CZECH POLAR REPORTS 10 (2): 226-235, 2020

New records of *Oleoguttula mirabilis* and *Rachicladosporium antarcticum* from James Ross Island, Antarctica

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Abstract

A group of seven isolates of black meristematic fungi was collected from rocks within the framework of mycological research focused on the study of diversity of rock-inhabiting fungi on James Ross Island in Antarctica. Their identification was based on ITS rDNA sequence comparisons supported by morphological data. Obtained results assigned four analysed strains as *Oleoguttula mirabilis* and three isolates as *Rachicladosporium antarcticum.* To the best of our knowledge this is the second report of isolation of these two psychrophilic species from different parts of James Ross Island which imply that they probably represent a common part of its environmental microbial flora.

Key words: black yeast, ITS rDNA region, meristematic fungi, polar region, rock-inhabiting fungi

DOI: 10.5817/CPR2020-2-17

Introduction

Rock-inhabiting fungi (RIF) represent a polyphyletic group of extremotolerant microorganisms which occur in different inhospitable environment such as cold or hot deserts (Ruibal et al. 2005, 2008; Selbmann et al. 2005, 2008, 2013, 2014; Egidi et al. 2014). Except natural habitats, a number of species have been isolated from marble monuments (Wollenzien et al. 1995, Sert et al. 2007, Isola et al. 2015) or radiation-ravaged places (Zhdanova et al. 2000).

Antarctic rocks represent harsh habitat due to the presence of various stress factors, including nutrient deficiency, intense sunlight, high UV radiation, osmotic stress, temperature fluctuations or low water availability (Sterflinger 1998, 2006; Selbmann et al. 2008, 2011). Despite those adverse conditions, they are inhabited by various

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Received November 26, 2020, *accepted* December 29, 2020.

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Acknowledgements: The author wish to thank the scientific infrastructure of the J. G. Mendel Czech Antarctic Station, part of the Czech Polar Research Infrastructure (CzechPolar2), and its crew for their assistance, supported by the Ministry of Education, Youth and Sports of the Czech Republic (LM2015078) and the Czech Antarctic Foundation for their support. Sincere thanks go to Dr. Pavel Švec for his valuable comments on the manuscript and Dr. Zdeněk Stachoň for providing topographic data.

microbial communities including algae, bacteria, cyanobacteria, lichenised and non-lichenised fungi. Fungi colonise rocks on the surface (epilithic fungi) and/or inside the rock (endolithic fungi)(Friedmann 1982, Selbmann et al. 2005, 2013; Gorbushina 2007, Zucconi et al. 2014).

The ability of these fungi to survive in extreme conditions is given by their morpho-physiological properties. They are characterized by restricted growth leading to formation of small compact black colonies. The black coloration of cells is given by production of high amount of pigment melanin, which protects them against UV radiation (Selbmann et al. 2005, 2011). Meristematic growth characterised by isodiametrically dividing cells contributes to their resistance as well and enable them to survive desiccation and extreme temperatures (Urzì et al. 2000, Selbmann et al. 2005).

Many novel genera of RIF, such as *Cryomyces*, *Elasticomyces, Extremus, Oleoguttula, Recurvomyces, Vermiconidia,* and endemic genus *Friedmanniomyces* have been described from the cold environment of Antarctica in taxonomic papers of Selbmann et al. (2005, 2008) and Egidi et al. (2014). They are classified into the class *Dothideomycetes,* mainly within the order *Capnodiales* (Ruibal et al. 2009, Egidi et al. 2014, Quaedvlieg et al. 2014).

The genus *Oleoguttula* belongs to the family *Teratosphaeriaceae* within the order *Capnodiales* (Egidi et. al. 2014, Quaedvlieg et al. 2014) The genus represented by a single psychrophilic species *Oleoguttula mirabilis* was proposed based on two isolates originated from rocks on James Ross Island by Selbmann and de Hoog (Egidi et. al. 2014) and the name was validated by Crous et al. (2019). Recently, this species has also been recorded from ice with high ice algae abundance (called dark ice) from Greenland Ice Sheet (Perini et al. 2019). Phialidic conidiogenesis is the important morphological feature of this genus, which has not been observed in other RIF taxa described from Antarctica and makes this species easy to distinguish from remaining RIF species (Egidi et. al. 2014).

