

# *Caudicicola gracilis* (Polyporales, Basidiomycota), a new polypore species and genus from Finland

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A new monotypic polypore genus, *Caudicicola* Miettinen, Kotir. & Kulju, is described for the new species *C. gracilis* Kotir., Kulju & Miettinen. The species was collected in central Finland from *Picea abies* and *Pinus sylvestris* stumps, where it grew on undersides of stumps and roots. *Caudicicola gracilis* is characterized by very fragile basidiocarps, monomitic hyphal structure with clamps, short and wide tramal cells, smooth ellipsoid spores, basidia with long sterigmata and conidiogenous areas in the margins of the basidiocarp producing verrucose, slightly thick-walled conidia. The genus belongs to the residual polyporoid clade of the Polyporales in the vicinity of Steccherinaceae, but has no known close relatives.

## Introduction

The species described here was found when Heino Kulju, the brother of the second author, was making a forest road for tractors. To make way for the road, pine and spruce stumps, cut in 1997 but still relatively hard, were grubbed up. Fruiting bodies of several species of polypores were growing on the undersides of the stumps and roots, and Heino Kulju brought samples of them to his brother for identification. The lifted stumps were colonized by poroid species such as *Trechispora hymenocystis*, *Porpomyces mucidus*, *Physisporinus vitreus*, and such less common corticioid species as *Chaetoporellus curvisporus* and *Jaapia ochroleuca*. Fallen spruce trunks at the same site harbored species such as *Meruliop-*

*sis taxicola*, *Pycnoporellus fulgens* and its successional predecessor *Fomitopsis pinicola*, and deciduous tree trunks had such seldom collected species as *Athelopsis glaucina* (on *Salix*) and *Ceraceomyces violascens* (on *Betula*).

Among the polypores collected from the underside of the stumps and their roots were also white, effused polypore specimens that the second author could not identify to any existing species, so he sent them to the first author who examined them and sent them further to the third author. Since none of the experts at the Finnish Museum of Natural History could identify them either, even to the genus, they were subjected to DNA analysis, which proved that the species was indeed unique.

## Material and methods

### Microscopy

Thirty spores per specimen were measured in Cotton Blue (CB) using phase contrast illumination and oil immersion with a subjective accuracy of 0.1  $\mu\text{m}$  (see Miettinen et al. 2006). Other mounting media used were Melzer's reagent (IKI), Cresyl Blue (CRB) and 5% potassium hydroxide (KOH). The following spore and conidium dimensions are reported:  $L$  = mean length,  $W$  = mean width,  $Q'$  = range of the variation in length-to-width ratio,  $Q$  = mean length-to-width ratio ( $L/W$  ratio). Conidium and spore measurements (length and width) are given as the whole range (in parentheses) and 90% range excluding 5% extreme values from both ends is given outside parentheses; when both values are identical, parentheses are omitted. None of the measurements is from spore prints.

Besides the geographical co-ordinates the biological province and collecting site are indicated also according to the Finnish national uniform grid system (27°E), applied to biological material by Heikinheimo and Raatikainen (1981). The nomenclature of fungi follows Kotiranta et al. (2009).

### Specimens examined

*Caudicicola gracilis*, see type specimens cited below. — *Hypochnicium bombycinum*. **Finland**. Kuusamo: Taivalkoski, Riihilehto, *Populus tremula*, 30 September 2004 Miettinen 9441 (H). — *Radulodon erikssonii*. **Norway**. Akershus: Asker, Brønnøya SØ, Slottsveien, *Malus pumila*, 28 October 2009 Hofton 09820 (O). — *Spongipellis delectans*. **China**. Liaoning: Anshan, Qianshan park, *Quercus*, 26 September 1998 Dai 3041 (H). — *Spongipellis spumea*. **Finland**. Uusimaa: Espoo, Träskända park, on *Acer platanoides*, 27 October 2005 Oksanen 100 (H).

