

## **New and Noteworthy Species of Helicogloea (Atractiellomycetes, Basidiomycota) from Europe**

Authors: Malysheva, Vera, Spirin, Viacheslav, Schoutteten, Nathan, De Lange, Ruben, Pennanen, Jorma, et al.

Source: *Annales Botanici Fennici*, 57(1-3) : 1-7

Published By: Finnish Zoological and Botanical Publishing Board

URL: <https://doi.org/10.5735/085.057.0101>

---

The BioOne Digital Library (<https://bioone.org/>) provides worldwide distribution for more than 580 journals and eBooks from BioOne's community of over 150 nonprofit societies, research institutions, and university presses in the biological, ecological, and environmental sciences. The BioOne Digital Library encompasses the flagship aggregation BioOne Complete (<https://bioone.org/subscribe>), the BioOne Complete Archive (<https://bioone.org/archive>), and the BioOne eBooks program offerings ESA eBook Collection (<https://bioone.org/esa-ebooks>) and CSIRO Publishing BioSelect Collection (<https://bioone.org/csiro-ebooks>).

Your use of this PDF, the BioOne Digital Library, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at [www.bioone.org/terms-of-use](http://www.bioone.org/terms-of-use).

Usage of BioOne Digital Library content is strictly limited to personal, educational, and non-commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

---

BioOne is an innovative nonprofit that sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

# New and noteworthy species of *Helicogloea* (Atractiellomycetes, Basidiomycota) from Europe

Vera Malysheva<sup>1</sup>, Viacheslav Spirin<sup>2,\*</sup>, Nathan Schoutteten<sup>3</sup>,  
Ruben De Lange<sup>3</sup>, Jorma Pennanen<sup>4</sup> & Karl-Henrik Larsson<sup>5</sup>

<sup>1</sup> Komarov Botanical Institute, Russian Academy of Sciences, Prof. Popova str. 2, RU-197376 St. Petersburg, Russia

<sup>2</sup> Finnish Museum of Natural History, University of Helsinki, P.O. Box 7, FI-00014 University of Helsinki, Finland (\*corresponding author's e-mail: viacheslav.spirin@helsinki.fi)

<sup>3</sup> Ghent University, Department of Biology, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium

<sup>4</sup> Keskuskatu 68A, FI-10800 Karjaa, Finland

<sup>5</sup> Natural History Museum, University of Oslo, P.O. Box 1172, Blindern, N-0318 Oslo, Norway

Received 28 May 2019, final version received 15 Aug. 2019, accepted 15 Aug. 2019

Malysheva V., Spirin V., Schoutteten N., De Lange R., Pennanen J. & Larsson K.-H. 2020: New and noteworthy species of *Helicogloea* (Atractiellomycetes, Basidiomycota) from Europe. — *Ann. Bot. Fennici* 57: 1–7.

Two new species of *Helicogloea*, *H. aseptata* V. Malysheva & Spirin and *H. insularis* Spirin & K.H. Larss. (Atractiellomycetes, Basidiomycota), are described based on morphological and molecular data from north-European collections. In addition, morphological flexibility and host specificity of *H. dryina*, *H. sebacea* and *H. subardosiaca* are discussed. A key for teleomorphic *Helicogloea* spp. found in Europe is provided.

## Introduction

The genus *Helicogloea* (Atractiellomycetes, Basidiomycota) comprises 25 species of resupinate fungi inhabiting rotten wood and other plant remnants. They all are characterized by semitranslucent, waxy or gelatinous basidiocarps, clampless hyphae, transversally septate, normally four-celled basidia provided with a probasidial sac, and medium-sized or large, variably shaped repetitive basidiospores (Spirin *et al.* 2018). The absence of cystidia is a main morphological feature distinguishing *Helicogloea* spp. from the recently described genus *Bourdotigloea* (Aime *et al.* 2018, Spirin *et al.* 2018). In turn, a few species with floccose, non-gelatinized basidiocarps and clamped hyphae were transferred from *Helicogloea* to *Saccosoma*

(Spirin *et al.* 2018). Two *Helicogloea* species recently introduced by Schoutteten *et al.* (2018), *H. jozefii* and *H. graminicola*, seem to belong to the latter genus, although at present no DNA data are available for them.

