Cryptogamie, Mycologie, 2016, 37 (3): 329-343

# Untangling the Central African Cantharellus sect. Tenues: Cantharellus minutissimus sp. nov. and epitypification of Cantharellus alboroseus

Bart BUYCK<sup>a\*</sup>, Eske DE CROP<sup>b</sup>, Annemieke VERBEKEN<sup>b</sup> & Valérie HOFSTETTER<sup>c</sup>

<sup>a</sup> Muséum National d'Histoire Naturelle, Dépt. Systématique et évolution, CP 39, ISYEB, UMR 7205 CNRS MNHN UPMC EPHE, 12 rue Buffon, F-75005 Paris, France; email: buyck@mnhn.fr

<sup>b</sup> Research Group Mycology, Department of Biology, Ghent University, K. L. Ledeganckstraat 35, 9000 Ghent, Belgium; e-mail: eske.decrop@ugent.be

<sup>c</sup> Department of plant protection, Agroscope Changins-Wadenswil Research Station ACW, Rte de Duiller, 1260, Nyon, Switzerland; email: valerie.hofstetter@agroscope.admin.ch

**Abstract** – *Cantharellus* section *Tenues* was originally created for four new, very small, redorange-yellow Central African chanterelles with a more or less fistulose stipe, short basidia and an omphaloid habit. The type species, *C. tenuis*, is here considered unrelated to the other three species as it is the only species having clamp connections. All four species remain poorly known and need to be recollected and epitypified with recently collected, sequenced specimens that comply to the original description. In this paper, *C. alboroseus* is epitypified, and an equally small species, *C. minutissimus*, is introduced. Both species are systematically placed using a multigene phylogeny.

Cantharellus floridulus / Cantharellus subg. Rubrinus / multigene phylogeny / taxonomy

### INTRODUCTION

Cantharellus section Tenues Heinemann presents several taxonomic problems, both as a group and at species level. It was originally described (Heinemann 1958) to harbor four new, very small, red-orange-yellow Central African chanterelles with a fistulose stipe, short basidia and an omphaloid habit (i.e resembling slender, very small Tricholomataceae with a relatively long stipe and decurrent gills). The new section was typified by C. tenuis, an entirely (cap, stipe and hymenophore) bright orange species with a cap measuring merely 10-15 mm diam. and having abundant clamp connections. As for the other three species, the presence of clamp connections was mentioned for C. pseudofriesii, but left unresolved for both Cantharellus floridulus Heinem. (ut C. floridula) and C. alboroseus Heinem. Upon

<sup>\*</sup> Corresponding author: buyck@mnhn.fr

his revision of the four type specimens, Eyssartier (2001) confirmed the presence of clamp connections in *C. tenuis*, but concluded that the other three species lacked clamp connections. Considering the importance of presence/absence of clamps in the systematic arrangement of the genus (Buyck *et al.* 2014), this feature therefore places *C. tenuis* most likely in subg. *Cinnabarinus* Buyck & V. Hofstetter, whereas the remaining three species of sect. *Tenues* are unrelated and most probably belong in subg. *Rubrinus* Buyck & Eyssart. As a consequence, sect *Tenues* does not correspond to a monophyletic concept.

A fifth species for which the original material had been lost (fide Eyssartier 2001), *Cantharellus addaiensis* P. Henn., was considered by Heinemann to be very closely related to his *C. floridulus* because of the very similar micro- and macromorphology, but the original description (Hennings, 1898) mentioned a concolorous hymenophore and the species was most likely associated with woodland vegetation. Although Eyssartier (2001) suggested that Heinemann's species could be a later synonym of *C. addaiensis* because of the highly similar descriptions, he had adopted the name *C. floridulus* for woodland collections with a highly similar macro- and micromorphology but a concolorous hymenophore. Eyssartier was followed herein by most other researchers (Buyck *et al.* 2000, Eyssartier & Buyck 1998, De Kesel *et al.* 2002, Härkönen *et al.* 1995, 2003).

The types of the chanterelles that were placed in sect. *Tenues* are kept at BR (Meise, Belgium) and have been collected by Mrs. Goossens-Fontana, now almost one century ago. With the exception of *C. floridulus*, none of these species has ever been mentioned again in the literature. Decennia passed since Heinemann described the collections of Goossens-Fontana and, during all these years, chanterelles had not been recollected from African rain forest until very recently. It were Eyi Ndong *et al.* (2011) who first illustrated new collections of chanterelles from this habitat, including specimens identified as *C. floridulus* showing a distinctly white hymenophore (corresponding to the original description), and thus quite different from the woodland collections identified as such. Consequently, Buyck (2012) neotypified *C. addaiensis* as a very similar but distinct species with a concolorous hymenophore and exclusively associated with woodland vegetation in tropical Africa. It was placed with strong molecular support in subg. *Rubrinus* sect. *Isabellinus* Eyssart. & Buyck, where it was the unique reddish species in a clade of otherwise entirely yellowish- brown and often much larger taxa (Buyck *et al.* 2014).

