

Study of not identified **Psathyrella** sp. 04-03-2022 = **indet 161**
= **Psathyrella senex - group A**
Deschuyteneer & Lothar Krieglsteiner



Small (young) specimens among woody and deciduous debris

Portugal – Algarve – Foia N – 04/03/2022

..... ??? , Castanea

Veil ++ at the cap margin of the young specimen – gill edge white

Photo in situ L. Krieglsteiner



Psathyrella
4-3-22 Indet 161
Po-Algarve Foia-N
Stru n Castanea Cu al
Sp-7-8/4-4,5
Pleuro G Chelos Elaphus

Basidia: 4-spored, clavate.

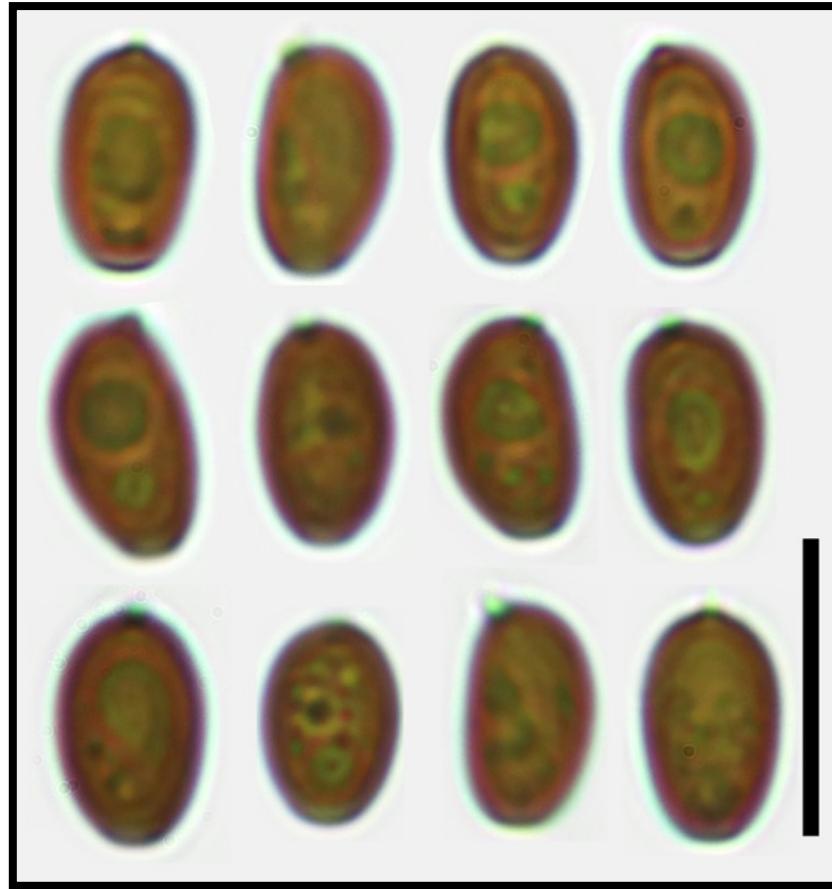
Clamps: present.

Pileipellis: usual globose and ob-pyriform cells.

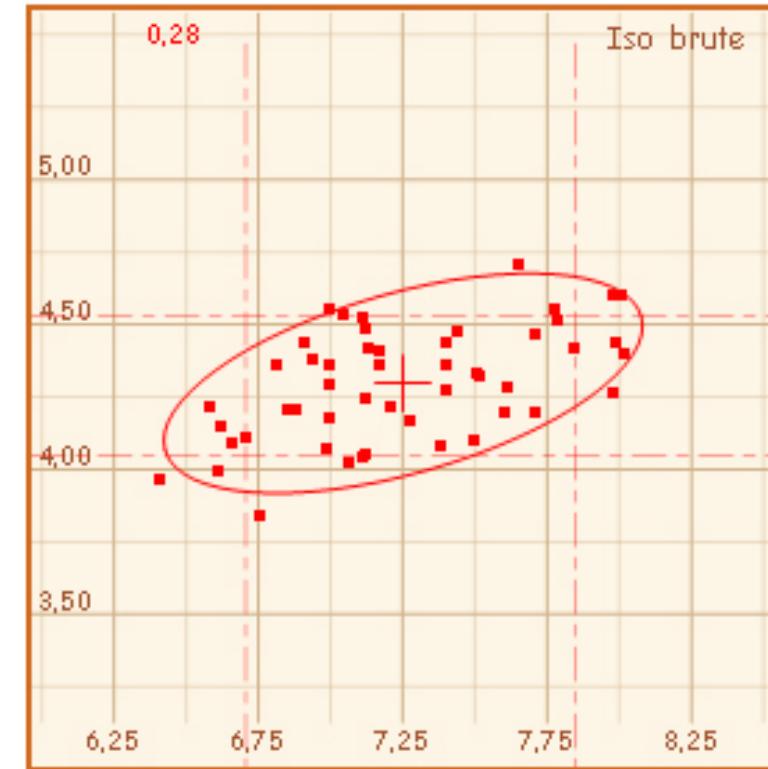


Spores: orange-brown, not opaque, ellipsoid in face view, adaxially flattened in profile, germ pore distinct, central.

Scale bar = 10 μm .

