***Coprinopsis canoceps* (C.H. Kauffman) Örstadius & E. Larss. 2015**
Mycological Progress 14(5/25) ; 1-42 : 37
{**MB**#551035}

Deschuyteneer daniel & Dieter Wächter

Basionyme : *Hypholoma canoceps* Kauffman, Papers of the Michigan Academy of Sciences 5 : 132 (1926).
Synonymes :
Psathyrella canoceps (C. H.Kauffman) A.H. Sm., Contributions from the University of Michigan Herbarium, 5 : 43 (1941) {MB#290025}.
Drosophila canoceps (C.H. Kauffman) Kühner & Romagn., Flore Analytique des champignons supérieurs : 366 (1953) {MB#296976} (non valide car le basionyme ne fut pas mentionné).
Psathyrella acutilamella J. Favre (Assoc. fong. Hauts–marais jurass.) Mater. Fl. Crypt. Suisse 10(3) : 150 (1948) (non valide, car absence de diagnose latine).
Psathyrella lanuginosa A.H. Sm. Mem. N. Y. bot. Gdn. 24 : 186 (1972).
Psathyra gordonii f. minor J.E Lange, 1939, Fl. Agar. Dan. 4 : 93 + Tab 151, fig. E (non valide).
Psathyra pennata ss. J. E. Lange 1939 in Fl. Agar. Dan. 4: 94 + Tab. 151, fig. C (nom erroné)
Famille : *Agaricales, Psathyrellaceae, Coprinopsis*, sous groupe *Marcescibilis*.

Ecologie

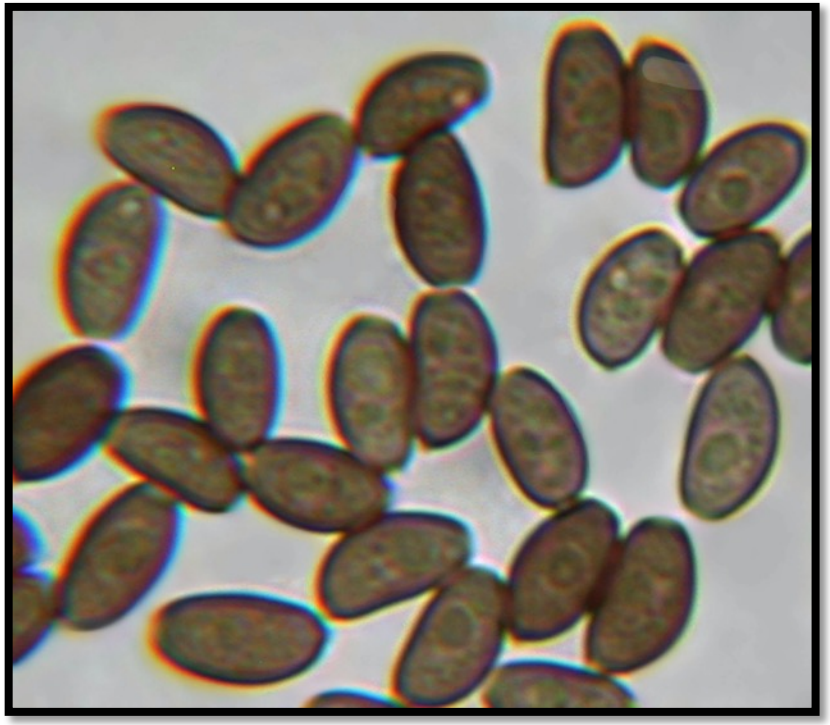
Cette espèce saprophyte a été récoltée en novembre 2017 à Kampenhout, Belgique, en lisière de feuillus divers dont de nombreux aulnes, peupliers et hêtres au sein de bois raméal fragmenté, ce qui correspond à son habitat habituel.
Örstadius la signale sous feuillus hygrophiles (aulnes, bouleaux, noisetiers, frênes) ainsi que sous hêtres et chênes, avec une préférence pour les sols calcaires, fixée à des fragments de bois, en milieu humide. Elle apparaît en général isolée ou subfasciculée comme dans ma récolte.

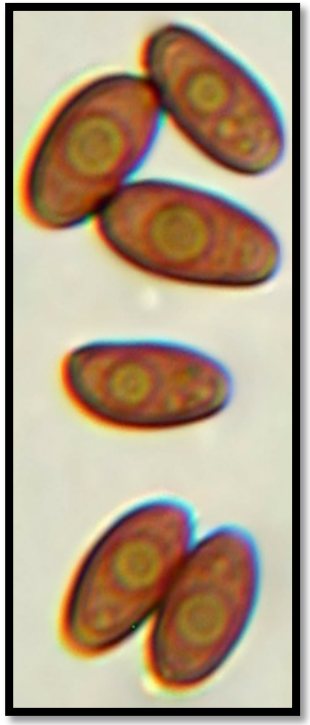
Chapeau de 6 à 20 mm de diamètre, initialement obtusément conique, devenant conico paraboloïde, parfois discrètement umboné ; couleur noisette à ocre grisâ-tre avec la marge légèrement striée jusqu'à mi-chapeau (ces caractères n'appa-raissant que lorsque le voile peu volatile se raréfie) ; hygrophane, il décolore à partir du disque en beige très pâle.