The genus *Rachicladosporium* belongs to the order *Capnodiales* and family *Cladosporiaceae* with phylogenetically closely related genera *Cladosporium, Dichocladosporium, Toxicocladosporium* and *Verrucocladosporium.* It was proposed by Crous et al. (2007) on a single isolate from leaf spots on *Luculia* sp. and assigned as *Rachicladosporium luculiae.* At present the genus comprise 14 species with validly published name that accommodate mainly epiphytic and rock-inhabiting fungi. A total, six new mostly psychrophilic species were described from rocks of which three species originated from the Italian Alps and two species from Antarctica, namely *Rachicladosporium mcmurdoi* and *Rachicladosporium antarcticum* (Egidi et al. 2014, Crous et al. 2019). *Rachicladosporium* is morphologically distinguishable from *Cladosporium s. str.* and related cladosporium-like genera by presence of apical rachis on conidiophores with inconspicuous to subconspicuous scars and unthickened, not darkened-refractive conidial hila (Crous et al. 2007). In contrast the rock-inhabiting species usually produce brown septate hyphae only, cladosporium-like cells are not observed (Egidi et al. 2014).

Morphological identification of many RIF species is difficult because some of them are highly pleomorphic or many species are morphologically scarcely differentiated and meristematic growth presents the only type of their reproduction (Urzì et al. 2000, Egidi et al. 2014). Therefore their identification is based primarily on phylogenetic analysis supported by morphological data.

In total, 115 isolates of black meristematic fungi were collected from rocks within the framework of mycological research focused on the study of diversity, taxonomy and phylogenetic relationships of rock-inhabiting fungi inhabiting James

Ross Island in Antarctica. For most isolates there were no phylogenetically close ITS rDNA sequences available in the GenBank nucleotide database enabling their reliable taxonomic identification (unpublished). Only seven RIF isolates described in this study showed high similarity with reference sequnces and could be indentified to the species level. Taxonomic position of the remaining isolates was unclear and require further investigation.

Material and Methods

Sampling sites

The investigated area was located in the northern deglaciated part of the Ulu Peninsula, James Ross Island (64° 10' S, 57° 45' W), which is situated close to the northeastern extremity of the Antarctic Peninsula. The climate of the island is semiarid with the mean annual temperature around -7°C (Ambrožová and Láska 2016). The vegetation is represented by a great variety of terrestrial algae, cyanobacteria, lichens and mosses as the main components of communities forming Antarctic vegetation oases (Barták et al. 2015).

Sampling and isolation

Seven isolates of RIF analysed in this study were obtained from five samples of rock fragments collected in February and March during the Czech polar expedition in 2018. The rock samples were aseptically collected into sterile plastic tubes and preserved at 8 °C until isolation. RIF were isolated by the direct inoculation of rock fragments on Petri dishes with Dichloran rose bengal chloramphenicol agar (DRBC, Difco) and Malt yeast extract agar (MYEA, Selbmann et al. 2005). The plates were incubated at 15°C under aerobic conditions and observed after four weeks. Axenic cultures of RIF were subcultured on agar plates with 2% Malt Extract Agar (MEA, Difco) and maintained at -70°C. Morphology of 12 weeks old isolates cultivated on MEA at 15°C was studied by microscopic observation in lactic acid using Olympus BX 50 light microscope. Microphotographs were done with a digital camera Artcam 500 MI.