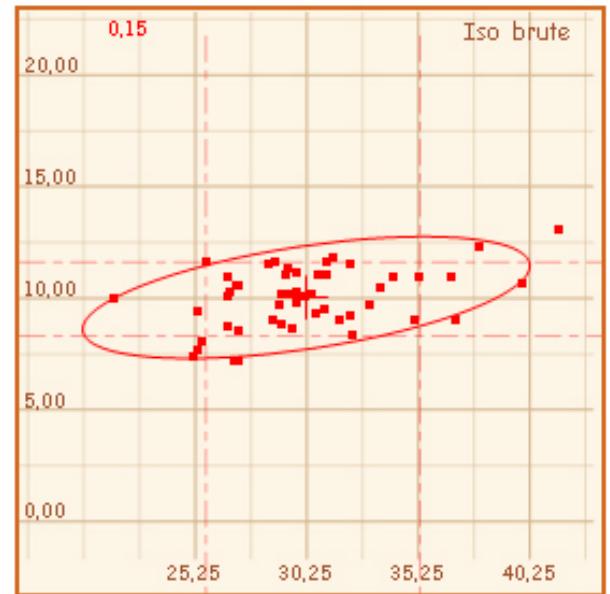
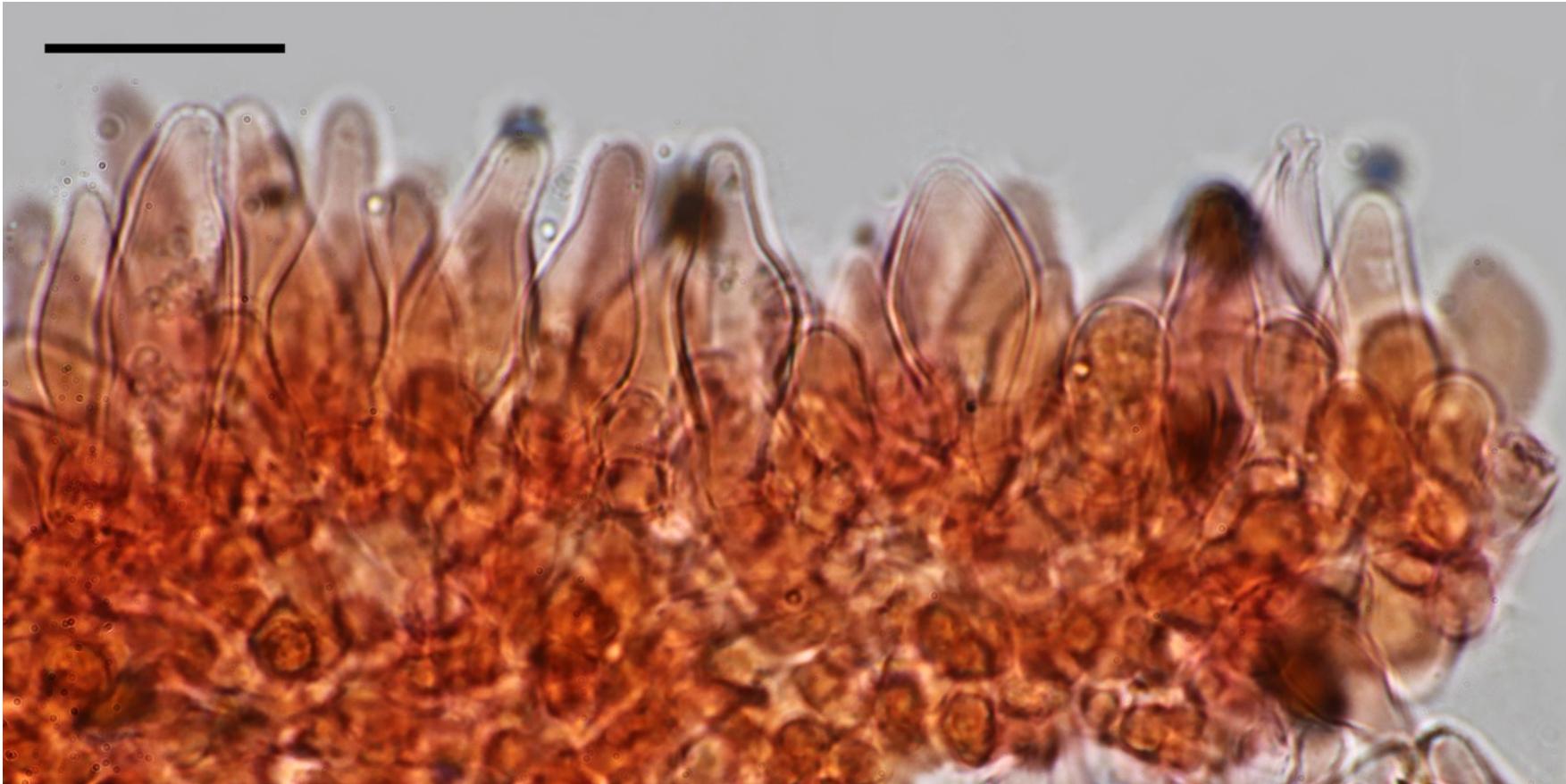


Spores measuring: N = 50
 $(6,7) 7,2 - 8,1 (8,5) \times (4,1) 4,4 - 4,9 (5,2) \mu\text{m}$
Me = $7,6 \times 4,6 \mu\text{m}$;
Q = (1,5) 1,52 - 1,8 (1,9) ; Qe = 1,6



Spores measuring on another specimen : N = 50
 $(6,4) 6,7 - 7,8 (8) \times (3,8) 4 - 4,5 (4,7) \mu\text{m}$
Me = $7,3 \times 4,3 \mu\text{m}$;
Q = (1,5) 1,6 - 1,8 (1,9) ; Qe = 1,7