In total, ten species of *Helicogloea s. stricto* have been found in Europe and eight are reported from northern Europe (Spirin *et al.* 2018). Almost all species seem to be host specific: seven of them have been found exclusively on angiosperm hosts and two only on conifers. In 2018, several specimens of *Helicogloea* spp. morphologically differing from the already described species were collected in Estonia, Finland, the Netherlands, Norway, and northwestern Russia. Subsequent DNA studies proved that two of them belonged to an undescribed species. One specimen from Finland belongs to *H. dryina* and

three collections from the Netherlands represent *H. sebacea*, although their basidiospores and basidia are quite different from those of the rest of the collections studied by Spirin *et al.* (2018). Additionally, a new record of *H. subardosiaca* on *Picea abies* is reported below.

## Material and methods

Type specimens and other collections treated in this study are stored in herbaria H, O, LE, TU and GENT. Herbarium acronyms are given according to *Index Herbariorum* (<http://sweetgum.nybg.org/ih>). Microscopic routines follow Miettinen *et al.* (2018). All measurements and line drawings were made from microscopic slides prepared in Cotton Blue, with oil immersion and phase contrast illumination ( $\times 1250$  magnification). The following abbreviations are used below:  $L$  = mean basidiospore length,  $W$  = mean basidiospore width,  $Q'$  = length-to-width ratio,  $Q$  = mean length-to-width ratio,  $n$  = number of measurements/specimens studied.

## DNA extraction and sequencing

In total, eight specimens were selected for molecular sampling. DNA was extracted using the NucleoSpin Plant II Kit (Macherey-Nagel GmbH & Co. KG) according to the manufacturer's instructions. PCR amplification and sequencing of the nrITS region was performed using primers ITS1F (Gardes & Bruns 1993) and ITS4 (White *et al.* 1990). Primers JS1 (Landvik 1996) and LR5 (Vilgalys & Hester 1990) were used to amplify and sequence part of nrLSU region. PCR products were purified applying the GeneJET Gel Extraction Kit (Thermo Scientific, Thermo Fisher Scientific Inc., MA, USA). Sequencing was performed with an ABI model 3130 Genetic Analyzer (Applied Biosystems, CA, USA). Raw data were edited and assembled in MEGA 7 (Kumar *et al.* 2016). Most steps of molecular studies were carried out at the center for collective use of scientific equipment "Cellular and molecular technology of studying plants and fungi" (Komarov Botanical Institute, Russian Academy of Sciences, St. Petersburg).

## Phylogenetic analyses

For this study, eight nrITS and five nrLSU sequences were newly generated. Additionally, 27 nrITS and 27 nrLSU sequences, including the outgroup were taken from Spirin *et al.* (2018). Sequences were aligned with MAFFT ver. 7 (<http://mafft.cbrc.jp/alignment/server/>) using the Q-INS-i option for both phylogenetic markers. One combined data set (nrITS + nrLSU) was prepared for the study. The final alignment contained 1580 characters (including gaps).

Phylogenetic reconstructions were performed with maximum likelihood (ML) and Bayesian (BA) analyses. Before the analyses, the best-fit substitution model for each phylogenetic marker was estimated based on the Akaike Information Criterion (AIC) using FindModel (<http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html>). The GTR model was chosen for all markers and was applied for the whole data set. ML analysis was carried out using PhyML ver. 3.0 (<http://www.atgc-montpellier.fr/phyml>; Guindon *et al.* 2010) with one hundred rapid bootstrap replicates.