DNA extraction and sequencing

Sequencing of the complete ITS rDNA region (ITS1-5.8S-ITS2) was used to delimit species of RIF's isolates and compare them with close relatives (de Hoog et al. 1999). Genomic DNA was isolated from 12 weeks old cultures grown on MEA plates at 15 °C. Mycelial fragments were disrupted using the FastPrep bead beating system (MP Biomedicals, Irvine, CA, USA) and purified with a High Pure PCR Template Preparation Kit (Roche, Germany). The ITS rDNA region was amplified with the primers SR6R and LR1 (Vilgalys and Hester 1990). PCR conditions and sequencing method were performed according to Marvanová and Laichmanová (2014). Sequences obtained in this study were submitted to NCBI's GenBank nucleotide database (Table 1).

Species	Strain No.	Locality	ITS GenBank accession No.
Aureobasidium subglaciale	CBS 123387	Svalbard and Jan Mayen Island	NR_147323.1
Cladosporium cladosporioides	CBS 112388	Germany	NR_119839.1
Cladosporium colombiae	CBS 274.80B	Colombia	NR_119729.1
Cladosporium verrucocladosporioides	CBS 126363	South Korea	MH863939.1
Oleoguttula mirabilis	**P10109**	**JRI, Antarctica (1)**	**MW222191**
Oleoguttula mirabilis	**P10406**	**JRI, Antarctica (2)**	**MW222211**
Oleoguttula mirabilis	**P10407**	**JRI, Antarctica (2)**	**MW222212**
Oleoguttula mirabilis	**P10444**	**JRI, Antarctica (1)**	**MW222225**
Oleoguttula mirabilis	CCFEE 5522	JRI, Antarctica	KF309972.1
Oleoguttula mirabilis	CBS 136102	JRI, Antarctica	NR_144974.1
Oleoguttula mirabilis	EXF-13077	Greenland Ice Sheet	MK460370.1
Oleoguttula mirabilis	EXF-13078	Greenland Ice Sheet	MK460369.1
Oleoguttula mirabilis	EXF-13080	Greenland Ice Sheet	MK460371.1
Rachicladosporium alpinum	CBS 136040	Monte Rosa, Italy	NR_144965.1
Rachicladosporium americanum	CBS 124774	Virginia, USA	MH863412.1
Rachicladosporium antarcticum	**P10108**	**JRI, Antarctica (3)**	**MW251711**
Rachicladosporium antarcticum	**P10377**	**JRI, Antarctica (5)**	**MW222195**
Rachicladosporium antarcticum	**P10413**	**JRI, Antarctica (4)**	**MW222216**
Rachicladosporium antarcticum	CCFEE 5527	Antarctic Peninsula, Antarctica	NR_144970.1
Rachicladosporium cboliae	CBS 125424	Virginia, USA	NR_156538
Rachicladosporium corymbiae	CBS 145087	Ghana	NR_161143
Rachicladosporium eucalypti	CPC 23241	Ethiopia	NR_155718.1
Rachicladosporium inconspicuum	CBS 136043	Monte Rosa, Italy	NR_144966
Rachicladosporium iridis	CBS 282.49	Netherlands	NR_169891.1
Rachicladosporium luculiae	CBS 121620	Auckland, New Zealand	NR_160222
Rachicladosporium mcmurdoi	CBS 119432	McMurdo Dry Valleys, Antarctica	NR_144967.1
Rachicladosporium monterosium	CBS 137178	Monte Rosa, Italy	NR_144968.1
Rachicladosporium paucitum	CBS 136041	Trento, Italy	NR_144969
Rachicladosporium pini	CBS 129525	Netherlands	JF951145.1
Toxicocladosporium banksiae	CBS 128215	Australia	NR_152322.1
Toxicocladosporium irritans	CBS 185.58	Suriname	NR_152316.1
Toxicocladosporium strelitziae	CBS 132535	South Africa	NR_111765.1
Pseudotaeniolina globosa	CBS 109889	Italy	MH862844.1

Table 1. List of isolates used in the study. Isolates investigated in this work are highlighted in bold. Strains isolated from the rock are highlighted in yellow. *Notes:* JRI - James Ross Island, Antarctica. Numbers in parentheses shows sampling sites displayed in Fig. 1.