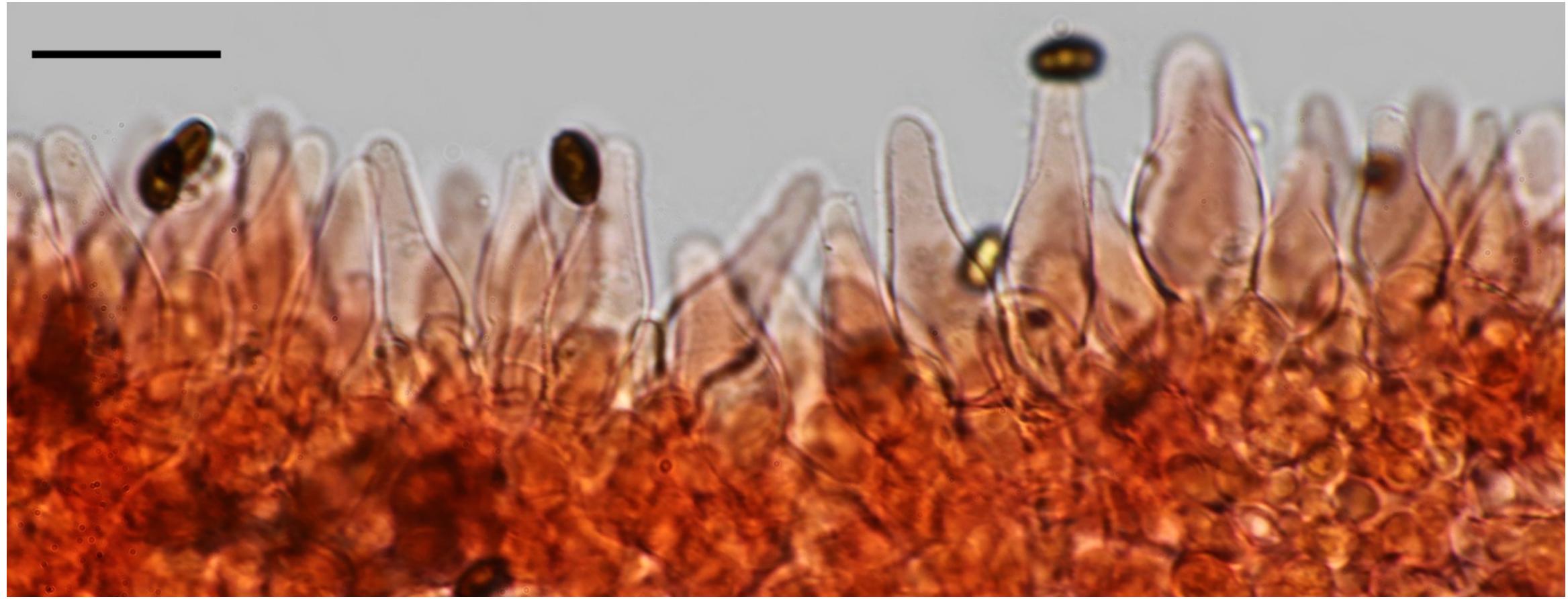
Cheilocystidia: N = 50; measuring (21,6) 25,7 - 35,3 (41,6) × (7,2) 8,3 - 11,6 (13,1) μm ; Me = **30,2 × 10 μm** ; thin walled, densely packed, lageniform and sub-ultriform with an obtuse apex. Paracystidia clavate, few in number, scattered.



