

# *Coprinopsis pannucioides* (J.E. Lange) Örstadius & E. Larss. 2008

in Myc. Research 112 : 1180

Daniel Deschuyteneer

## Synonymes :

*Drosophila pannucioides* (J.E. Lange) Kühner & Romagn. 1953, in Fl. anal. Champ. sup.: 362 (inval.)

*Psathyrella pannucioides* (J.E. Lange) M.M. Moser 1967, in Gams, Kl. Krypt.fl. 2b/2, 2. éd. : 220

La description de cette espèce est basée sur plusieurs récoltes réalisées en Belgique en Brabant Flamand.

Trois récoltes ont été réalisées à Bertem, fin octobre et mi novembre 2017, ainsi que le 10/10/2018, dans le Bertembos un bois humide de feuillus divers essentiellement hygrophiles. L'une d'entre elle (DD2216 - GPS: 50.884158, 4.632601) a fait l'objet d'un séquençage.

Les basidiomes se présentaient en petits groupes de quelques exemplaires connés par leur base émergeant le long de rondins pourrissants utilisés pour stabiliser le chemin boueux. Le long de celui-ci dans l'humus on pouvait observer de grandes touffes denses de spécimens réunis en faisceaux soudés par la base du stipe.

Une récolte complémentaire d'un trentaine d'exemplaires fasciculés a été effectuée le 24/11/2018 à la base d'un vieux saule vivant, à Zemst (Mechelen - GPS: 50. 998266, 4.479677).



Voucher DD2216 – Bertembos – GPS : 50.885479 - 4.634351  
Bertem- Belgique





**Chapeau** mesurant 20(40) x 15 mm, non strié, conico-paraboloïde devenant sur le tard plan convexe, pourvu d'un large mamelon presque lisse, obtus et beige pâle, contrastant avec le reste de la surface du chapeau qui, étant largement recouverte par un voile aranéeux constitué de fibrilles à orientation radiaire, apparaît feutrée, soyeuse et brillante. Le voile déborde de la marge et reste appendiculé à celle-ci, lui donnant un aspect cotonneux.

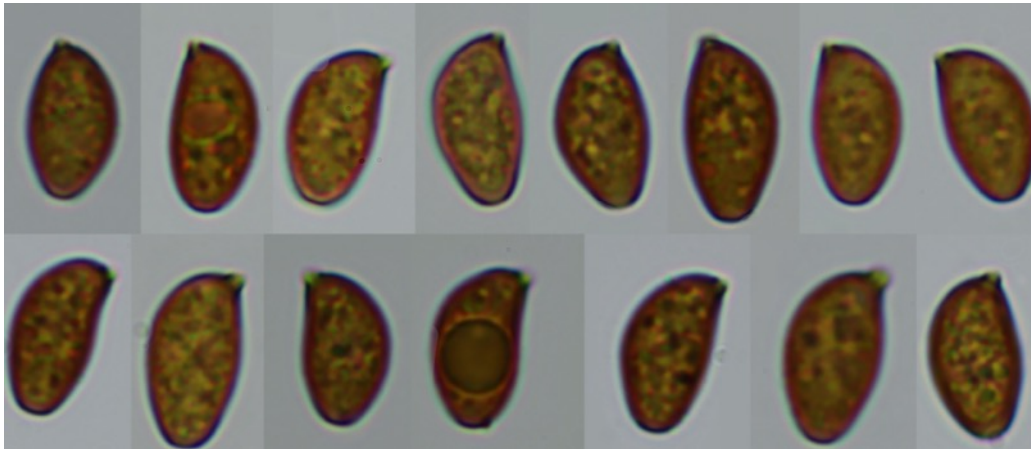
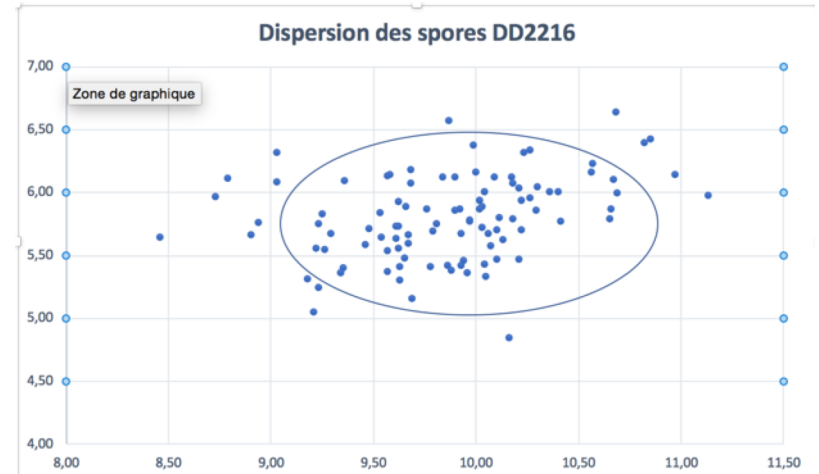
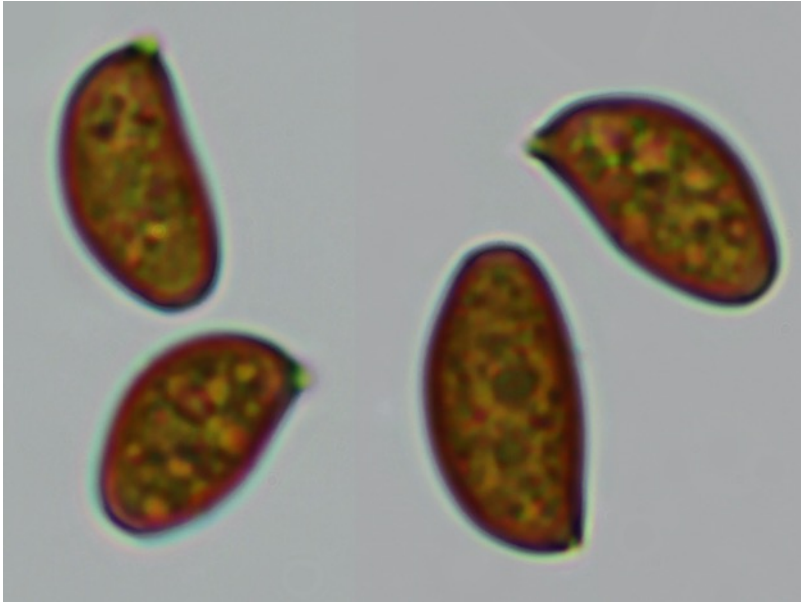


**Lames** alternant avec lamelles et lamellules, serrées, largement adnées, brunes devenant brun grisâtre; arête fimbriée concolore ou blanche. La trame lamellaire est nettement pigmentée de brun.