In the present paper, the authors discuss identification problems and systematic placement of some of the species that were previously assigned to sect. *Tenues* on the basis of several recent collections that were made only some 350 km away from the holotype locality and in their original habitat, the *Gilbertiodendron dewevrei* rain forest. Considering the poor state of the type specimens and the impossibility of obtaining good DNA sequence data from these types, it is important to epitypify each of the names introduced by Heinemann, a process that started only recently (De Kesel *et al.* 2016, this issue; Buyck et al, 2016a,b this issue). Therefore specimens have to be collected that correspond to the original description and, more importantly, they have to be sequenced for the most important gene regions used in current fungal phylogenies to reliably fix their future identification. In particular the future epitypification of *C. floridulus* would be an important step as the species was selected as type of subg. *Rubrinus* Buyck & Eyssart. (in Eyssartier & Buyck 2001).

#### MATERIAL AND METHODS

Taxon sampling, DNA isolation, amplification and sequencing

Genomic DNA isolation, amplification and sequencing of the here newly included Cantharellus samples were performed as described in Buyck et al. (2014) and the analysis is based on the same four loci but includes now 94, instead of 82 specimens. Compared to the original sampling in Buyck et al. (l.c.), we replaced some collections for which we had missing data in order to maximize molecular support in our analyses (Table 1): Cantharellus appalachiensis (previously sampled from GenBank) is replaced by our collection 1084; both samples of C. congolensis (247 and 512) were replaced by samples 1645 and 1676 (now both from the original rain forest habitat); the single sample for C. friesii (481) is now represented by two new, fully sequenced collections of the same species (1001 and 1004); the sample for C. subpruinosus (484) by two more recent collections (1110 and 1115; here renamed as C. pallens, see Olariaga et al., in press); the sample 267 for C. addaiensis is replaced by the fully sequenced sample 1630; the new samples 1608, 1609 and 1533 were added for C. miomboensis, C. cf subcyanoxanthus and C. subamethysteus respectively; the holotype sample for C. conspicuus is replaced by the fully sequenced sample 1629. Finally, samples for previously not included taxa were added for C. guyanensis (samples 1501 and 1517; see Buyck et al. 2016b, this issue) and C. miniatescens (samples 1671, 1682 and 1683, see Buyck et al. 2016a, this issue), together with representative samples for the here discussed taxa (samples 1670, 1659 and 1621). We used a single taxon as the outgroup: Craterellus tubaeformis.

All in all, 59 sequences were newly generated for this study (Table 1): 15 mitochondrial small subunit (mitSSU), 15 nuclear large subunit (nucLSU), 15 RNA polymerase II second largest subunit (*RPB*2) and 14 translation elongation factor 1-alpha (*TEF*1) partial locus sequences.

## Phylogenetic analyses

After the introduction of the newly produced sequences in single locus alignments of Buyck *et al.* (2014) using MacClade 4.05 (Maddison and Maddison, 2002) and the removal of five taxa (replacements; see Materials and Methods section), the final 4 loci dataset included 94 taxa. The full alignment included 5916 characters. After exclusion of introns and ambiguously aligned regions, the combined dataset included 3326 characters. In-depth congruence tests have been conducted for individual locus sequence data by Buyck *et al.* (2014) for 82 out of the 94 taxa analyzed in the present study. Therefore we did not repeat congruence tests for the 4 loci-94 taxa dataset: for taxa replacements, but the newly introduced data were checked for sequence similarity with previously obtained sequence data for the same species; for additional sequence data, represented by more than one collection, we checked for sequence similarity between collections of the same species.

Searches for optimal trees and branch robustness for the four loci used in combination were conducted with the program PhyML (Guindon & Gascuel, 2003) under the "best-fit" model (Lio & Goldman, 1998) estimated using Modeltest v. 3.06 (Posada & Crandall, 1998), with the search starting from a distance-based tree and with the proportion of invariable sites, the gamma shape parameter and the number of substitution categories estimated during the search. Three of these searches were implemented to check for convergence to the same likelihood value. Phylogenetic

Table 1. Voucher table showing additional or replaced Cantharellus sequence data compared to the voucher table in Buyck et al. 2014

	TEF1	KX857073	I	KX857032	KX857075	KX857078	KX857073	KX857076	KX857077	KX857015	KX857016	KX857071	KX857035	KX857036	KX857072	KX857062
Genbank accession numbers	RPB2	KX857004	KX857003	KX856994	KX857006	KX857010	KX857004	KX857007	KX857008	KX856987	KX856988	KX857001	KX856995	KX856996	KX857002	KX857000
	nucLSU	KX857100	KX857099	KX857090	KX857102	KX857106	KX857100	KX857103	KX857104	KX857083	KX857084	KX857097	KX857091	KX857092	KX857098	KX857096
	mitSSU	KX857126	KX857125	KX857116	KX857128	KX857132	KX857126	KX857129	KX857130	KX857109	KX857110	KX857123	KX857117	KX857118	KX857124	KX857122
Herbarium		GENT	GENT	PC 0142451	PC 0142445	PC 0142446	GENT	PC 0142441	PC 0142442	PC 0142447	PC 0142448	GENT	PC 0142449	PC 0142450	GENT	GENT
Provenance		Togo	Cameroon	USA	C-African Rep.	C-African Rep.	Togo	C-African Rep.	C-African Rep.	Italy	Italy	Zambia	Italy	Italy	Zambia	Thailand
Voucher		1630/EDC14.414	1621/EDC14.281	1084/JJ MOCant3	1645/BB16.044	1676/BB16.123	1629/EDC14.407	1659/BB16.086	1670/BB16.108	1001/EC09.16	1004/EC09.43	1608/EDC14.018	1110/BB12.077	1115/BB12.082	1609/EDC14.034	1533/AV12.003
Тахоп		Cantharellus addaiensis	C. minutissimus	C. appalachiensis	C. congolensis	C. congolensis	C. conspicuus	C. alboroseus	C. alboroseus	C. friesii	C. friesii	C. miomboensis	C. pallens	C. pallens	C. cf subcyanoxanthus	C. cf subamethysteus

