Botanica SERBICA

(2023) 47 (1): 55–63

DOI: https://doi.org/10.2298/BOTSERB2301055I
journal homepage: botanicaserbica.bio.bg.ac.rs

Original Scientific Paper

Pseudoxenochalara gen. nov. (Dermateaceae, Helotiales), with *P. grumantiana* sp. nov. from the Svalbard archipelago

Vadim Alexandrovich Iliushin* and Irina Yuryevna Kirtsideli

Komarov Botanical Institute of the Russian Academy of Sciences, 197022, St. Petersburg, Russia
* Correspondence: ilva94@yandex.ru

ABSTRACT:
The family Dermateaceae belongs to the Helotiales order, the class Leotiomycetes, and consists of 14 genera. In this study, we introduce the new genus *Pseudoxenochalara* gen. nov. to the Dermateaceae family, which is supported by morphological observations and multilocus phylogenetic analysis. Partial sequences of the loci encoding β-tubulin (BenA), ribosomal polymerase II second largest subunit (RPB2), 28S rDNA (LSU) and internal transcribed spacer rDNA region (ITS1-5.8S-ITS2) were analysed. This genus comprises one new species, *P. grumantiana*, isolated from the soil of the Arctic tundra near the settlement of Barentsburg (the Svalbard archipelago). The asexual morph of *P. grumantiana* was described. The sequences data, as well as the macro- and micromorphological characteristics distinguish *P. grumantiana* from all known species in the Dermateaceae family.

Keywords:
Dermateaceae, Helotiales, multi-gene phylogeny, Arctic tundra, Svalbard

UDC: 561.28(984)

Received: 04 August 2022
Revision accepted: 25 November 2022

INTRODUCTION

According to polyphasic taxonomy, the Dermateaceae family includes the genera *Coleophoma* Höhn., *Corniculariella* P. Karst., *Cryptosporiopsis* Bubák & Kabát, *Davidhawksworthia* Crous, *Dermea* Fr., *Neodermea* W.J. Li, D.J. Bhat & K.D. Hyde, *Neofabraea* H.S. Jacks., *Neogloeosporidina* W.J. Li, Camporesi & K.D. Hyde, *Pezicula* Tul. & C. Tul., *Phlyctema* Desm., *Pseudofabraea* Chen Chen, Verkley & Crous, *Rhizodermea* Verkley & Zijlstra, *Verkleyomyces* Y. Marín & Crous, and *Xenochalara* M.J. Wingf. & Crous (Coetsee *et al*. 2000; Chen *et al*. 2016; Crous & Groenewald 2016; Li *et al*. 2020). The fungi of the Dermateaceae family are predominantly reported from temperate regions of the world and occupy various ecological niches. Most species are endophytes, plant pathogens, wood destroyers, saprobes and soil inhabitants (Domsch *et al*. 2007; Chen *et al*. 2016; Crous & Groenewald 2016). Although the fungi belonging to the Dermateaceae family are morphologically distinct, the data based on molecular studies confirmed a monophyletic clade (Ekanayaka *et al*. 2019; Johnston *et al*. 2019). In this paper, an unidentified fungal isolate of the Dermateaceae family from the soil of the Arctic tundra (the Svalbard archipelago) is described using a multi-locus molecular phylogenetic approach and morphological characteristics and it is proposed here as a novel species belonging to a new genus.

MATERIAL AND METHODS

Collection and preservation. Soil samples were collected from the Arctic tundra near the settlement of Barentsburg on the Svalbard archipelago (N 78°05′50″, E 14°13′05″). The samples were collected in individual sterile plastic tubes and stored frozen (-18°C) before use. The fungi were cultivated on Czapek yeast agar (CZA). Single spore isolation was used to obtain pure cultures. The plates were inoculated with a spore suspension made in a 0.2% agar and 0.05% Tween 80 solution as described by Samson *et al*. (2014).

The isolated strain was deposited in the CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands, under No. CBS 148028. A dried type culture was also preserved in the Mycological Herbarium of the Komarov Botanical Institute, St. Petersburg, Russia (acronym LE), under No. LE F-341004.

Morphological characterisation. The isolate was cultivated on Czapek agar (CZA), malt extract agar (MEA), and potato dextrose agar (PDA) for morphological observations [according to Samson *et al.* (2014) and Mongkolsamrit *et al.* (2020)]. The isolate was inoculated on 9-cm Petri dishes and incubated for 21 days at 2, 4, 8, 12, 16, 18, 21, 25, and 27°C. Colour determination was performed according to the ISCC-NBS Centroid Color Charts (Kelly 1964), based on the recommendations of Nováková *et al.* (2012). The Zeiss Axio Imager A1 was used for micro-morphological examination.