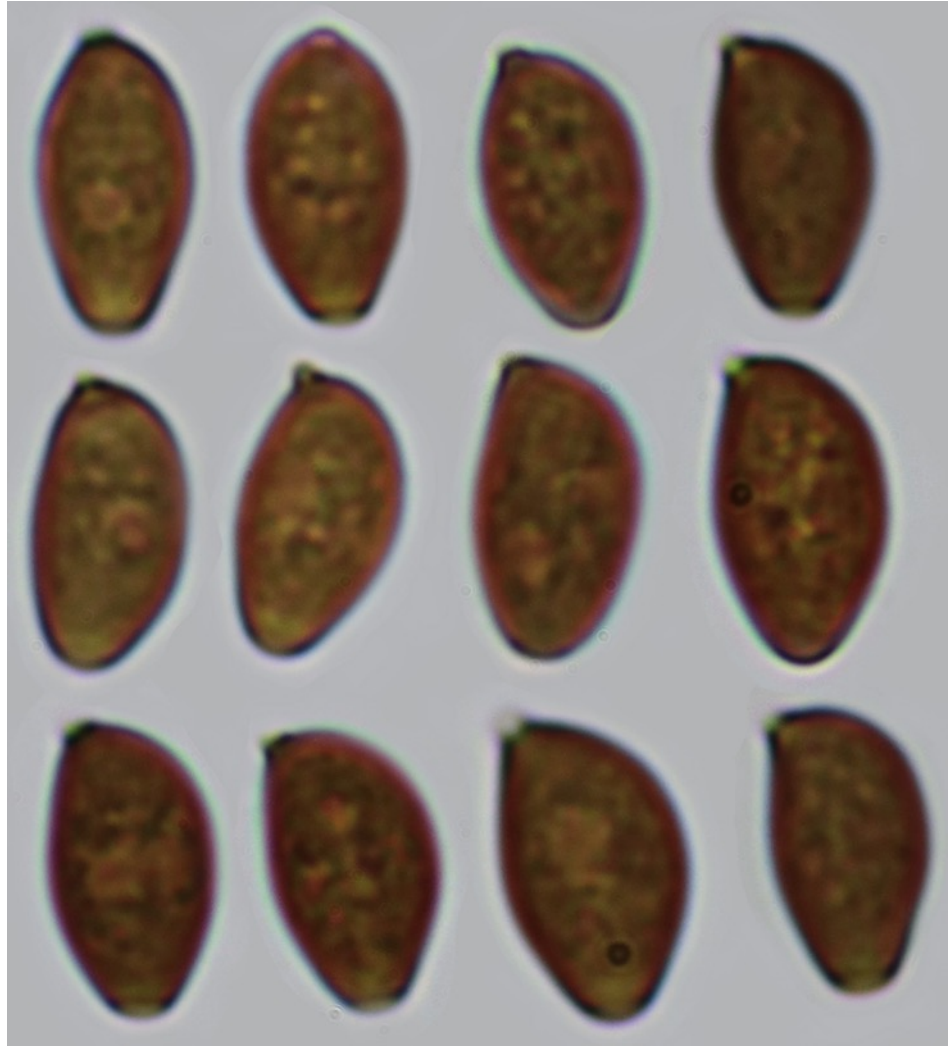
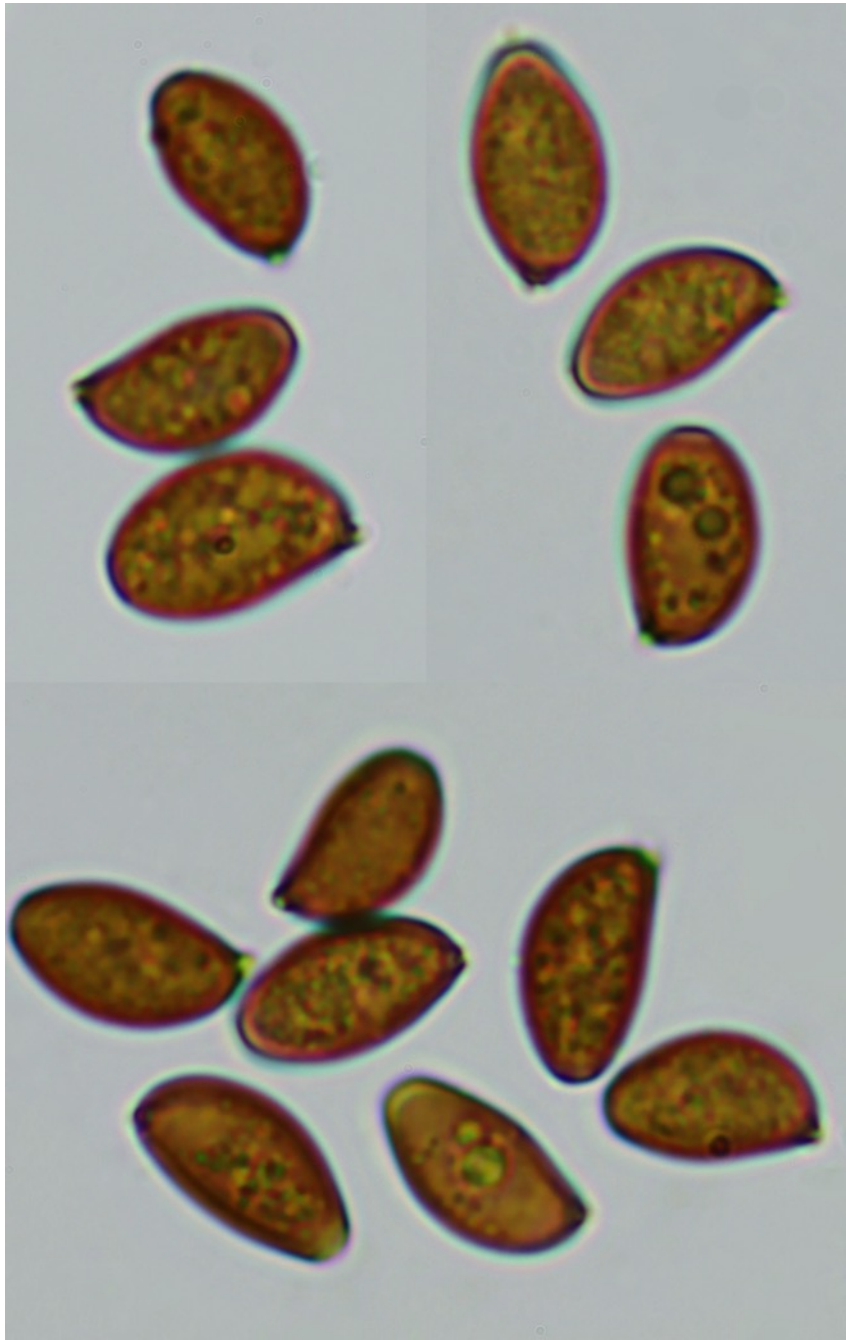
**Stipe** mesurant 35-60 x 2-3 mm (Örstadius : 30-60 x 2-6 mm), cylindrique, creux, fragile, se brisant aisément, pruineux au sommet et conné par la base qui est parfois légèrement dilatée. Le voile abondant persiste sur certains exemplaires sous forme de fibrilles gris noirâtres teintées par la sporée.