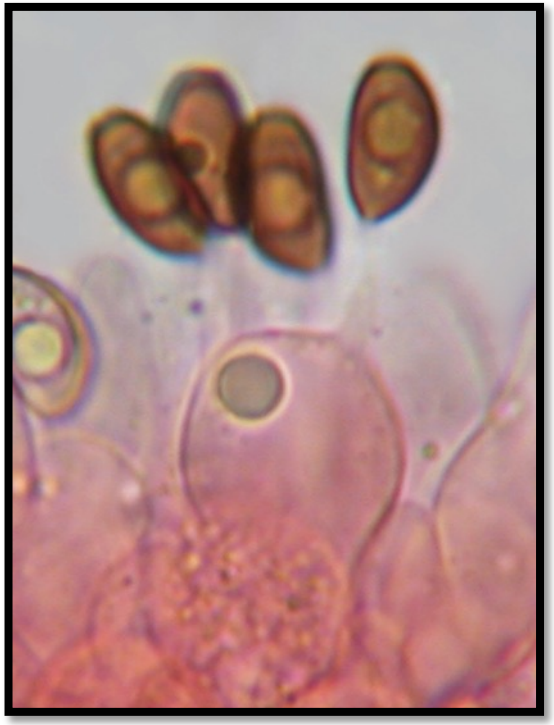
Voile très abondant et de ce fait pouvant parfois sembler inné, recouvrant au début la totalité du chapeau ; constitué de fibrilles blanches apprimées à orientation radiaire ou de mèchules ayant tendance à se retrousser, formant une épaisse couche aranéeuse appendiculée à la marge, qui apparaît barbue ; s'étendant sur les deux tiers inférieurs du stipe.

Lames larges de 2-3 mm, alternant avec des lamelles ; droites à légèrement ventrues, serrées, largement adnées ; beige devenant gris brun foncé (sporée) ; arête fimbriée blanche. Médiostrate pigmentée de brun jaunâtre.
Stipe 20-60 x 1,5-2,5 mm, fistuleux, cylindrique mais un peu clavé, à la base parfois strigueuse ; glabrescent blanchâtre devenant ochracé ; pruineux fibrilleux dans le tiers supérieur, cotonneux blanchâtre et ensuite longitudinalement fibrilleux dans les deux tiers inférieurs.
Chair 1-1,5 mm au disque, beige grisâtre ; odeur et saveur sans particularités.

Basides : 16-25(32) x 8,5-11 µm, clavées, tétrasporiques.
Spores : 7,5-**8,53**-9 x 4,5-**4,85**-5 µm ; Qav 1,7-2 ; lisses, brunes avec souvent une grosse goutte hileuse dans le NH_4OH 10%, beige grisâtre dans le KOH 10% ; non opaques ; ellipsoïdes à oblongues de face, asymétriques de profil et alors très légèrement amygdaliformes ou phaséoliformes ; pore germinatif central distinct (1-1,5 µm) et tronqué.
(Kits van Waveren : moyenne 8,8-9,8 x 4,9-5,4 µm ; Örstadius : 8-11 x 4,5-6 µm).