### DNA extraction and phylogenetic analysis

We produced 5 new nuclear ribosomal DNA internal transcribed spacer (ITS) sequences, 5 large subunit (nLSU, 28S) sequences, 4 mitochondrial small subunit (mtSSU) sequences, 4 ATP synthase 6 (*atp6*) sequences, and 1 RNA

Polymerase II Largest Subunit (*rpb1*) sequence. They have been deposited in INSDC (Cochrane et al. 2016; see also Table 1). We also used sequences of 50 specimens retrieved from INSDC (Table 1). They were chosen based on similarity searches and the results in Miettinen et al. (2012), Binder et al. (2013) and Zhao et al. (2014). DNA was extracted using an E.Z.N.A. forensic DNA kit (Omega Bio-Tek, Norcross, GA, USA) or a DNeasy plant mini kit (Qiagen, Hilden, Germany). PCR primers included ITS1F, ITS5, ITS1, ITS4 and LR22 for ITS; CTB6, LR0R and LR7 for the partial nLSU; MS1 and MS2 for mtSSU (White et al. 1990, <http://biology.duke.edu/fungi/mycolab/primers.htm>); ATP6-2 and ATP6-3 for *atp6* (Kreutzer & Bruns 1999), and RPB1-Af and RPB1-Cr for *rpb1* (Matheny et al. 2002). Sequencing primers were the same with the addition of primers LR5 and LR3R for nLSU and RPB1-Int2.2f (Binder et al. 2009) for *rpb1*.

A concatenated data set of the residual polyporoid clade of the Polyporales was constructed containing 55 species and five loci (ITS, partial nLSU, partial mtSSU, partial *rpb1* and partial *atp6*). Phylograms were built for the concatenated data set as well as each of the loci separately. The ITS data set contained 53 species, 226 characters of which 52 parsimony informative after excluding apparently non-homologous characters from the alignment (5.8S: 156 characters, 16 parsimony informative; ITS1 + ITS2: 70 characters, 36 parsimony informative). LSU data set had 55 species, 979 characters of which 209 parsimony informative, mtSSU data set 34 species, 527 characters of which 168 parsimony informative, *atp6* data set 25 species, 633 characters of which 260 parsimony informative, *rpb1* data set 20 species, 1079 characters of which 383 parsimony informative, and concatenated data set 55 species, 3444 characters of which 1072 parsimony informative.

Sequences were aligned using MAFFT online version 7.244 with the strategy E-INS-I (<http://mafft.cbrc.jp>; Katoh & Standley 2013) and adjusted manually using PhyDE 0.9971 (see <http://phyde.de>). Numbers of informative characters were calculated in MEGA6 (Tamura et al. 2013). Trees were rooted based on information from Binder et al. (2013). In the case of the con-

**Table 1.** INSDC accession numbers for DNA sequences used in this study. Specimens provided with collector and collection number information were sequenced for this study, the rest retrieved from the INSDC database. Province/state abbreviations follow Guobiao standards for China and ISO 3166 for other countries.

