

Psathyrella pseudogracilis (Romagn.) Moser (1967)

in Gams, Kl ; Kryptogam. Fl. , 2b/2,3 , p. 214.

Daniel Deschuyteneer et Dieter Wächter

Basionyme : *Drosophila pseudogracilis* Romagn. (1952), Romagn., Bull. Soc. Linn. Lyon, 21, p. 152.

La description de cette espèce est basée sur plusieurs récoltes effectuées en Brabant flamand (Belgique) ainsi qu'en Allemagne dont l'une (DSD9111) a été séquencée.

The description of this species is based on several harvests from Flemish Brabant (Belgium) and Germany, one of which (DSD9111) has been sequenced.

Habitat : Cette espèce gracile est observée dans les forêts de feuillus, parcs, buissons, parmi le bois raméal fragmenté ainsi que dans l'humus liée à des débris ligneux.

Habits: This gracile species is found in deciduous forests, parks, shrubs, among mulch on the ground and in humus associated with woody debris.

Description macroscopique

Chapeau mesurant de 10 à 25(30) mm de diamètre, lisse, parfois discrètement mamelonné ; initialement conico-campanulé, de couleur noisette avec une marge plus pâle, devenant par la suite plan-convexe, beige terne à grisâtre pâle, strié par transparence jusqu'à mi-rayon. Très hygrophane, il devient presque totalement blanc, avec souvent des tonalités roses.

Lames ventrues, adnées, larges de 2 à 4 mm, moyennement à peu serrées, blanches au début, devenant sous l'effet de la sporée, grisâtres à gris cendré. Arête blanche, mais discrètement et entièrement surlignée de manière continue de rouge-brun. Cette pigmentation de l'arête peut être masquée par la sporée et nécessite parfois un examen sous la loupe binoculaire, après détersion des spores. La **trame** lamellaire est presque hyaline.

Voile très volatile, présent uniquement sur les primordia sous forme de fibrilles blanchâtres au niveau de la marge et sur le stipe, disparaissant totalement sur les sujets adultes.

Stipe : 40-90 x 1-2,5 mm, cylindrique, creux, blanc, lisse, légèrement pruveux au sommet ; base un peu dilatée et strigieuse par le mycélium blanc, parfois courtement radicaux, parfois avec un pseudorhize pouvant atteindre 25 mm selon Melzer et Örstadius.

Chair : 1-2 mm d'épaisseur, concolore au chapeau, blanche ; saveur et odeur sans particularités.

Description microscopique

Basides : clavées, tétrasporiques.

Spores mesurant (11,9-)12,1-12,8 13,5(-15,1) × (6,1-)6,3-6,7(-7,6) µm ; Q = (1,7)1,8-2(2,1) ; N = 70 ; brun-rouge foncé, opaques à subopaques, oblongues à ellipsoïdes de face, asymétriques et légèrement amygdaliformes de profil, avec un large pore germinatif central, parfois tronqué, mesurant 1,5-2 µm.

Cheilocystides abondantes, clairessemées ou groupées en « cluster », nettement versiformes, majoritairement largement utriformes, à paroi fine ou discrètement épaissie, mesurant 25-52 x 13-22 µm mais également lagéniformes, mesurant alors 23-42 x 8-13 µm, ainsi que de nombreuses formes intermédiaires, mêlées à de nombreuses cellules marginales clavées et sphéropédonculées (= paracystides) généralement de petite taille, dont la paroi est souvent épaissie et pigmentée de brun-jaune. A proximité de la marge du chapeau les cheilocystides se font plus rares, sont davantage lagéniformes et la marge est alors occupée essentiellement par des cellules « marginales clavées et sphéropédonculées » à paroi pigmentée (= paracystides).

Pleurocystides mesurant 32-60(-70) x 13-17(-22) µm, nombreuses, le plus souvent lagéniformes et pédicellées, mais également utriformes comme les cheilocystides et alors à parois souvent légèrement épaissies et teintées. A noter la présence erratique de pleurocystides de tailles hors norme, à parois épaisses teintées et à sommet parfois fourchu.

Pileipellis banal, composé de cellules globuleuses, clavées et sphéropédonculées.

Boucles présentes.



Cette récolte (DSD9111), illustrant l'espèce à différents stades d'évolution, a été séquencée.
[This harvest \(DSD9111\) illustrating the species at different stages of evolution was sequenced.](#)
Genbank Accession number/Version: **MK045739.1**



Récolte de Bergnersreuth du 21/09/2015 - 95659 Arzberg – Allemagne - 50°04'04.5"N 12°09'08.9"E

Photo-montage Dieter Wächter

Cap: measuring 10 to 25(30) mm in diameter, smooth, sometimes with a small umbo; initially conico-campanulate, hazelnut colored with a paler margin, later becoming plane-convex, dull beige to pale greyish, striate by transparency halfway to centre. Highly hygrophanous, it becomes almost totally white, drying sometimes with pink tinges.

Veil: present only in very young fruitbodies as very fugacious whitish fibrils near the margin and on the stipe, disappearing completely on mature specimens.



Stem: 40-90 x 1-2,5 mm, cylindrical, hollow, white, smooth, pruinose at apex; slightly thickening toward base which is more or less strigose by white mycelium, sometimes shortly rooting or with up to 25 mm pseudorrhiza according to Melzer and Örstadius.

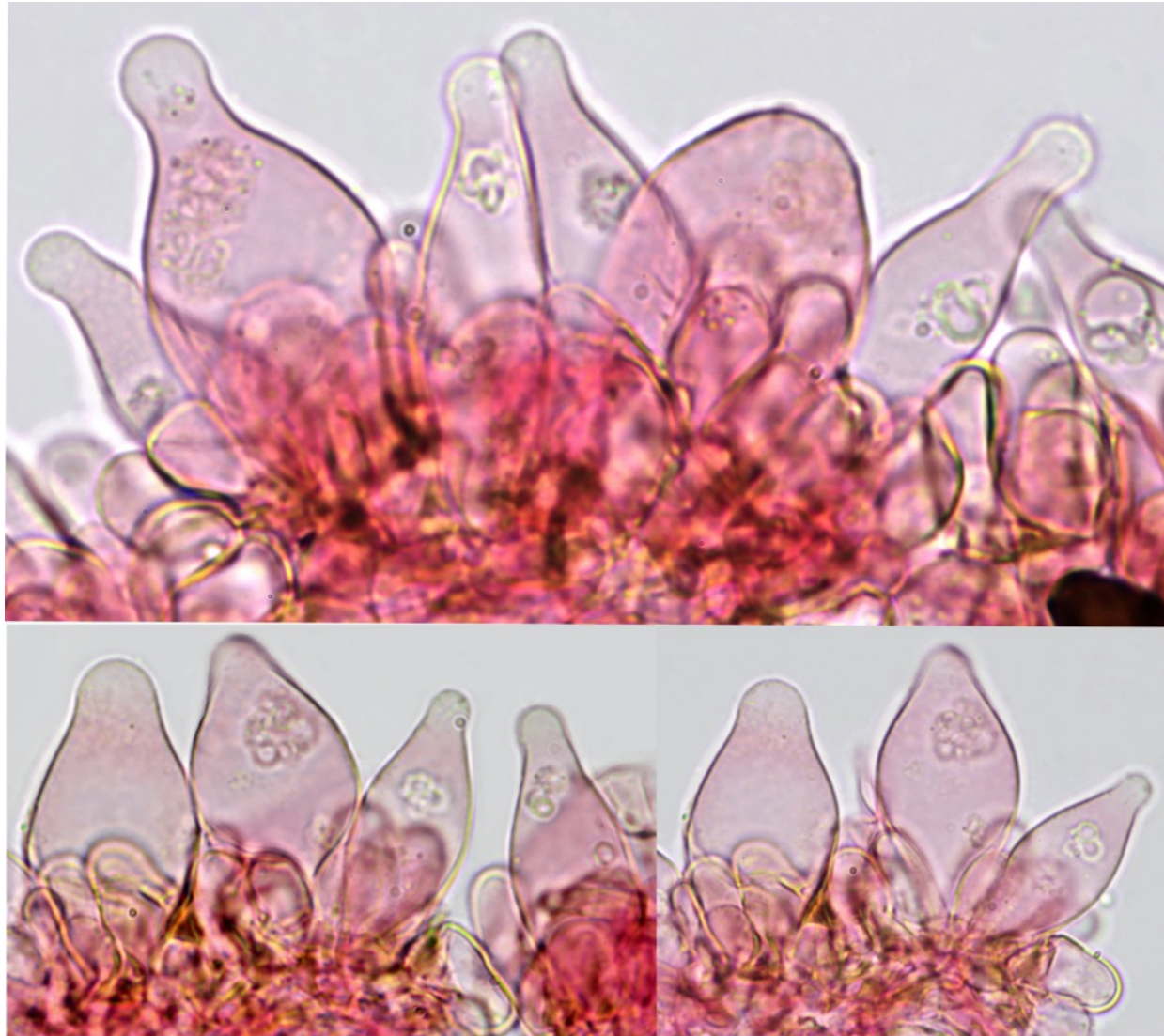
Flesh: 1-2 mm thick, concolorous to the cap; taste and smell not distinctive.