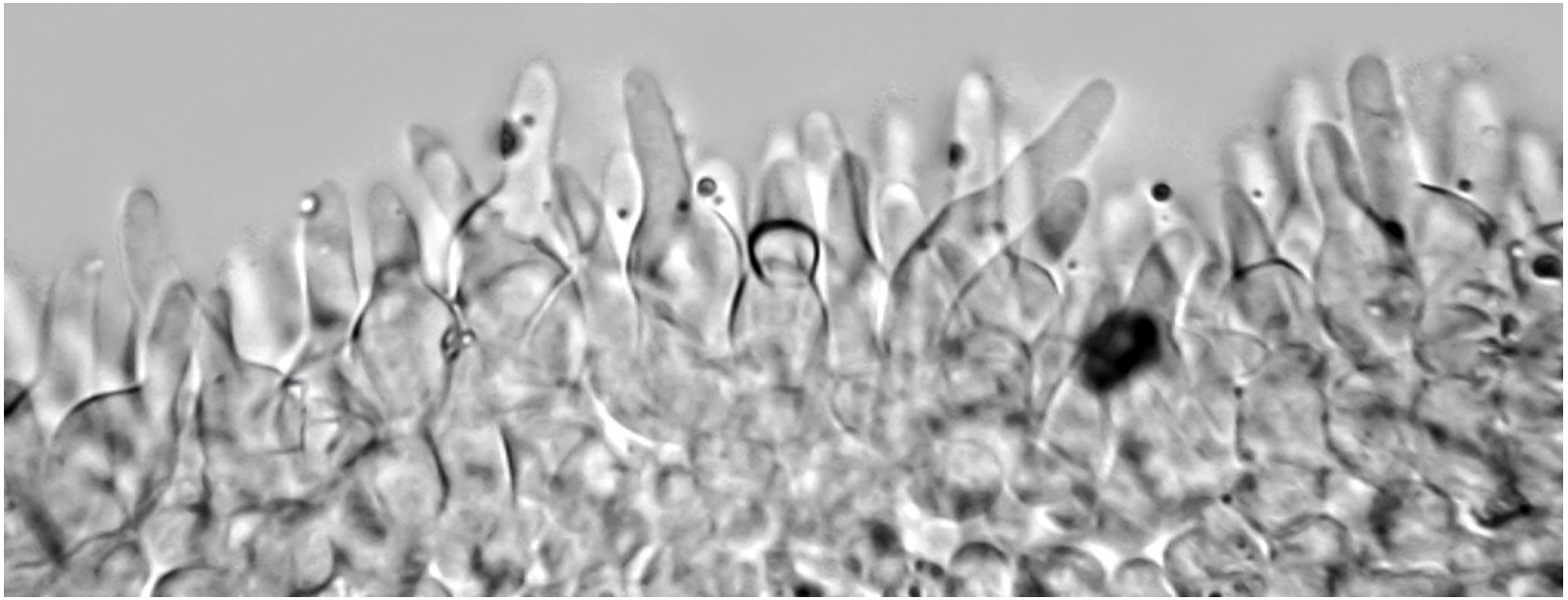


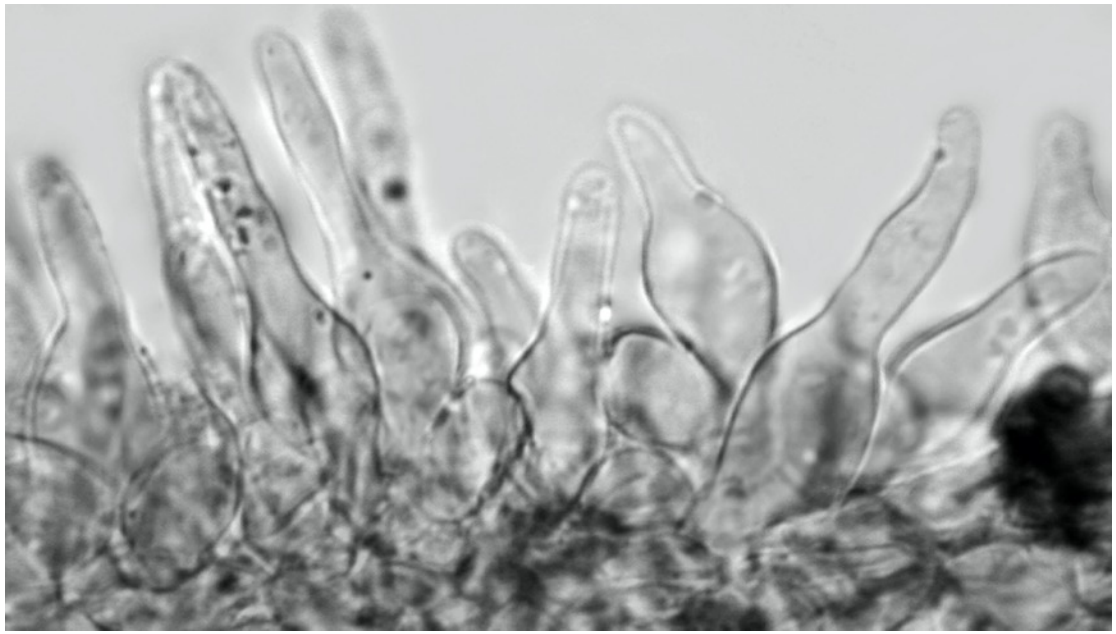
Chéilocystides : 23-35(40) x 9-12(14) µm, à paroi fine, et densément accolées, de différents types :

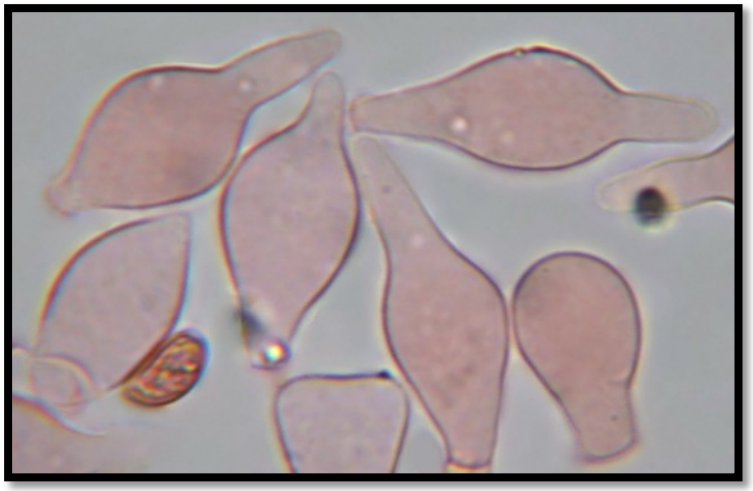
- soit majoritairement et typiquement courtes, avec un corps globuleux à base droite, prolongé de manière abrupte par un col généralement court (aspect parfois rostré), assez large à sommet obtus ;
- soit fusilagéniformes à long col assez large, à sommet obtus à subaigu et parfois flexueux ;
- plus rarement subcylindriques à sommet fourchu ou clavées.

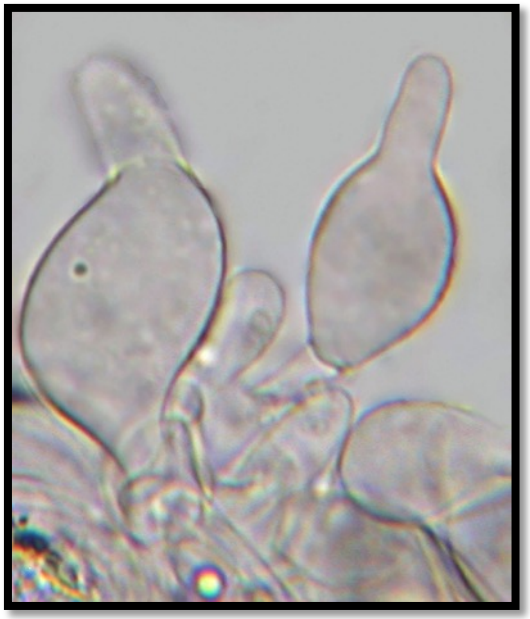
(Kits van Waveren : 25-40 x 9-15 µm ; Örstadius : 25-50 x 8-16 µm).

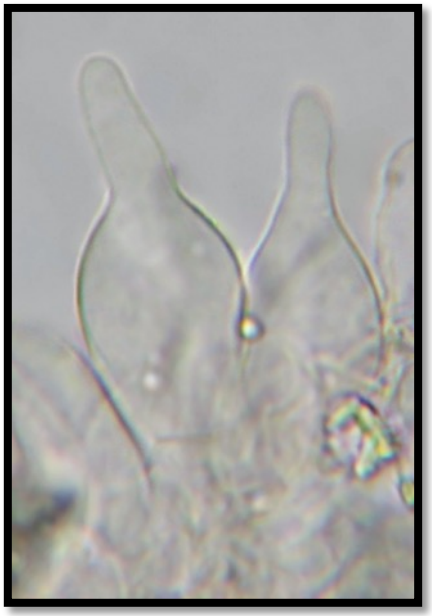
Cellules « marginales » clavées et sphéropédonculées de petite taille, à paroi fine, assez nombreuses mais masquées par la densité des cheilocystides.