DNA extraction, PCR amplification, sequencing and phylogenetic analysis. The pure culture was grown on MEA at 16°C for 14 days for molecular analysis. DNA was extracted by using a DiamondDNA Plant kit (ABT, Russia, Barnaul) according to the manufacturer's instructions. The internal transcribed spacer rDNA region (ITS1-5.8S-ITS2) was amplified using the PCR-primers ITS1 (5'-TCCGTAGGTGAACCTTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') (White *et al.* 1990). The D1/D2 region of 28S rDNA (LSU) was amplified using the PCR-primers NL-1 (5′-GCATATCAATAAGCGGAGGAAAAG-3′) and NL-4 (5′-GGTCCGTGTTTCAAGACGG -3′) (O'Donnell 1993). For partial β-tubulin gene (BenA) amplification, Bt2a (5'-GGTAACCAAATCGGTGCTGCTTTC-3') and Bt2b (5'- ACCCTCAGTGTAGTGACCCTTGGC-3') primers were used (Glass & Donaldson 1995). For the amplification of the partial ribosomal polymerase II second largest subunit (RPB2) primers 5F_Eur (5'-GAY-GAY-CGK-GAY-CAY-TTC-GG-3') and 7CR_Eur (5'- CCCA-TRGCYTGYTTRCCCAT-3') were used (Houbraken & Samson 2011). After amplification, the agarose gel electrophoretic method was applied to separate the DNA in the samples; the sequencing of the obtained DNA fragments was carried out using the Sanger method.

The sequences were edited in BioEdit version 7.1.9. The obtained sequences were submitted to the NCBI GenBank (see Table 1 for the GenBank accession numbers). The obtained sequences were compared to the available sequences in the GenBank database (NCBI) by using BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi). The sequences were aligned with other Dermateaceae species sequences using the multiple sequence alignment programme ClustalW (Larkin *et al.* 2007). A combined ITS+LSU+RPB2+BenA data matrix containing 55 species was constructed. Datasets were generated by combining the obtained sequences with reference sequences (preferably ex-type or holotype) from previous studies (Coetsee *et al.* 2000; Pangallo *et al.* 2013; Chen *et al.* 2016; Crous & Groenewald 2016; Ekanayaka *et al.* 2019; Crous *et al.* 2020; Li *et al.* 2020; Suija *et al.* 2020).

The phylogenetic analysis was performed by using the maximum likelihood method and the Tamura-Nei model (Tamura & Nei 1993). Single locus trees were also constructed. Evolutionary analyses were conducted in MEGA X (Kumar *et al.* 2018). Initial tree(s) for the heuristic search were obtained by applying the neighbor-joining method to a matrix of pairwise distances estimated using the maximum composite likelihood approach. A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 0.4548)]; the rate variation model allowed for some sites to be evolutionarily invariable ([+I], 27.70% sites) (for the combined locus tree). A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 0.2587)]; the rate variation model allowed for some sites to be evolutionarily invariable ([+I], 30.20% sites) (for the ITS locus tree). A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 0.4179)]; the rate variation model allowed for some sites to be evolutionarily invariable ([+I], 36.37% sites) (for the LSU locus tree). A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 0.9762)]; the rate variation model allowed for some sites to be evolutionarily invariable ([+I], 26.12% sites) (for the RPB2 locus tree). A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 0.6329)]; the rate variation model allowed for some sites to be evolutionarily invariable ([+I], 9.20% sites) (for the BenA locus tree). The codon positions included were 1st+2nd+3rd+Noncoding. The confidence levels in the nodes were determined using bootstrap analyses of 1000 replicates.

RESULTS

According to the BLAST analysis of the ITS region sequences of the Dermateaceae family, *Pseudoxenochalara grumantiana* is related to *Coleophoma camelliae* Crous [Identities = 457/513(89%), 15 gaps (2%)], *Coleophoma cylindrospora* (Desm.) Höhn. [Identities = 452/512(88%), 14 gaps (2%)], and *Xenochalara juniperi* M.J. Wingf. & Crous [Identities = 451/513(88%), 25 gaps (4%)]. The closest hits using the LSU sequence are *Coleophoma ericicola Crous* [Identities = 548/578(95%), 2 gaps (0%)], *Coleophoma coptospermatis* Crous [Identities = 548/578(95%), 2 gaps (0%)], and *Neofabraea malicorticis* (Cordley) H.S. Jacks. [Identities = 547/578(95%), 2 gaps (0%)]. According to the BLAST analysis of the partial β-tubulin gene, *P. grumantiana* is most closely related to *Coleophoma*

Table 1. The specimens used in the phylogenetic analyses of the Dermateaceae species. The *P. grumantiana* sequences are in bold