**Spores** mesurant (8,5) 9,2 - **9,9**- 10,6 (11,1) × (0,6) 5,4 – **5,7**- 6,2 (6,6) μm (Örstadius : 9-11,5 x 5-6,5 μm, Qav 1,7 -1,9) ; non opaques, brunes dans l'ammoniaque et grise dans le KOH, oblongues à ellipsoïdes, asymétriques de profil et légèrement amygdaliformes ; dépression suprahilaire fréquente, pore germinatif large de 2 μm, souvent tronqué.



Mesures réalisées avec Piximètre  
 (8,5) 9,2 - 10,6 (11,1) × (0,6) 5,4 - 6,2 (6,6) μm  
 Q = (1,4) 1,6 - 1,8 (2,1) ; N = 100  
 Me = 9,9 × 5,7 μm ; Qe = 1,7

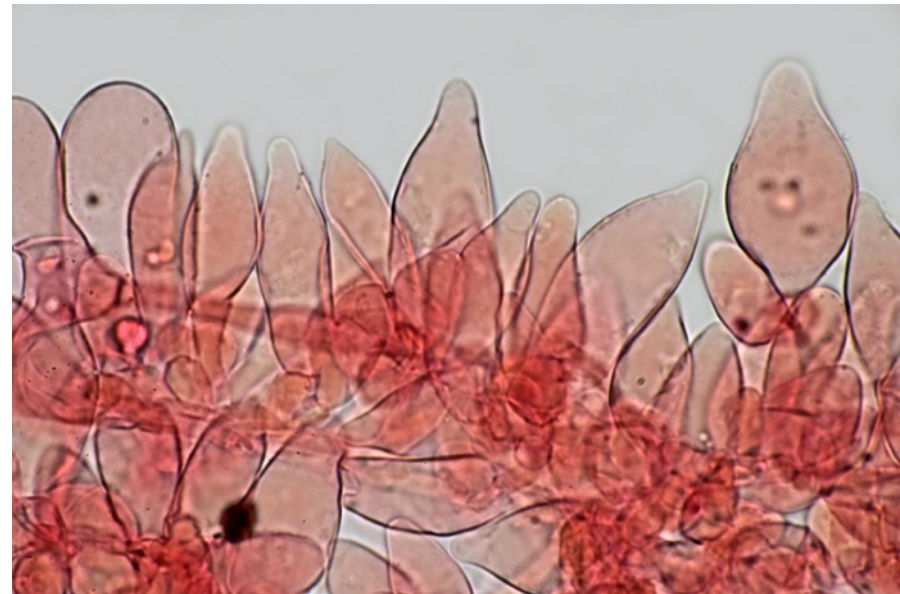
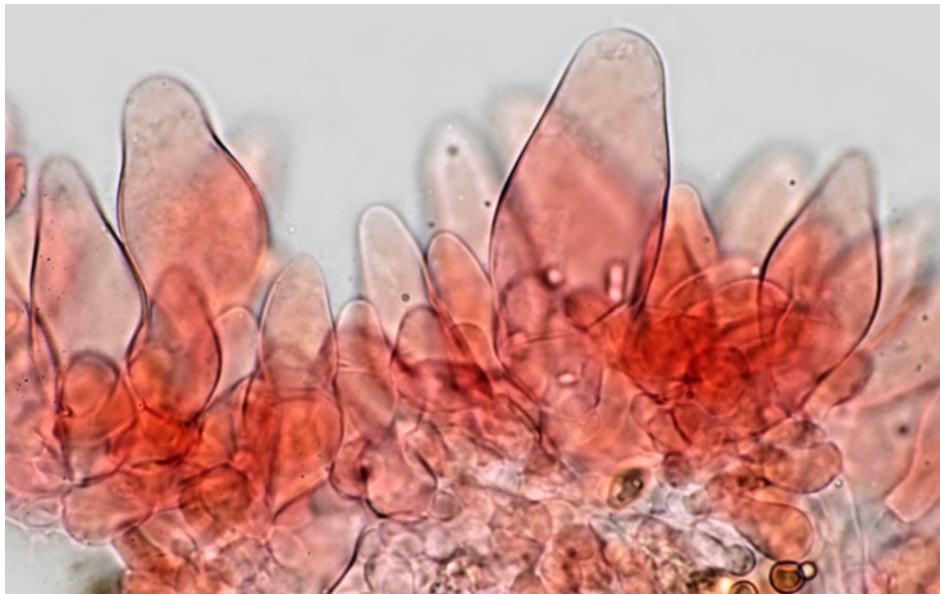
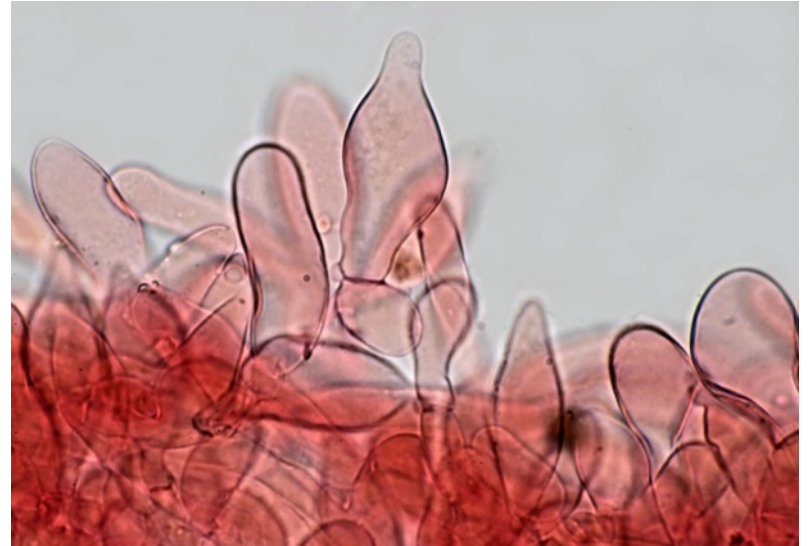