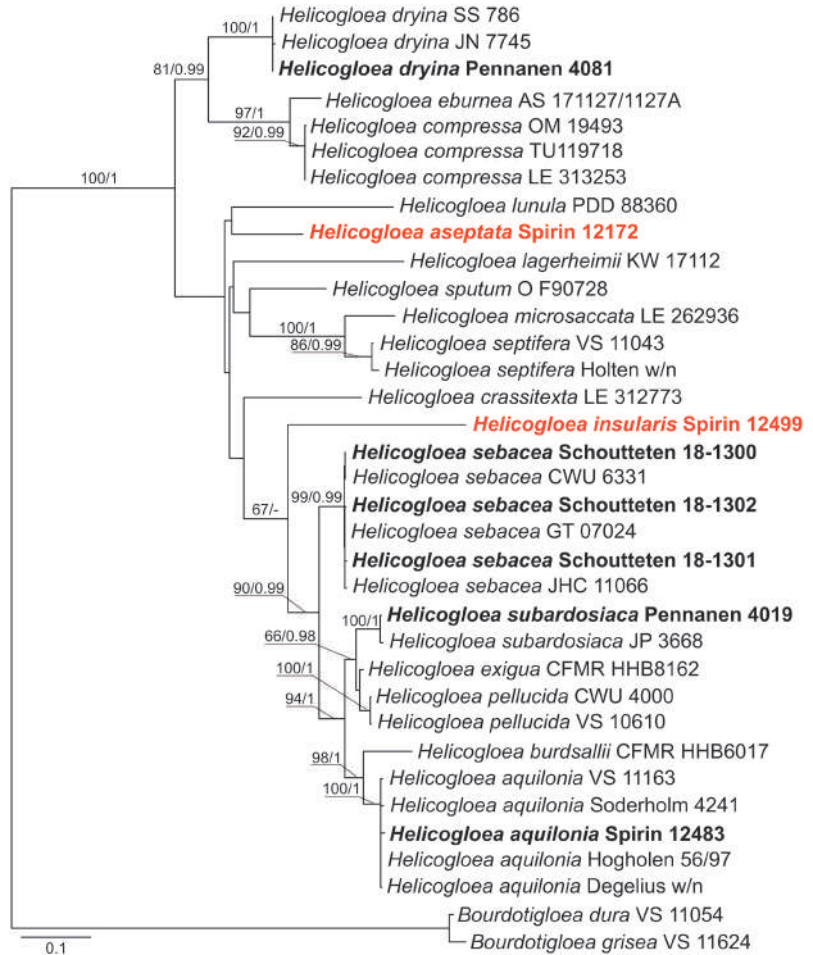
Bayesian analyses were performed with MrBayes ver. 3.2.5 (Ronquist *et al.* 2012). There were two independent runs, each with 5 million generations under described model, and four chains with sampling every 100 generations. To check for convergence of MCMC analyses, and to obtain estimates of the parameter-value posterior distribution, Tracer ver. 1.6 was used (<http://tree.bio.ed.ac.uk/software/tracer/>). We accepted the result if ESS (Effective Sample Size) was greater than 200 and PSRF (Potential Scale Reduction Factor) was close to 1. The smallest ESS in our analysis equalled 3782.94.

Newly generated sequences are deposited in GenBank. The alignments are deposited in TreeBASE (S24377).

## Results

ML and BA analyses produced nearly the same topologies for the combined ITS–nrLSU data set (Fig. 1). The specimen *Spirin 12172* from northwestern Russia clustered with *H. lunula* described from New Zealand although without

**Fig. 1.** Combined phylogenetic nrITS + nrLSU topology from maximum likelihood analysis showing interspecific relationships within *Helicogloea*. All sequences generated for this study are set in boldface. Newly described species are in red. Collection numbers of specimens are given for all sequences. Support values (ML/BA) are given above the branches. Scale bar shows expected changes per site.



adequate support. It is interpreted as belonging to a new species, introduced below. Another problematic collection, *Spirin 12499* from Norway, is only distantly related to the microscopically similar species *H. exigua* distributed in North America and Europe. As a consequence, a new species is described based on that specimen. Six other sequences resolved in strongly supported clades representing *H. dryina* (*Pennanen 4081* from Finland), *H. sebacea* (*Schoutteten 18-1300*, *1301*, *1302* from the Netherlands), *H. aquilonia* (*Spirin 12483* from Norway), and *H. subardosiaca* (*Pennanen 4019* from Finland).