Species	Collection No.	Isolation source	GenBank Accession Number			
			LSU	ITS	BenA	RPB2
Coleophoma caliginosa	CBS 124806	Leaves of *Eucalyptus caliginosa,* Australia	KR858881	GU973505	KR859293	KR859330
Coleophoma camelliae	CBS 101376	Rotting petals *of Camellia japonica*, New Zealand	KU728521	KU728481	KU728597	nd
Coleophoma coptospermatis	CBS 251.39	Leaves of *Coptosperma littorale*	KU728523	KU728483	KU728599	nd
Coleophoma ericicola	CBS 301.72	Leaves of *Erica cinerea,* UK	KU728528	KU728488	KU728605	nd
Coleophoma eucalypticola	CBS 124810	*Eucalyptus globulus,* Australia	GQ303310	GQ303279	KR859294	KR859331
Coleophoma eucalyptorum	CPC 19294	Leaves of *Eucalyptus piperita*, Australia	KF251743	KF251240	KF252725	KR859331
Coleophoma paracylindrospora	CBS 109074	Leaves of *Hypericum* sp., New Zeland	KU728531	KU728491	KU728609	nd
Coleophoma parafusiformis	CBS 132692	Leaves of *Rhododendron* sp., Sweden	KU728534	KU728494	KU728612	nd
Coleophoma proteae	CBS 132532	Leaves of *Protea caffra,* South Africa	JX069850	JX069866	KU728613	nd
Corniculariella rhamni	HKAS:101649	Decaying wood of *Rhamnus alpinus*, Italy	MT183459	MT185497	nd	MT432218
Davidhawksworthia ilicicola	CBS 734.94	Fruit of *Ilex aquifolium,* Netherlands	NG_067307	NR_154008	KU728631	nd
Davidhawksworthia quintiniae	CPC 38153	Leaves of *Quintinia sieberi,* Australia	MW175378	MW175338	MW173132	MW173113
Dermea cerasi	MFLU:16-0929	Decaying wood of *Prunus avium*, Italy	MT183464	MT185502	nd	MT432221
Dermea libocedri	CBS:138.46	*Darlingtonia californica*, USA, California	MH867661	MH856142	nd	nd
Neodermea rossica	MFLU 15-2190	Decaying wood of *Acer tataricum,* Russia, Rostov region	MT183493	MT185530	nd	MT432236
Neofabraea krawtzewii	CBS 102867	*Populus* × *berolinensis*, Norway	KR858875	KR859084	AF281459	KR859324
Neofabraea malicorticis	CBS 122030	*Malus* sp., USA, Oregon	KR858877	KR859086	KR859291	KR859326
Neofabraea actinidiae	CBS 121403	*Actinidia deliciosa*, New Zealand	KR858870	KR859079	KR859285	KR859319
Neofabraea inaequalis	CBS 326.75	*Chamaecyparis* sp., France	KR858872	KR859081	KR859287	KR859321
Neofabraea kienholzii	CBS 126461	*Malus domestica* cv. Fuji, USA	KR858873	KR859082	KR859288	KR859322
Neofabraea perennans	CBS 275.29	*Malus sylvestris*, UK	KR858879	KR859088	KR859292	KR859328
Neofabraea perennans	CBS 453.64	*Malus sylvestris*, UK	KR858880	KR859089	AF281474	KR859329
Neogloeosporidina pruni	MFLU 16-2153	Decaying wood of *Prunus avium*, Italy	MT183501	NR_169721	nd	MT432239
Pezicula neocinnamomea	CBS 100248	*Abies alba*, Denmark	KR859005	KR859213	KF376328	KF376209
Pezicula pseudocinnamomea	CBS 101000	*Castanea sativa*, Netherlands	KR859027	KR859235	KR859303	KR859340
Pezicula neoheterochroma	CBS 127388	*Sorbus aucuparia,* Austria	KR859013	KR859221	KR859301	KR859338
Pezicula acericola	CBS 239.97	*Acer spicatum,* Canada, Ontario	KR858884	KR859093	KF376283	KF376214
Pezicula aurantiaca	CBS 201.46	*Alnus crispa* var. *mollis,* Canada	KR858893	KR859102	KF376335	KF376210
Pezicula californiae	CBS 124805	*Eucalyptus* sp., USA, California	KR858895	KR859104	KR859295	KR859332
Pezicula carpinea	CBS 923.96	*Carpinus betulus,* Germany	KR858899	KR859108	KF376279	KF376158
Pezicula cinnamomea	CBS 239.96	*Fagus sylvatica*, France	KR858915	KR859124	KF376323	KF376165
Pezicula cinnamomea	CBS 240.96	*Fagus sylvatica*, France	KR858916	KR859125	KF376325	KF376163
Pezicula cornina	CBS 285.39	*Cornus circinata*, Canada, Ontario	KR858955	KR859163	KR859296	KR859333
Pezicula eucrita	CBS 259.97	*Pinus sylvestris*, USA, New York	KR858971	KR859179	KF376333	KF376205
Pezicula fagacearum	CBS 112400	*Fagus sylvatica,* Italy	KR858993	KR859201	KR859298	KR859335
Pezicula frangulae	CBS 100244	*Rhamnus frangula,* Denmark	KR858996	KR859204	KF376285	KF376211
Pezicula microspora	CBS 124641	*Berberis vulgaris,* Italy	KR859004	KR859212	KR859300	KR859337
Pezicula neosporulosa	CBS 101.96	*Abies alba*, Netherlands	KR859015	KR859223	KF376305	KF376193
Pezicula ocellata	CBS 268.39	*Salix* sp., Germany	KR859024	KR859232	KR859302	KR859339
Pezicula rubi	CBS 253.97	*Rubus* sp., USA, New York	KR859042	KR859250	KF376329	KF376204
Pezicula sporulosa	CBS 224.96	*Larix decidua*, Netherlands	KR859053	KR859261	KF376326	KF376201
Phlyctema vagabunda	CBS 109875	*Fraxinus americana*, USA, Michigan	KR859069	KR859275	AY064702	KR859346