Species	Collector, coll. no. (herbarium)	Country (province/state)	ITS	LSU	mtSSU	ATP6	RPB1
<i>Abortiporus biennis</i>		USA	KP135300	KP135195			KP134783
<i>Antella americana</i>		USA (TN)	KP135316	KP135196			KP134885
<i>Antrodiella pallenscens</i>		Sweden	JN710518	JN710518	JN710661	JN710612	
<i>Antrodiella semisupina</i>		USA (MA)	KP135314	KP135197			KP134886
<i>Bulbillomyces farinosus</i>		Spain	DQ681201	DQ681201			
<i>Butyrea japonica</i>		Japan	JN710556	JN710556	JN710680	JN710629	KP134887
<i>Butyrea luteoalba</i>		USA (MD)	KP135320	KP135226			KY415972
<i>Caudicicola gracilis</i>	Heino Kulju 15/14 (H 6013927), holotype	Finland	KY415962	KY415962	KY415967	KY415970	
<i>Ceriporiopsis consobrina</i>		Finland	FJ496663	FJ496715	FJ496745		
<i>Cerrena unicolor</i>		Sweden	JN710525	JN710525	JN710663	JN710614	
<i>Cerrena unicolor</i>		USA (MA)	KP135304	KP135209			KP134874
<i>Citripora afroctrina</i>		Uganda	JN710507	JN710507	JN710655		
<i>Climacocystis borealis</i>		USA (MA)	KP135308	KP135210			KP134882
<i>Cymatoderma caperatum</i>		Venezuela	JN710529	JN710529	JN710666	JN710617	
<i>Diplomitoporus crustulinus</i>		USA (MA)	KP135299	KP135211			KP134883
<i>Etheirodon fimbriatum</i>		Sweden	JN710530	JN710530	JN710667	JN710618	
<i>Fibricium subceraceum</i>		Germany	JN710531	JN710531	JN710668	JN710619	
<i>Flaviporus cf. brownii</i>		Australia	JN710538	JN710538	JN710670	JN710620	
<i>Flaviporus sp.</i>		Brazil	JN710542	JN710542	JN710671		
<i>Hyphoderma granuliferum</i>		Costa Rica	JN710545	JN710545	JN710673	JN710622	
<i>Hyphoderma litschaueri</i>		USA	KP135295	KP135219			KP134868
<i>Hyphoderma medioburicense</i>		USA	KP135298	KP135220			KP134869
<i>Hyphoderma mutatum</i>		USA	KP135296	KP135221			KP134870
<i>Hyphoderma setigerum</i>		USA	KP135297	KP135222			KP134871
<i>Hypochnicium bombycinum</i>	Otto Miettinen 9441 (H)	Finland	KY415959	KY415959	KY415965		
<i>Hypochnicium polonense</i>		Russia	EU118635	EU118635			
<i>Hypochnicium subigescens</i>		Norway	JN710546	JN710546	JN710674	JN710623	
<i>Ischnoderma resinosum</i>		USA (MD)	KP135303	KP135225			KP134884
<i>Junghuhnia crustacea</i>		Indonesia (SB)	JN710553	JN710553	JN710678	JN710627	
<i>Loweomyces fractipes</i>		USA (NY)	JN710569	JN710569	JN710689		
<i>Meripilus giganteus</i>		United Kingdom	KP135307	KP135228			KP134873
<i>Meripilus giganteus</i>				AF287874	U27053	EU339259	
<i>Metuloides cf. murashkinskyi</i>		China (YN)	JN710586	JN710586	JN710698		

continued

Table 1. Continued.

Species	Collector, coll. no. (herbarium)	Country (province/state)	ITS	LSU	mtSSU	ATP6	RPB1
<i>Mycorrhaphium adustum</i>		USA (TN)	JN710573	JN710573	JN710692	JN710640	
<i>Panus conchatus</i>		Finland	JN710579	JN710579	JN710695	JN710643	
<i>Panus lecomtei</i>		USA (AZ)	KP135328	KP135233			KP134877
<i>Physisporinus sanguinolentus</i>		Slovakia	FJ496671	FJ496725	FJ496750		
<i>Physisporinus vitreus</i>		Norway	JN710580	JN710580	JN710696	JN710644	
<i>Podoscypha bolleana</i>		Central African Republic	JN649354	JN649354			
<i>Podoscypha multizonata</i>		Germany	JN710581	JN710581	JN710697	JN710645	
<i>Podoscypha petaloides</i>		Puerto Rico	AF518639	AF518639	AF518688		
<i>Podoscypha venustula</i>		Venezuela	JX109851	JX109851			
<i>Podoscypha vespillonea</i>			JN649368	JN649368			
<i>Pouzarporia subrufa</i>		Czech Republic	FJ496662	FJ496724	FJ496751		
<i>Radulodon erikssonii</i>	Tom Helliik Hofton 09820 (O)	Norway	KY415963	KY415963	KY415964	KY415971	
<i>Rickiopora latemarginata</i>		Brazil	KU521770	KU521770			
<i>Spongipellis delectans</i>		USA (MI)	KP135301	KP135287			KP134876
<i>Spongipellis delectans</i>		China (LN)	KY415961	KY415961	KY415966	KY415969	
<i>Spongipellis pachyodon</i>	Yu-Cheng Dai 3041 (H)	USA	DQ249277	AY629322	AFTOL705	EU339271	
<i>Spongipellis pachyodon</i>		USA (MA)	KP135302	KP135288			KP134875
<i>Spongipellis spumea</i>		Finland	KY415960	KY415960		KY415968	
<i>Steccherinum collabens</i>	Marjukka Oksanen 100 (H)	Sweden	JN710552	JN710552	JN710677	JN710626	
<i>Steccherinum fimbriatellum</i>		Russia (LEN)	JN710555	JN710555	JN710679	JN710628	
<i>Steccherinum litschaueri</i>		Russia (NIZ)	JN710587	JN710587	JN710699	JN710646	
<i>Steccherinum nitidum</i>		USA (MD)	KP135323	KP135227			KP134888
<i>Steccherinum ochraceum</i>		Sweden	JN710589	JN710589	JN710700	JN710647	
<i>Steccherinum sp.</i>		USA (MA)	KP135322	KP135289			KP134889
<i>Xanthoporus syringae</i>		China	AY789078	AY684166	AFTOL774	EU339242	AY788846