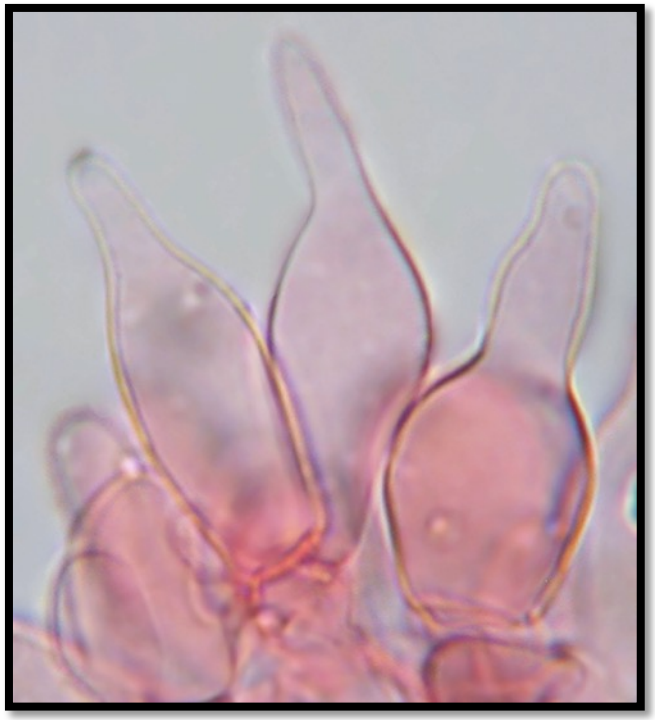


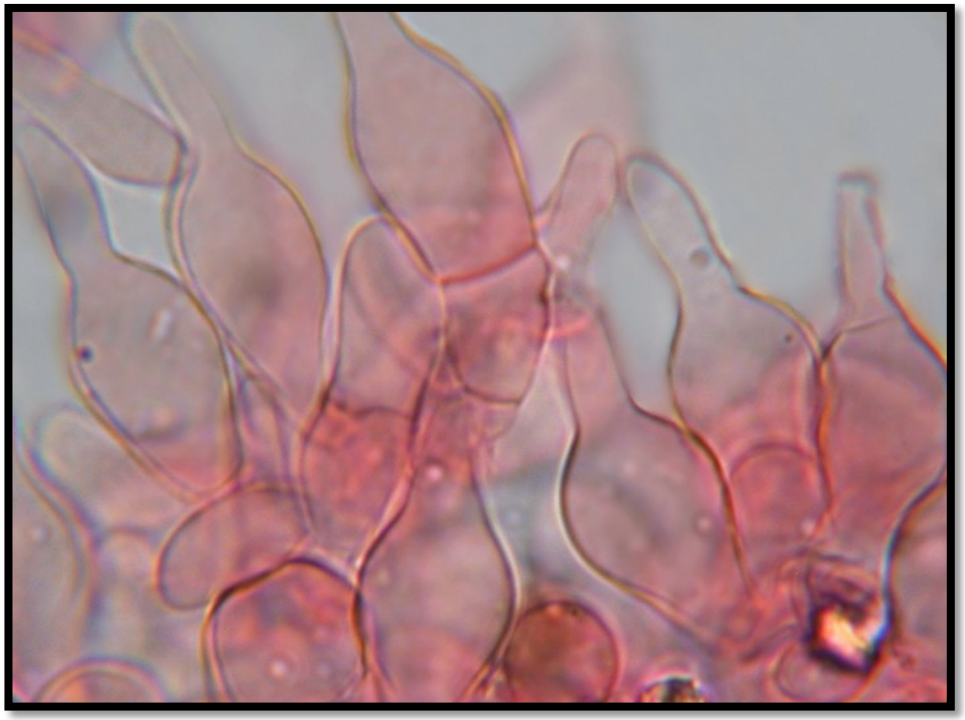


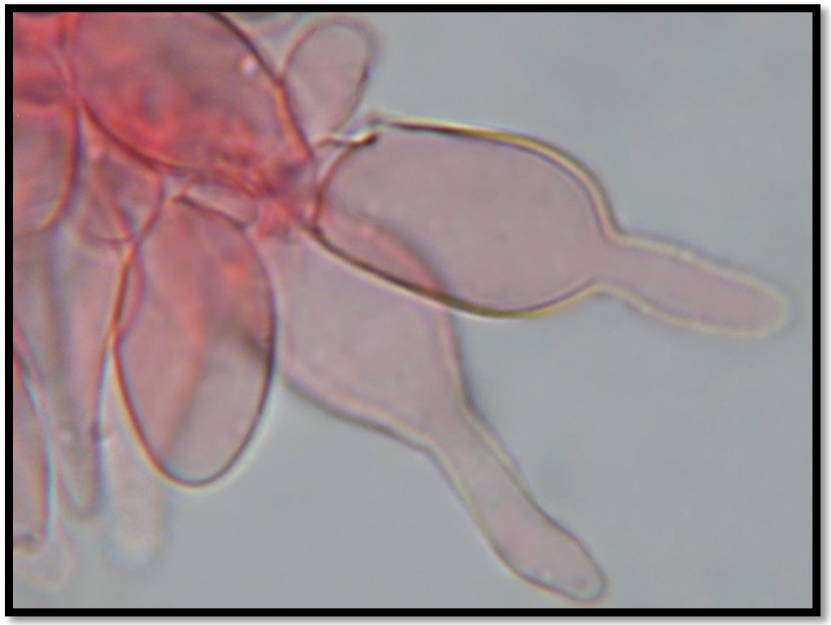


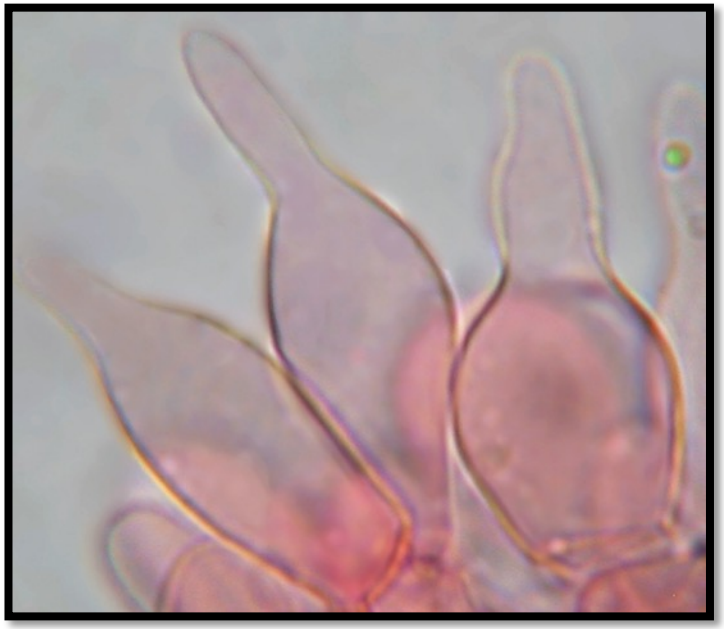


cheilocystides

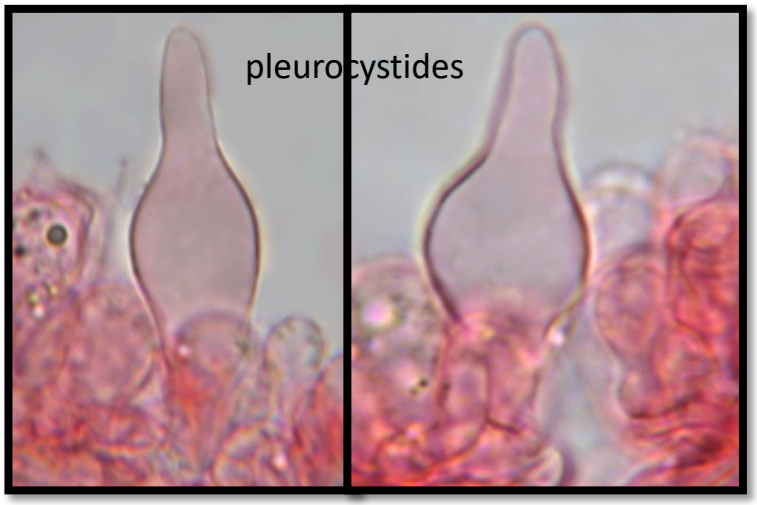




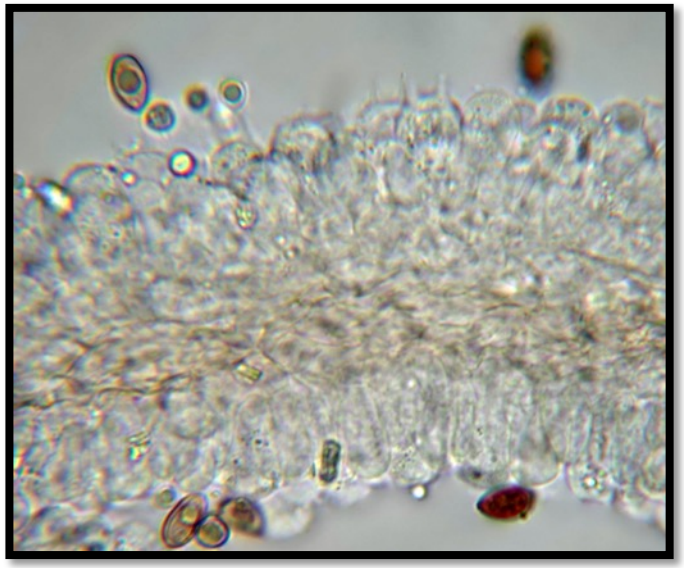


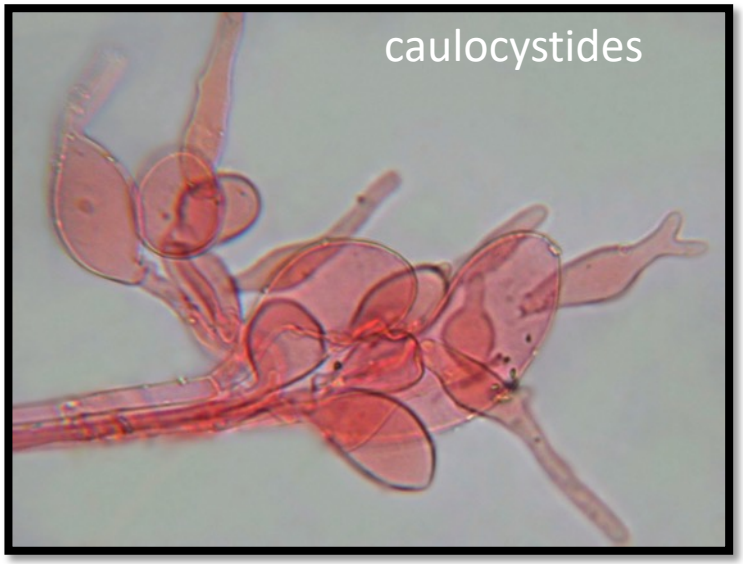


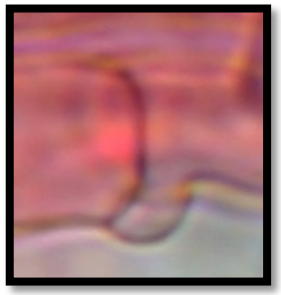
Pleurocystides réputées pour être **<u>absentes</u>,** mais peut-être à considérer comme étant plutôt très rares, puisque j'ai eu l'occasion, après examen patient d'une dizaine de lames, d'en observer deux, d'aspect analogue aux cheilocystides. Melzer (communication personnelle) a fait la même observation.
Boucles présentes entre autres à la base de certaines basidioles, ainsi qu'au niveau des hyphes du stipe.
Caulocystides abondantes, analogues aux cheilocystides, sublagéniformes, souvent à sommet fourchu et clavées.