Phlyctema vagabunda	CBS 304.62	*Malus sylvestris*, South Africa	KR859070	KR859276	KR859310	KR859347
Phlyctema vincetoxici	CBS 102469	*Paeonia* sp., New Zealand	KR859071	KR859277	KR859311	KR859348
Phlyctema vincetoxici	CBS 123727	*Vincetoxicum officinale*, Czech Republic	KR859072	KR859278	KR859312	KR859349
Pseudofabraea citricarpa	CBS 130297	*Citrus unshiu*, China	KR859073	KR859279	KR859313	KR859350
Pseudofabraea citricarpa	CBS 130532	*Citrus unshiu*, China	KR859074	KR859280	KR859314	KR859351
Pseudoxenochalara grumantiana	**CBS 148028**	**Soil of arctic tundra, Norway, Svalbard Archipelago**	**OM776920**	**OM774424**	**OM782292**	**OM782293**
Rhizodermea veluwensis	CBS 110605	Roots of *Erica tetralix,* Netherlands	KR859076	KR859282	KR859316	KR859353
Rhizodermea veluwensis	CBS 110615	Roots of *Vaccinium myrtillus,* Netherlands	KR859077	KR859283	KR859317	KR859354
Trichosporiella cerebriformis	CBS 244.68	Soil from a constantly used tracked vehicle road rut near a diesel power station, Antarctica, King George Island	MH870838	MH859126	nd	nd
Xenochalara juniperi	MEA-B5-SW	Funeral clothes in the crypt, Slovakia, Bratislava	nd	JX869564	nd	nd
Xenochalara juniperi	CBS 670.75	Decaying needles of *Juniperus communis,* Netherlands	nd	AF184887	nd	nd
Outgroup: *Infundichalara microchona*	CBS 175.74	Decaying wood of *Pinus sylvestris*	HQ609479	KR859078	KR859284	KR859318

nd—no data

paracylindrospora Crous [Identities = 293/365(80%), 21 gaps (5%)], and *Davidhawksworthia quintiniae* Crous [Identities = 300/376(80%), 24 gaps (6%)]. The closest hits using the RPB2 sequence are *Pezicula chiangraiensis* Ekanayaka & K.D. Hyde [Identities = 813/1013(80%), 8 gaps (0%)], and *Pezicula cinnamomea* (DC.) Sacc. [Identities = 812/1013(80%), 8 gaps (0%)].

For the examination of the *Pseudoxenochalara grumantiana* phylogeny the sequence data from the ITS, LSU, BenA, and RPB2 loci were analysed. The sequence data of 53 isolates including the outgroup (*Infundichalara microchona* CBS 175.74) were used to construct the phylogenetic relationships of the new species of the new genera with other species of the Dermateaceae family. The ITS region (457 sites/329 variable), the partial 28S rDNA gene (LSU) (521 sites/332 variable), the partial RPB2 (868 sites/641 variable) and the BenA (212 sites/193 variable) sequences were combined. There were a total of 2058 positions in the final dataset. Single locus trees were also constructed. The final dataset for the ITS, LSU, RPB2 and BenA, contained a total of 457, 521, 868, and 212 positions, respectively.

The combined maximum likelihood phylogenetic tree based on the ITS, LSU, BenA, and RPB2 is shown in Fig. 1 and demonstrates the relationships between the novel isolate and all the other Dermateaceae species. Based on the combined tree, *P. grumantiana* formed a strongly supported clade with *Xenochalara juniperi*.

Based on the ITS locus individual tree, *P. grumantiana* formed a strongly supported clade with *Xenochalara juniperi,* which in turn, combined into a common clade with the genera *Coleophoma, Davidhawksworthia, Phlyctema* and *Neofabraea*. *P. grumantiana* was shown to form a separate clade in the LSU individual tree with the rest of the Dermateaceae species. Based on the RPB2 individual tree, *P. grumantiana* formed a weakly supported clade with the genus *Coleophoma*. *P. grumantiana* was found to form a strongly supported clade in the partial β-tubulin (BenA) tree with the species of the genera *Coleophoma* and *Davidhawksworthia*. Individual trees are not shown, due to less representativeness, compared to the combined tree.

Taxonomy

***Pseudoxenochalara* V.A. Iliushin & I.Y. Kirtsideli, gen. nov.**

MycoBank MB 843171

Etymology. Morphologically similar to *Xenochalara*.

Type species. *Pseudoxenochalara grumantiana* V.A. Iliushin & I.Y. Kirtsideli

***Pseudoxenochalara grumantiana* V.A. Iliushin & I.Y. Kirtsideli, sp. nov.** MycoBank MB 843172

Generic-specific diagnosis. The mycelium consists of branched, seplate, hyaline and smooth hyphae. The conidiogenous cells are phialidic, cylindrical to ampulliform, grouped on penicillately branched micronematous conidiophores or single on undifferentiated hyphae. The collarettes are short 1.5–3.5 × 1.5–3.0 µm. The conidia are formed in unbranched chains, hyaline, smooth, ellipsoidal to ovoid, 6.4–8.9 × 4.4–4.6 µm.

Holotype. NORWAY: the Svalbard archipelago, near the settlement of Barentsburg, on soil from the Arctic tundra, 2019, *V. A. Iliushin* (LE F-341004 holotype, cul-