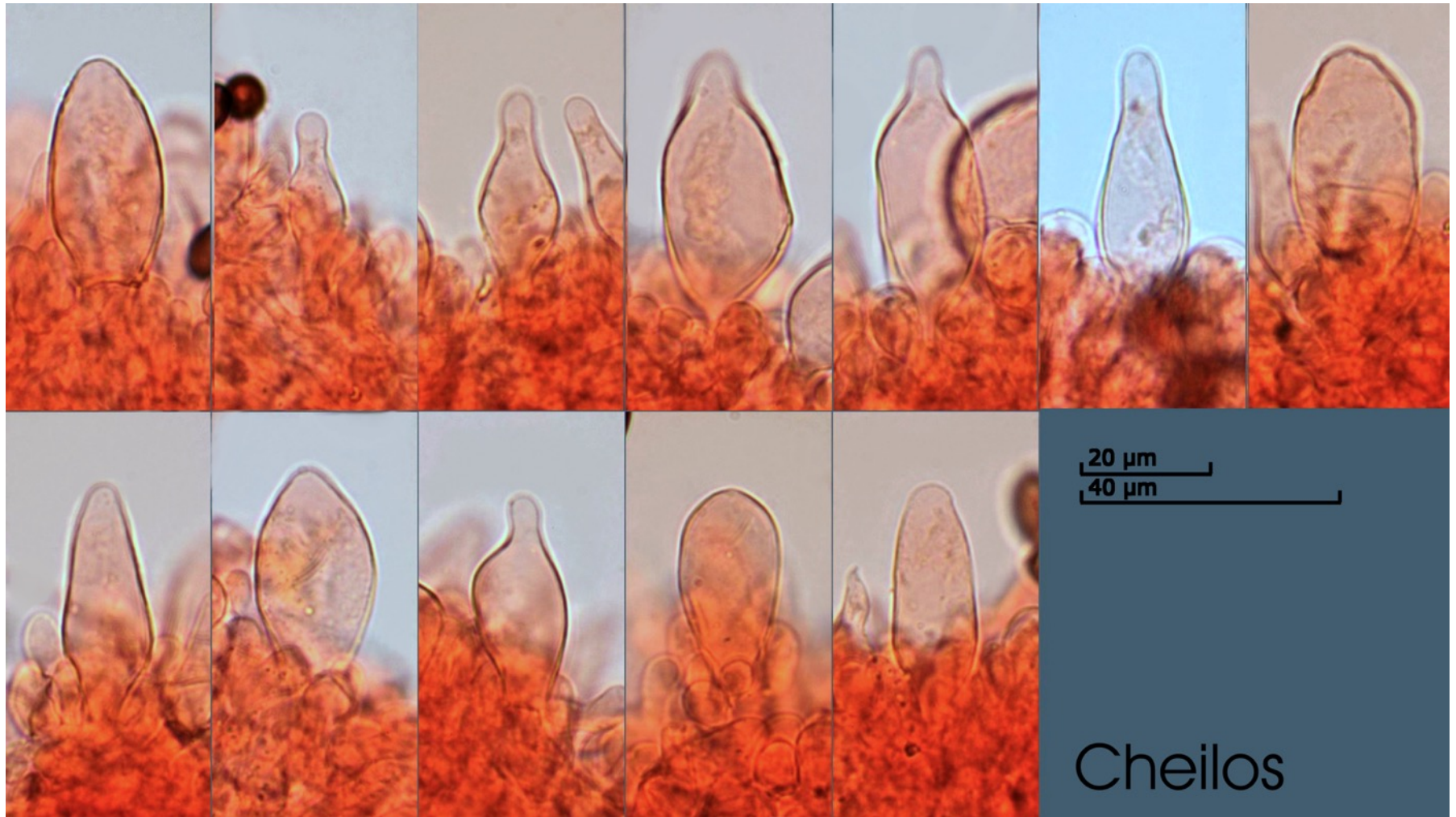


Gills: ventricose, adnate, 2 to 4 mm broad, moderately distant, initially white becoming, greyish to ash-grey. Edge white, but discretely and continuously red-brown underlined. This pigmentation of the edge can be hidden by the spores and sometimes requires an examination under a binocular magnifying glass, of « washed » gills. The trama of « washed » gills is nearly hyaline.



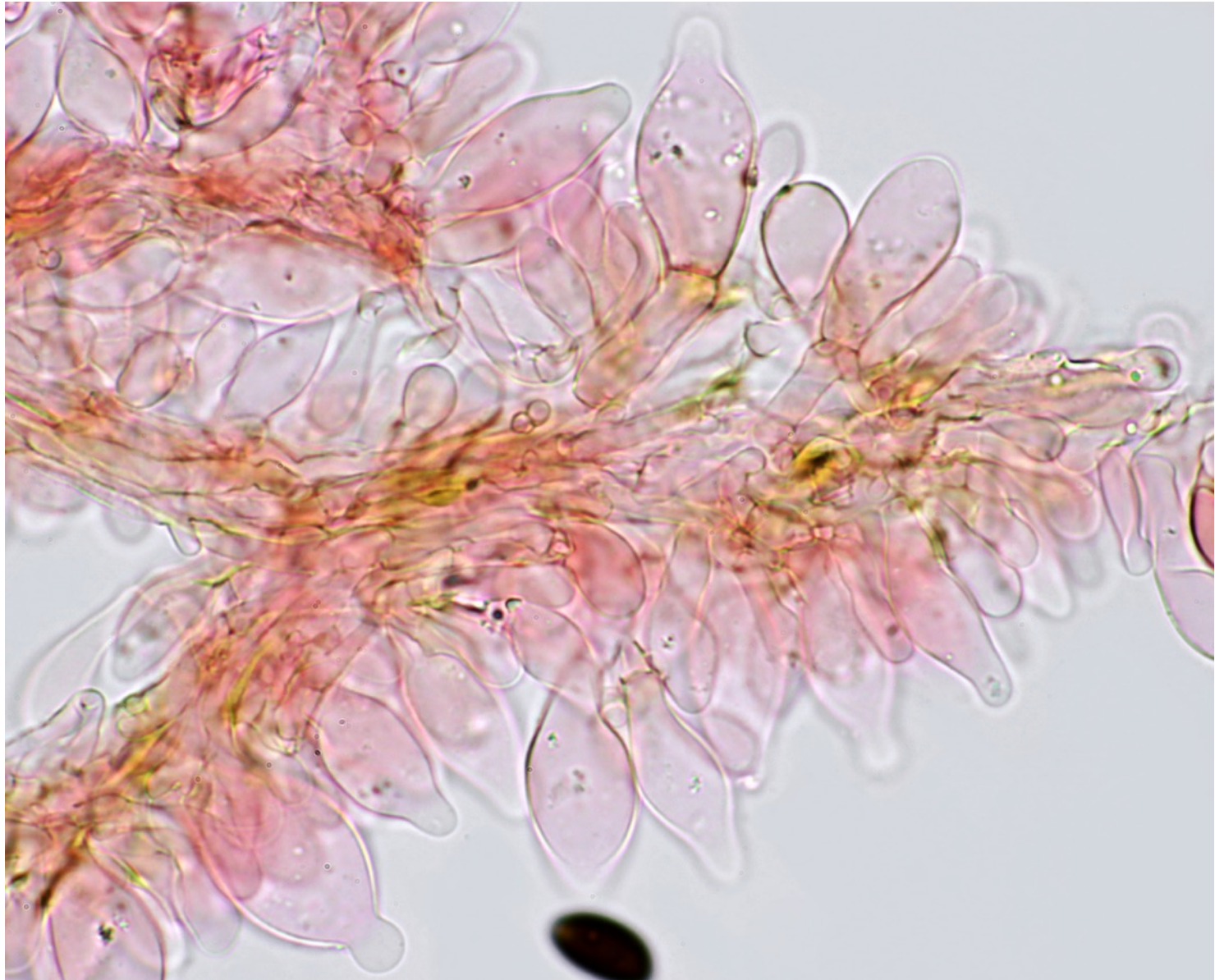
Cheilocystidia abundant, scattered or most often grouped in clusters, versiform, mostly utriform, thin-walled or discretely thickened, measuring 25-52 x 13-22 μm but also lageniform, measuring 23-42 x 8-13 μm , as well as many intermediary shapes, mixed with many clavate to obpyriform marginal cells (= paracystidia) generally of small sizes whose wall is often slightly thickened and yellow-brown pigmented. Near the cap margin, the cheilocystidia are rarer, more often lageniform and paracystidia predominate.