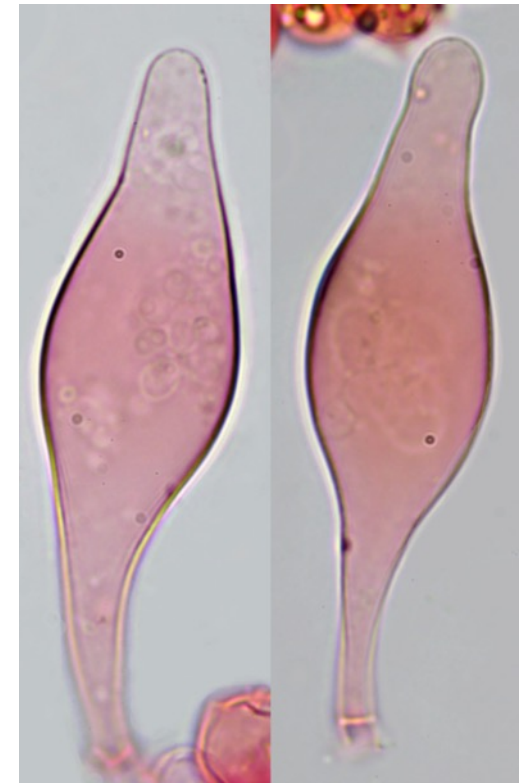
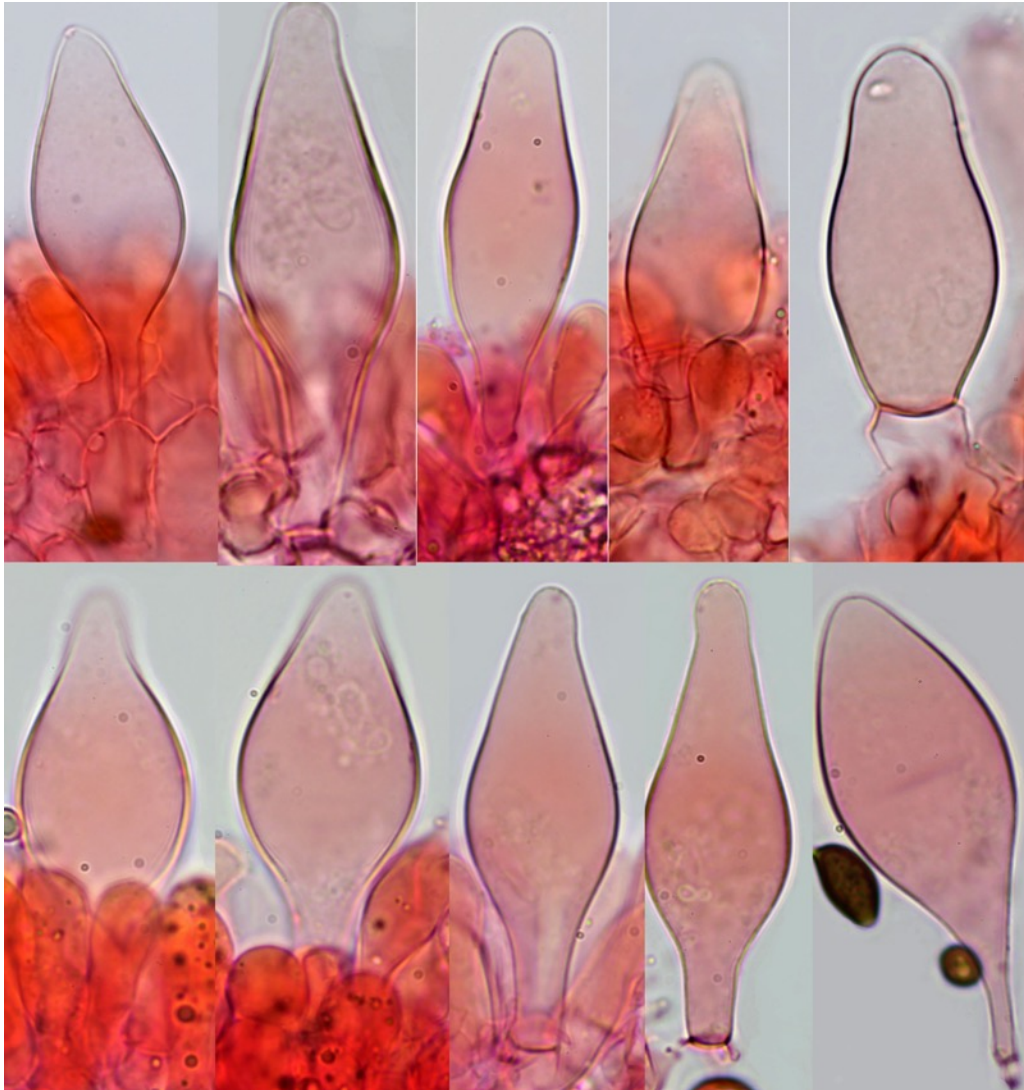
**Cheilocystides** nombreuses ventrues, sublagéniformes, spatulées, mesurant 40-65 x 13-26  $\mu\text{m}$  ; (Örstadius : 30-80 x 11-25  $\mu\text{m}$ ) ; mêlées à de nombreuses basidioles et basides, les cellules marginales clavées et sphéropédonculées étant peu fréquentes.