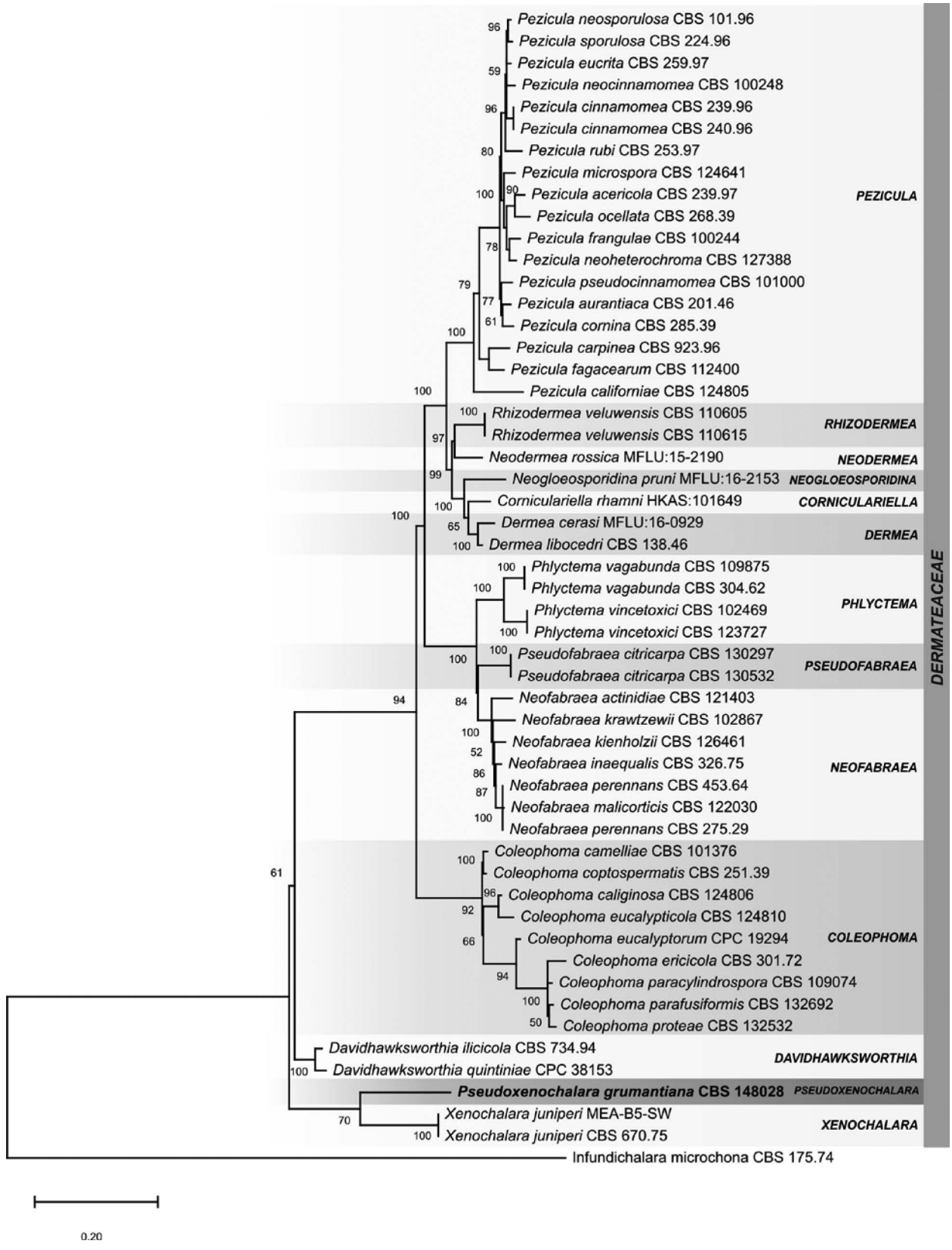

Fig. 1. Phylogenetic tree based on maximum likelihood (ML) analysis of the combined ITS+LSU+ RPB2+BenA sequences showing the relationships between *Pseudoxenochalara grumantiana* and the other species in *Dermateaceae*. The tree is rooted with *Infundichalara microchona* CBS 175.74. The bootstrap percentages > 50% are given at the nodes.

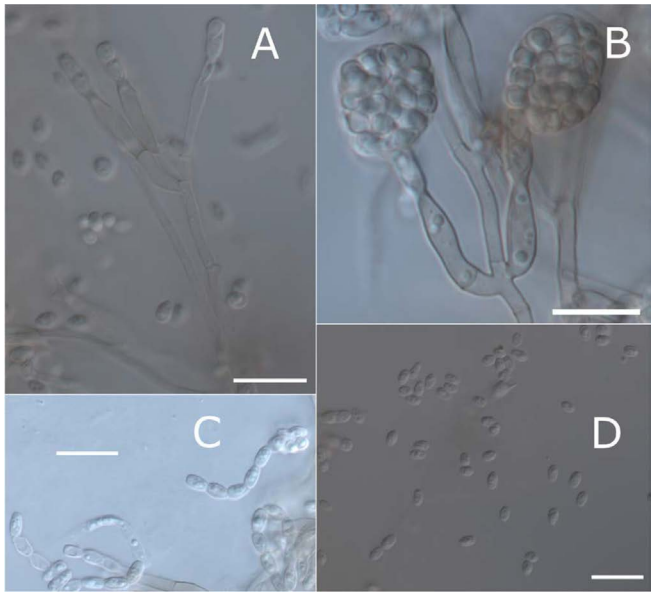

Fig 2. Micromorphology of *Pseudoxenochalara grumantiana*. A, B - conidiophores, with phialidic conidiogenous cells; C - chains of conidia; D - conidia. Scale bar = 20 µm.