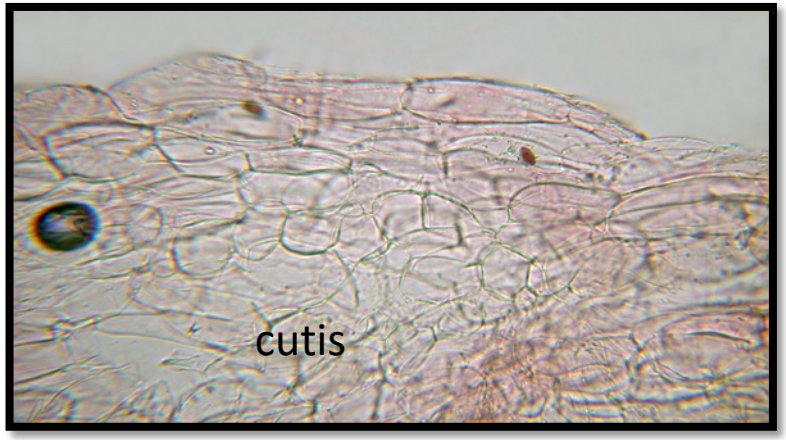


Trame lamellaire









Sequencing and phylogenetic analysis

DNA Extraction, Amplification and Sequencing of the fungus was performed by Alvalab (Oviedo, Spain). The phylogenetic analysis was done by Dieter Wächter (Thiersheim, Germany). The genomic DNA was extracted from dried fruiting bodies. Amplification of the ITS region was performed with the ITS4 primer [1], amplification of the LSU region was performed with the LR0R primer [2]. The initial base calling was done with FinchTV [3]. The nucleotide sequences were checked manually for errors, as well as the base calling at unsafe regions (trails, low confidence scores, stutters and polymorphs) on the basis of existing sequences of the /*canoceps*-clade by divergence matrix and corrected if necessary. In the present case only a trimming of the trails and som minor corrections were necessary. The following molecular phylogenetic markers were used for the phylogenetic analysis: ITS1 (Internal Transcribed Spacer 1), 5.8S (5.8S rRNA Gene), ITS2 (Internal Transcribed Spacer 2), LSU (Large Subunit 28S rRNA Gen), β-tub (exons of the β-tubulin gene), ef-1α (exons of the ef-1α gene). The nucleotide sequences for the tree inference were taken from NCBI [4] and Unite [5] (essential ones of the /*cortinata*, /*Nivei*, /*canoceps* and /*Fragilissimae*-clades see Table 1). Region boundaries for the ITS- and LSU-region were carried out with ITSx [6] and HMMER [7] including the databases. As outgroup, the sequence sets of the most closely related clades of the ingroup were used, i.e. from the Genera *Lacrymaria*, *Homophron* and *Parasola*. Due to the rapidly evolving, indel-rich areas of the ITS region, it can only be aligned veridical by using an iterative multigene-guide tree. The initial alignment of the ITS region was performed with Mafft [8] using the FFT-NS-2 method. The initial alignments of the LSU-, β-tub and ef-1α genes was carried out using E-INS-i method. The indel matrices for the ITS and LSU regions were each coded with SeqState [9] using the SIC = "Simple Indel coding" [10] method. After each alignment step, an ML analysis with RAxML [11] (model: GTRCAT, refining under GTR+G for DNA, GTR2+G with acquisition bias correction according to Lewis [12] for indel partitions) was carried out and the resulting best tree was used as a guide tree for the refinement of the ITS1 and ITS2 MSA. The iterative alignments were done with Prank [13], whereby the switches -once and -uselogs were set. Tracing values were recorded, evaluated statistically and thus the end of the iteration loop of the alignment was determined. The partitioning of all alignments and the indel matrices as well as the model selection for the DNA alignments was done with Partitionfinder [14]. For the final partitioning, the guide tree of the last iteration step was used. As information criterion the Bayesian Information Criterion (BIC) [15] used was after comparison with the Corrected Akaike Information Criterion (AICc) [16] and evaluation with respect to over- or under-partitioning. The partitioning scheme of the final phylogeny was:

•DNA-partition 1: ITS1 + ITS2
•DNA-partition 2: 5.8S
•DNA-partition 3: LSU + β-tub Codon 1
•DNA-partition 4: β-tub Codon 1 + ef-1α Codon 1 + ef-1α Codon 2
•DNA-partition 5: β-tub Codon 3 + ef-1α Codon 3
•Binary partition (gap matrices): ITS1 + ITS2 + LSU

The final maximum likelihood analysis was done with RAxML 8.2.10 [11]. For all DNA partitions, the GTR substitution matrix [17] under the CAT model [11] was used. The final optimization took place under gamma distribution [11]. For the binary partitions, the "Two State Time-Reversible Model" with acquisition bias correction [12] was used. 1000 ML bootstrap inferences were calculated. Of these, 1000 trees were sampled and the best tree was labeled with the ML bootstrap support values and collapsed to the ML bootstrap value of 50%. The phylogram in Fig 1 was edited with Treegraph [18]. The Outgroup and the upper Coprinopsis clades has been collapsed for a better view.

Discussion:

Cette espèce faisait anciennement partie du genre *Psathyrella*. Les études biomoléculaires qui ont été réalisées ont abouti au transfert de cette espèce dans la section *Marcescibilis* du genre *Coprinopsis*.

Elle se caractérise par sa préférence pour les feuillus hygrophiles, sa croissance isolée ou subfasciculée sur fragments de bois enfouis, sa petite taille, son voile blanchâtre très abondant masquant le chapeau et formant un filet aranéeux au niveau de la marge, et son stipe fibrillo-cotonneux légèrement clavé à la base.

Sur le plan microscopique, elle se caractérise par des spores de longueur moyenne inférieure à 10 µm, l'absence (ou plutôt l'extrême rareté) des pleurocystides, des cheilocystides très nombreuses dont l'aspect ventru-fusiforme est assez caractéristique, et la présence de boucles.

Macroscopiquement, elle peut être confondue avec *Coprinopsis pannucioides*, mais les caractères microcopiques bien différents permettent de distinguer aisément ces deux espèces.

Etude biomoléculaire

Bien que ma récolte soit typique tant sur le plan macroscopique que microscopique, la séquence ITS de l'ADN ribosomal effectuée par le laboratoire Alvalab (Pablo Alvarado Garcia), a révélé une correspondance à seulement 95% avec la séquence de GenBank (KC992964) ; Voucher LO148-95 de Örstadius.