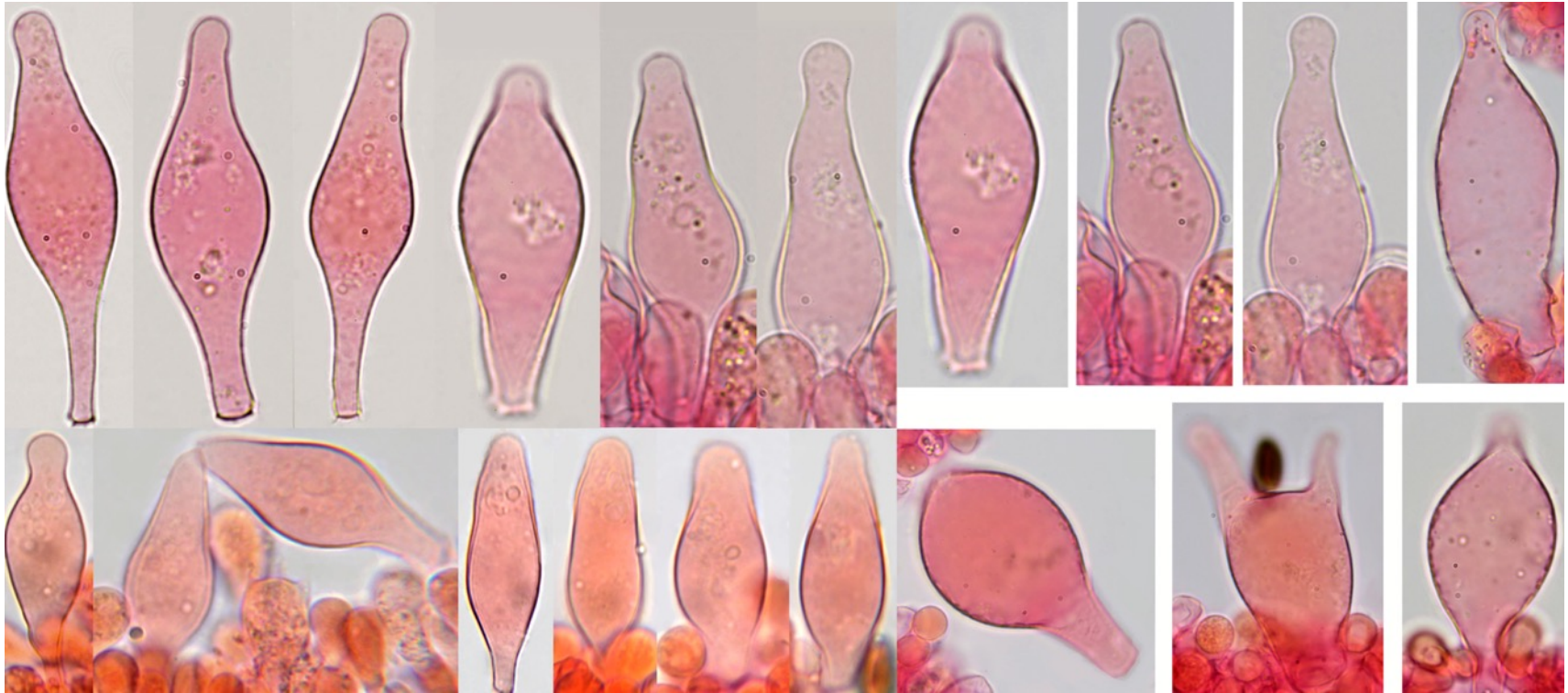


Cheilocystidia from D. Wächter specimens.





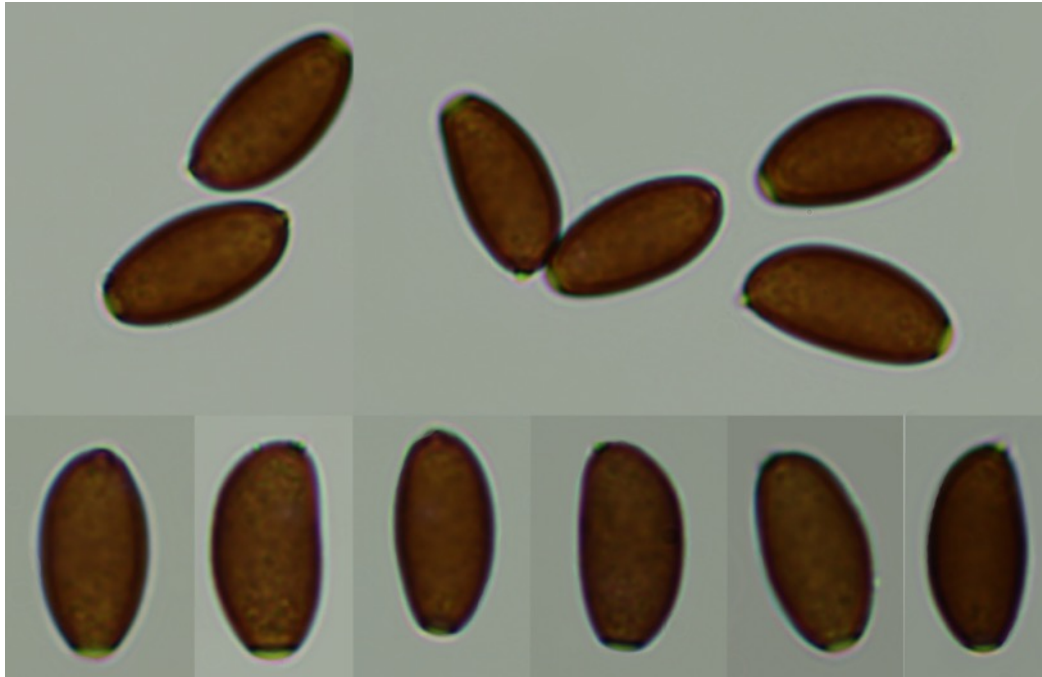
Pleurocystidia measuring 32-60(-70) x 13-17(-22) μm , numerous, most often lageniform and pedicellate, but also utriform like the cheilocystidia and then often with slightly thickened and tinted walls. To be noted the erratic presence of pleurocystidia of unusual sizes with thick light brown coloured walls and sometimes forked apex.



Spores: measuring (11,9-)12,1-12,8-13,5(-15,1) \times (6,1-)6,3-6,7-7(-7,6) μm ; Q = (1,7)1,8-2(2,1) ; N = 70, dark red-brown, opaque to subopaque, oblong to ellipsoidal in face view, asymmetric and slightly amygdaloid in profile, with a broad central and sometimes truncate germinal pore measuring 1.5-2 μm .

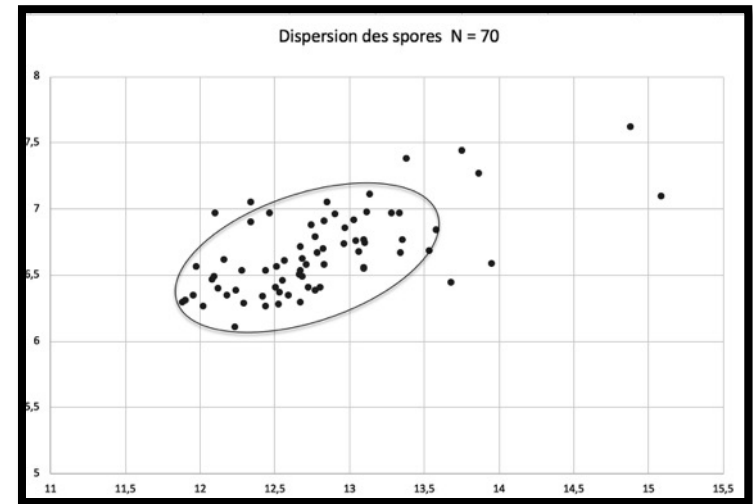
Pileipellis banal formed of globular, clavate and obpyriform .