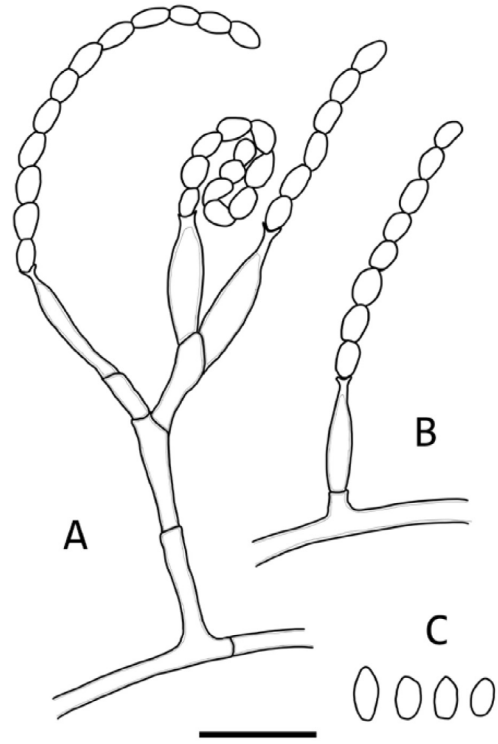

Fig 3. The growth curve of the micromorphology of *Pseudoxenochalara grumantiana*. A – conidiophore with phialidic conidiogenous cells; B - conidiogenous cell on undifferentiated hyphae; C - conidia. Scale bar = 20 µm.

ture ex-type CBS 148028; ITS, LSU, BenA and RPB2 sequences GenBank OM774424, OM776920, OM782292, OM782293).

Hyphae branched, hyaline, septate, smooth-walled, and 2.5–3.0 µm wide. *Conidiophores* micronematous, arising from aerial mycelium or submerged hyphae, 20–80 × 3.0–5.0 µm. **Conidiogenous cells** phialidic, terminal, cylindrical to ampulliform, grouped on penicillately branched micronematous conidiophores or single on undifferentiated hyphae, 15–25 × 3.0–5.0 µm. **Collarettes** short, cup-shaped, 1.5–3.5 × 1.5–3.0 µm. **Conidia** hyaline, ellipsoidal to ovoid, with a truncate base, single, 6.4–8.9 × 4.4–4.6 µm, forming unbranched twisted chains up to 25 at the apices of the phialides. **Chlamydospores** absent. Sexual state not observed. The micromorphology is shown in Figs. 2 & 3.

Culture characteristics (Fig. 4) Colony diameter 34–39 mm in 14 d at 16°C on MEA, velvety, zonal, yellowish grey (#bfb8a5; ISCC-NBS Centroid Color Charts) with a colourless marginal zone of 4–6 mm, exudate is absent; sporulation is profuse; the reverse is light olive grey (#8a8776), rapidly darkening. Colony diameter 25–35 mm in 14 d at 16°C on CZA, velvety, yellowish grey (#bfb8a5) and light greyish olive (#8c8767), exudate is absent; sporulation is not very profuse; the reverse is greyish olive (#5b5842), rapidly darkening. Colony diameter 35–45 mm in 14 d at 16°C on PDA, flat, limited, zonal, successively yellowish grey (#bfb8a5), dense and dark olive brown (#3b3121), velvety from the centre towards the edge, no exudate; sporulation is not very profuse; the reverse is dark greyish olive (#363527). Growth temperature range: 2–25°C. Optimum: 16°C. The growth curve is shown in Fig. 5.

Habitat and distribution. The new species was isolated from soil in the Arctic tundra (willow grass and moss tundra) of the Svalbard archipelago (N 78°03′35.0″, E 14°12′22.9″).

Etymology. The name refers to the former Russian name of Svalbard, "Grumant".

DISCUSSION

The Dermateaceae family was separated into 14 genera. A combined tree based on *ITS+LSU+BenA+RPB2* partial sequences showed *P. grumantiana* is also included in Dermateaceae and is most closely related to *Xenochalara juniperi* M.J. Wingf. & Crous. This species was isolated from coniferous trees *Juniperus* and the roots of *Pinus densiflora*, but it was also found in an exotic habitat - on the funeral clothes of Cardinal Peter Pázmány in an ancient crypt (Coetsee *et al.* 2000; Pangallo *et al.* 2013; Park *et al.* 2020). The finds were made in Europe (the Netherlands and Slovakia) and South Korea.

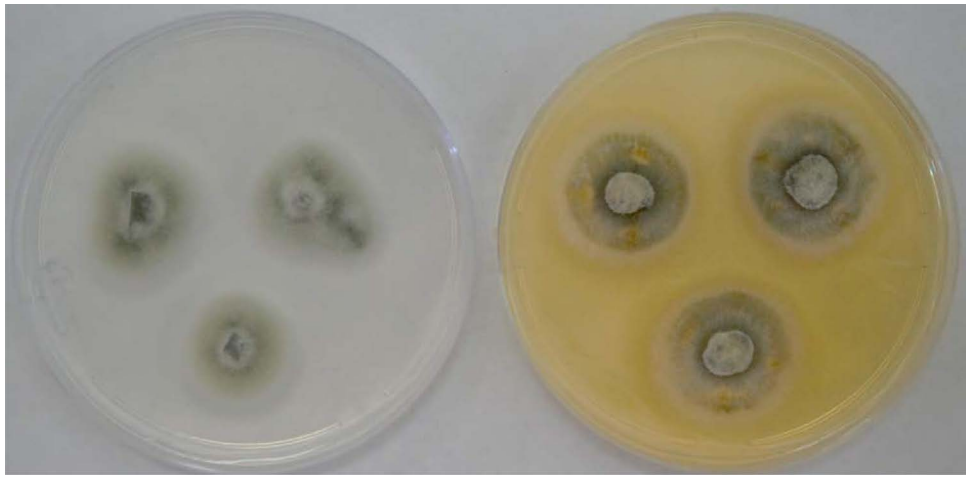

Fig 4. Colony of *Pseudoxenochalara grumantiana* on CZA (left) and MEA (right) after 2 weeks at 16°C.