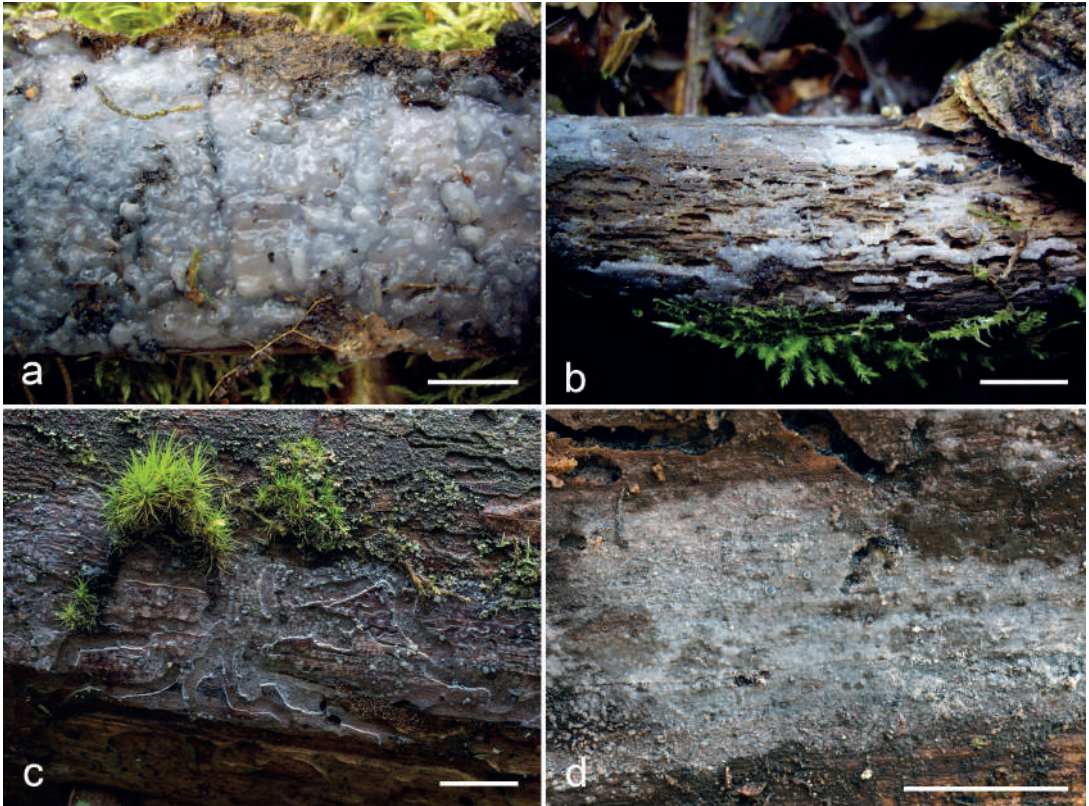
***Helicogloea aseptata* V. Malysheva & Spirin, sp. nova** (Figs. 2a and 3a)

(GenBank MK880145, MK880143) MB 831162. — HOLO-

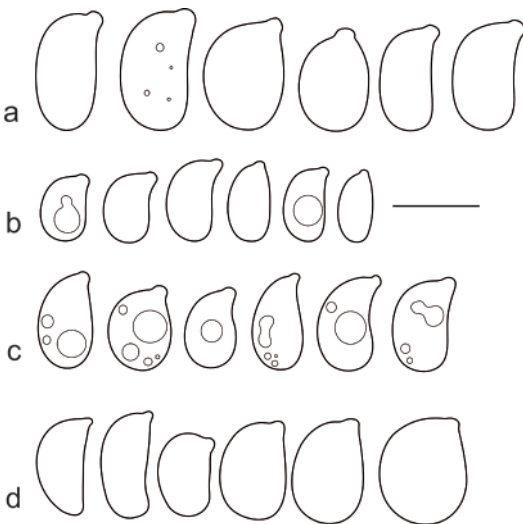
TYPE: Russia. Leningrad Reg.: Boksitogorsk Dist., Ostrechka, *Betula pubescens*, 18 August 2018 *Spirin 12172* (H; isotype LE) (N59.693 E34.6075).

ETYMOLOGY. *Aseptatus* (Lat., adj.), in reference to aseptate basidiospores.