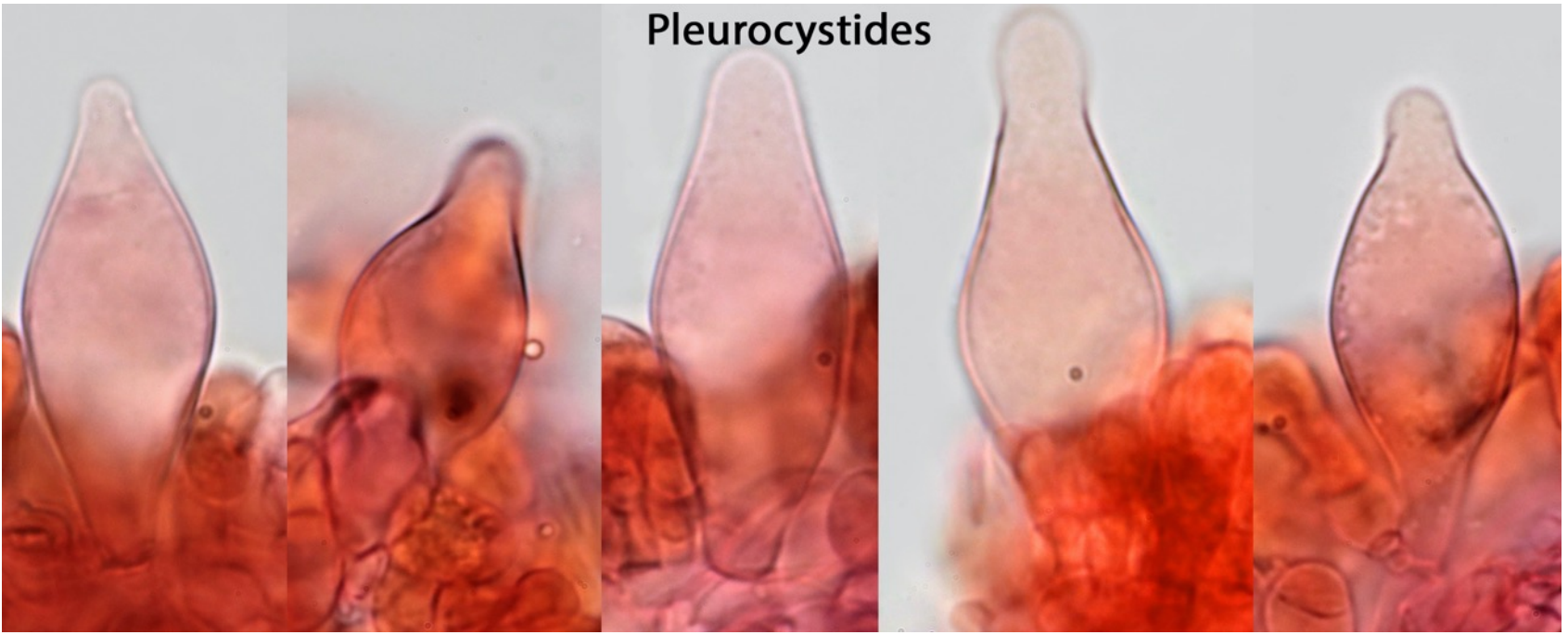
cheilocystides



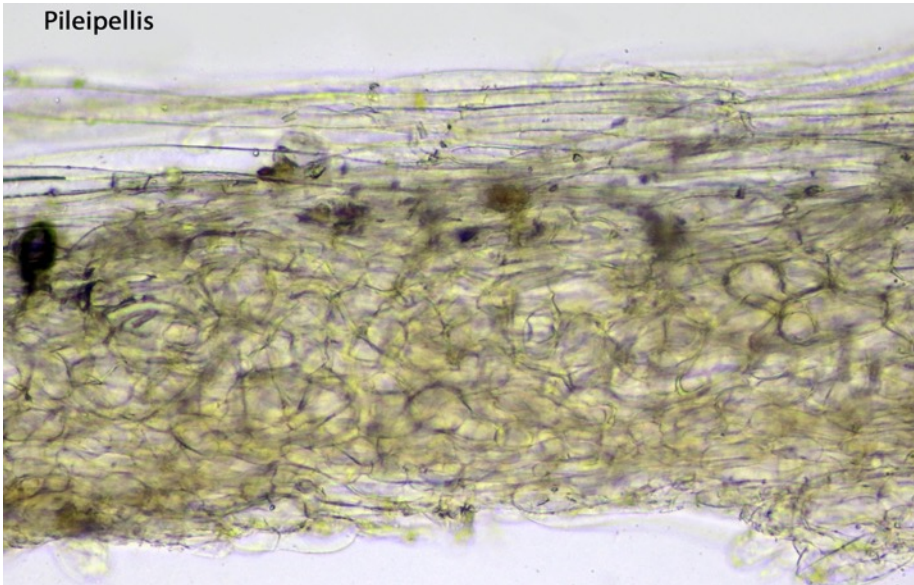
**Pleurocystides** peu nombreuses à nombreuses suivant les lames examinées, essentiellement utriformes, ventrues et spatulées, ainsi que parfois lagéniformes, stipitées ou non, semblables aux cheilocystides ; mesurant 40-83 x 16-30  $\mu\text{m}$  ; (Örstadius : 35-90 x 12-24  $\mu\text{m}$ ).