Phylogenetic analysis

The megablast search (Zhang et al. 2000) of ITS rDNA sequences was used to identify highly similar species to RIF isolates in the NCBI's GenBank nucleotide database. The ITS rDNA sequences dataset for phylogenetic analysis involved 33 nucleotide sequences of which 26 sequences of close related taxa were retrieved from the NCBI's GenBank (Table 1). They were aligned by the ClustalW program (Thompson et. al. 1994) and manually checked and assembled. The phylogenetic analysis and dendrogram construction was conducted using MEGA X software (Kumar et al. 2018). The evolutionary history was inferred by using the Maximum Likelihood method and Jukes-Cantor model and genetic distances were estimated using the Maximum Composite Likelihood (MCL) method (Jukes and Cantor 1969). Branch support was tested by 1000 replications in the bootstrap test (Felsenstein 1985).

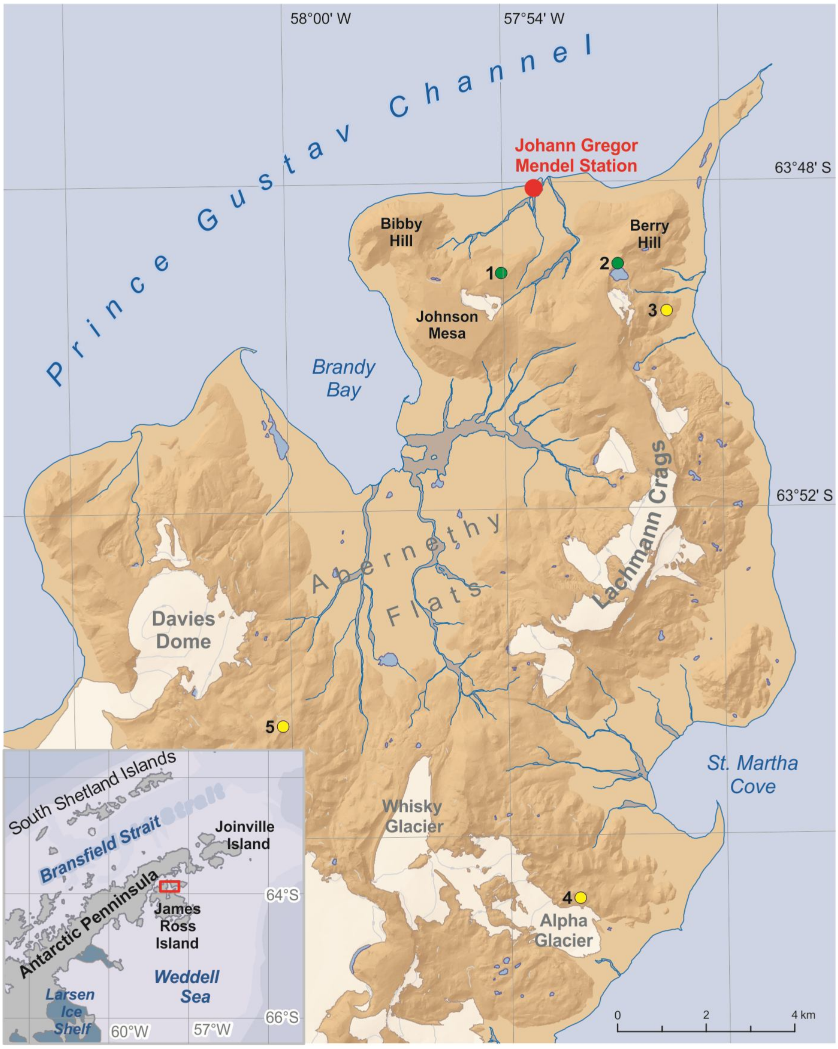

Fig. 1. Modified map of James Ross Island - Northern part ([1] - Czech Geological Survey 2009) showing the sampling sites of *Oleoguttula mirabilis* (green points) and *Rachicladosporium antarcticum* (yellow points) analysed strains. *Notes*: (1) – northeast side of Johnson Mesa, (2) – southeast side of Lachman Crags, (3) – rock outcrop of Sekyra Peak, (4) – Panorama Pass, (5) – near Alpha Glacier.