Basidiocarps whitish, gelatinous, widely effused, up to 10 cm in widest dimension, 0.1–0.5 mm thick, hymenial surface uneven, indistinctly tuberculate, drying to a semitranslucent vernicose crust. Hyphae simple-septate; subicular hyphae interwoven, unevenly thick-walled, (4.0)4.1–7.4(7.8)  $\mu\text{m}$  in diam. ( $n = 20/1$ ), subhymenial hyphae interwoven or ascending, thin to slightly thick-walled, (2.8)3.2–4.9(5.0)  $\mu\text{m}$  in diam. ( $n = 20/1$ ). Basidia tubular-clavate, 4-celled, more or less clearly twisted or curved, 47–72  $\times$  (5.0)5.1–7.2(7.3)  $\mu\text{m}$  ( $n = 20/1$ ), with sharp-pointed sterigmata up to 8  $\times$  4  $\mu\text{m}$ ; basidia saccate-clavate, 14–42  $\times$  7–11  $\mu\text{m}$ . Basidio-



**Fig. 2.** Basidiocarps. — **a:** *Helicogloea aseptata* (holotype). — **b:** *Helicogloea insularis* (holotype). — **c:** *Helicogloea dryina* (Pennanen 4081). — **d:** *Helicogloea subardosiaca* (Pennanen 4019). Scale bar = 10 mm.



**Fig. 3.** Basidiospores. — **a:** *Helicogloea aseptata* (holotype). — **b:** *Helicogloea insularis* (holotype). — **c:** *Helicogloea dryina* (Pennanen 4081). — **d:** *Helicogloea sebacea* (Schoutteten 18-1302). Scale bar = 10  $\mu$ m.

spores thin-walled, cylindrical, mostly curved, more rarely ellipsoid, aseptate,  $(10.2)10.3\text{--}13.8(14.2) \times (5.7)5.8\text{--}8.1(9.1) \mu\text{m}$  ( $n = 30/1$ ),  $L = 11.97$ ,  $W = 6.57$ ,  $Q' = (1.3)1.4\text{--}2.3(2.4)$ ,  $Q = 1.84$ .

The largely effused and rather thick, gelatinous basidiocarps of *H. aseptata* are strongly reminiscent of those of *H. septifera* distributed in northern Europe. Microscopically, these species are also very similar, and therefore the specimen *Spirin 12172* was treated by Spirin *et al.* (2018) under *H. septifera*. However, no septate basidiospores were detected in it, and this difference prompted us to undertake a DNA study. It seems the presence of septate basidiospores is the only reliable character distinguishing *H. septifera* from *H. aseptata*. The latter species also possesses slightly wider subicular hyphae and shorter and narrower basidia than in *H. septifera*, although the taxonomic value of these traits

should be confirmed based on a wider sampling of both species.

*Helicogloea aseptata* is so far known from the type locality in northwest Russia. It was collected from a large, decorticated but still hard birch log. The habitat where it was found represented an undisturbed, about 160 years old spruce-dominated forest of *Sphagnoso-myrtillusum* type.

***Helicogloea insularis* Spirin & K.H. Larss., sp. nova** (Figs. 2b and 3b)

(GenBank MK880144) MB 831163. — HOLOTYPE: Norway. Buskerud: Lier, Stokkerinden, *Ulmus glabra*, 29 September 2018 *Spirin 12499* (O; isotypes H, LE) (N59.891 E10.263). — PARATYPES: Estonia. Viljandimaa: Pääsma, *U. glabra*, 18 September 2018 *Spirin 12372, 12379* (H), *Spirin 12383* (H, TU).

ETYMOLOGY. *Insularis* (Lat., adj.), insular, isolated, referring to the basidiocarp shape.