catenated, ITS, LSU and RPB1 data sets we used *Ischnoderma resinotum*, which is outside the residual polyporoid clade. We rooted mtSSU and *atp6* data sets with *Hyphoderma granuliferum* since no sequence data for *I. resinotum* were available.

MrBayes 3.2 (Ronquist *et al.* 2012) was used for inferring Bayesian consensus trees. The LSU and *rpb1* data sets were partitioned as follows: ITS1 and ITS2 in one partition, 5.8S and LSU in another, and *rpb1* separately. The nucleotide substitution model GTR + I + G was used for all partitions, chosen based on the AIC scoring produced in *jmodeltest* 2.1.6 (Darriba *et al.* 2012). Bayesian analyses were run with eight chains in three parallel runs, temp = 0.1. Single-locus data sets were run for 4 million generations sampling every 2000 generations. The concatenated data set was run for 6 million generations sampling every 2500 generations. All runs converged to below 0.01 average standard deviation of split frequencies. A burn-in of 25% was used before computing the consensus tree. The alignments and phylogenies are available in TreeBase (<http://purl.org/phylo/treebase/phyloids/study/TB2:S20389>).

## Results

Our phylogenetic analyses place *Caudicicola gracilis* in the residual polyporoid clade. Depending on the genetic locus, *Caudicicola* is within Steccherinaceae (mitochondrial genes mtSSU and *atp6*), a sister to the rest of the Steccherinaceae (*rpb1*) or its position remains unresolved within the residual polyporoid clade (ITS, LSU). The concatenated data set places *Caudicicola* as a sister to the Steccherinaceae clade with good support (Fig. 1). For now the best family placement for *Caudicicola* is in Steccherinaceae, where it has no close relatives.

## Taxonomy

***Caudicicola* Miettinen, Kotir. & Kulju, gen. nov.**

MB 819547. — ETYMOLOGY: *Caudicicola* (Latin) from *caudex* = stump or trunk, and *cola* = where the fungus lives