Abbreviations for collectors are as follows: AV Annemieke Verbeken, BB Bart Buyck, EC Emanuele Campo, EDC Eske de Crop, JJ Jay Justice.

confidence was evaluated based on 500 ML bootstrap replicates using the same settings as for the searches for the most likely trees. Bootstrap values  $\geq$  70% were considered significant (Alfaro *et al.*, 2003).

#### **RESULTS**

Phylogenetic analyses

The most likely tree  $(-\ln = 78507.437)$  out of the three runs conducted under the estimated GTR "best fit" substitution model, is depicted in Figure 1. The topology of the recovered phylogeny is quite similar to the topology recovered by Buyck et al. (2014). Cantharellus alboroseus is part of subclade 2b sensu Buyck et al. (2014 = Cantharellus subg. Rubrinus sect. Heinemannianus Eyssart. & Buyck) and highly supported by ML bootstrap values (ML-bs) to be monophyletic with (ML-bs = 90%) and sister taxon (ML-bs = 100%) to C. ibitvensis. Phylogenetic analyses place C. minutissimus in subclade 2b sensu Buyck et al. (2014, = Cantharellus subg. Rubrinus sect. Isabellinus Eyssart. & Buyck) and our new species nests with maximum support (ML-bs = 100%) in the subclade including all reddish-greyish to dark brown species of subclade 2b with the exception of C. miomboensis which is suggested to be sister to this clade but without significant support. Also the internal relationships within the subclade containing C. minutissimus remain poorly supported and our species is not resolved from the other closely related species. The whitish, more yellowish to pale brown species of sect. *Isabellinus* constitute a third, significantly supported subclade (ML-bs 74%).

*Taxonomy* 

Cantharellus alboroseus Heinem., Bull. Jard. Bot. État, 28 (4): 420. 1958 Figs 2-4, 8-10

Original diagnosis: "Pileus tenuis, depressus, rubeolus. Stipes breviusculus, fistulosus, pileo concolor. Lamellae pliciformes, distantes, albidae vel luteolae, ramosae. Caro rubeola, odore C. cibarii. Sporae ellipsoideae,  $7-8 \times 4,5-5,5$  µm."

Original description (freely translated from French): "Pileus ca 1 cm diam., thin, soon depressed-concave with rounded-incurved and slightly lobed margin; surface glabrescent, reddish pink. Stipe  $10\text{-}20\times1$  mm, cylindrical, sometimes a bit flexuous or curved, narrowly fistulose (?), concolorous. Lamellae fold-like, spaced, narrow (0.5 mm), white with very faint yellow tinges, forked or unequal, subsmooth in between. Context reddish pink. Smell of *C. cibarius* when boiling a part of the exsiccatum. Spore print white. Exsiccatum entirely pale orange brown. Spores yellowish,  $7\text{-}8\times4.5\text{-}5.5~\mu\text{m}$ , shortly ellipsoid or a bit ovoid, finely rugose in ammonium, appearing inamyloid and smooth in Melzer's reagent; apiculus small. Basidia long, claviform, measuring  $53\times9$  for ex., at least four-spored. Pseudoparenchyma well characterized at least in the stipe."

*Holotype*: Democratic Republic of the Congo. district forestier central, Binga, oct. 1925, Mrs. Goossens-Fontana 946 (BR).