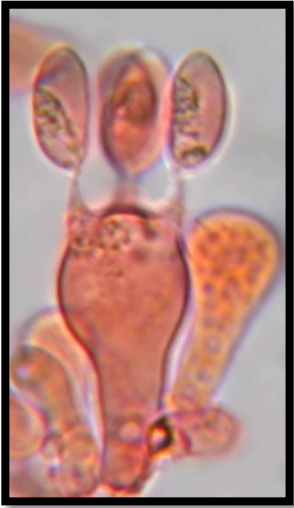
Clamps present.



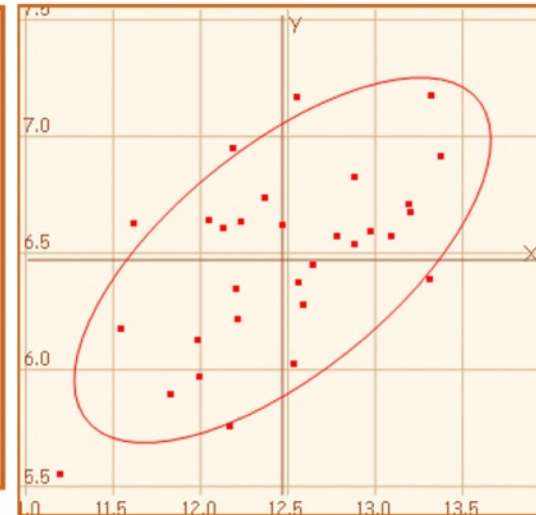
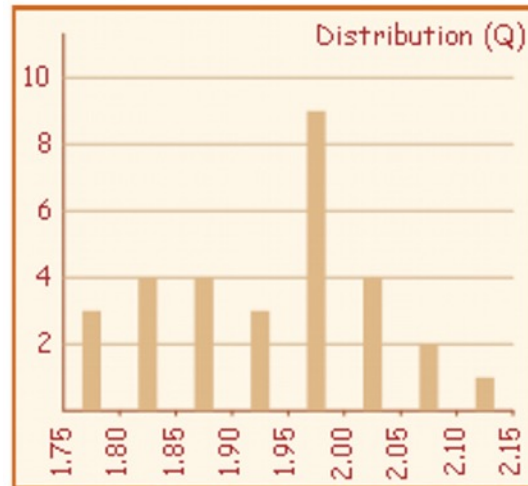
Spores in NH_4OH 10%

Mesures des spores des récoltes belges avec Piximètre
 (11,9)12,1-13,5(15,1) \times (6,1)6,3-7(7,6) μm
 Q = (1,7)1,8-2(2,1) ; N = 70
 Me = 12,8 \times 6,7 μm ; Qe = 1,9





Basidia clavate, 4-spored



Dispersion des spores – Spores dispersion - D. Wächter - Piximètre

Molecular part

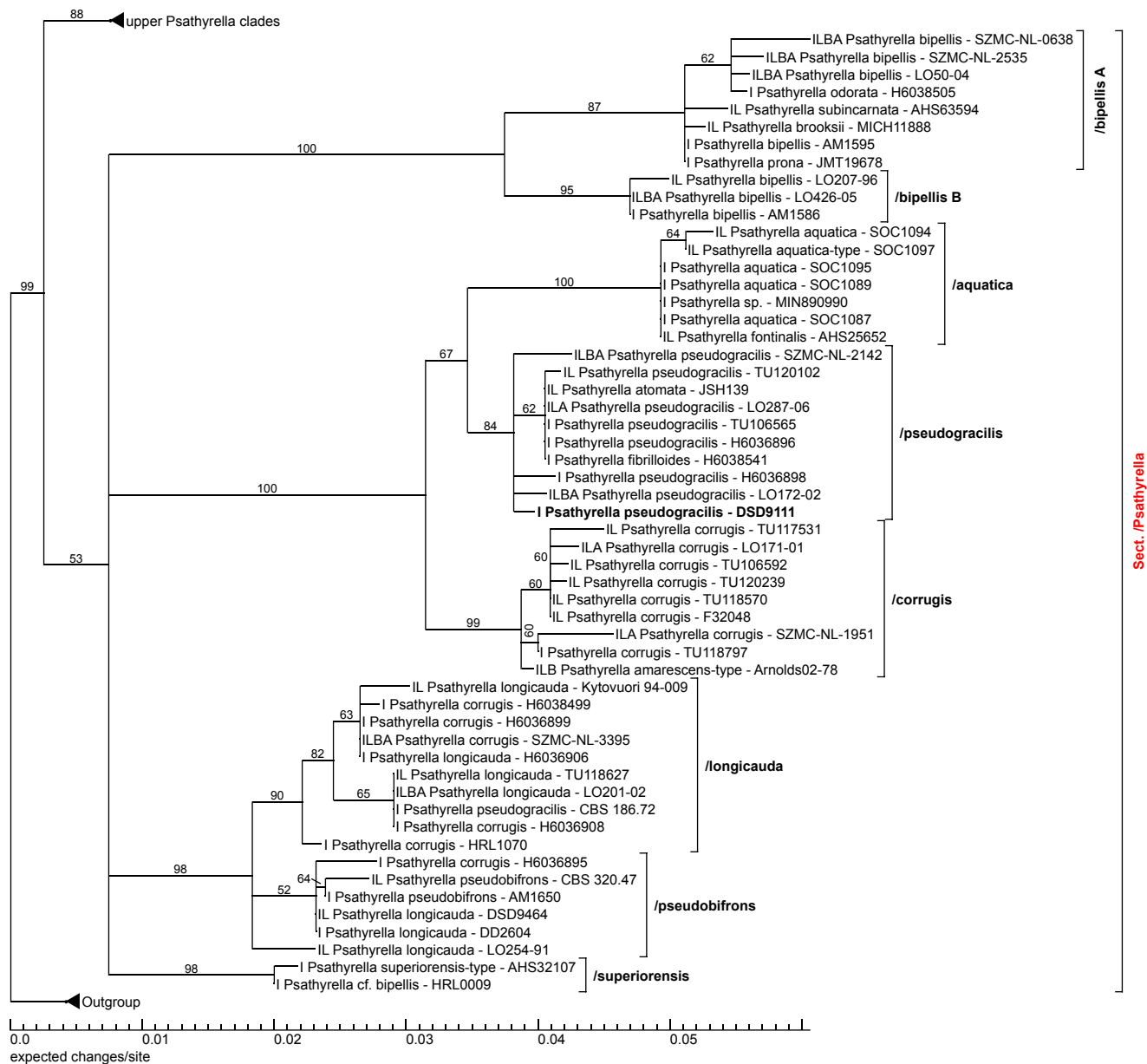
Séquençage ADN de *Psathyrella pseudogracilis* DSD9111 - Alvalab 12973_ITS

Genbank Accession number/Version: **MK045739.1**

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]. The initial base calling was done with FinchTV [2]. 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 *IPsathyrella*-clade (section) 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), β -tub (exons of the β -tubulin gene), ef-1 α (exons of the ef-1 α gene). The nucleotide sequences for the tree inference were taken from NCBI [3] and Unite [4] (essential ones of the partial *IPsathyrella*-clade see Table 1). Region boundaries for the ITS- and LSU-region were carried out with ITSx [5] and HMMER [6] including the databases. As outgroup, the sequence sets of the most closely related clades of the ingroup were used, i.e. the *prona*-clade down to the *candolleana*-clade. 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 [7] using the FFT-NS-2 method. The initial alignments of the LSU-, β -tub and ef-1 α genes was carried out using E-INS-i method. The indel matrices for the ITS and LSU regions were each coded with SeqState [8] using the SIC = "Simple Indel coding" [9] method. After each alignment step, an ML analysis with RAXML [10] (model: GTRCAT, refining under GTR+G for DNA, GTR2+G with acquisition bias correction according to Lewis [11] 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 [12], 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 [13]. For the final partitioning, the guide tree of the last iteration step was used. As information criterion the Bayesian Information Criterion (BIC) [14] used was after comparison with the Corrected Akaike Information Criterion (AICc) [15] 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: LSU + 5.8S + β -tub-Codon 1 + ef-1 α -Codon 1
- DNA-partition 3: β -tub-Codon 2 + ef-1 α -Codon 2
- DNA-partition 4: β -tub-Codon 3 + ef-1 α -Codon 3
- Binary partition (gap matrices): ITS1 + ITS2 + LSU

The final maximum likelihood analysis was done with RAXML 8.2.10 [10]. For all DNA partitions, the GTR substitution matrix [16] under the CAT model [10] was used. The final optimization took place under gamma distribution [10]. For the binary partitions, the "Two State Time-Reversible Model" with acquisition bias correction [11] 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 [17].