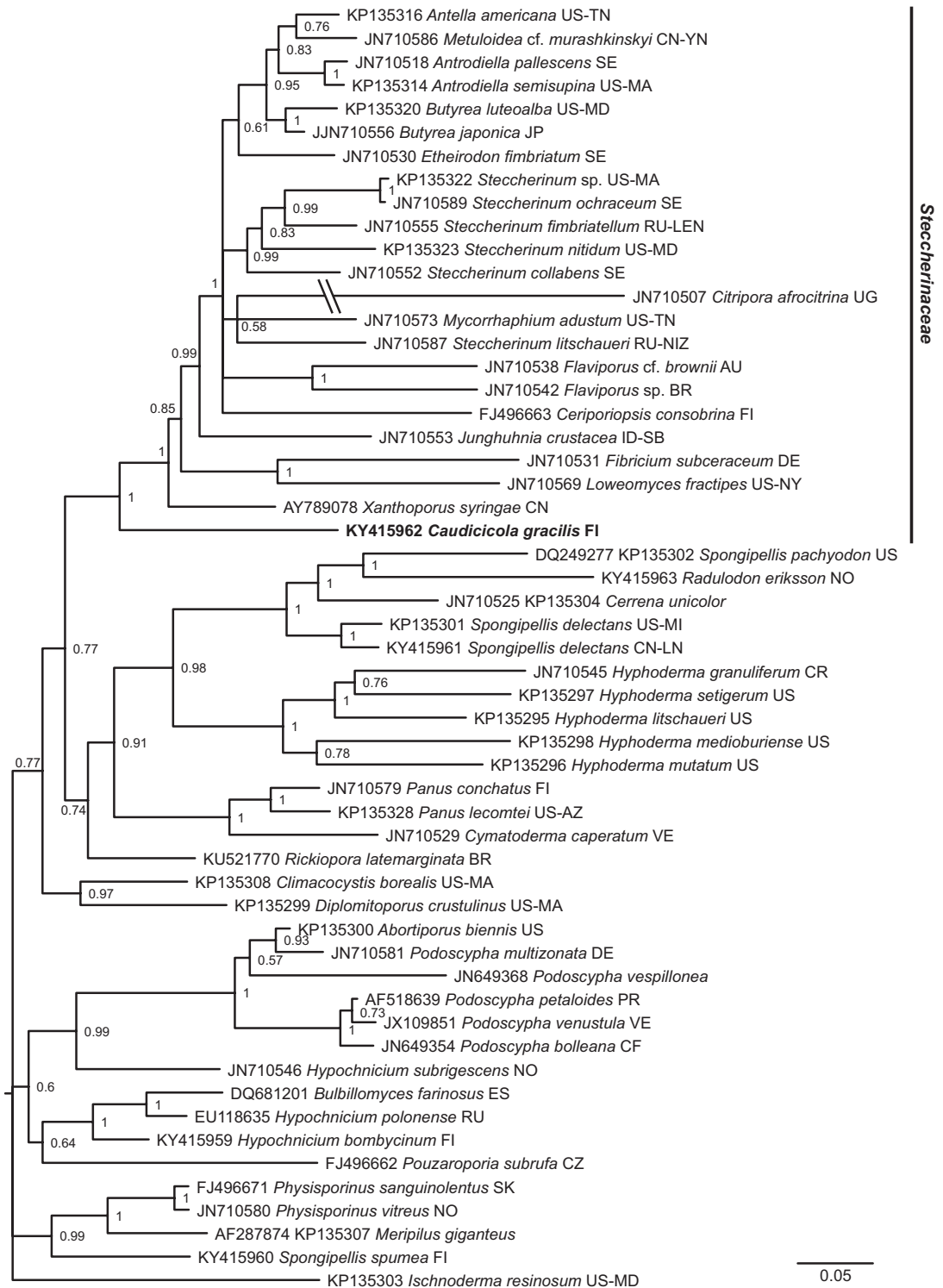
Basidiocarp white, resupinate, very fragile, poroid, hyphal system monomitic, clamped, partly with ampullaceous-looking septa. Basidia subcylindrical with long sterigmata and born on bladder-like large cells. Spores ellipsoid, small, smooth.