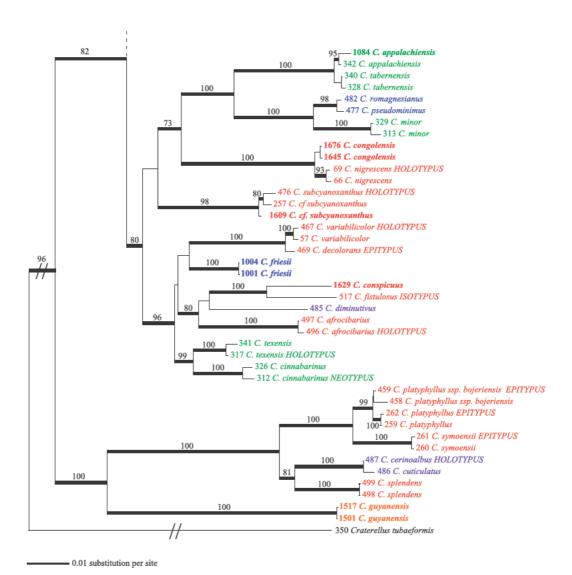
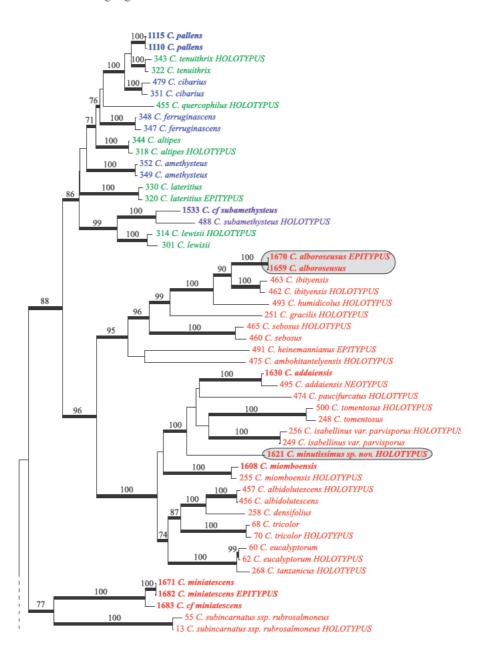
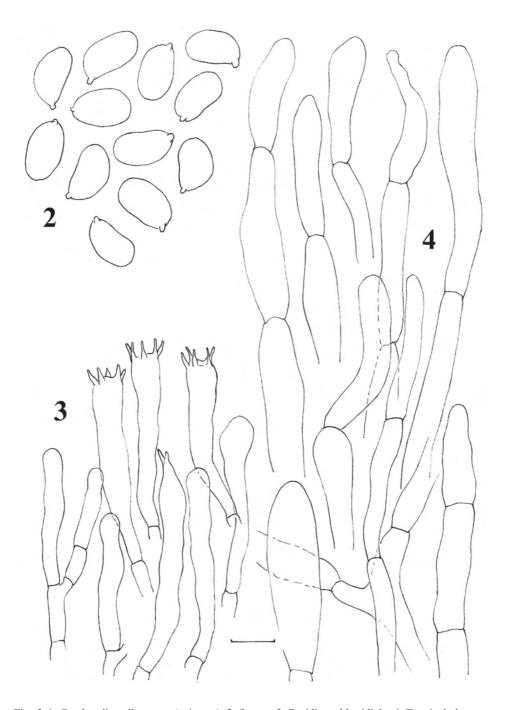


Fig. 1. Most likely tree (-ln = 22902.011) inferred from maximum likelihood (ML) analyses of the 96 taxa-4 loci dataset. Branches that received significant bootstrap values (MLbs ≥ 70%) are in bold with bootstrap values indicated along branches. Colors refer to geographic origin of the collections following Buyck *et al.* (2014), viz.: red = Africa+Madagascar, orange = South America, green = North America, blue = Europe, lilac = Asia.



0.01 substitution per site

Fig. 1. (continued)



Figs 2-4. *Cantharellus alboroseus* (epitypus). **2.** Spores. **3.** Basidia and basidiola. **4.** Terminal elements of the pileipellis. Scale bar =  $10 \mu m$  but  $5 \mu m$  for spores. (drawings B. Buyck).

# Epitype description

Fruiting bodies few, widely dispersed. Pileus 10-15 mm diam., convexplane to slightly depressed in the center, bright orange (5A8), hygrophanous and becoming pale pink when drying out, smooth, dull to waxy; cap margin remaining inrolled for a long time. Stipe up to 23 mm high, 2-3 mm diam., subcylindrical to slightly widening at the base, smooth, tinged with orange (5A3-5) but usually paler than cap, with yellowish tinges near the stipe base, solid inside. Hymenophore decurrent, composed of spaced, low veins (< 1 mm), unequal to sparsely forking, without interstitial anastomosing veins, not well delimited from the sterile stipe surface, off-white. Context thin, fibrous, distinctly staining pinkish red (6A3-4) when cut. Smell agreeable, fruity. Taste mild. Spore print not obtained, but certainly very pale.

*Examined material*: CENTRAL AFRICAN REPUBLIC. Dzanga-Sangha Forest Reserve, near Bayanga, in Bai-Hakou base camp, N 02.859934- E 16.467492, under monospecific upper story *Gilbertiodendron dewevrei* forest, on bare sandy soil, 21 May 2016, Buyck 16.086 (PC 0142441); ibid., Buyck 16.108 (PC 0142442, epitypus hic designatus).