Results and Discussion

Comparison of obtained ITS rDNA sequences within the nucleotide NCBI database showed *R. antarcticum* CCFEE 5527 (NR_144970.1) as 100% identical with RIF isolate P10108 and highly similar with RIF isolates P10377 and P10413 (99.59%), followed by *Rachicladosporium monterosium* CBS 137178 (NR_144961.1, 98.56%) and *R. mcmurdoi* CBS 119432 (NR_144967.1, 97.33%). The remaining four RIF isolates (P10109, P10406, P10407, P10444) showed 100% sequence similarity with *O. mirabilis* CCFEE 5522 (KF309973.1) and 99% sequence similarity with *O. mirabilis* CBS 136102 (NR_144974.1) and *O. mirabilis* strains EXF-13077, EXF-13078, EXF-13080. The genus *Oleoguttula* displayed very distinct ITS sequences from other sequences in the nucleotide NCBI database and *Pseudotaeniolina globosa* CBS 109889 (MH862844) isolated from stone of church in Italy was found as the phylogenetically closest relative (similarity 89.77%).

Phylogenetic analysis and Maximum Likelihood phylogenetic tree constructed using ITS rDNA sequences (Fig. 3) clearly showed the phylogenetic relation of three RIF isolates P10108, P10377 and P10413 from James Ross Island to *R. antarcticum* (*Rachicladosporium* clade) and P10109, P10406, P10407 and P10444 RIF isolates to *O. mirabilis* (*Oleoguttula* clade).

The three RIF isolates assigned in the *Rachicladosporium* clade clustered with the reference ITS sequences of 13 *Rachicladosporium* species. *Cladosporium* spp. and *Toxicocladosporium* spp. were included in the phylogenetic tree construction as closely related genera of the family *Cladosporiaceae*. Analysed RIF isolates P10108, P10377 and P10413 were clustered with *R. antarcticum* CCFEE 5527 (NR_144970.1) described from Antarctic Peninsula (Egidi et al. 2014) with 91% bootstrap support. The evolutionary divergences among strains placed in the separate subbranch, including *R. antarcticum, R. monterosium* and *R. mcmurdoi* varied from 1.1 to 2.2%, while the evolutionary divergences among all *Rachicladosporium* species were in the range of 1.1 – 15.4% (data not showed). Pairwise distance calculation showed a minor percentage of nucleotide differences (0 – 0.5%) in the case of intraspecific variation in *R. antarcticum.*

Rachicladosporium antarcticum isolates were collected from three distant localities of James Ross Island (Fig. 1). The closest related species *R. monterosium* was isolated from Monte Rosa in the Italian Alps and *R. mcmurdoi* was collected from McMurdo Dry Valleys in Southern Victoria Land, Antarctica. These species are difficult to identify based on morphology because they are scarcely differentiated. They all develop brown, branched hyphae but *R. monterosium* often forms hyphae in strands with anastomosis and *R. antarcticum* produces torulose hyphae enteroblastically proliferating. *Rachicladosporium mcmurdoi* develops 1 – 2-celled conidia by arthric secession, while the formation of conidia or chlamydospor-like cells were not observed even after prolonged incubation of *R. monterosium* and *R. antarcticum* (Egidi et al. 2014). Studied isolates developed brown, branched, torulose hyphae (Fig. 2). Colonies on MEA attained 20 mm in diam. after 12 weeks at 15 °C. They were compact, elevated with folds, dark brown in observe and black in reverse (Fig. 2).