***Caudicicola gracilis* Kotir., Kulju & Miettinen, sp. nova** (Figs. 2 and 3, Tables 2 and 3)

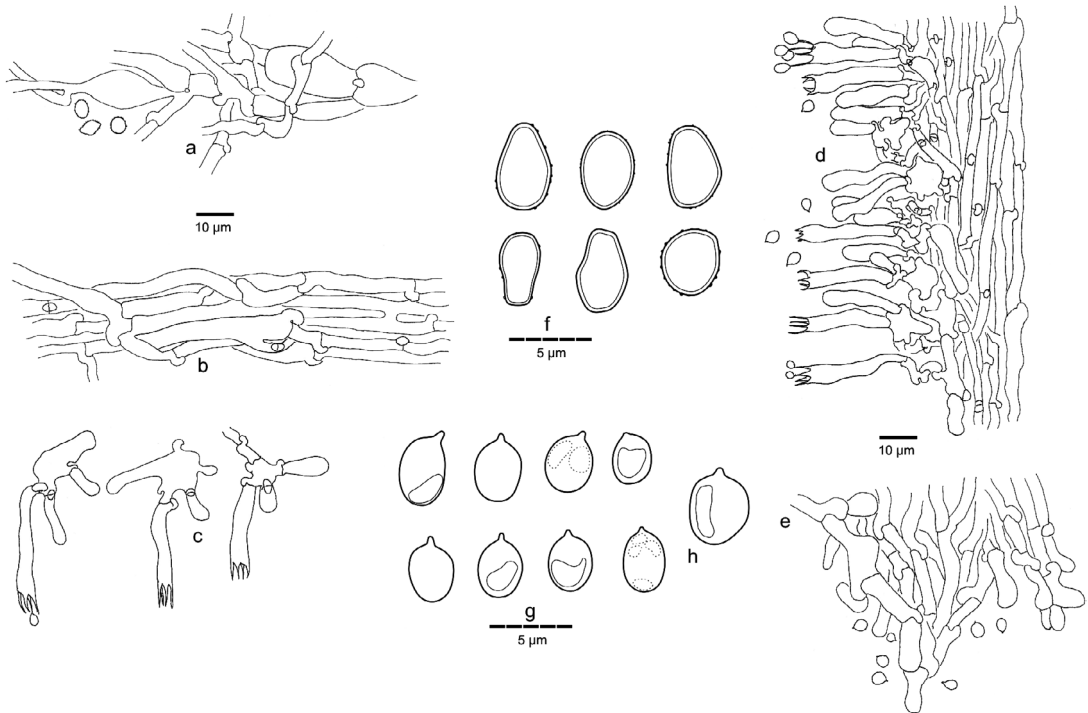
MB 819548. — HOLOTYPE: Finland. Keski-Pohjanmaa: Pyhäjärvi, Jokikylä, Varpusuo, *Picea abies* dominated swampy forest, on *Picea abies* stump, alt. 146 m a.s.l., 63°45'N, 25°58'E (grid 27°E 707253:344988), 6 October 2014 *H. Kulju* 15/14 (H 6013927; isotype OULU). — PARATYPES: Finland. Keski-Pohjanmaa: Pyhäjärvi, Jokikylä, Varpusuo, *Picea abies* dominated swampy forest, alt. 146 m a.s.l., 63°45'N, 25°58'E (grid 27°E 707253:344988), 18 October 2014 on *Picea abies*, *H. Kulju* 14/14 (OULU, H), on *Pinus sylvestris*, *H. Kulju* 16/14 (OULU, H), on *Picea abies*, *H. Kulju* 17/14 (OULU, H), 20 October 2014, on coniferous stump, *H. Kulju* 13/14 (OULU, H), 9 September 2015 on *Picea abies*, *M. Kulju* 48/15, *H. Kulju* & *P. Helo* (OULU).

ETYMOLOGY: *gracilis* (Latin) = fragile.

Basidiocarp annual, resupinate, very fragile, pale creamish white or pale yellow when dry, total thickness up to 2.5 mm, with a very thin white subiculum, pores angular, 3–4 per mm, after drying partly shrinking and partly widening, up to 1 mm, with thin, partly lacerate dissepiments. Old fruit bodies have sometimes pulverulent areas at margin, which contain masses of conidia, but no rhizomorphs. No particular smell observed, taste mild. Hyphal system monomitic, hyphae relatively thin-walled, CB–, IKI–, CRB lilac. Subiculum consists of narrow hyphal strands and loosely arranged randomly orientated hyphae (2.5)3–5  $\mu\text{m}$  wide, mostly with normal clamps, but ampullaceous, up to 10  $\mu\text{m}$  wide septa fairly common as well as hyphae 9–11(15)  $\mu\text{m}$  wide; conidiogenous hyphae double walled, in some parts of subiculum common; tramal hyphae subparallel, 2.5–3.5  $\mu\text{m}$  wide, clamped, with a few ampullaceous septa and vesicle-looking cells 8–15  $\mu\text{m}$  in diam.; dissepimental hyphae often, but not always, wide, winding, up to 9  $\mu\text{m}$ ; subhymenial hyphae mostly originate from large, often roundish cells, 8–18  $\mu\text{m}$  in diam., with some protuber-



**Fig. 1.** Phylogeny of the residual polyporoid clade of the Polyporales. Bayesian consensus tree based on ITS, nLSU, mtSSU, *atp6* and *rpb1* sequences. Numbers denote posterior probabilities.