Commentary: Our identification of the abovementioned collections is based on a comparison and evaluation of observed differences and similarities with the type specimens of the various species. The absence of clamp connections in our collections immediately excludes *C. tenuis*, which is unrelated to the other species (see introduction). Because of the very pale-coloured hymenophore of our collections, it is also possible to rapidly exclude *C. pseudofriesii*, which has also much smaller spores compared to the remaining two species. In contrast, the attribution of our collections to either *C. alboroseus* or *C. floridulus* appeared to be much more difficult, even though the identification key provided by Heinemann (1958) seems straightforward:

```
I. Gills crowded (20-25/cm), well differentiated; cap and stipe vermillon; spores 6.5-7.7 \times 4.5-5.6 \mu m C. floridula. II. Gills spaced (L+1:\pm 15 total), fold-like; cap and stipe reddish pink; spores 7-8 \times 4.5-5.5 \mu m C. alboroseus
```

Among the used criteria in this key, the size of spores is of little use and, the first author having a longstanding experience with the genus worldwide, also the subtle differences in color seem insignificant considering the enormous differences observed in most other "small red chanterelles" (Buyck in Ariyawansa *et al.* 2015, Buyck *et al.* 2016 this issue corralinus). This leaves only features of the hymenophore: crowded and well-differentiated versus spaced and vein-like. However, even the hymenophore configuration in *Cantharellus* is very variable as again illustrated in Buyck *et al.* (2016 this issue c.antillanus + miniatescens).

Due to the pity state of the type specimens (already noted by Heinemann), anatomical characters can hardly be exploited to distinguish between both types.

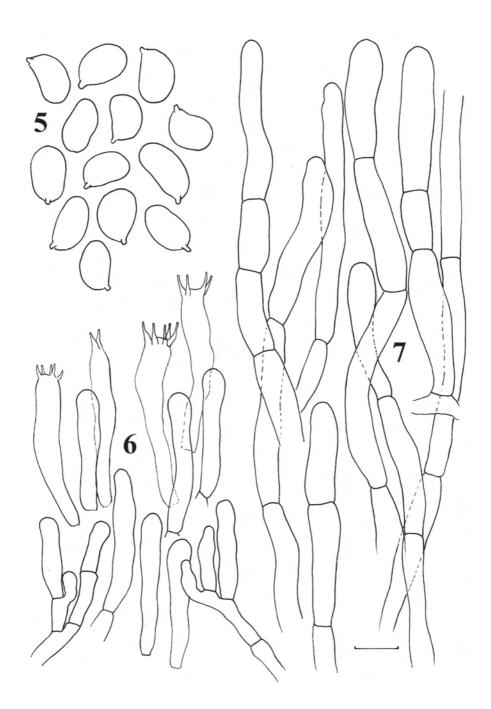
Table 2. Comparison of spore values and basidium size among the studied collections. Asterisk (*)
indicating measurements from holotype fide Eyssartier (2001)

	Basidium size	Spore length	Spore width	Length-width ratio
C. alboroseus Holotype	53×9 40-50 (55)×8-10*	7- <b>7.69</b> -9*	4 <b>-4.94</b> -5.5*	1.4- <b>1.56</b> -2.0*
C. alboroseus BB 16.108	$40-53 \times 7-8$	(6.9)7.1-7 <b>.39</b> -7.7(7.9)	(4.0)4.1 <b>-4.42</b> -4.7(5.0)	(1.4)1.56- <b>1.68</b> -1.80(1.9)
C. alboroseus BB 16.086	$40-55 \times 7-8$	(6.2)6.6- <b>6.93-</b> 7.3	(3.5)3.9- <b>4.18</b> -4.4(4.6)	(1.5)1.57 <b>-1.66</b> -1.75(1.9)
C. minutissimus Holotype	38-47×5-7	(6.0)6.2 <b>-6.80-</b> 7.4(8.1)	(3.5)3.9- <b>4.15</b> -4.4(4.6)	(1.36)1.48- <b>1.65</b> - 1.82(1.95)
C. floridulus Holotype	35×10	6- <b>6.68-</b> 7*	4 <b>-4.85</b> -5.5*	1.2- <b>1.38</b> -1.55*
C. floridulus Eyi Ndong 2011	28-34×7-9	(5.7)5.6- <b>6.5</b> -7.3(8.1)	(3.4)3.5-4.0-4.5(4.7)	1.4- <b>1.61</b> -1.8(1.9)

Does the above implicate then that both names refer to a single species? Perhaps... but not certain, as there exists at least one other, probably more important microscopical difference between both type specimens as also suggested by the identification in Eyi Ndong et al. (2011): C. floridulus has distinctly shorter basidia (Table 2). Yet, Eyi Ndong et al. point out a relatively important difference in cap size between their collection, i.e. 10-15 mm diam. (exactly as in C. alboroseus) versus the 40 mm diam. mentioned for the cap diam. in the type description of C. floridulus and attribute this divergence to the fact that Mrs. Goossens-Fontana forgot to mention that she had applied an exceptional enlargement of the original size when representing the type specimen in her watercolor, an explanation that seems a bit farfetched as no enlargement was used by the same artist to represent other, equally small chanterelles.

Finally, there is one feature that definitely argues in favor of *C. alboroseus* as the correct name for our collections: the original description (Heinemann 1958) mentions a "reddish pink context". For such small species, the reddish color of cap and stipe automatically influences the color of the context immediately underneath (as observed in nearly all chanterelles) and we initially assumed that the very small size of this species was responsible for the mention of "reddish pink context" as nearly all context is situated in such small species is situated immediately beneath the surface. However, our collections now demonstrate a clear reddish pink staining of the entire context. Such a color change is unique among all known species in section Heinemannianus and therefore constitutes probably the best feature to characterize this tiny chanterelle. The fistulose aspect of the stipe was mentioned with a question mark in the original description (see above) and does indeed correspond to our specimens which clearly have a solid stipe in the epitype collection (Fig. 8), but show a near-fistulose stipe in the second collection obviously due to injuries caused by insect larvae (Fig. 10). It is in our opinion a second important difference with the other species originally placed in sect. *Tenues*.