The *Oleoguttula* clade was composed of four analysed RIF isolates (P10109, P10406, P10407, P10444) collected from two different sampling sites on James Ross Island while strains of *O. mirabilis* (CBS 136102, CCFEE 5522) described by Selbmann and de Hoog and originated form James Ross Island (Egidi et al. 2014) were isolated from another locality than our isolates.

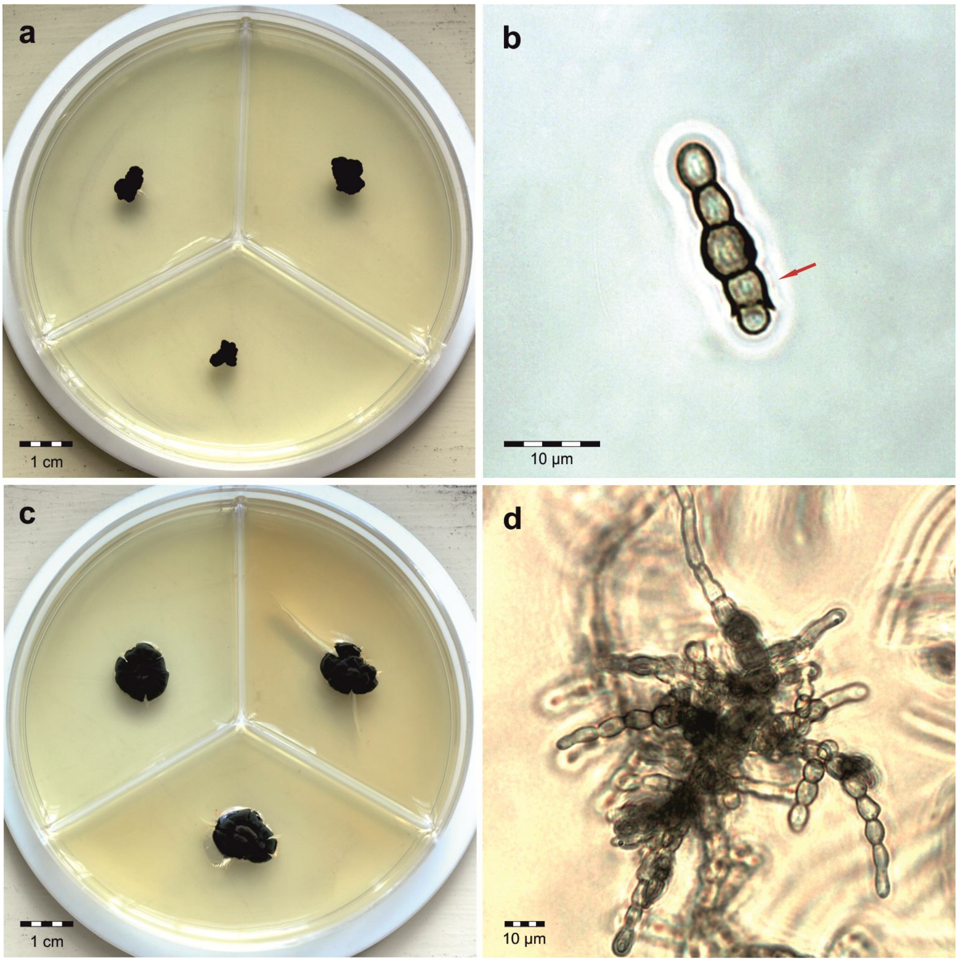

Fig. 2. a-b *Oleoguttula mirabilis* P10407; **a** – colony appearance on MEA after 12 weeks, **b** – wide opening, terminal phialide with conidia; **c-d** *Rachicladosporium antarcticum* P10108, **c** – colony appearance on MEA after 12 weeks, **d** – torulose, branched hyphae.