Basidiocarps semitranslucent, first pustulate, 0.05–0.1 mm in diam., partly fusing together and producing reticulate compound fruitbodies, then totally coalescent, tuberculate, covering a few cm, 0.05–0.1 mm thick, drying to a hardly visible vernicose crust. Hyphae simple-septate, interwoven; subicular hyphae thin- or slightly thick-walled, irregularly distributed, (2.7)2.8–4.0(4.2)  $\mu\text{m}$  in diam. ( $n = 20/1$ ), subhymenial hyphae thin-walled, quickly collapsing, (2.0)2.2–3.2(3.3)  $\mu\text{m}$  in diam. ( $n = 20/1$ ). Basidia tubular-clavate, 4-celled, more or less clearly twisted or curved, 28–63  $\times$  (3.9)4.0–6.1(6.3)  $\mu\text{m}$  ( $n = 40/3$ ), with sharp-pointed sterigmata up to 10  $\times$  2  $\mu\text{m}$ ; probasidia saccate-clavate, 13–24  $\times$  4.5–6.0  $\mu\text{m}$ . Basidiospores thin-walled, cylindrical, mostly curved, more rarely narrowly ellipsoid, (7.2)7.4–11.1(12.0)  $\times$  (3.8)4.0–6.6(6.7)  $\mu\text{m}$  ( $n = 112/4$ ),  $L = 8.81\text{--}9.77$ ,  $W = 4.81\text{--}5.89$ ,  $Q' = (1.4)1.5\text{--}2.1(2.2)$ ,  $Q = 1.63\text{--}1.84$ .

The rather narrow, cylindrical basidiospores and slender basidia make *H. insularis* microscopically similar to *H. exigua*. The latter species possesses extremely thin and totally smooth basidiocarps. Those of *H. insularis* are initially represented by numerous, small, gelatinous pustules then fusing together in crust-like fructifications with tuberculate hymenophore. Another similar-

looking species in Europe is *H. pellucida*, but it differs from *H. insularis* in having on average broader basidiospores and slightly shorter basidia, as well as very thin, nearly smooth basidiocarps (Spirin *et al.* 2018). *Helicogloea insularis* is so far known only from two localities in Estonia and Norway where it was collected from strongly rotten elm logs.

***Helicogloea dryina* Spirin & Miettinen** (Figs. 2c and 3c)

Fungal Systematics and Evolution 2: 332. 2018.

*Helicogloea dryina* is a common species in northern Europe, occurring exclusively on fallen, usually decorticated spruce logs. It differs from the angiosperm-dwelling *H. aquilonia* by having narrower (4–5.5  $\mu\text{m}$  wide) basidia and shorter and slightly narrower basidiospores (7–10  $\times$  6–8  $\mu\text{m}$  in *H. dryina* versus 8.5–13  $\times$  5.5–9.5  $\mu\text{m}$  in *H. aquilonia*) (Spirin *et al.* 2018). However, a newly collected specimen *Pennanen 4081* has basidia up to 7.5  $\mu\text{m}$  wide and predominantly ellipsoid-lacrymoid basidiospores, (8.3)8.7–11.2(12.0)  $\times$  (5.6)5.9–7.2(7.3)  $\mu\text{m}$  ( $n = 30/1$ ),  $L = 9.71$ ,  $W = 6.58$ ,  $Q' = (1.2)1.3\text{--}1.7(1.9)$ ,  $Q = 1.48$ . These dimensions fit better to *H. aquilonia* although ITS sequence of the new collection is identical to those of *H. dryina*, thus indicating higher morphological variation of the latter species than earlier assumed. Different host preferences, i.e. spruce *versus* hardwoods, seem to be the only reliable trait to recognize *H. dryina* and *H. aquilonia* in such critical cases.

SPECIMENS EXAMINED. — *Helicogloea aquilonia*. Norway. Vestfold: Larvik, *Fraxinus excelsior*, *Spirin 12521* (O). Akershus: Asker, *F. excelsior*, *Spirin 12464* (O). Buskerud: Lier, *Ulmus glabra*, *Spirin 12483* (O, H) (infected by *Achroomyces chlamydospora*) (GenBank MK880148), *Spirin 12493* (H). — *Helicogloea dryina*. Finland. Uusimaa: Vantaa, *Picea abies*, *Pennanen 4081* (H) (GenBank MK880147, MK880142). Norway. Hedmark: Løten, *P. abies*, *Spirin 12410* (O).

***Helicogloea sebacea* (Bourdot & Galzin) Spirin & Trichies** (Fig. 3d)

Fungal Systematics and Evolution 2: 335. 2018.