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-1 α region.

Table 1 List of relevant sequences used in this publication

Species	Voucher	ITS	LSU	β -Tub	ef-1 α
<i>Psathyrella amarescens</i>	Arnolds02-78	KC992852.1	KC992852.1	KJ664842.1	
<i>Psathyrella aquatica</i>	SOC1094	EU259194.2	EU259195.1		
<i>Psathyrella aquatica</i>	SOC1089	EU664990.1			
<i>Psathyrella aquatica</i>	SOC1095	EU259196.2			
<i>Psathyrella aquatica</i>	SOC1097	EU259192.2	EU259193.1		
<i>Psathyrella aquatica</i>	SOC1087	EU664989.1			
<i>Psathyrella atomata</i>	JSH139	FJ899610.1	DQ986230.1		
<i>Psathyrella bipellis</i>	SZMC-NL-0638	FN396108.1	FN396160.1	FN396303.1	FN396216.1
<i>Psathyrella bipellis</i>	SZMC-NL-2535	FN430689.1	FM160688.1	FN396297.1	FN430691.1
<i>Psathyrella bipellis</i>	LO50-04	DQ389680.1	DQ389680.1	KJ664847.1	KJ732761.1
<i>Psathyrella bipellis</i>	AM1595	MK045706.1			
<i>Psathyrella bipellis</i>	LO207-96	DQ389679.1	DQ389679.1		
<i>Psathyrella bipellis</i>	LO426-05	KC992865.1	KC992865.1	KJ664848.1	KJ732762.1
<i>Psathyrella bipellis</i>	AM1586	MK045708.1			
<i>Psathyrella brooksii</i>	MICH11888	EU664993.1	EU664995.1		
<i>Psathyrella cf. bipellis</i>	HRL0009	KX897437.1			
<i>Psathyrella corrugis</i>	SZMC-NL-1951	FM878015.1	FM876272.1		FM897220.1
<i>Psathyrella corrugis</i>	TU118797	UDB019572			
<i>Psathyrella corrugis</i>	TU117531	UDB034043	UDB034043		
<i>Psathyrella corrugis</i>	LO171-01	DQ389674.1	DQ389674.1		KJ732757.1
<i>Psathyrella corrugis</i>	TU106592	UDB011818	UDB011818		
<i>Psathyrella corrugis</i>	TU120239	UDB024631	UDB024631		
<i>Psathyrella corrugis</i>	TU118570	UDB017986	UDB017986		
<i>Psathyrella corrugis</i>	F32048	KX236128.1	KX236128.1		
<i>Psathyrella corrugis</i>	H6038499	UDB021180			
<i>Psathyrella corrugis</i>	H6036899	UDB021162			
<i>Psathyrella corrugis</i>	SZMC-NL-3395	FN430692.1	FN396205.1	FN396344.1	FN396240.1
<i>Psathyrella corrugis</i>	H6036908	UDB021171			
<i>Psathyrella corrugis</i>	HRL1070	KX897407.1			
<i>Psathyrella corrugis</i>	H6036895	UDB021158			
<i>Psathyrella fibrilloides</i>	H6038541	UDB021219			
<i>Psathyrella fontinalis</i>	AHS25652	FJ899614.1	FJ899629.1		
<i>Psathyrella longicauda</i>	Kvtovuori 94-009	DQ389677.1	DQ389677.1		

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] **FinchTV 1.4.0**: Geospiza, Inc.; Seattle, WA, USA; <http://www.geospiza.com>
- [3] **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/>
- [4] **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
- [5] **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)
- [6] **HMMER 3.1b2** (February 2015): <http://hmmer.org/> - Copyright (C) 2015 Howard Hughes Medical Institute. Freely distributed under the GNU General Public License (GPLv3)
- [7] **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.
 - KATOH, ROZEWICKI, YAMADA 2017 (Briefings in Bioinformatics, in press) - MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization.
 - YAMADA, TOMII, KATOH 2016 (*Bioinformatics* 32:3246-3251) additional information - Application of the MAFFT sequence alignment program to large data-reexamination of the usefulness of chained guide trees.
 - KATOH, STANDLEY 2016 (*Bioinformatics* 32:1933-1942) - A simple method to control over-alignment in the MAFFT multiple sequence alignment program.
 - KATOH, STANDLEY 2013 (*Molecular Biology and Evolution* 30:772-780) - MAFFT multiple sequence alignment software version 7: improvements in performance and usability.
 - KURAKU, ZMASEK, NISHIMURA, KATOH 2013 (*Nucleic Acids Research* 41:W22-W28) - aLeaves facilitates on-demand exploration of metazoan gene family trees on MAFFT sequence alignment server with enhanced interactivity.
 - KATOH, FRITH 2012 (*Bioinformatics* 28:3144-3146) - Adding unaligned sequences into an existing alignment using MAFFT and LAST.
 - KATOH, TOH 2010 (*Bioinformatics* 26:1899-1900) - Parallelization of the MAFFT multiple sequence alignment program.
 - KATOH, ASIMENOS, TOH 2009 (*Methods in Molecular Biology* 537:39-64) - Multiple Alignment of DNA Sequences with MAFFT. In *Bioinformatics for DNA Sequence Analysis* edited by D. Posada
 - KATOH, TOH 2008 (*BMC Bioinformatics* 9:212) - Improved accuracy of multiple ncRNA alignment by incorporating structural information into a MAFFT-based framework.
 - KATOH, TOH 2008 (Briefings in Bioinformatics 9:286-298) - Recent developments in the MAFFT multiple sequence alignment program.
 - KATOH, TOH 2007 (*Bioinformatics* 23:372-374) Errata - PartTree: an algorithm to build an approximate tree from a large number of unaligned sequences.
 - KATOH, KUMA, TOH, MIYATA 2005 (*Nucleic Acids Res.* 33:511-518) - MAFFT version 5: improvement in accuracy of multiple sequence alignment.
 - KATOH, MISAWA, KUMA, MIYATA 2002 (*Nucleic Acids Res.* 30:3059-3066) - MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform.
- [8] **SeqState 1.4.1**: MÜLLER, K (2005), SeqState - primer design and sequence statistics for phylogenetic DNA data sets. *Applied Bioinformatics*, 4, 65-69
- [9] **SIC (Simple Indel Coding)**: SIMMONS MP AND OCHOTERENA H (2000): Gaps as characters in sequence-based phylogenetic analyses. *Syst Biol* 49: 369–381
- [10] **RAXML Version 8.2.10**: A. STAMATAKIS: "RAXML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies". In *Bioinformatics*, 2014, open access link: <http://bioinformatics.oxfordjournals.org/content/early/2014/01/21/bioinformatics.btu033.abstract?keytype=ref&ikey=VTEqgUJYCDcf0kP>
- [11] **Two parameter model & Acquisition Bias Correction**: PAUL O. LEWIS: A Likelihood Approach to Estimating Phylogeny from Discrete Morphological Character Data - *Systematic Biology*, Volume 50, Issue 6, 1 November 2001, Pages 913–925
- [12] **Prank 140603**:
- LÖYTYNOJA A, GOLDMAN N: AN ALGORITHM FOR PROGRESSIVE MULTIPLE ALIGNMENT OF SEQUENCES WITH INSERTIONS. *PROC NATL ACAD SCI USA* 2005, 102: 10557–10562. 10.1073/PNAS.0409137102
 - LÖYTYNOJA A, GOLDMAN N: A MODEL OF EVOLUTION AND STRUCTURE FOR MULTIPLE SEQUENCE ALIGNMENT. *PHILOS TRANS R SOC LOND B BIOL SCI* 2008, 363: 3913–3919. 10.1098/RSTB.2008.0170
 - PHYLOGENY-AWARE ALIGNMENT WITH PRANK (ARI LÖYTYNOJA), [METHODS MOL BIOL.](#) 2014;1079:155-70
- Prank - F Option**: LÖYTYNOJA A, GOLDMAN N: Phylogeny-aware gap placement prevents errors in sequence alignment and evolutionary analysis. *Science* 2008, 320: 1632–1635. 10.1126/science.1158395
- [13] **Partitionfinder 2.1.1**:
- LANFEAR, R., FRANDSEN, P. B., WRIGHT, A. M., SENFELD, T., CALCOTT, B. (2016) PartitionFinder 2: new methods for selecting partitioned models of evolution formolecular and morphological phylogenetic analyses. *Molecular biology and evolution*. DOI: [dx.doi.org/10.1093/molbev/msw260](https://doi.org/10.1093/molbev/msw260)
 - greedy algorithm used with Partitionfinder: LANFEAR, R., CALCOTT, B., HO, S. Y., & GUINDON, S. (2012). PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Molecular biology and evolution*, 29(6), 1695-1701
- [14] **Bayesian Information Criterion (BIC)**: SCHWARZ, G. (1978). Estimating the dimension of a model. *The Annals of Statistics*, 6, 461–464
- [15] **Corrected Akaike Information Criterion (AICc)**:
- AKAIKE, H. (1974). A new look at the statistical model identification. *IEEE Transactions on Automatic Control*, 19, 716–723
 - HURVICH, C. AND TSAI, C. (1989). Regression and time series model selection in small samples. *Biometrika*, 76, 297–307
 - SUGIURA, N. (1978). Further analysis of the data by akaike's information criterion and the finite corrections. *Communications in StatisticsTheory and Methods*, A7,13–26
 - MARK J. BREWER, ADAM BUTLER, SUSAN L. COOKSLEY 2016- The relative performance of AIC, AICC and BIC in the presence of unobserved heterogeneity
 - BROWN, J.M., LEMMON, A.R. 2007 - The importance of data partitioning and the utilityof Bayes factors in Bayesian phylogenetics. *Syst. Biol.* 56, 643–655
- [16] **GTR-Modell**: TAVARÉ S. Some probabilistic and statistical problems in the analysis of DNA sequences, *Lectures on mathematics in the life sciences*, vol. Volume 17 Providence (RI) American Mathematical Society
- [17] **Treegraph 2.14.0-771 beta**: STÖVER B C, MÜLLER K F: TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses. *BMC Bioinformatics* 2010, 11:7 - DOI: 10.1186/1471-2105-11-7