The use of statistics on spore measurements reveals no important differences, although *C. alboroseus* appears to have slightly longer spores compared to *C. floridulus*. Spore measurements for the holotype conform very well to the original



Figs 5-7. Cantharellus minutissimus (holotypus). 5. Spores. 6. Basidia and basidiola. 7. Terminal elements of the pileipellis. Scale bar =  $10~\mu m$  but  $5~\mu m$  for spores. (drawings B. Buyck).



Fig. 8. Cantharellus alboroseus (epitypus). Photo B. Buyck.



Fig. 9. Cantharellus alboroseus (epitypus). Showing progressive discoloring when drying out. Photo B. Buyck.



Fig. 10. Cantharellus alboroseus. (BB 16.086). Photo B. Buyck.



Fig. 11. Cantharellus minutissimus (holotypus).

description and also to the holotype measurements given by Eyssartier (2001), but are nearly identical to those for *C. minutissimus* (Table 2). The somewhat smaller spore size for our second collection (BB 16.086) is probably due to its more immature nature as we found only few mature spores.

There is, however, yet another aspect about these species that raises questions: both the first author's collections on specimens that resemble *C. floridulus* in size, as well as the collection illustrated by Eyi Ndong *et al.* (2011) for *C. floridulus* concern prolific fruitings, consisting of many fruiting bodies dispersed over a considerable surface of the soil, and belong to a species that is apparently not rare in the rain forest (the first author has seen hundreds of such fruitings in hardly two weeks of collecting). So why did Mrs Goossens-Fontana, who lived there for so many years, illustrate so few specimens and only made a single collection for these small species while she usually has several collections for other rain forest chanterelles? We will probably never have the answer to this question, but our collections for *C. alboroseus* suggest that this extremely small species is easily overlooked, particularly because it occurs mixed with these prolific fruitings and fruiting bodies could easily be mistaken for young, immature specimens of this larger species.

So, in conclusion, our collections from Central African Republic match the description of *C. alboroseus* in context color change, in size of fruiting bodies and basidia, in spacing and color of the hymenophore, but differ because of the slightly smaller spores (yet shorter than in *C. floridulus*) and the orange instead of reddish pink color of the fruiting bodies.

Our phylogenetic analyses (Fig. 1) now confirm the assumed placement of *C. alboroseus* in subg. *Rubrinus*, more precisely as sister-species to the Malagasy *C. ibityensis* Buyck & V. Hofstetter in sect. *Heinemannianus* Eyssart. & Buyck. Within this clade it is difficult to confuse it with the other already known species by the combination of its macro- and microscopic features – compare with species described in Buyck *et al.* 2013, 2015).

# Cantharellus minutissimus Buyck & V. Hofstetter, sp. nov. Figs 5-7, 11

Mycobank: MB 818372

Diagnosis: Differs from the equally small C. alboroseus in the absence of reddening context and slightly smaller spores, but even more in obtained sequence data from TEF-1, LSU, RPB2 and mitSSU, placing it in a different section of the genus.

Etymology: The name refers to its extremely small size, even compared to other small chanterelles.

*Holotypus*: Cameroon. Eastern region, Haut-Nyong Department, Somalomo Commune, Dja Biosphere Reserve, 641 m, N-3°19'53" E 12°45'25", in rainforest with *Uapaca* sp. on terra firma, 17 May 2014, legunt Annemieke Verbeken and Eske de Crop, EDC 14-281 (GENT, **holotypus**).

**Pileus** very small, less than 8 mm diam., triangular in lateral view, with an almost plane cap surface but slightly depressed in the center; surface pinkish red, smooth. **Stipe** very slender, 10-15 × 2mm, subcylindrical, concolorous or slightly paler than the cap surface, pinkish, fistulose. **Hymenophore** strongly decurrent, composed of surprisingly well-developed gill folds considering its small size, white. **Context** extremely thin, almost inexistent, white. **Taste** and **smell** not observed. **Spore print** certainly very pale (white?).

**Spores** narrowly ellipsoid,  $(6.0)6.2-6.80-7.4(8.1) \times (3.5)3.9-4.15-4.4(4.6)$  μm, Q = (1.36)1.48-1.65-1.82(1.95), smooth, with a short, relatively wide apiculus. **Basidia** rather short,  $38-47\times5-7$  μm, clavulate, (2-)4-5-spored; basidiola subcylindrical, not remarkable undulate nor wavy in outline. **Subhymenium** filamentous, with diam. of subhymenial cells equal to the basal part of the basidium. **Cystidia** none. **Pileipellis** composed of very loosely interwoven hyphae that are larger than these of the thin underlying context (mostly 2-4(5) μm thick) and subhymenium; hyphal extremities with frequent septa, thin-walled or walls refringent but never thick-walled, composed of subcylindrical cells, (5)6-9(12) μm diam.; the terminal cell obtuse rounded, of variable length, but mostly < 50 μm long. **Clamp connections** absent.