*Helicogloea sebacea* was originally described from France by Bourdot and Galzin (1909) as *Saccoblastia sebacea*. Spirin *et al.* (2018) recombined it in the genus *Helicogloea*, based on morphological and DNA data. The species is known from Europe, the Russian Far East and North America. However, the sequence data have not yet confirmed whether the collections from outside Europe belong to the same taxon. European collections are from Denmark, Estonia, France, Germany, Russia and Ukraine. Here, we report three collections from the Netherlands, found at two locations. Various deciduous trees (*Acer*, *Corylus*, *Fagus*, *Fraxinus*, *Populus*, *Salix*, *Tilia*) grow at both locations. It was impossible to unravel the identity of the substrates of these three collections. Like other *Helicogloea* species, the specimens have thin (< 0.5 mm) gelatinous basidiocarps and clampless hyphae. The collections reported here are slightly different from the description in Spirin *et al.* (2018). Basidiospores are considerably larger, (10.3)10.5–13.5(14.2) × (4.6)4.8–7.9(8.0) μm ( $n = 30/1$ ),  $L = 12.24$ ,  $W = 6.31$ ,  $Q' = (1.5)1.6–2.3(2.6)$ ,  $Q = 1.97$ , and they exhibit a larger variability in size and shape. The shape of secondary spores resulting from the basidiospore repetition is often more cylindrical to allantoid. Basidia were also found to be larger than earlier described (up to 70 μm long), and sterigmata were up to 24 μm long. The observed intraspecific variation may be age-dependent and it is likely that this applies to other *Helicogloea* species as well (and by extension also to *Saccosoma* and *Bourdotigloea* species). Therefore, it is important to continue reporting and describing additional collections of the effused *Atractiellomyces*.

**SPECIMENS EXAMINED.** **The Netherlands.** Groningen: De Starckenborg, deciduous wood, *Schoutteten 18-1300* (GENT) (GenBank MK908010, MK908014), *Schoutteten 18-1301* (GENT) (GenBank MK908008, MK908013); Lauwersmeer, *Schoutteten 18-1302* (GENT) (GenBank MK908009).

### *Helicogloea subardosiaca* (Bourdot & Galzin) Donk (Fig. 2d)

Persoonia 4: 213. 1966.

*Helicogloea subardosiaca* is the second conifer-dwelling representative of the genus in

Europe. While re-introducing it, Spirin *et al.* (2018) mentioned several collections on *Pinus sylvestris* from Finland and France. One of these specimens was used for the DNA study. To date, there have been no verified records from *Picea abies*, although spruce was mentioned as a potential host of *H. subardosiaca* based on two French specimens (DNA extraction from both of them was unsuccessful). The newly collected Finnish specimen from spruce (*Pennanen 4019*) was sequenced for the present study and confirmed as belonging to *H. subardosiaca*.

**SPECIMEN EXAMINED.** **Finland.** Etelä-Häme: Hämeenlinna, *Picea abies*, *Pennanen 4019* (H) (GenBank MK880146, MK880141).

### Key to teleomorphic *Helicogloea* spp. in Europe

1. Basidiospores subfusiform,  $Q > 4$ ; on various plant remnants ..... *H. angustispora*
1. Basidiospores cylindrical, ellipsoid or subglobose,  $Q < 2.5$ ; on wood ..... 2
2. On conifers ..... 3
2. On deciduous trees ..... 4
3. Basidiospores broadly ellipsoid to subglobose, rarely lacrymoid, 7–11 × 6–8 μm; on *Picea* ..... *H. dryina*
3. Basidiospores cylindrical to narrowly ellipsoid, 11–18 × 5.5–8.5 μm; mostly on *Pinus* ..... *H. subardosiaca*
4. Basidiocarps largely effused, gelatinous, up to 0.5 mm or thicker ..... 5
4. Basidiocarps usually rather small-sized, waxy, up to 0.1 mm thick ..... 6
5. Basidiospores aseptate, 10.5–14 × 6–8 μm ... *H. aseptata*
5. At least some basidiospores 1–2-septate, 11–16 × 6–9 μm ..... *H. septifera*
6. Basidiospores 12–16 × 6.5–8.5 μm,  $L > 13$  ... *H. sputum*
6. Basidiospores shorter,  $L < 12$  ..... 7
7. Basidiospores predominantly cylindrical,  $W < 5$  ..... 8
7. Basidiospores cylindrical to ellipsoid,  $W > 5$  ..... 9
8. Basidiocarps continuous, effused, smooth ..... *H. exigua*
8. Basidiocarps first pustular, then fusing together, reticulate or tuberculate ..... *H. insularis*
9. Basidiospores 7.5–11 × 4.5–6.5 μm,  $W = 5.19–5.51$  ..... *H. pellucida*
9. Basidiospores wider,  $W > 5.7$  ..... 10
10. Hemiboreal/boreal species; basidiospores 8.5–13 × 5.5–9.5 μm,  $W = 6.50–8.03$  ..... *H. aquilonia*
10. Temperate species; basidiospores 7.5–13.5 × 5–8 μm,  $W = 5.78–6.31$  ..... *H. sebacea*