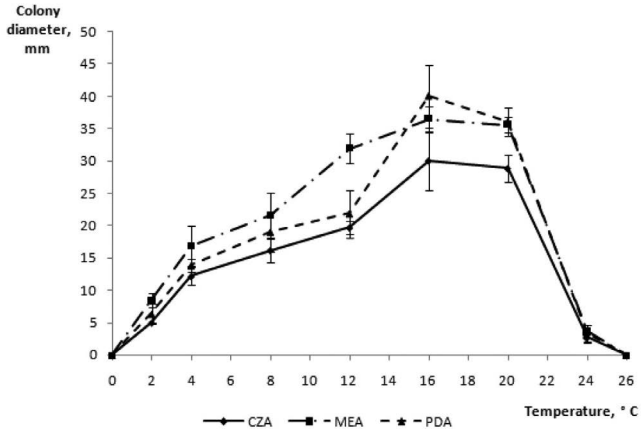

Fig 5. The growth curve of *Pseudoxenochalara grumantiana* on different media after 2 weeks at 16°C.

However, *P. grumantiana* has unique sequences. The low percentage of sequence similarity and the formation of a separate subclade make it possible to separate the fungus into a separate genus. *Pseudoxenochalara* represents a new genus in Dermateaceae and is morphologically similar to *Xenochalara* (Coetsee *et al.* 2000), but distinguished from *Xenochalara* based on its penicillately branched conidiophores, cylindrical to ampulliform phialidic conidiogenous cells, wider hyphae, and 2–3 times larger ellipsoidal to ovoid conidia.

The vast majority of the species of the Dermateaceae family are inhabitants of plants in the temperate zone (Chen *et al.* 2016; Crous & Groenewald 2016). *Pseudoxenochalara grumantiana* is an inhabitant of the soil in the Arctic tundra. Various studies have been devoted to the Svalbard fungal communities in the soils of the Arctic tundra (Kurek *et al.* 2007; Singh *et al.* 2012; Ali *et al.* 2013; Iliushin *et al.* 2022). The optimum growth temperature (16°C) confirmed the high adaptability of *P. grumantiana* to low Arctic temperatures.

Thus, our data indicate that the fungus can be clearly distinguished from the other species in Dermateaceae based on phylogenetic and morphologic analyses and represents the novel species *Pseudoxenochalara grumantiana* in the genus *Pseudoxenochalara*.

Acknowledgement – The work was carried out at the Komarov Botanical Institute RAS with the financial support of the Ministry of Education and Science of the Russian Federation under Agreement No. 075-15-2021-1056 dated September 28, 2021. The research was conducted using equipment from The Core Facilities Center "Cell and Molecular Technologies in Plant Science" at the Komarov Botanical Institute RAS (St. Petersburg, Russia).

REFERENCES

Ali SH, Alias SA, Siang HY, Smykla J, Pang K-L, Guo S-Y & Convey P. 2013. Studies on diversity of soil microfungi in the Hornsund area. Spitsbergen. *Polish Polar Research* **34**: 39–54.

Chen C, Verkley GJ, Sun G, Groenewald JZ & Crous PW. 2016. Redefining common endophytes and plant pathogens in *Neofabraea, Pezicula*, and related genera. *Fungal Biology* **120**(11): 1291–1322.

Coetsee C, Wingfield MG, Crous PW & Wingfield BD. 2000. *Xenochalara*, a new genus of dematiaceous hyphomycetes for chalara-like fungi with apical wall building conidial development. *South African Journal of Botany* **66**: 99–103.

Crous PW, Cowan DA, Maggs-Kölling G, Yilmaz N, Larsson E, Angelini C, Brandrud TE, Dearnaley JD, Dima B, Dovana F & Fechner N. 2020. Fungal Planet description sheets: 1112–1181. *Persoonia* **45**: 251–409.

Crous PW & Groenewald JZ. 2016. They seldom occur alone. *Fungal Biology* **120**: 1392–1415.

Domsch KH, Gams W & Anderson TH. 2007. *Compendium of soil fungi, 2nd taxonomically revised edition by W. Gams.* IHW, Eching.

Ekanayaka A, Hyde KD, Gentekaki E, McKenzie EHC, Zhao Q, Bulgakov TS & Camporesi E. 2019. Preliminary classification of Leotiomycetes. *Mycosphere* **10**: 310–489.

Glass NL & Donaldson GC. 1995. Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Applied and Environmental Microbiology* **61**: 1323–1330.

Houbraken J & Samson RA. 2011. Phylogeny of *Penicillium* and the segregation of *Trichocomaceae* into three families. *Studies in Mycology* **70**: 1–51.

Iliushin VA, Kirtsideli IY & Vlasov DY. 2022. Diversity of culturable microfungi of coal mine spoil tips in Svalbard. *Polar Science* **32**: 100793.