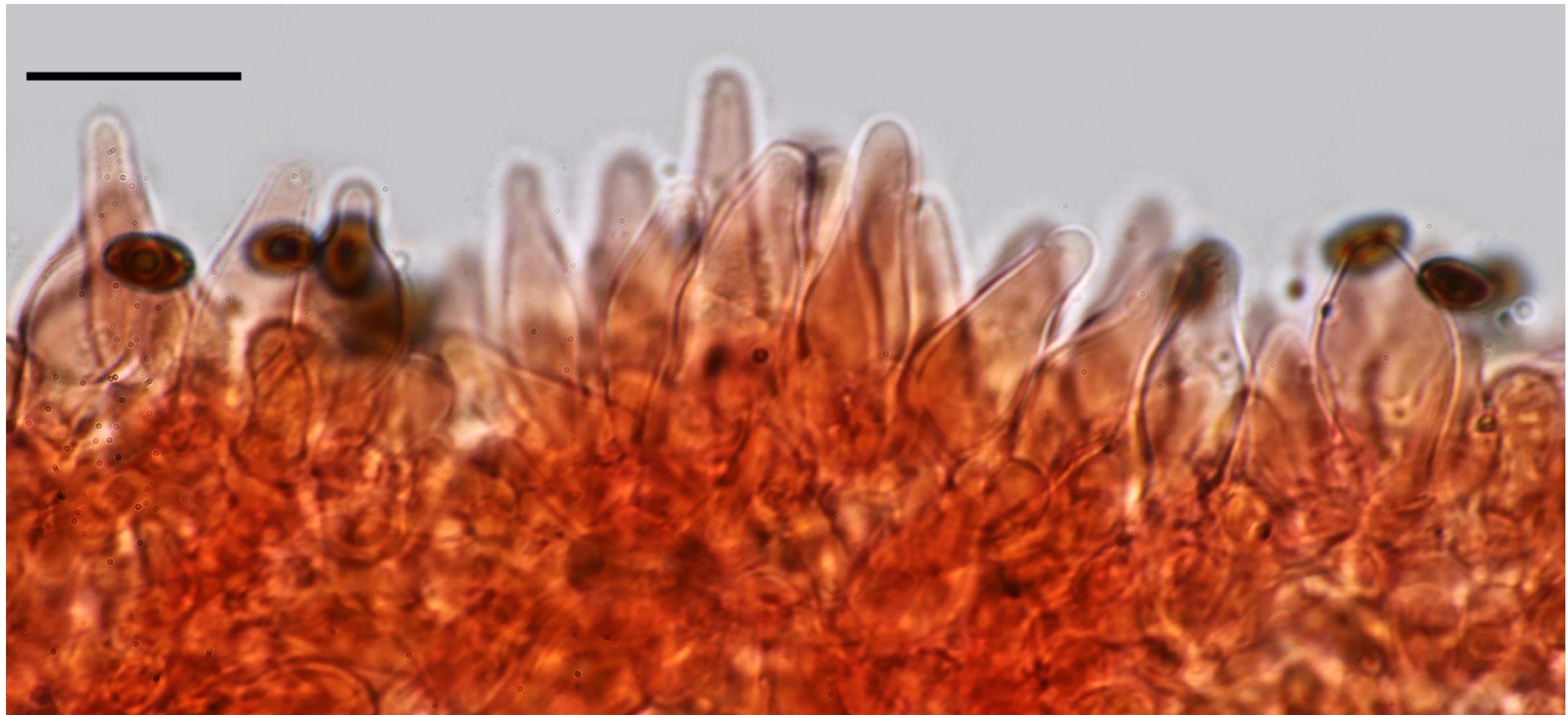
Cheilocystidia: scale bar = 20 μ m



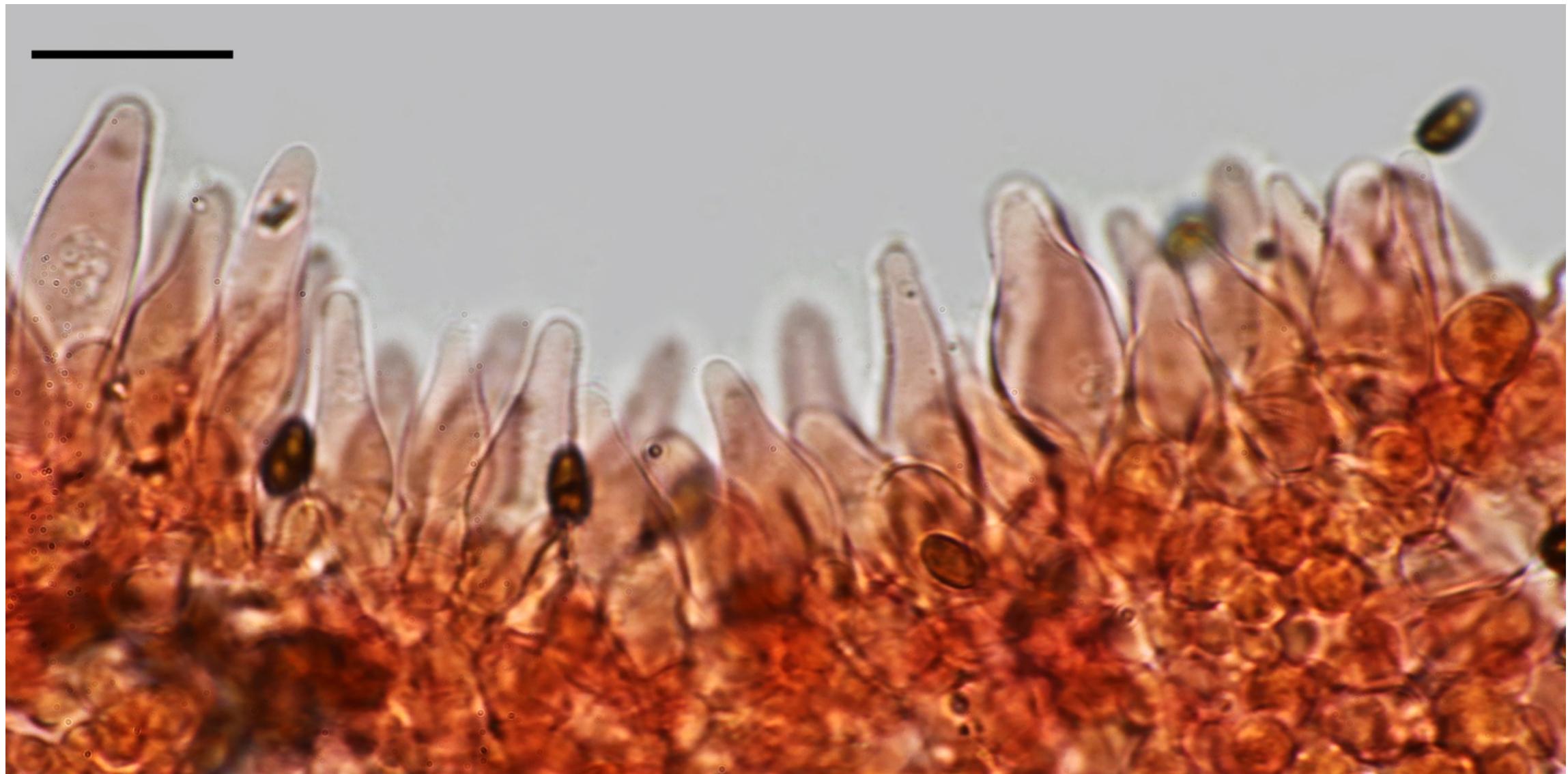
Cheilocystidia: scale bar = 20 μ m



Cheilocystidia: scale bar = 20 μ m



Cheilocystidia: scale bar = 20 μ m



Cheilocystidia: scale bar = 20 µm



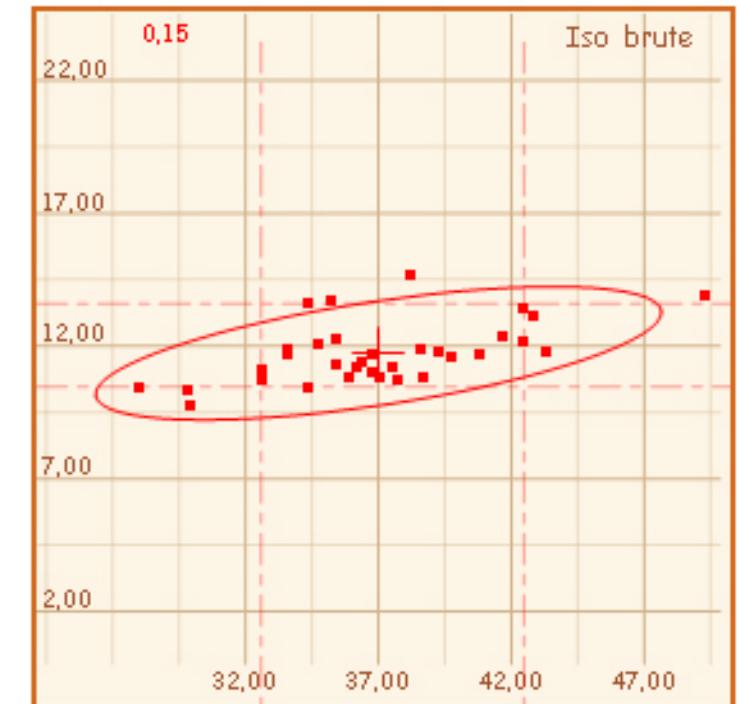