### Acknowledgements

The research was supported by Norwegian Biodiversity

Information Centre (the project “A survey of Norwegian jelly fungi”, grant no. knr. 44-15, the authors KHL and VS) and by Finnish Academy of Sciences (project 315927, the author VS). The molecular work was partly financially supported by the Russian Foundation for Basic Researches, project no. 19-04-00024 (the author V. Malysheva) and the Research Group Mycology, Ghent University. Roeland Enzlin, Nico Dam and other contributing members of ‘the phragmoproject’ are thanked for sharing *Helicogloea* collections and their valuable opinions during the 2018 autumn Cristella weekend in Lauwersmeer.

## References

- Aime M.C., Urbina H., Liber J.A., Bonito G. & Oono R. 2018: Two new endophytic Atractiellomycetes, *Atractiellum hillariae* and *Proceropycnis hameedii*. — *Mycologia* 110: 136–146.
- Bourdot H. & Galzin A. 1909: Hyménomycètes de France. I. Hétérobasidiés. — *Bulletin de la Société Mycologique de France* 25: 15–36.
- Gardes M. & Bruns T.D. 1993: ITS primers with enhanced specificity for basidiomycetes — applications to the identification of mycorrhizae and rusts. — *Molecular Ecology* 2: 113–118.
- Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W. & Gascuel O. 2010: New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. — *Systematic Biology* 59: 307–321.
- Kumar S., Stecher G. & Tamura K. 2016: MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. — *Molecular Biology & Evolution* 33: 1870–1874.
- Landvik S. 1996: *Neolecta*, a fruit-body producing genus of the basal ascomycetes, as shown by SSU and LSU rDNA sequences. — *Mycological Research* 100: 199–202.
- Miettinen O., Vlasák J., Rivoire B. & Spirin V. 2018: *Postia caesia* complex (Polyporales, Basidiomycota) in temperate northern hemisphere. — *Fungal Systematics & Evolution* 1: 101–129.
- Ronquist F., Teslenko M., van der Mark P., Ayres D.L., Darling A., Höhna S., Larget B., Liu L., Suchard M.A. & Huelsenbeck J.P. 2012: MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. — *Systematic Biology* 61: 539–542.
- Schouteten N., Roberts P., van de Put K. & Verbeken A. 2018: New species in *Helicogloea* and *Spiculogloea*, including a type study of *Helicogloea graminicola* (Bres.) G.E. Baker (Basidiomycota, Pucciniomycotina). — *Cryptogamie Mycologie* 39: 311–323.
- Spirin V., Malysheva V., Trichies G., Savchenko A., Põldmaa K., Nordén J., Miettinen O. & Larsson K.-H. 2018: A preliminary overview of the corticioid Atractiellomycetes (Pucciniomycotina, Basidiomycota). — *Fungal Systematics & Evolution* 2: 311–340.
- Vilgalys R. & Hester M. 1990: Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. — *Journal of Bacteriology* 172: 4238–4246.
- White T.J., Bruns T., Lee S. & Taylor J. 1990: Amplification and sequencing of fungal ribosomal RNA genes for phylogenetics. — In: Innis M.A., Gelfand D.H., Sninsky J.J. & White T.J. (eds.), *PCR protocols. A guide to methods and applications*: 315–322. Academic Press, San Diego.