Commentary: Because of its extremely small size, this African Cantharellus can only be confused with the species described in sect. Tenues sensu Heinemann (1958). Because of the absence of clamps and the reddish pink color, the confusion can actually be narrowed down to either C. floridulus or C. alboroseus, but the specimen does not fit either description. It was a real surprise to find out that our phylogenetic analyses did not even place this species in the same section as C. alboroseus considering the obvious similarity of their microscopic features.

Acknowledgements. The first author thanks the ATM of the Paris' Museum and "l'Institut Ecologie et Environnement" (CNRS-INEE) for funding the field trip with Shelly Masi to Africa: Shelly is thanked for all the practical help and sharing her experience. Terence Fuh and the staff of the Primate Habituation Program of the Dzanga-Ndoki National Park of the "Réserve spéciale de Foret Dense de Dzanga-Sangha at Bayanga, as well as all staff, Aka guides and visitors of the Bai hakou field station for logistical support, field assistance and the very enjoyable company during our stay. This research was made possible through research permit 034/MENESR/DIRCAB/DGESRSTI/DRSTSPI/SSSTI/16 from the "Ministère de l'éducation nationale, de l'enseignement supérieur et de la recherche scientifique" of the Central African Republic. E. De Crop is supported by the "Special Research Fund Ghent University" (BOF, grant B/13485/01). The survey in Zambia was financially supported by the Research Foundation Flanders (FWO, grant K202014N). The survey in Cameroon and Togo was financially supported by the Research Foundation Flanders (FWO, grant V416214N) and by the Leopold III Fund. We would like to express our gratitude to André-Ledoux Njouonkou for his help during field work in Cameroon.A. De Kesel (BR, Belgium) is thanked for critically reading an earlier version of the manuscript. The Molecular Service of the Paris' Natural History Museum (USM2700) is thanked for assistance with procedures for sequencing.

#### REFERENCES

- ALFARO M., ZOLLER S. & LUTZONI F., 2003 Bayes or bootstrap? A simulation study comparing the performance of Bayesian Markov chain Monte Carlo sampling and bootstrapping in assessing phylogenetic confidence. *Molecular Biology and Evolution* 20: 255-266.
- ARIYAWANSA H.A., HYDE K.D., JAYASIRI S.C., BUYCK B., CHETHANA K.W.T., DAI D.Q., DAI Y.C., DARANAGAMA D.A., JAYAWARDENA R.S., LUCKING R., GHOBAD-NEJHAD M., NISKANEN T., THAMBUGALA K.M., VOIGT K., ZHAO R.L., LI G.J., DOILOM M., BOONMEE S., YANG Z.L., CAI Q., CUI Y.Y., BAHKALI A.H., CHEN J., CUI B.K., CHEN J.J., DAYARATHNE M.C., DISSANAYAKE A.J., EKANAYAKA A.H., HASHIMOTO A., HONGSANAN S., JONES E.B.G., LARSSON E., LI W.J., LI O.R., LUO Z.L., MAHARACHCHIKUMBURA S.S.N., MAPOOK MCKENZIE E.H.C., NORPHANPHOUN C., KONTA S., PANG K.L., PERERA R.H., PHOOKAMSAK R., PHUKHAMSAKDA C., PINRUAN U., RANDRIANJOHANY E., SINGTRIPOP C., TANAKA K., TIAN C.M., TIBPROMMA S., ABDEL-WAHAB M.A., WANASINGHE D.N., WIJAYAWARDENE N., ZHANG J.F., ZHANG H., ABDEL-AZIZ F.A., WEDIN M., WESTBERG M., AMMIRATI J.F., BULGAKOV T.S., LIMA D.X., CALLAGHAN T.M., CALLAC P., CHANG C.H., COCA L.F., DAL-FORNO M., DOLLHOFER V., FLIEGEROVA K., GREINER K., GRIFFITH G.W., HO H.M., HOFSTETTER V., JEEWON R., KANG J.C., WEN T.C., KIRK P.M., KYTÖVUORI I., LAWREY J.D., XING J., LI H., LIU Z.Y., LIU X.Z., LIIMATAINEN K., LUMBSCH H.T., MATSUMURA M., MONCADA B., NUANKAEW S., PARNMEN S., DE AZEVEDO SANTIAGO A.L.C.M., SOMMAI S., SONG Y., DE SOUZA C.A.F., DE SOUZAMOTTA C.M., SU H.Y., SUETRONG S., WANG Y., WEI S.F., WEN T.C., YUAN H.S., ZHOU L.W., RÉBLOVÁ M., FOURNIER J., CAMPORESI E., LUANGSA-ARD J.J., TASANATHAI K., KHONSANIT A., THANAKITPIPATTANA D., SOMRITHIPOL S., DIEDERICH P., MILLANES A.M., COMMON R.S., STADLER M., YAN J.Y., LI X.H., LEE H.W., NGUYEN T.T.T., LEE H.B., BATTISTIN E., MARSICO O., VIZZINI A., VILA J., ERCOLE E., EBERHARDT U., SIMONINI G., WEN H.A. & CHEN X.H., 2015 — Fungal Diversity Notes 111-252: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 75: 1-197.
- BOA E., 2004 Wild edible fungi. A global overview of their use and importance to people. *Non-wood forest products*. 17. FAO, Rome.
- BUYCK, B., 2012a. One neo- and four epitypifications in *Cantharellus* from tropical African savannah woodland. *Cryptogamie, Mycologie* 33(1): 11-17.
- BUYCK B., EYSSARTIER G. & KIVAISI A., 2000 Addition to the inventory of the genus *Cantharellus* (Basidiomycotina, Cantharellaceae) in Tanzania. *Nova Hedwigia* 71(3/4): 491-502.