Johnston PR, Quijada L, Smith CA, Baral HO, Hosoya T, Baschien C, Pärtel K, Zhuang WY, Haelewaters D, Park D, Carl S, López-Giráldez F, Wang Z & Townsend JP. 2019. A multigene phylogeny toward a new phylogenetic classification of *Leotiomycetes*. *IMA Fungus* **10**: 1.

Kelly KL. 1964. *Color Name Charts Illustrated with Centroid Colors.* Inter-Society Color Council – National Bureau of Standards. Government Printing Office, Washington, DC.

Kumar S, Stecher G, Li M, Knyaz C & Tamura K. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution* **35**: 1547–1549.

Kurek E, Kornillowicz-Kowalska T, Slomka A & Melke J. 2007. Characteristics of soil filamentous fungi communities isolated from various micro-relief forms in the high Arctic tundra (Bellsund region, Spitsbergen). *Polish Polar Research* **28**: 57–73.

Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, Valentin F, Wallace IM, Wilm A, Lopez R, Thompson JD, Gibson TJ & Higgins DG. 2007. Clustal W and Clustal X version 2.0. *Bioinformatics* **23**: 2947–2948.

Li W, McKenzie EH, Liu J, Bhat DJ, Dai D, Camporesi E, Tian Q, Maharachchikumbura SS, Luo Z, Shang Q, Zhang J, Tangthirasunun N, Karunarathna SC, Xu J & Hyde KD. 2020. Taxonomy and phylogeny of hyaline-spored coelomycetes. *Fungal Diversity* **100**(1): 279–801.

Mongkolsamrit S, Khonsanit A, Thanakitpipattana D, Tasanathai K, Noisripoom W, Lamlertthon S, Himaman W, Houbraken J, Samson RA & Luangsa-Ard J. 2020. Revisiting *Metarhizium* and the description of new species from Thailand. *Studies in Mycology* **95**: 171–251.

Nováková A, Hubka V, Saiz-Jimenez C & Kolarik M. 2012. *Aspergillus baeticus* sp. nov. and *Aspergillus thesauricus* sp. nov., two species in section *Usti* from Spanish caves. *International Journal of Systematic and Evolutionary Microbiology* **62**: 2778–2785.

O'Donnell K. 1993. *Fusarium* and its near relatives. In: Reynolds DR & Taylor JW (eds.), *The Fungal Holomorph: Mitotic, Meiotic and Pleomorphic Speciation in Fungal Systematics*, pp. 225–233, CABI Publishing, Wallingford.

Pangallo D, Kraková L, Chovanová K, Bučková M, Puškarová A & Simonovičová A. 2013. Disclosing a crypt: microbial diversity and degradation activity of the microflora isolated from funeral clothes of Cardinal Peter Pázmány. *Microbiological Research* **168**: 289–299.

Park KH, Oh S-Y, Yoo S, Park MS, Fong JJ & Lim YW. 2020. Successional change of the fungal microbiome pine seedling roots inoculated with *Tricholoma matsutake*. *Frontiers in Microbiology* **11**: 574146.

Samson RA, Visagie CM, Houbraken J, Hong SB, Hubka V, Klaassen CHW, Perrone G, Seifert KA, Susca A, Tanney JB, Varga J, Kocsubé S, Szigeti G, Yaguchi T & Frisvad JC. 2014. Phylogeny, identification and nomenclature of the genus *Aspergillus*. *Studies in Mycology* **78**: 141–173.

Singh SM, Singh SK, Yadav LS, Singh PN & Ravindra R. 2012. Filamentous soil fungi from ny-alesund, spitsbergen, and screening for extracellular enzymes. *Arctic* **65**: 45–55.

Suija A, Haldeman M, Zimmermann E, Braun U & Diederich P. 2020. Phylogenetic placement and lectotypification of *Pseudotryblidium neesii* (Helotiales, Leotiomycetes). *Fungal Systematics and Evolution* **5**: 139–149.

Tamura K & Nei M. 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* **10**: 512–526.

White TJ, Bruns TD, Lee SB & Taylor JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ & White TJ (eds.), *PCR protocols: a guide to methods and applications*, pp. 315–322, Academic Press, London, UK.

REZIME

Botanica SERBICA

Pseudoxenochalara gen. nov. (Dermateaceae, Helotiales), sa *P. grumantiana* sp. nov. sa arhipelaga Svalbard

Vadim Alexandrovich Iliushin i Irina Yuryevna Kirtsideli

Familija Dermateaceae pripada redu Helotiales, klasi Leotiomycetes, i obuhvata 14 rodova. U ovoj studiji predstavljamo novi rod *Pseudoxenochalara* gen. nov. u okviru familije Dermateaceae, što je podržano morfološkim analizama i analizom multilokusne filogenije. Analizirane su parcijalne sekvence lokusa koji kodiraju β-tubulin (BenA), drugu po veličini podjedinicu ribozomalne polimeraze II (RPB2), 28S rDNK (LSU) i interno transkribovani spejser rDNK region (ITS1-5.8S-ITS2). Ovaj rod obuhvata jednu novu vrstu *P. grumantiana*, izolovanu iz zemljišta arktičke tundre u blizini naselja Barencburg (arhipelag Svalbard). Opisana je aseksualna morfologija *P. grumantiana*. Podaci o sekvencama, makro- i mikromorfološke karakteristike izdvajaju *P. grumantiana* od svih poznatih vrsta iz porodice Dermateaceae.

Ključne reči: Dermateaceae, Helotiales, multigenska filogenija, arktička tundra, Svalbard