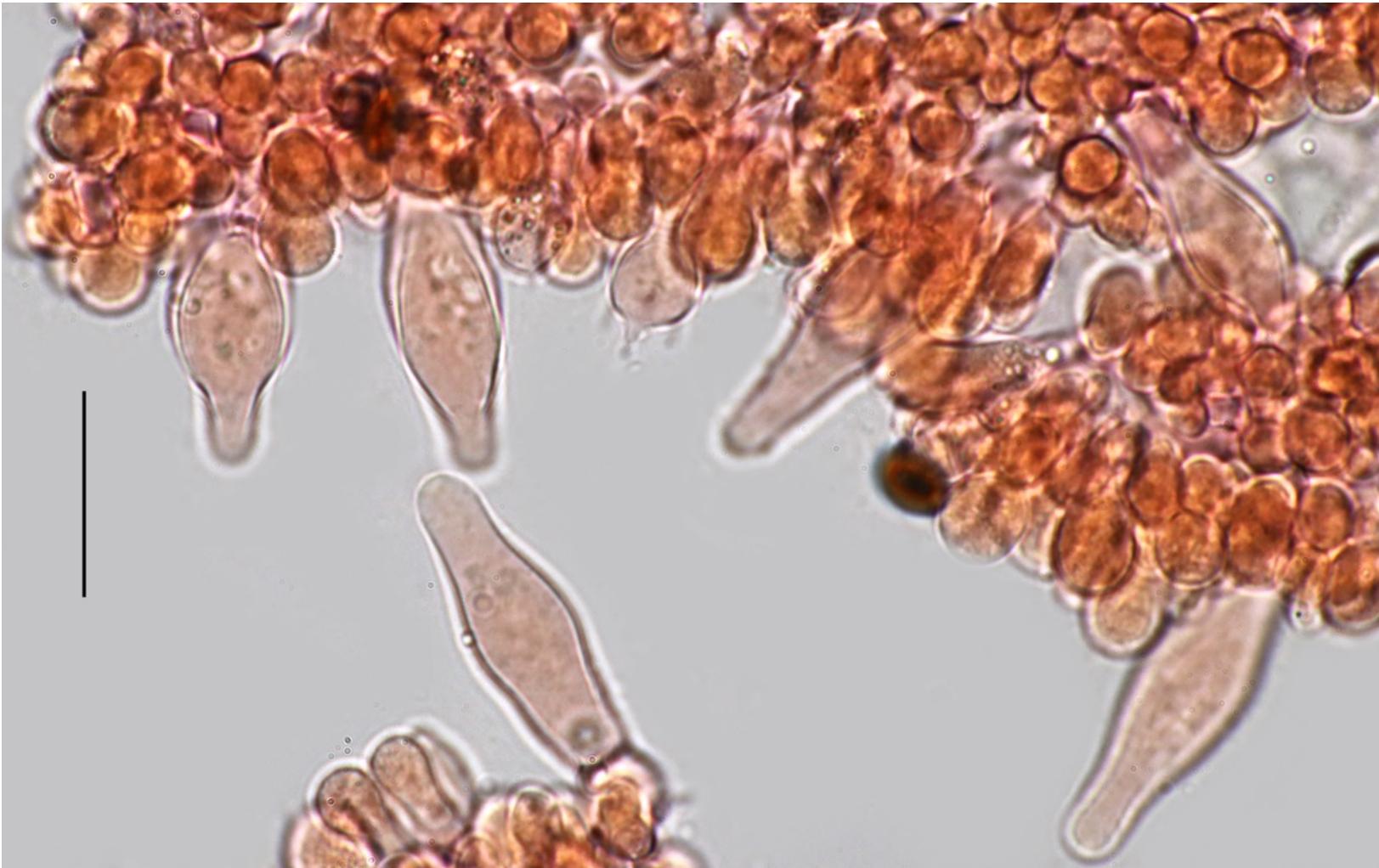


Cheilocystidia: scale bar = 20 µm



Pleurocystidia measuring $N = 33$; (28) $32,6 - 42,5$ (49,2) \times (9,7) $10,5 - 13,6$ (14,7) μm ; **Me = 37 \times 11,7 μm** ; numerous, thin walled, mostly lageniform, nearly similar to the cheilocystidia.