**Fig. 2.** Microscopy of *Caudicicola gracilis*. — **a**: Subicular hyphae with ampullaceous septa, wide hyphae and conidia. — **b**: Subicular strand with ampullaceous septa. — **c**: Bladder-like cells which give rise to basidioles and basidia. — **d**: Section trough trama and hymenium showing the bladder-like cells in subhymenium, basidia and spores. — **e**: Dissepiment edge with wide hyphae. — **f**: Conidia. — **g**: Basidiospores (from the holotype).

ances, thin-walled, richly clamped and branched, 2–3  $\mu\text{m}$  wide. Cystidia and cystidioles absent. Hymenial cells with inclusion that stains in IKI and CB, gloecystidia-looking. Basidia basally clamped (normally), subcylindrical, (15)20–28  $\times$  4.5–5  $\mu\text{m}$ , with (2)4 sterigmata, which are exceptionally long, typically 5  $\mu\text{m}$  but even up

to 8  $\mu\text{m}$ . Spores smooth, subglobose, broadly ellipsoid or pip-shaped, fairly thin-walled, with a relatively large apiculus, commonly with one or many shiny, irregular bodies inside, CB–, IKI–, 3.0–4.1(4.5)  $\times$  (2.1)2.3–3.1(3.6)  $\mu\text{m}$ ,  $L = 3.50 \mu\text{m}$ ,  $W = 2.69 \mu\text{m}$ ; conidia ellipsoid, often broadly fusiform, reminding a protozoan

**Table 2.** Spore dimensions of the studied *Caudicicola gracilis* specimens.  $L$  = mean length,  $W$  = mean width,  $Q'$  = range of the variation in length-to-width ratio,  $Q$  = mean length-to-width ratio ( $L/W$  ratio),  $n$  = number of measured spores. Length and width are given as the whole range (in parentheses) and 90% range excluding 5% extreme values from both ends is given outside parentheses; when both values are identical, parentheses are omitted.

	Length	$L$	Width	$W$	$Q'$	$Q$	$n$
<i>Caudicicola gracilis</i>	3.0–4.1(4.5)	3.50	(2.1)2.3–3.1(3.6)	2.69	1.1–1.5(1.7)	1.30	211*
Holotype	(3.0)3.1–4.2	3.54	(2.2)2.4–3.0(3.2)	2.78	1.1–1.5(1.6)	1.28	61
<i>H. Kulju 13/14</i>	3.0–4.0(4.3)	3.44	2.2–2.8(2.9)	2.50	(1.1)1.2–1.7	1.38	30
<i>H. Kulju 14/14</i>	3.0–4.0(4.2)	3.64	(2.1)2.2–3.4(3.5)	2.70	1.1–1.7	1.35	30
<i>H. Kulju 16/14</i>	(3.4)3.5–4.2(4.5)	3.81	2.5–3.4(3.6)	2.87	1.1–1.5	1.32	30
<i>H. Kulju 17/14</i>	3.0–3.6(3.7)	3.30	(2.2)2.3–2.8(3.0)	2.55	1.1–1.5	1.29	30
<i>M. Kulju 48/15</i>	3.0–3.8(4.0)	3.21	(2.2)2.3–3.0(3.1)	2.65	1.1–1.4(1.6)	1.21	30

\* from all specimens listed below.



**Fig. 3.** Mature basidiome of *Caudicicola gracilis* on *Picea abies* stump. Photographed *in situ* by Pekka Helo. Specimen Kulju, M. 48/15, Kulju, H. & Helo, P (OULU).

ciliate, slightly thick-walled, finely ornamented or more rarely smooth, CB+, IKI–, (4.0)4.5–7.0(8.0) × (2.7)3.0–4.5(5.2) μm,  $L = 5.44$  μm,  $W = 3.60$  μm.