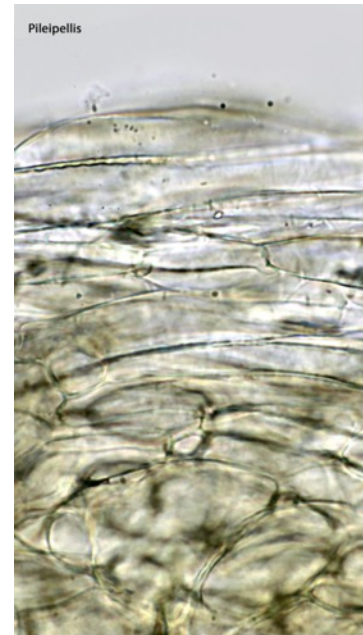
# Pleurocystides



# Pileipellis



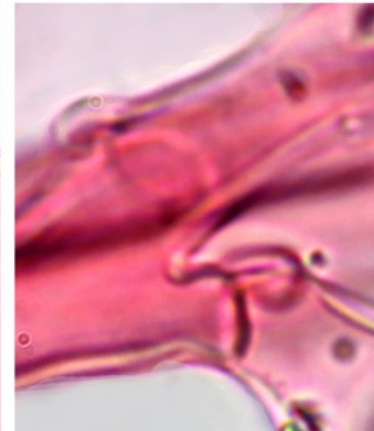
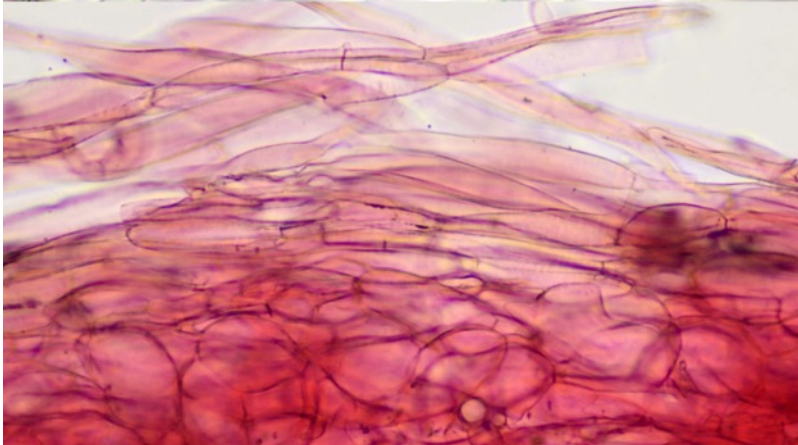
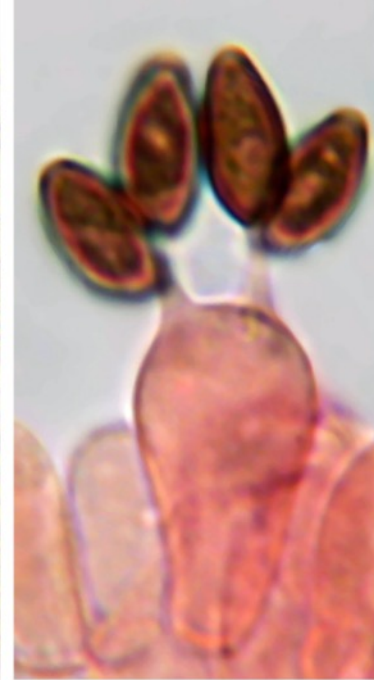
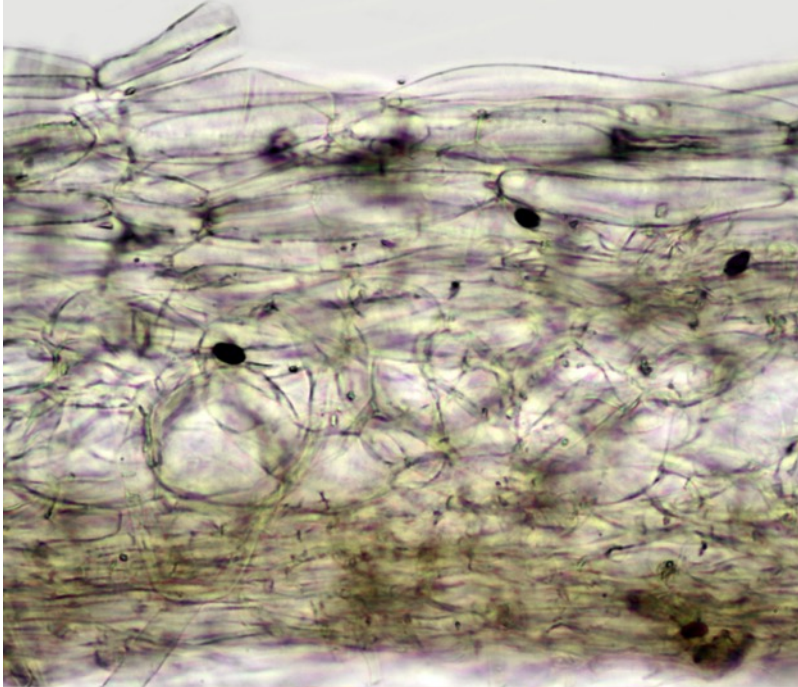
# Pileipellis