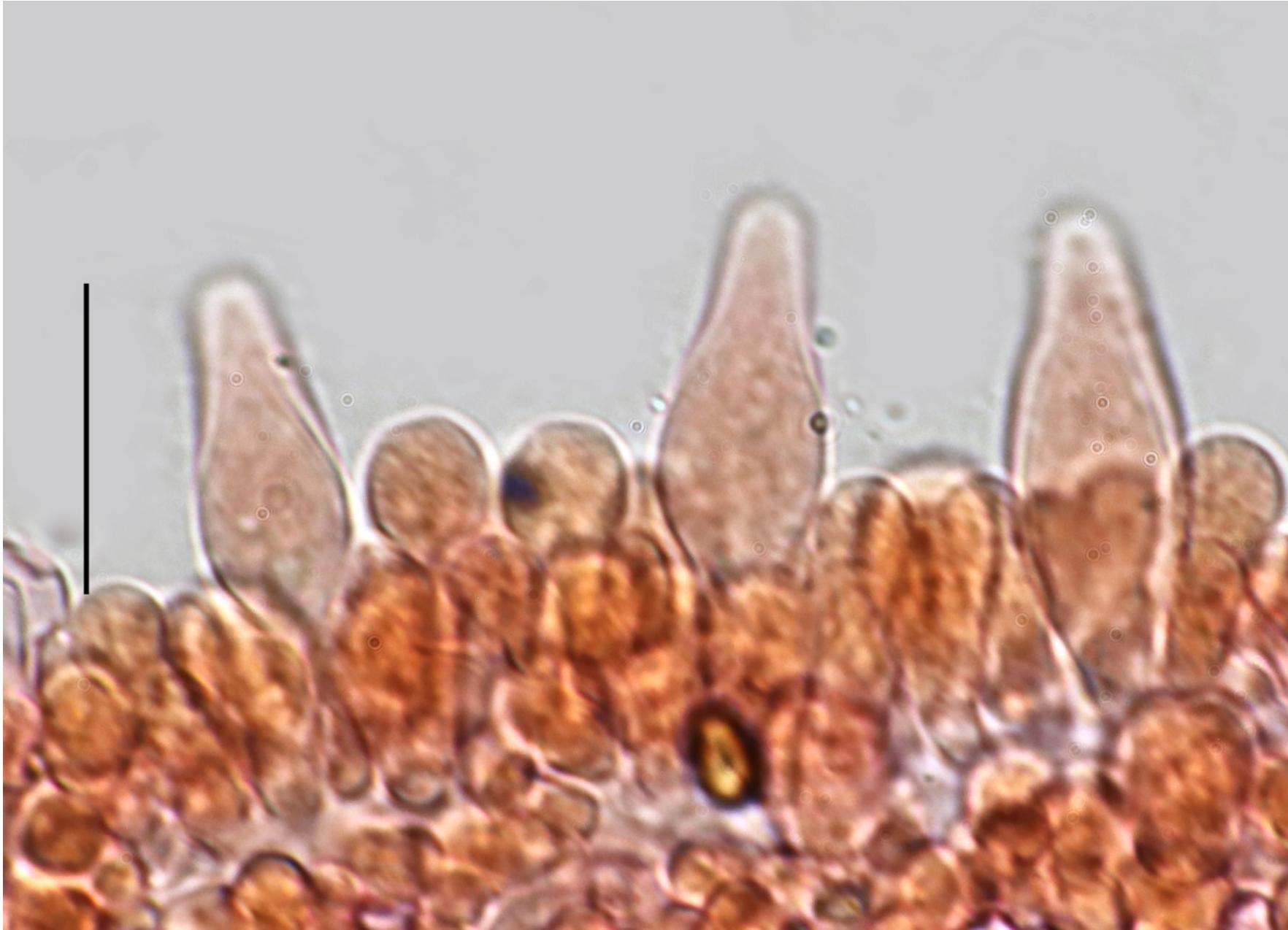
Scale bar = 20 μm



Pleurocystidia numerous, lageniform and sub-ultriform. Scale bar = 20 μ m



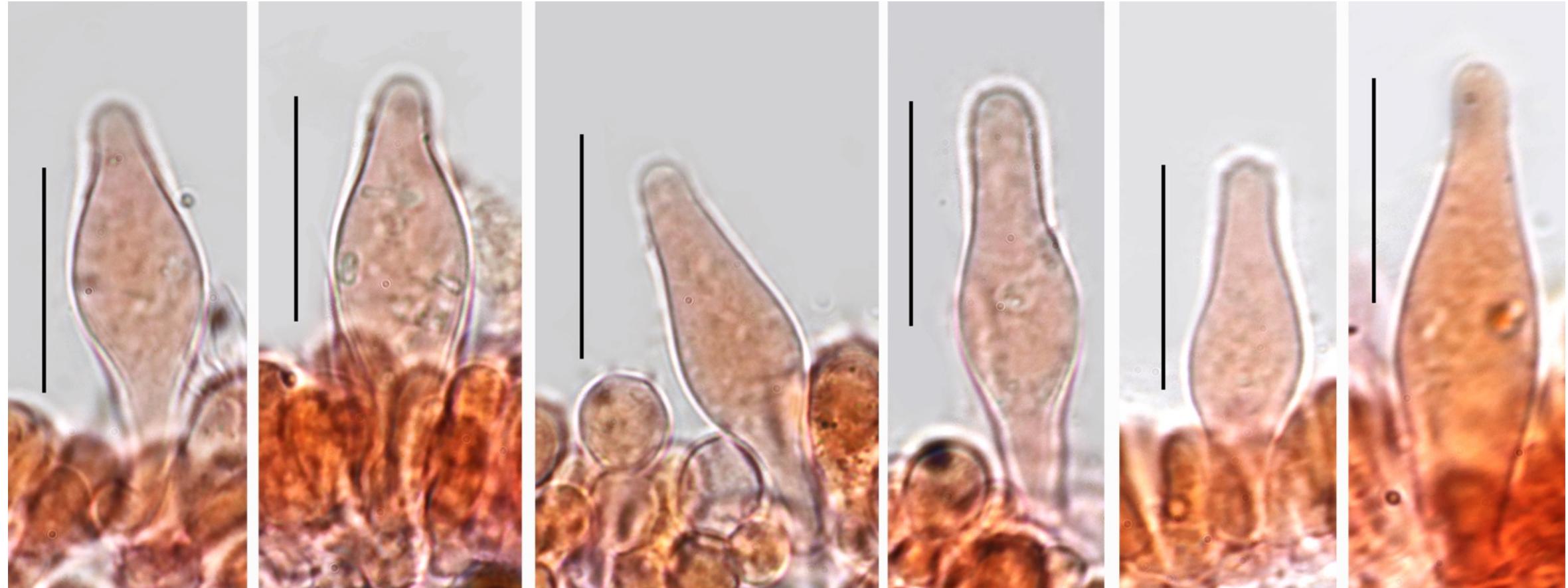
Pleurocystidia numerous, lageniform and sub-utriform. Scale bar = 20 µm