Discussion : sur le terrain, cette espèce peu fréquente est très difficile à distinguer de *Psathyrella corrugis*. Ceci est bien illustré sur les photos ci-après

Discussion: In situ, this infrequent species is very difficult to differentiate from *Psathyrella corrugis*. This is well illustrated in the photos below.



Psathyrella pseudogracilis



Psathyrella corrugis

L'aspect général de l'arête apporte néanmoins de précieux renseignements permettant de séparer les deux espèces.

En effet, si les deux espèces possèdent bien une arête blanche fimbriée surlignée de rouge-brun, son aspect apparaît bien différent pour chacune. La pigmentation de l'arête de *P. pseudogracilis* est continue et apparaît peu marquée à l'examen microscopique et les cellules « marginales clavées et sphéropédonculées = paracystides », à paroi légèrement pigmentée, sont petites et ne sont présentes en grand nombre qu'à proximité de la marge du chapeau.

Nevertheless, the general appearance of the edge provides valuable information to separate the two species.

Indeed, if the two species do have a white fimbriate edge underlined with reddish-brown, its aspect appears significantly different for each.

The pigmentation of the edge of *P. pseudogracilis* is continuous and appears not very marked on microscopic examination and the "marginal clavate and spheropedonculate cells (paracystidai), with slightly pigmented walls, are small and only present in large numbers near the cap margin.

Par contre, l'arête de *P. corrugis* (illustrée ci-après) est surlignée de manière très nette et discontinue, surtout dans sa moitié proche de la marge du chapeau.

Cet aspect est évident au microscope dès le plus faible grossissement et un œil avisé peut déjà le visualiser sous la loupe binoculaire.

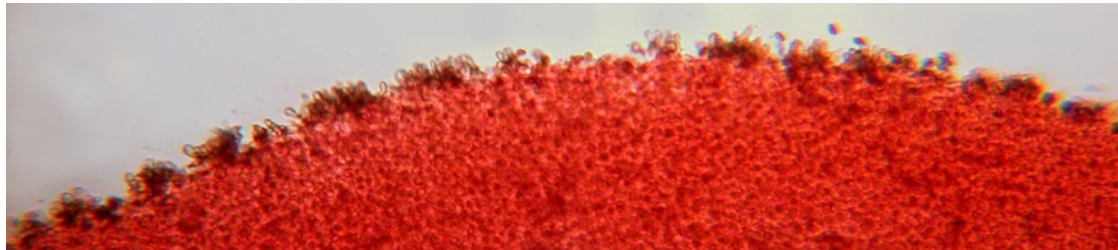
De plus, les cellules marginales sont très développées, de grande taille, souvent irrégulières, nettement pigmentées de brun jaunâtre et à paroi très épaisse.

On the other hand, the edge of *P. corrugis* (illustrated below) is very clearly and discontinuously underlined, especially in its half near the cap margin.

This is evident under the microscope at the lowest magnification and a keen eye can already visualize this character under a binocular magnifying glass. In addition, the marginal cells are well-developed, large in size, often irregular, strongly yellowish-brown pigmented and very thick walled.

L'aspect des cystides est également bien différent dans les deux espèces et permet alors de les différencier facilement.

The appearance of the cystidia is also very different in the two species and allows then to easily differentiate them.



Arête de *P. corrugis* - Edge of *P. corrugis*

Remerciements à

Pablo Alvarado Garcia (Alvalab) pour le séquençage de l'ADN ribosomal (fraction ITS),
Marcel Lecomte pour la relecture de cette fiche sur le plan de la forme,
François Corhay qui assure sa publication sur le site de l'AMFB.

Littérature et iconographie

ENDERLE M., 1993 - *Studien in der Gattung Psathyrella* III, p. 57

EYSSARTIER G., 2004 - *Notes sur quelques espèces de cortinaires et de psathyrelles rares ou nouvelles* : pp. 23-24

EYSSARTIER G. & ROUX P. - *Le guide des champignons, France et Europe*, p. 894

EYSSARTIER G. & ROUX P., 2017 - *Le guide des champignons, France et Europe*, 4^{ème} éd., p. 924

LUDWIG E., 2007 - *Pilzkompendium Band 2 Abbildungen* : Tafel 390 – plate 98.73 A-B-C

ÖRSTADIUS L. & KNUDSEN H., 2008 : *Funga Nordica*, p. 590

ÖRSTADIUS L. & KNUDSEN H., 2012 : *Funga Nordica*, p. 694

Auteurs - Authors

Daniel Deschuyteneer, Spreeuwenhoek 12, 1820 Perk, Belgique.

danieldeschuyteneer@gmail.com

Dieter Wächter, Burgstrasse 5, 95707 Thiersheim, Germany.

info@nocrotec.com

Récolte du 19/07/2020 le long d'un chemin herbeux dans un parterre de bois raméal fragmenté sous jacent.

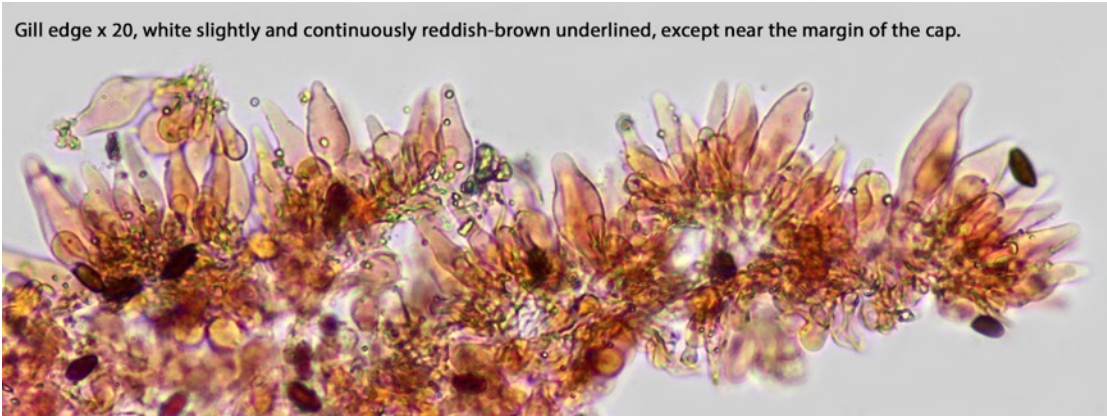
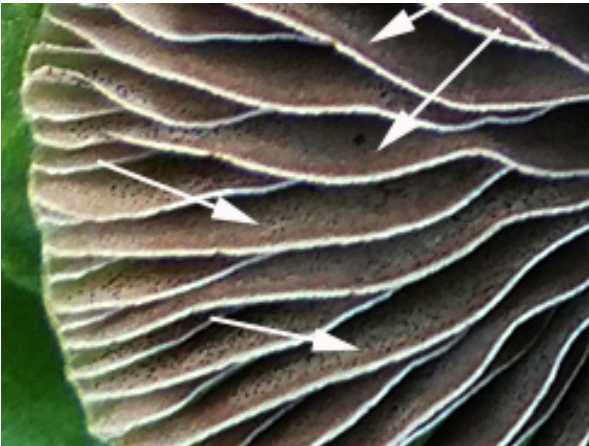
Collection of 19/07/2020 along a grassy path in an underlying mulch bed.