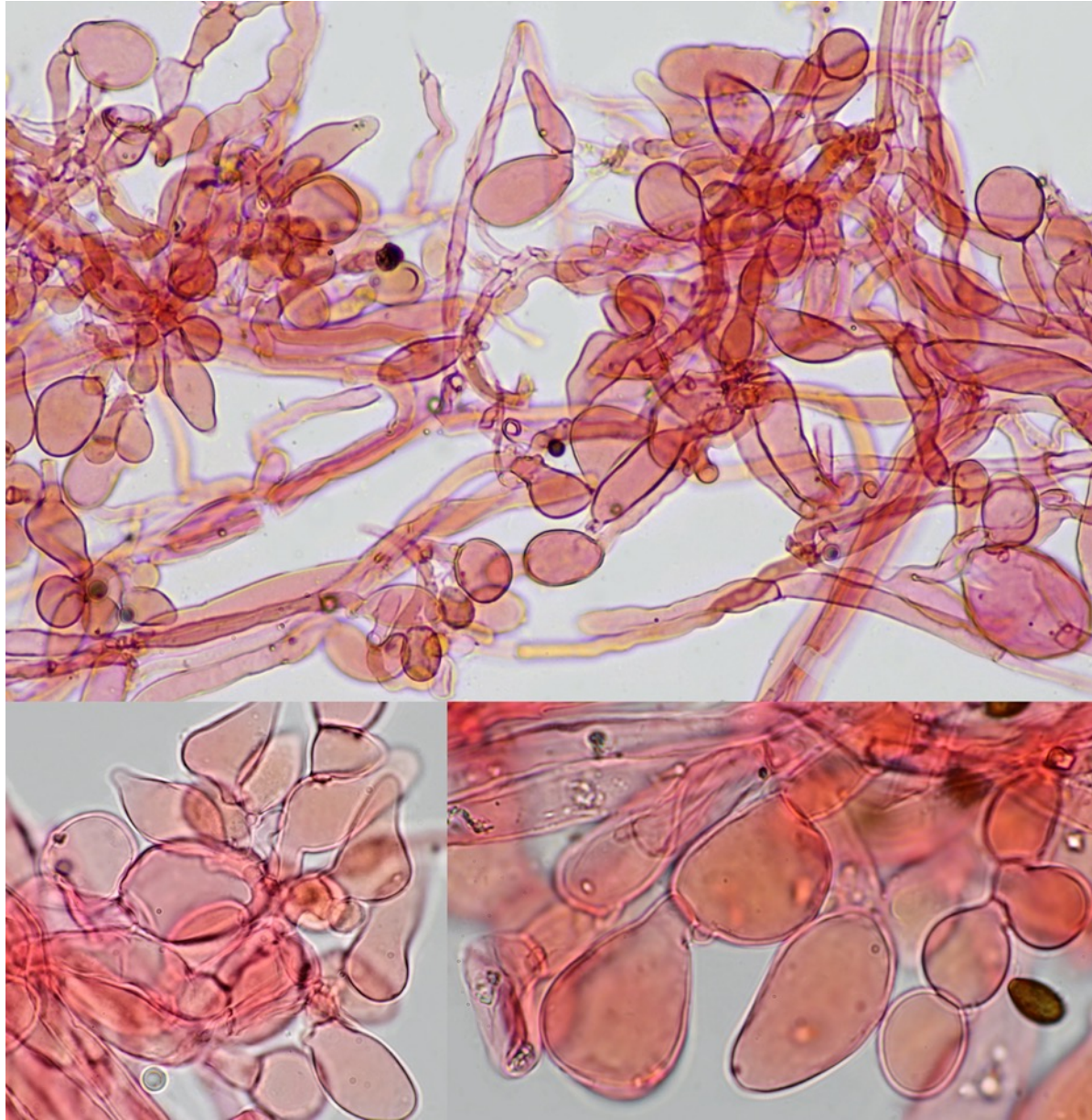
**Pileipellis** constitué de cellules subglobuleuses, irrégulières et entremêlées, recouvertes d'une fine couche d'hyphes cylindriques légèrement pigmentées.

**Basides** tétrasporiques, mesurant 20-30 x 10-12  $\mu\text{m}$ .

**Boucles** présentes.



**Caulocystides** très nombreuses, clavées ou analogues aux cystides.



**Le séquençage ADN** (ITS & LSU) été effectué par Pablo Alvarado Garcia ; laboratoire Alvalab référence: 2017-803-ALV13310 - DD2216.

Genbank Accession number/Version: **MK400695.1**

## DD2216\_Coprinopsis\_pannucioides\_ITS\_final

GTAGCTGGCTCTCCAAGAGTATGTGCACACCTGTCACCTTTATCTTTCTCCCTGTGCACATCTGTAGGCCTGGATAACTCTCGTCGCAAGGCGGATGCAGAGA  
TTGCTGCATGCAGCCTTCTTTGAATTTTCAGGTCTATGACTTTATATACCCCAAACAAATGTTATAGAATGTATTCATAAGGTCTTGTGCCTATAAATTTAAACAA  
CTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAAC  
GCACCTTGCCTCTTGGTATTCCGAGGAGCATGCCTGTTTGTGAGTGCATTAATTTCTCAACCTATTTTTTGAAGCTATAAGGCTTGGATATGGGGGGCTG  
CAGGTCCACAATTATGGTCTGCTCCTCTGAAATGCATTAGTGGGTTAGGCTCCTGTCTGTTAGTGTGATAATTATCTACACTATGGACTAGAGCTTTAATTAACC  
TGCTTATAACATGTCCCTAGGACAATTTTGACAATTT

## DD2216\_Coprinopsis\_pannucioides\_LSU

ACAAGGATTCCCCTAGTAACTGCGAGTGAAGCGGGAAAAGCTCAAATTTAAAATCTGGCAGTCTTTGGCTGTCCGAGTTGTAATCTAGAGAAAGTGTACCCG  
TGCTGGACCGTGTATAAGTCTCCTGGAATGGAGTGTGCATAGAGGGTGAGAATCCCGTCTTTGACATGGACTACCAGTGCTTTTGTGGTGCGCTCTCAAAGAG  
TCGAGTTGTTTGGGAATGCAGCTCAAATGGGTGGTAAATTCATCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACCGTGAGGGAAAGAT  
GAAAAGAAGTTTGGAAAGAGAGTTAAACAGTACGTGAAATTGCTGAAAGGGAAACGCTTGAAGTCAGTCATGTTGACTGGAAATCAACCTTGCTTTTGCTG  
GGTGTACTTTCTGGTTGACGGGCCAGCATCAGTTTTGCTCAATGGAAAAAGTCTAAGGGAATGTGGCATCTTTGGATGTGTTATAGCCCTTGGTTGTATACAT  
TGGTTGGGACTGAGGAATTCAGCACGCCGAAAGGCCGGGTCTTTGACCACGTTTCGTGCTTAGGATGCTGGCATAATGGCTTTAATCGACCCGTCTTGAAAC  
ACGGACCAAGGAGTCTAACATGCCTGCGAGTATTTGGGTGTAAACTCGGATGCGTAATGAAAGTGAAAGTTGGGATCCCTGTCATGGGGAGCACTGACGC  
CCGGACCAGAAGTATTCTGATGGCCCCGCGGTAGAGCATGTATGTTGGGACCCGAAAGATGGTGAAGTATGCCTGAATAGGGTGAAGCCAGAGGAAACTCT  
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## Sequencing and phylogenetic analysis