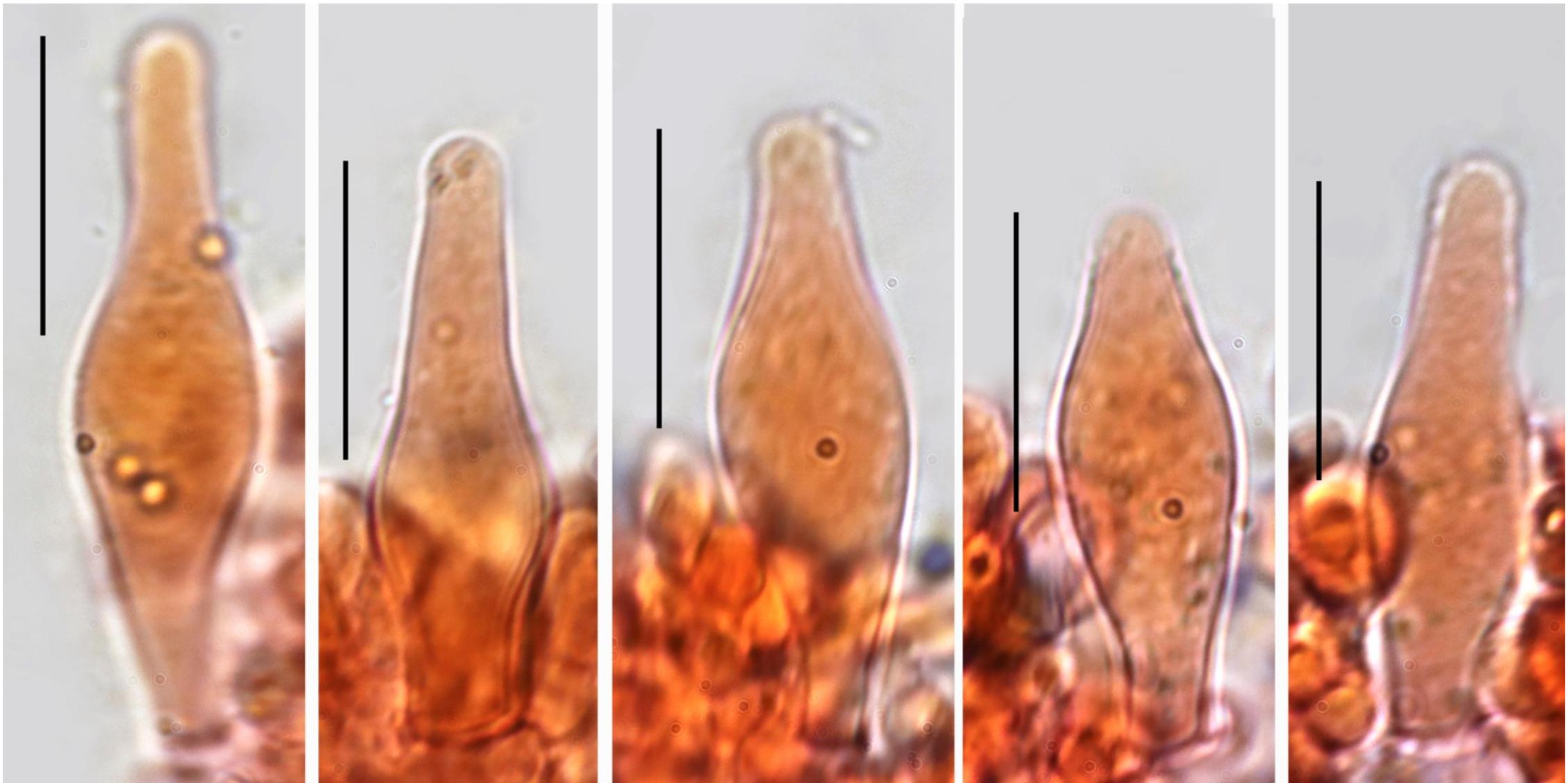
Pleurocystidia numerous, lageniform and sub-utriform. Scale bar = 20 µm



Pleurocystidia numerous, lageniform and sub-ultriform. Scale bar = 20 µm



Pleurocystidia numerous, lageniform and sub-ultriform. Scale bar = 20 μ m



2022-2329-ALV35383 DD-KRIEG-030422= indet 161

ITS = ok, 99.53% Psathyrella sp. MN017259, 99.38% P. borealis NR_175197, **P. senex MG734732 = Psathyrella senex HMJAU 4450**

TEF1 = ok, 97.80% Psathyrella amygdalinospora MW410999, 97.28% P. fagetophila FM897222

ITS

NNNNNNNNNNNACCTNATTGAGGTCAATTGTAAAAAT
TGTCTTGAGACGGTTAGAAGCAAGTCTAACAGCTCCATCC
ACGGCGTAGATAATTATCACACCAATAGACGGAGCTCAGT
TTGAACTCGCTAATCCATTGAGAGGGAGCAGTCAGCAGTT
AAGCGTTCTGCACAACCCCCACATCCAAGCTCACGCAGT
TTCATAACAAAATGATGAAGTTGAGAATTAAATGACACT
CAAACAGGCATGCTCCTCGGAATACCAAGGAGCGCAAGGT
GCGTTCAAAGATTGATGATTCACTGAATTCTGCAATTCA
CATTACTTATCGCATTTCGCTGCGTTCTCATCGATGCGA
GAGCCAAGAGATCCGTTGCTGAAAGTTGTATTTGTTTA
TAGGCTAAAAGCCCATTGACTACATTCTTCATTATAACAT
TGGGGTTGTAAAGATAACATAGACCTGAAAATTCAAAGAG
AGCTGGCCTTGCACCCAGCAATCCTGCATCCGCTCAA
AGAACGAGAGTTATCCAGGCCTACATTAAGTGCACAGGTG
GAAAGATAAAAATGACGGGTGTGCACATGCTCCTAGAAGC
CAGCTACAACCAACGCCATAAGTATTCTTAATGATCCTT
CCGCAGGTTCACCTACGGAAACCTTGTACGACTTTACT
TCCTCTAATGGAACCAAGAAAA

| Descriptions | Graphic Summary | Alignments | Taxonomy | | | | | | | | | | |
|---|---|----------------------|-----------|-------------|-------------|---------|------------|----------|-------------|----------|----------------|--------------------------|------------|
| Sequences producing significant alignments | | | | | | | | | | Download | Select columns | | |
| <input checked="" type="checkbox"/> select all 100 sequences selected | | | | | | | | | | 100 | ? | | |
| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession | GenBank | Graphics | Distance tree of results | MSA Viewer |
| <input checked="" type="checkbox"/> | Psathyrella senex voucher HMJAU 4450 small subunit ribosomal RNA gene, partial sequence: internal transcribed spacer 1 a... Psathyrella senex | Psathyrella senex | 1225 | 1225 | 97% | 0.0 | 98.84% | 717 | MG734732.1 | | | | |
| <input checked="" type="checkbox"/> | Psathyrella borealis MICH Smith 43743 ITS region; from TYPE material | Psathyrella borealis | 1186 | 1186 | 92% | 0.0 | 99.39% | 652 | NR_175197.1 | | | | |
| <input checked="" type="checkbox"/> | Psathyrella borealis MICH:Smith 43743 small subunit ribosomal RNA gene, partial sequence: internal transcri... Psathyrella borealis | Psathyrella borealis | 1186 | 1186 | 92% | 0.0 | 99.39% | 652 | MZ895470.1 | | | | |
| <input checked="" type="checkbox"/> | Psathyrella limicola var. subspicinata voucher MICH11965 small subunit ribosomal RNA gene, partial sequence: intern... Psathyrella limico... | Psathyrella limicola | 1184 | 1184 | 98% | 0.0 | 97.68% | 721 | MF325980.1 | | | | |
| <input checked="" type="checkbox"/> | Psathyrella seminuda voucher Smith34091 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene ... Psathyrella semin... | Psathyrella seminuda | 1184 | 1184 | 95% | 0.0 | 98.37% | 1596 | KC992907.1 | | | | |
| <input checked="" type="checkbox"/> | Psathyrella sp. voucher JLF2657 small subunit ribosomal RNA gene, partial sequence: internal transcribed spacer 1 a... Psathyrella sp. | Psathyrella sp. | 1182 | 1182 | 92% | 0.0 | 99.39% | 653 | MN017259.1 | | | | |