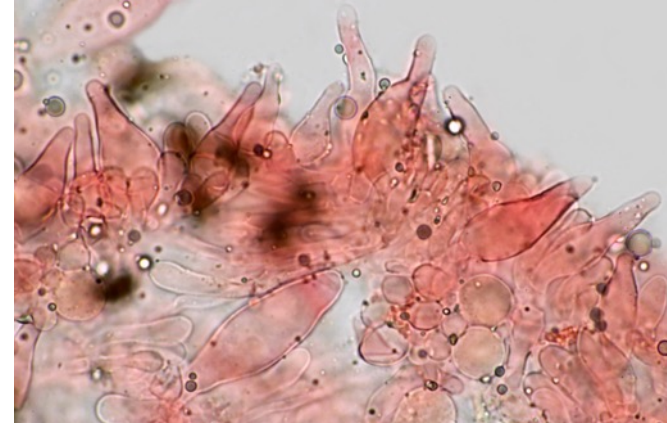
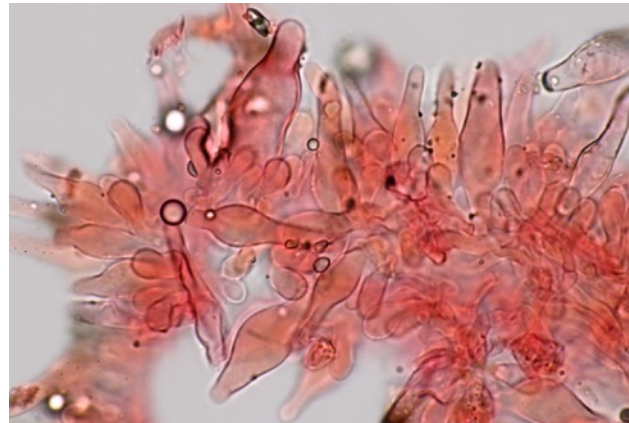
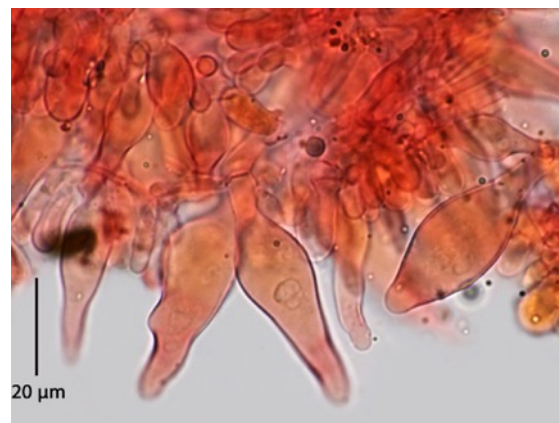
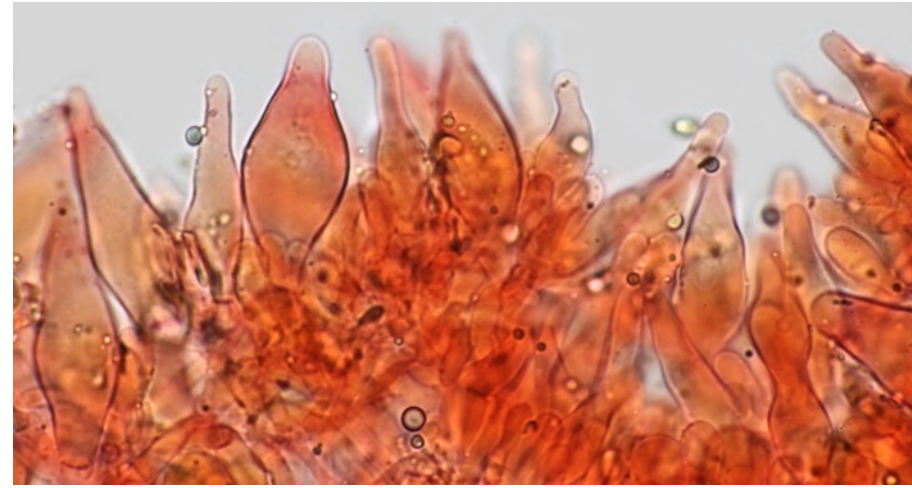
Deschuyteneer Daniel – Perk – 19/07/2020

Base du stipe non radicante, strigieuse fixée à des débris de bois – Arête des lames blanche délicatement surlignée de rouge brun de manière continue sauf à proximité de la marge du chapeau.

Base of stipe not rooting, strigous, attached to wood debris – Gill edge white, delicately and continuously underlined with red-brown except near the margin of the cap.

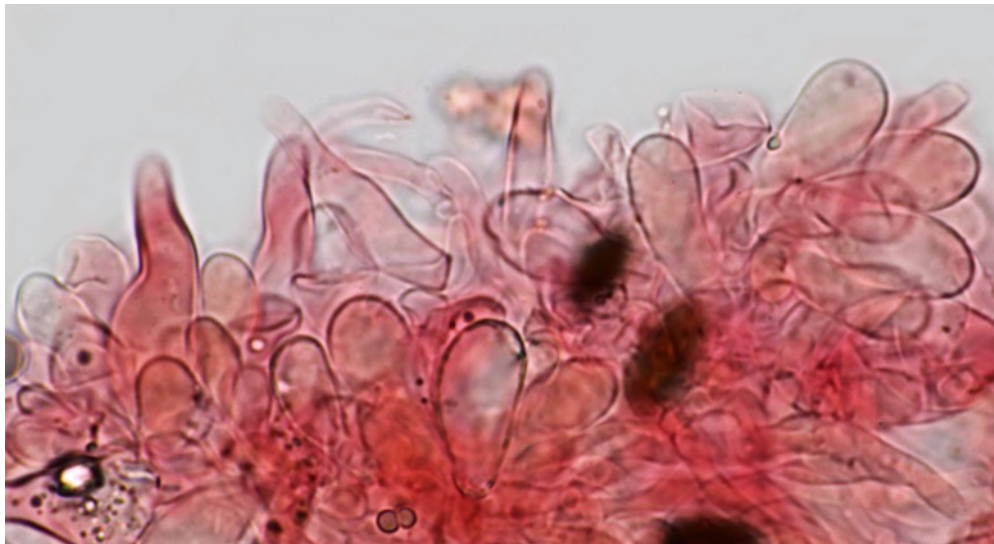
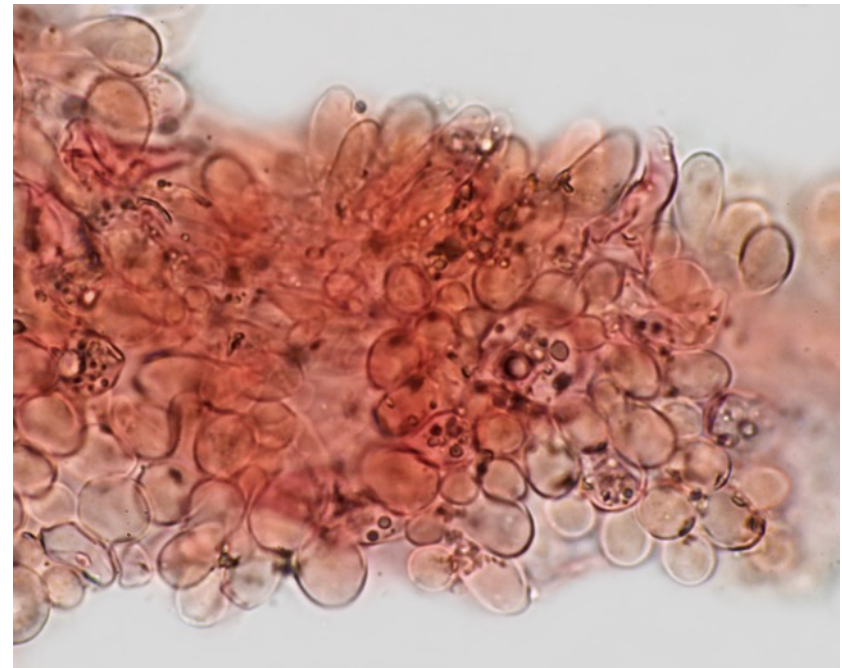
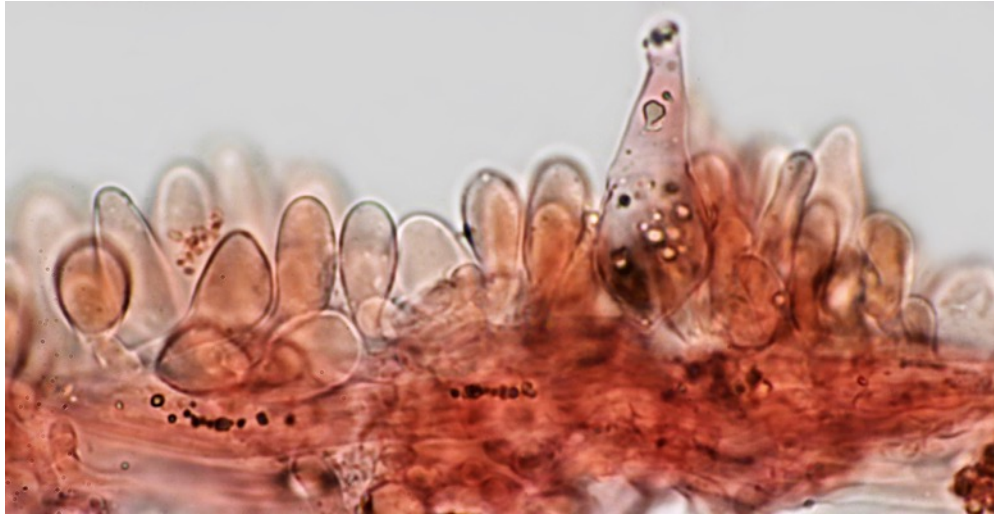