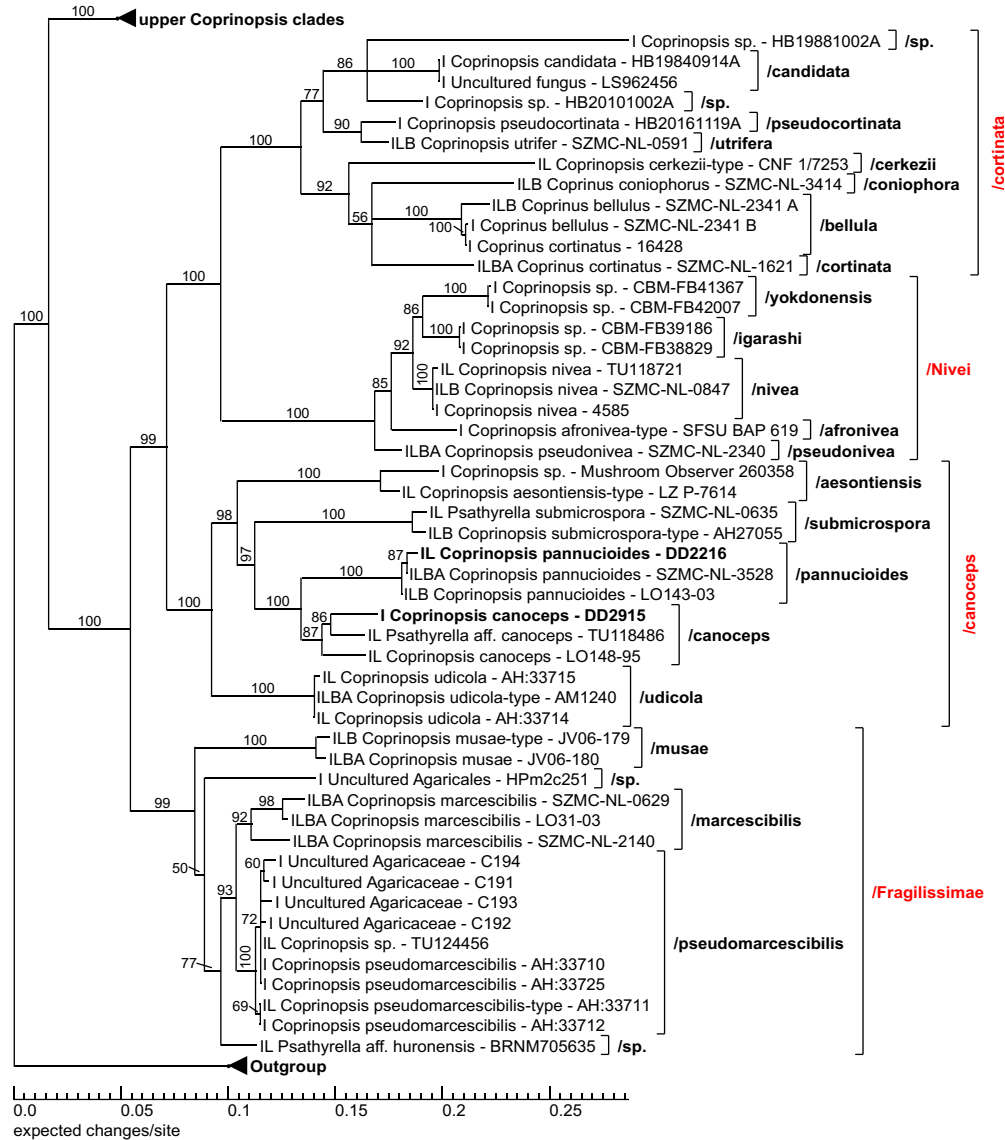
DNA Extraction, Amplification and Sequencing of the fungus was performed by Alvalab (Oviedo, Spain). The phylogenetic analysis was done by Dieter Wächter (Thiersheim, Germany). The genomic DNA was extracted from dried fruiting bodies. Amplification of the ITS region was performed with the ITS4 primer [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 *Icanoceps*-clade by divergence matrix and corrected if necessary. In the present case only a trimming of the trails and some 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),  $\beta$ -tub (exons of the  $\beta$ -tubulin gene), ef-1 $\alpha$  (exons of the ef-1 $\alpha$  gene). The nucleotide sequences for the tree inference were taken from NCBI [4] and Unite [5] (essential ones of the *Icortinata*, *INivei*, *Icanoceps* and *Ifragilissimae*-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-,  $\beta$ -tub and ef-1 $\alpha$  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 +  $\beta$ -tub Codon 1
- DNA-partition 4:  $\beta$ -tub Codon 1 + ef-1 $\alpha$  Codon 1 + ef-1 $\alpha$  Codon 2
- DNA-partition 5:  $\beta$ -tub Codon 3 + ef-1 $\alpha$  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.



# Arbre phylogénétique précisant la position de ma récolte de *Coprinopsis pannuoides*- DD2216



**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:  $\beta$ -tubulin region, A: ef-1 $\alpha$  region.

**Table 1** List of relevant sequences used in this publication

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

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## **Note:**

Le présent article ainsi que d'autres, relatifs aux *Psathyrellaceae* sont disponibles au format pdf sur le site de l'Association des Mycologues francophones de Belgique (AMFB) :

<http://www.amfb.eu/Myco/Psathyrelles/psathyrella.html>

Je suis intéressé par l'examen de toute récolte de *Psathyrelle* que vous voudrez bien me confier.

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