TEF1#

NNNNNNNNNNNTACTTCCCAGNGCTGNNNNTGCCATCC
 TCATCATCGCTGCTGGTACTGGTGAATTCAAAGCTGGTAT
 CTCCAAGGATGGTCAAACCCGTGAACACGCCTGCTCGCC
 TTCACCCTCGGTGTGCGTCAGCTCATCGTCGCCGTCAACA
 AGATGGACACCACCAAGGTATAACGGTTAGCTTCACTTA
 ATAATGTAACACTTCTCAACTTCCTTATTAGTGGAA
 GCGAAGATCGTTCAATGAAATCATTAAGGAGACTTCCAG
 CTTTATCAAGAAGGTCGGTTACAACCCCCAAGGCTGTCGCC
 TCGTCCCCATCTCCGGATGGCACGGAGAACATGTTGG
 AGGAGTCCAAGAAGTAAGCGCCTGGCTTTTACTCGTC
 AACTTTCTCACATCTCTAGCATGACCTGGTTCAAGGG
 TTGGTCCCGCGAAGGCAAGACCGGTACCCCTCAAGGGCAAG
 ACCTTGTGGATGCTATCGATGCTATCGAGCCCCCTGTCC
 GTCCCTCCGACAAGCCCCCTCCGTCTCCCCCTCCAGGACGT
 CTACAAGATTGGTGGTATCGGAACTGTGCCGTGGTCGT
 GTTGAGACTGGTATCATCAAGGCCGGTATGGTCGTCAACT
 TCGCTCCCTCCAACGTCACCAACCGAAGTCAAGTCCGTGA
 AATGCATCACGAGCAGCTCGAGCAGGGTAACCCCGGTGAC
 AACGTCGGCTTCAACGTCAAGAACGTTCCGTCAAGGATA
 TCCGTGAAACGTCGCCTCCGACTCCAAGAACGACCC
 TGCCAAGGAAGCCGCCTTTCAACGCACAGGTACGTGTC
 CTCAACCACCCCTGGACAGATCGGTGCCGGCTACGCACCCG
 TCCTCGATTGCCACACTGCTCACATTGCTGCAAGTTCGC
 TGAGCTCATCGAGAAGATCGATGCCGAACTGGTAAATCC
 CTCGAAGACGCACCCAAGTCGTCAAGTCTGGTGACGCCG
 CCATCGTCAAGCTTATCCCCAGCAAGCCCAGGTACGTAA
 AGAGGCCGCTTACTCCCAAACCTATACTAACTATATGTCT
 AGTGTGTGAGTCCTACAACGAGTACCCCTCTGGTCGTT
 TCGCTGTCGTGACATGAAACAAACGTCCCCCTTTGGGG
 TAAAAAAA

| Sequences producing significant alignments | | | | | | | | | | Download | Select columns | Show 100 | ? |
|--|--|---------------------------------------|---|----------------------|-------------|-------------|---------|------------|----------|-----------|----------------|--------------------------|------------|
| | | | | | | | | | | GenBank | Graphics | Distance tree of results | MSA Viewer |
| | Description | | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession | | | |
| <input checked="" type="checkbox"/> | Psathyrella amygdalinopora | voucher HMJAU37952 | translation elongation factor 1-alpha gene, partial cds | Psathyrella amyg... | 1807 | 1807 | 90% | 0.0 | 97.63% | 1053 | MW410999.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella romagnesii | isolate 4324 | translation elongation factor 1-alpha gene, partial cds | Psathyrella roma... | 1520 | 1520 | 85% | 0.0 | 94.04% | 1006 | KJ732802.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella fennoscandica | voucher HMJAU37918 | translation elongation factor 1-alpha gene, partial cds | Psathyrella feno... | 1513 | 1513 | 89% | 0.0 | 92.68% | 1055 | MW411000.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella sp. 1 | EL-2013 isolate 9201 | translation elongation factor 1-alpha gene, partial cds | Psathyrella sp. 1... | 1491 | 1491 | 85% | 0.0 | 93.53% | 1004 | KJ732790.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella pseudocorrigis | isolate 9198 | translation elongation factor 1-alpha gene, partial cds | Psathyrella pseu... | 1323 | 1323 | 85% | 0.0 | 90.58% | 1001 | KJ732801.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella microrhiza | isolate 4217 | translation elongation factor 1-alpha gene, partial cds | Psathyrella micro... | 1238 | 1238 | 85% | 0.0 | 89.03% | 1006 | KJ732765.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella hirta | isolate 4319 | translation elongation factor 1-alpha gene, partial cds | Psathyrella hirta | 1236 | 1236 | 85% | 0.0 | 89.10% | 998 | KJ732800.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella pennata | isolate 5190 | translation elongation factor 1-alpha gene, partial cds | Psathyrella pennata | 1234 | 1234 | 85% | 0.0 | 88.94% | 1008 | KJ732813.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella microspora | isolate 5190 | translation elongation factor 1-alpha gene, partial cds | Psathyrella micro... | 1208 | 1208 | 85% | 0.0 | 88.47% | 1009 | KJ732764.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella sp. 9 | partial cds | partial cds | Psathyrella sp. 9... | 1199 | 1199 | 85% | 0.0 | 88.33% | 1003 | KJ732792.1 | | |
| <input checked="" type="checkbox"/> | Psathyrella fagetophila | tef1 gene region, strain SZMC-NL-2530 | | Psathyrella faget... | 1197 | 1197 | 61% | 0.0 | 96.54% | 740 | FM897222.1 | | |

Genbank accession code
 ITS 35383 = OP006264
 TEF 35383 = OP021858

It seems well that this species is well *Psathyrella senex* from the group A

To see the two groups, A & B read my publication which is online :

<http://www.amfb.eu/Myco/Psathyrelles/Pdf/Psathyrella-senex.pdf>

The identification of this species was not easy and several propositions were made by specialists of this genre :

P. senex, *P. rubiginosa*, *P. arenosa* and *P. ichnusae*.