Cheilocystides denses, très polymorphes, de lagéniforme à essentiellement utriformes et parfois à sommet fouchu, hyalines, à paroi fine ou très légèrement épaissie.
Cheilocystidia densely packed,, very polymorphic, lageniform to essentially utriform and sometimes with a forked apex, hyaline, thin-walled or slightly thickened.

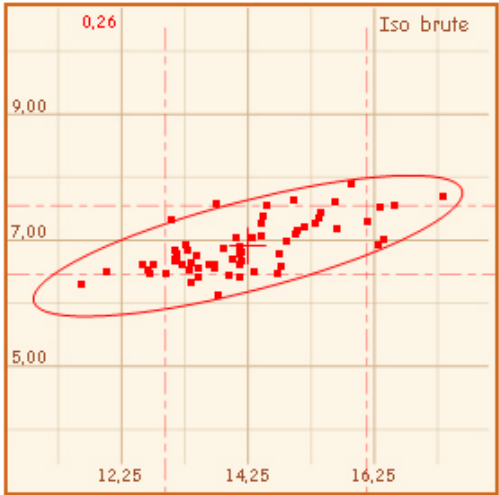
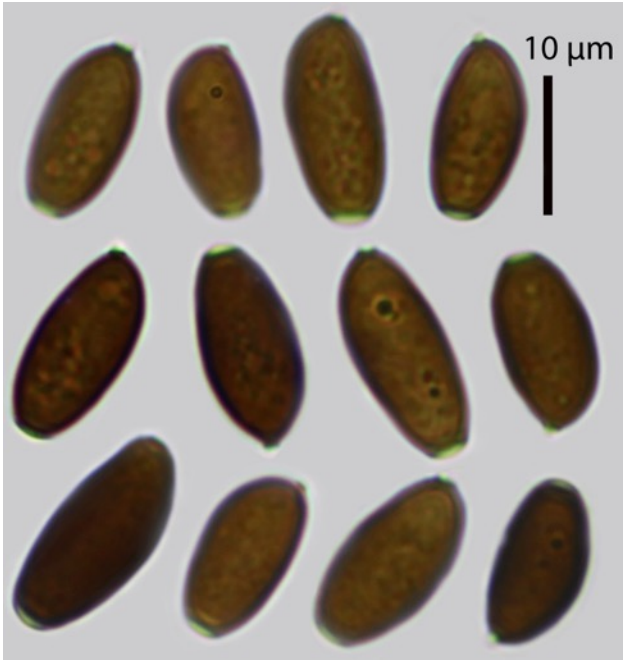
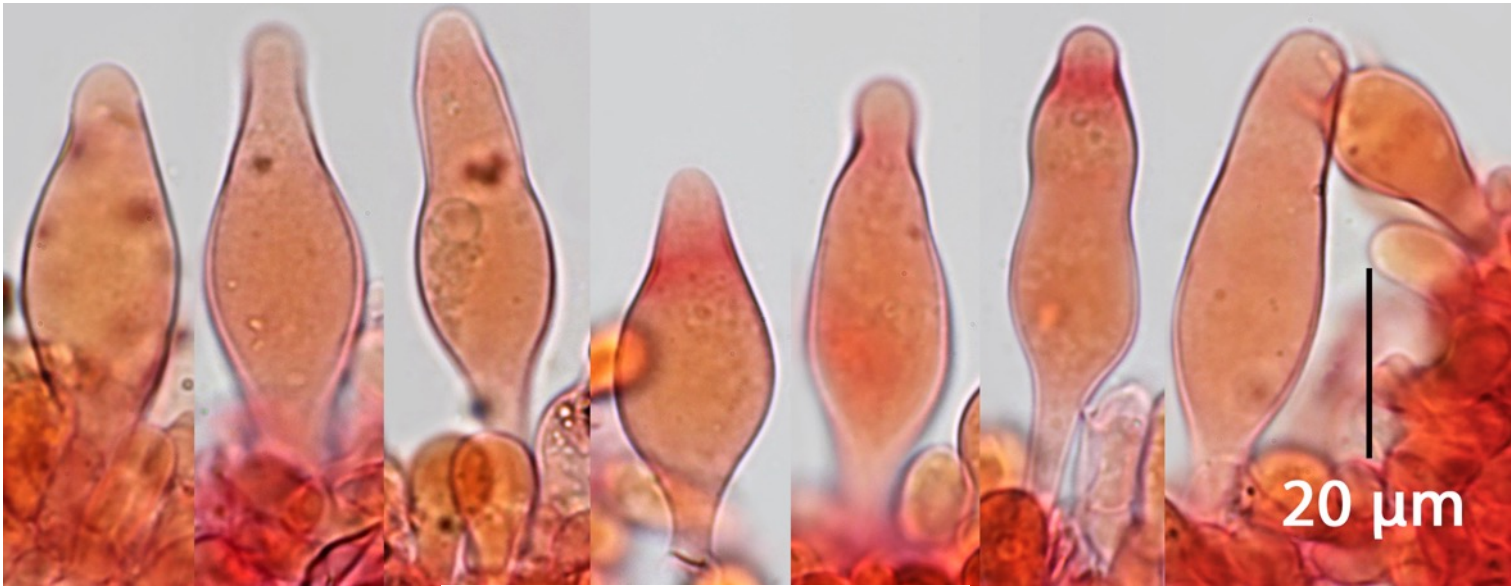


A proximité de la marge du chapeau les cheilocystides se raréfient et cèdent la place à de nombreuses paracystides clavées, souvent pigmentées de rouge-brun et à paroi épaisse.

Near the cap margin the cheilocystidia become scarce and are replaced by numerous clavate paracystidia, often reddish-brown pigmented and with thickened walls.



Pleurocystides nombreuses lagéniformes à utriformes - Pleurocystidia numerous lageniform to utriform.



Spore dimensions: N = 64
(11,6) 12,9 - 16,1 (18,4) × (6,1) 6,5 - 7,5
(8,1) μm
Me = 14,2 × 6,9 μm ;
Q = (1,8) 1,9 - 2,2 (2,4) ; Qe = 2,1