- BUYCK B., HENKEL T.W., DENTINGER B.T.M., SÉNÉ O. & HOFSTETTER V., 2016a Multigene sequencing provides a suitable epitype, barcode sequences and a precise systematic position for the enigmatic, African Cantharellus miniatescens. Cryptogamie Mycologie 37(3): 269-282.
- BUYCK B., KAUFF F., COULOUX A. & HOFSTETTER V., 2013 Molecular evidence for novel Cantharellus (Cantharellales, Basidiomycota) from tropical African miombo woodland and a key to all tropical African chanterelles. Fungal Diversity 58: 281-298.
- BUYCK B., KAUFF F., EYSSARTIER G., COULOUX A. & HOFSTETTER V., 2014 A multigene world phylogeny for Cantharellus. Fungal Diversity 64: 101-121.
- BUYCK B., KAUFF F., RANDRIANJOHANY E. & HOFSTETTER V., 2015 Sequence data reveal a high diversity of endemic Cantharellus associated with native vegetation in Madagascar. Fungal Diversity 70(1): 189-208.
- BUYCK B., MOREAU P.-A., COURTECUISSE R., ROY M., KONG A. & HOFSTETTER V., 2016b - Cantharellus coccolobae sp. nov. and Cantharellus garnieri, two tropical members of Cantharellus subg. Cinnabarinus. Cryptogamie, mycologie 37(3): 391-403.
- BUYCK B., RANDRIANJOHANY E. & HOFSTETTER V., 2016c Almost one century later...
- *Cantharellus avellaneus* finally rediscovered! *Cryptogamie, mycologie* 37(3): 259-268. DE KESEL A., AMALFI M., KASONGO B., YOROU N.S., RASPÉ O., DEGREEF J. & BUYCK B., 2016 — New and interesting Cantharellus from tropical Africa. Cryptogamie, Mycologie 37(3): 283-327
- DE KESEL A., CODJIA J.T.C. & YOROU S.N., 2002 Guide des champignons comestibles du Benin. Centre International d'Ecodeveloppement Integre (CECODI). Coco-Multimedia, Cotonou, Republique du Benin. Jardin Botanique National de Belgique, Meise.
- EYI NDONG H.E., DEGREEF J. & DE KESEL A., 2011 Champignons comestibles des forêts denses d'Afrique Centrale. Taxonomie et identification. ABC Taxa 10, 253 pp. Brussels.
- EYSSARTIER G., 2001 Vers une monographie du genre Cantharellus Adans.:Fr. 259 p. Dissertation, National History Museum, Paris.
- EYSSARTIER G. & BUYCK B., 1998 Contribution à la systematique du genre Cantharellus en Afrique tropicale: étude de quelques espèces rouges. Belgian Journal of Botany 131(2): 139-149.
- EYSSARTIER G. & BUYCK B., 2001 Novitates. Note nomenclaturale et systématique sur le genre Cantharellus. Documents Mycologiques 31(121): 55-56.
- GUINDON S. & GASCUEL O., 2003 A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Systematic Biology 52(5): 696-704.
- HÄRKÖNEN M., NIEMELA T. & MWASUMBI L., 2003—Tanzanian mushrooms. Edible, harmful and other fungi. Norrlinia 10: 1-200.
- HÄRKÖNEN M., ŠAARIMÄKI T. & MWASUMBI L., 1995 Edible mushrooms of Tanzania. Karstenia 35 suppl., 52 pp.

  HEINEMANN P., 1958 — Champignons récoltés au Congo Belge par Madame Gossens-Fontana.
- III. Cantharellineae. Bulletin du jardin botanique de l'État Bruxelles 28: 385-438.
- HEINEMANN P., 1959 Cantharellineae. Flore iconographique des champignons du Congo 8: 153-165, pl. 26-28.
- KORNERUP A. & WANSCHER J.H., 1978 Methuen handbook of colour. 3rd ed. London: Methuen & Co. Ltd. 252 pp, 30 pl.
- LIO, P. & GOLDMAN N., 1998 Models of molecular evolution and phylogeny. Genome Research 8: 1233-1244.
- MADDISON D.R. & MADDISON W.P., 2002 MacClade: Analysis of Phylogeny and Character Evolution. (Sinauer, Sunderland, v. 4.05).
- POSADA D. & CRANDALL K. A., 1998 ModelTest: testing the model of DNA substitution. Bioinformatics 14: 817-818.