2017-835-ALV13825 DD2915

GTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTATTGAATAAATCTGACATGGTTGTAGCTGGCTCTCTGGAGTATGTGCACACCGGTC
ACCTTTATCTTTCTCCCTGTGCACACCTGTAGGCCTGAATAACTCTCGTCGCAAGGCGGATGCAGAGATTGCTGCTTGCAGCTCTCTTTGAATTTTTAGGTCTATGA
CTTTATATACCCCAAATGAATGTTATAGAATGTATTCATAAGGCCTTGTGCCTATAAAYTTAAACAACTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAA
CGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCTTGGTATTCCGAGGAGCATGCCTGTATGA
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Etude biomoléculaire : Dieter Wächter

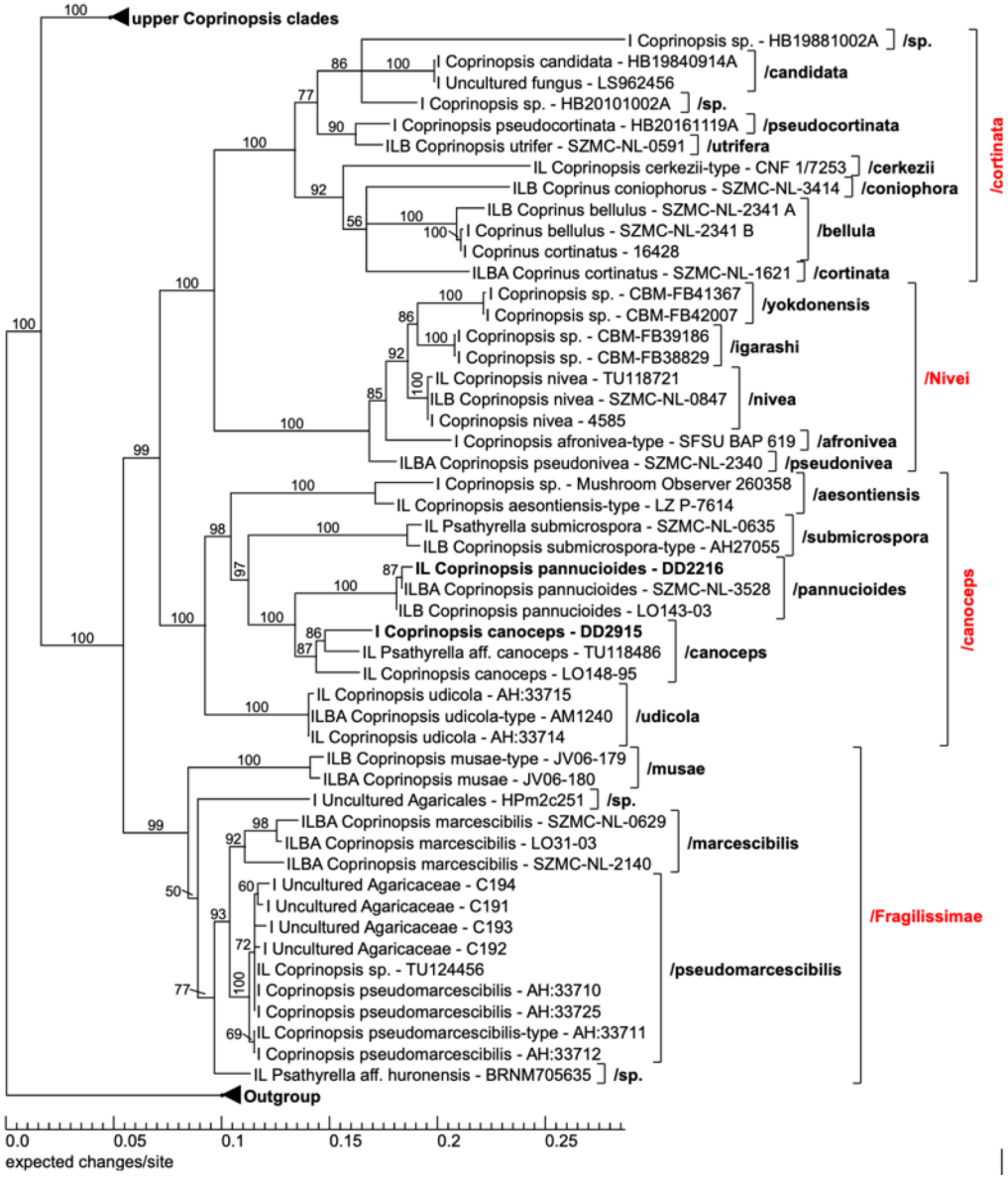

Fig 1 50% collapsed maximum likelihood consensus phylogram. The values on the branches are ML bootstrap values. Abbreviations: I: ITS region, L: LSU region, B: β-tubulin region, A: ef-1α region.

Table 1 List of relevant sequences used in this publication.