**HABITAT ECOLOGY AND DISTRIBUTION:** Found only in one location in central Finland. Its habitat was a boreal wooded, drained minerotrophic

mire. The dominant tree species was spruce (*Picea abies*) intermixed with pine (*Pinus sylvestris*), birches (*Betula* spp.) and some willows (*Salix* spp.). The site was selectively cut about 20 years earlier, but has otherwise no intensive forest management history. The ground vegetation consists of mosses, *Dryopteris carthusiana* and *Equisetum sylvaticum*, and in dryer places of *Vaccinium vitis-idaea*. Basidiocarps grew on the underside of spruce and pine stumps and their roots, so basically underground. *Caudicicola gracilis* is apparently a wood- or litter decomposer, since there are no mycorrhizal species in Steccherinaceae or in Polyporales (Hibbett *et al.* 2014).

The basidiocarps of *C. gracilis* mostly resemble those of *Trechispora hymenocystis*, which, however, has normally hyphal cords at the margins (see Niemelä 2016: 374). Also *Anomoporia kamtschatica* is very similar looking in being white and fragile. *Oligoporus sericeomollis* is as well relatively similar even if not so fragile, and when fresh, it has a strong pungent smell and the taste is very bitter.

Microscopically the ampullaceous septa, especially in subicular cords, resembles those of *Porpomyces mucidus* and many *Trechispora* species, whereas the subcylindrical basidia are almost like those in the genus *Ceraceomyces*. If the ampullate septa are really homologous with the similar looking septa in e.g. *Trechispora* is not confirmed. Small spores are often pip-shaped and many have the shape of the spores of *Sistotrema muscicola*. The number of conidia varies; in some specimens they are few, in some others quite numerous and the shape varies from ellipsoid to broadly fusiform and in rare cases some

**Table 3.** Conidium dimensions of the studied *Caudicicola gracilis* specimens.  $L$  = mean length,  $W$  = mean width,  $Q'$  = range of the variation in length-to-width ratio,  $Q$  = mean length-to-width ratio ( $L/W$  ratio),  $n$  = number of measured conidia. Length and width are given as the whole range (in parentheses) and 90% range excluding 5% extreme values from both ends is given outside parentheses; when both values are identical, parentheses are omitted.

	Length	$L$	Width	$W$	$Q'$	$Q$	$n$
<i>Caudicicola gracilis</i>	(4.0)4.5–7.0(8.0)	5.44	(2.7)3.0–4.5(5.2)	3.60	(1.1)1.2–1.9(2.1)	1.51	130*
Holotype	(4.3)4.5–7.1(8.0)	6.03	(2.7)3.3–5.0(5.2)	4.04	(1.1)1.2–1.9(2.0)	1.49	40
H. Kulju 14/14	(4.4)4.5–5.7	4.94	(2.8)3.0–4.0(4.5)	3.31	(1.1)1.3–1.8(1.9)	1.49	30
H. Kulju 17/14	5.0–7.0(7.5)	5.65	3.0–3.8(4.0)	3.47	(1.3)1.4–2.0(2.1)	1.63	30
M. Kulju 48/15	(4.0)4.3–5.3(5.5)	4.95	3.1–3.9(4.0)	3.42	1.2–1.6(1.7)	1.45	30

\* from all specimens listed below.



are almost like in *Trechispora stevensonii* (see Bernicchia & Gorjón 2010: 681). For the mode of formation of conidia of *C. gracilis* see Kirk *et al.* (2008: 32, fig. 22).

The combination of characteristics, a resupinate, very fragile basidiocarp, monomitic hyphal system with ampullaceous septa, subcylindrical basidia which arise from bladder-like cells and small pip-shaped spores plus smooth or rough conidia is unique, and we do not know any other species microscopically resembling *C. gracilis*. The closest relatives of *Caudicicola* in the Steccherinaceae do not resemble it morphologically, though many of them are soil inhabiting or root-rotting such as *Caudicicola* may be (e.g. *Xanthoporus syringae*, *Tyromyces wynnae*, *Loweomyces fractipes*).

All the basidiocarps grew on undersides of spruce or pine stumps and could be seen only after the stumps were lifted from the ground. If this is a typical growth habit of this species, then it is no wonder that *C. gracilis* has never before been found during extensive polypore inventories carried out in Finnish old-growth forests. It may be more common than a single known location suggests.

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