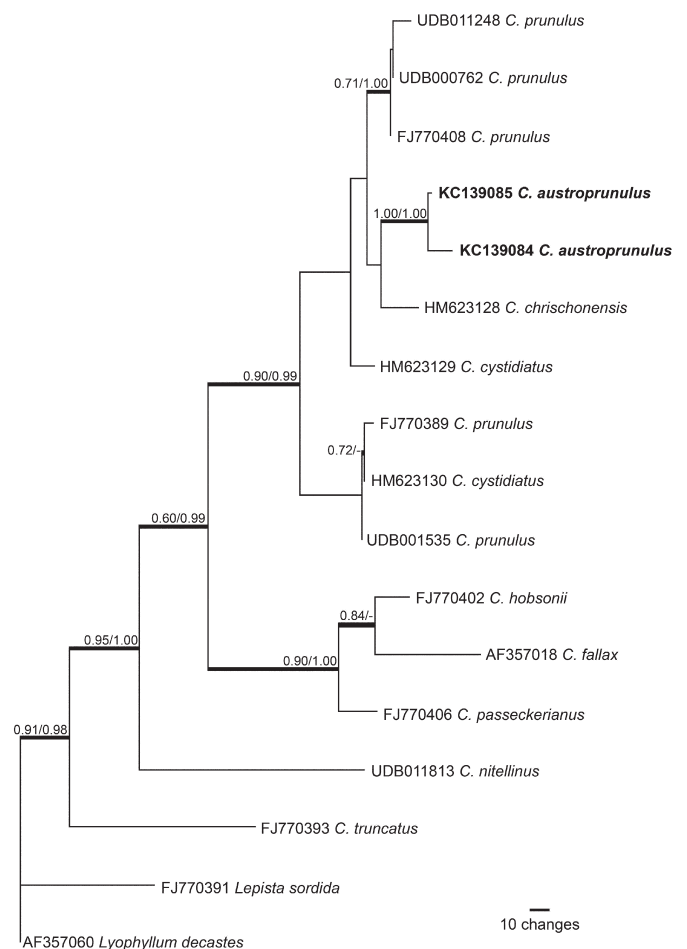
Notes — The morphospecies *Clitopilus prunulus* is widespread in Europe and North America. A number of closely related species have been described in literature (Hausknecht & Noordeloos 1998, Yang 2007, Vizzini et al. 2011). Species limits are however often difficult to define due to the lack of good morphological characters. Recent studies confirm that the current concept of *C. prunulus* is polyphyletic (Hartley et al. 2009, Vizzini et al. 2011). *Clitopilus austroprunulus* is very similar morphologically to *C. prunulus* from Europe, and therefore Noordeloos & Gates (2012) initially listed it as *Clitopilus* cf. *prunulus*. However, a phylogenetic analysis based on internal transcribed spacer (ITS) sequences derived from two *C. austroprunulus* isolates and previously published data (Co-David et al. 2009, Hartley et al. 2009, Vizzini et al. 2011) clearly showed that the collections of *C. austroprunulus* cluster together as a clade of their own, phylogenetically distinct from the rest of the *C. prunulus* clade. The other closely re-

Colour illustrations. Australia, Tasmania, Kermantie Falls, Lower Track, type-locality. *Clitopilus austroprunulus*, holotype (photo's M.E. Noordeloos).

lated species, *C. cystidiatus* and *C. chrischonensis* are phylogenetically distinct and differ from *C. austroprunulus* in morphology by the abundant presence of cheilocystidia. Although judging from the phylogeny presented here, the occurrence of cheilocystidia may well be of limited value in the systematics of this group. *Clitopilus amygdaliformis* described from China (Yang 2007) is also closely related, but differs in spore and stipe morphology. Unfortunately, sequences for this species are not available in public databases and therefore it was not included in the phylogenetic analysis.

A multi-gene maximum-likelihood phylogeny based on four independent genetic markers (data not shown) yielded the same conclusions as the ITS phylogeny presented here. Therefore *C. austroprunulus* is phylogenetically distinct from all sequenced species and morphologically distinct from all described species without available sequences.

Maximum-likelihood phylogram (-ln L = 3770.9401) of ITS sequence analysis with general-time-reversible model using Garli 2.0 (Zwickl 2006), showing the phylogenetic position of *Clitopilus austroprunulus* (in **bold**) generated in this study among representatives of closely related taxa with sequences deposited in GenBank and the UNITE database. Branches with bootstrap support (BS) ≥ 0.70 (based on 100 replicates) and/or bayesian posterior probability (PP) ≥ 0.95 (based on 5 000 generations) (Ronquist et al. 2012) are thickened with BS/PP values indicated above the branches. The tree was rooted with *Lepista sordida* and *Lyophyllum decastes*.



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