Art	Beleg	ITS1	LSU	β-Tub	ef-1α
Coprinopsis aesontiensis	LZ P-7614	KY554753.1	KY554752.1		
Coprinopsis afronivea	SFSU BAP 619	NR_148105.1			
Coprinopsis candidata	HB19840914A	follows			
Coprinopsis canoceps	LO148-95	KC992964.1	KC992964.1		
Coprinopsis cerkezii	CNF 1/7253	KX869912.1	KX869913.1		
Coprinopsis marcescibilis	SZMC-NL-0629	FM878021.1	FM876278.1	FN396267.1	FM897256.1
Coprinopsis marcescibilis	LO31-03	DQ389728.1	DQ389728.1	KJ664919.1	KJ732829.1
Coprinopsis marcescibilis	SZMC-NL-2140	FM878020.1	FM876277.1	FN396271.1	FM897257.1
Coprinopsis musae	JV06-179	KC992965.1	KC992965.1	KJ664920.1	
Coprinopsis musae	JV06-180	KC992966.1	KC992966.1	KJ664921.1	KJ732830.1
Coprinopsis nivea	TU118721	UDB019531	UDB019531		
Coprinopsis nivea	4585	JF907848.1			
Coprinopsis nivea	SZMC-NL-0847	HQ847032.1	HQ847117.1	HQ847182.1	
Coprinopsis pannucioides	SZMC-NL-3528	FN396143.1	FN396202.1	FN396341.1	FN396238.1
Coprinopsis pannucioides	LO143-03	DQ389727.1	DQ389727.1	KJ664917.1	
Coprinopsis pseudocortinata	HB20161119A	follows			
Coprinopsis pseudomarcescibilis	AH:33725	KY698006.1			
Coprinopsis pseudomarcescibilis	AH:33710	KY698009.1			
Coprinopsis pseudomarcescibilis	AH:33711	KY698008.1	MF033345.1		
Coprinopsis pseudomarcescibilis	AH:33712	KY698007.1			
Coprinopsis pseudonivea	SZMC-NL-2340	FM163181.1	FM160728.1	FN396288.1	FN430698.1
Coprinopsis sp.	CBM-FB41367	LC259499.1			
Coprinopsis sp.	CBM-FB42007	LC259498.1			
Coprinopsis sp.	CBM-FB39186	AB854626.1			
Coprinopsis sp.	CBM-FB38829	AB854625.1			
Coprinopsis sp.	Mushroom Observer 260358	MF163178.1			
Coprinopsis sp.	TU124456	UDB028407	UDB028407		
Coprinopsis sp.	HB19881002A	follows			
Coprinopsis sp.	HB20101002A	follows			
Coprinopsis submicrospora	AH27055	KC992959.1	KC992959.1	KJ664918.1	
Coprinopsis udicola	AH:33715	KY698002.1	KY698003.1		
Coprinopsis udicola	AM1240	KC992967.1	KC992967.1	KJ664922.1	KJ732831.1
Coprinopsis udicola	AH:33714	KY698004.1	KY698005.1		
Coprinopsis utrifer	SZMC-NL-0591	FN396140.1	FN396209.1	FN396356.1	
Coprinus bellulus	SZMC-NL-2341 A	FM163176.1	FM160680.1	FN396274.1	
Coprinus bellulus	SZMC-NL-2341 B	FN430682.1			
Coprinus coniophorus	SZMC-NL-3414	FN396122.1	FN396207.1	FN396354.1	
Coprinus cortinatus	16428	JF907847.1			
Coprinus cortinatus	SZMC-NL-1621	FN396121.1	FN396171.1	FN396346.1	FN396224.1
Psathyrella aff. canoceps	TU118486	UDB017928	UDB017928		
Psathyrella aff. huronensis	BRNM705635	AM712291.1	AM712291.1		
Psathyrella submicrospora	SZMC-NL-0635	HQ847053.1	HQ847133.1		
Uncultured Agaricaceae	C194	AM076653.1			
Uncultured Agaricaceae	C191	AM076650.1			
Uncultured Agaricaceae	C193	AM076652.1			
Uncultured Agaricaceae	C192	AM076651.1			
Uncultured Agaricales	HPm2c251	JN802317.1			
Uncultured fungus	LS962456	LS962456.1			

References

[1] White TJ, Bruns T, Lee L, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: InnisMA, GelfandDH, Sininski JJ,White TJ (eds) PCR protocols, a guide to methods and applications. Academic Press, New York, pp 315–322

[2] Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of Gliocladium analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98: 625-634

[3] **FinchTV 1.4.0**: Geospiza, Inc.; Seattle, WA, USA; http://www.geospiza.com

[4] **NCBI**: National Center for Biotechnology Information, U.S. National Library of Medicine 8600 Rockville Pike, Bethesda MD, 20894 USA - https://www.ncbi.nlm.nih.gov/

[5] **Unite:** Kõljalg U, Nilsson RH, Abarenkov K, Tedersoo L, Taylor AFS, Bahram M, Bates ST, Bruns TD, Bengtsson-Palme J, Callaghan TM, Douglas B, Drenkhan T, Eberhardt U, Dueñas M, Grebenc T, Griffith GW, Hartmann M, Kirk PM, Kohout P, Larsson E, Lindahl BD, Lücking R, Martín MP, Matheny PB, Nguyen NH, Niskanen T, Oja J, Peay KG, Peintner U, Peterson M, Põldmaa K, Saag L, Saar I, Schüßler A, Scott JA, Senés C, Smith ME, Suija A, Taylor DL, Telleria MT, Weiß M, Larsson K-H. 2013. Towards a unified paradigm for sequence-based identification of Fungi. Molecular Ecology, DOI: 10.1111/mec.12481

[6] **ITSx 1.1b**: JOHAN BENGTSSON-PALME 2012-2017; Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences of fungi and other eukaryotes for use in environmental sequencing. JOHAN BENGTSSON-PALME, VILMAR VELDRE, MARTIN RYBERG, MARTIN HARTMANN, SARA BRANCO, ZHENG WANG, ANNA GODHE, YANN BERTRAND, PIERRE DE WIT, MARISOL SANCHEZ, INGO EBERSBERGER, KEMAL SANLI, FILIPE DE SOUZA, ERIK KRISTIANSSON, KESSY ABARENKOV, K. MARTIN ERIKSSON, R. HENRIK NILSSON: Methods in Ecology and Evolution, 4: 914-919, 2013 - (DOI: 10.1111/2041-210X.12073)

[7] **HMMER 3.1b2** (February 2015): http://hmmer.org/ - Copyright (C) 2015 Howard Hughes Medical Institute. Freely distributed under the GNU General Public License (GPLv3)

[8] **Mafft 7.372** (used over mafft.cbrc.jp)

- NAKAMURA, YAMADA, TOMII, KATOH 2018 (Bioinformatics 34:2490–2492) - Parallelization of MAFFT for large-scale multiple sequence alignments.
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Iconographie

Lange : Flora Agaricina Danica (1939), planche 151 fig. E (*Psathyra gordonii f. minor*) et fig. C (P*sathyrella pennata*).
Ludwig : Pilzkompendium tome 2 (2007), fig. 98.30 A & B.

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