The remaining three strains (EXF-13077, EXF-13078, EXF-13080) of *Oleoguttula* clade were originated from the Greenland ice sheet (Perini et al. 2019). The intraspecific variability of ITS sequences in *O. mirabilis* varied from 0 to 0.5%. The morphology of studied isolates corresponded with the description of the type culture *O. mirabilis* CBS 136102^T from Selbmann and de Hoog (Egidi et al. 2014). Colonies on MEA attained 9 mm in diam. after 12 weeks at 15°C. They were black in obverse and reverse, cerebriform with irregular margin. Unicellular, micronematous phialides with wide collorattes and brown conidia were observed (Fig. 2).

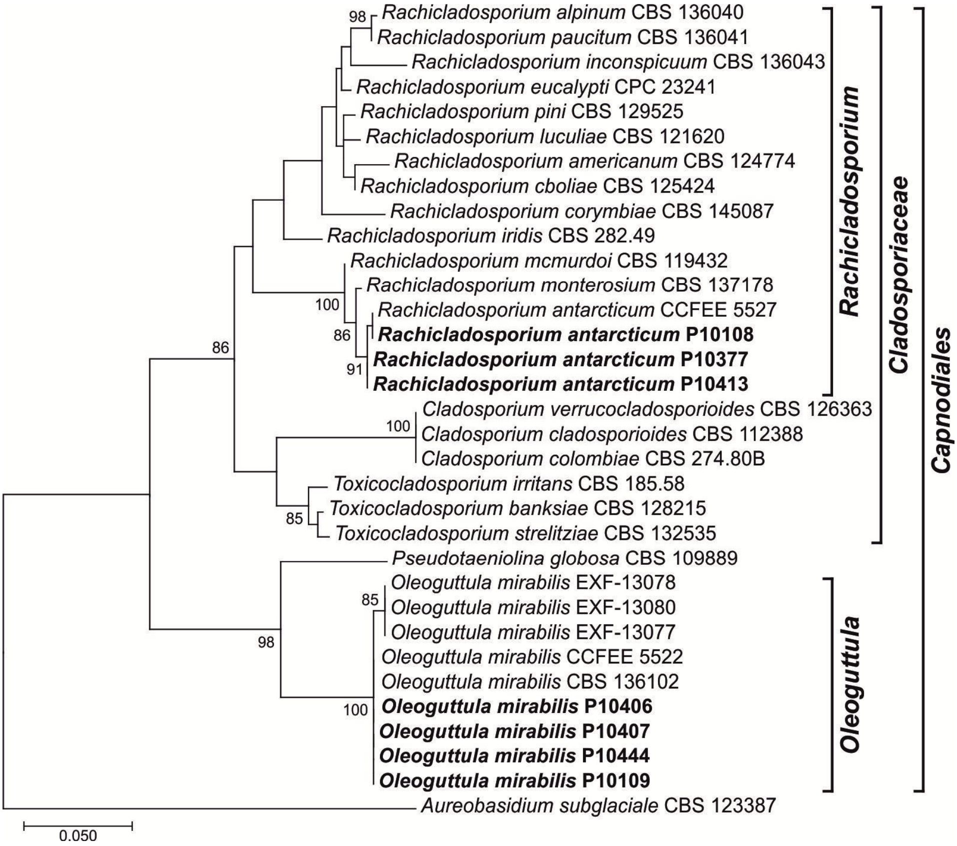

Fig. 3. Maximum Likelihood phylogenetic tree constructed using ITS rDNA sequences shows the phylogenetic position of studied *Oleoguttula mirabilis* and *Rachicladosporium antarcticum* isolates (in bold) among representaive strains of the genera *Rachicladosporium* and *Oleoguttula.* All positions containing gaps and missing data were eliminated. There were a total of 391 positions in the final dataset. Bootstrap probability values (percentages of 1000 tree replications) greater than 85 % are indicated at branch points. *Aureobasidium subglaciale* CBS 123387 (NR 147323.1) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

Conclusion

Oleoguttula mirabilis and *Rachicladosporium antarcticum,* two psychrophilic species inhabiting rocks in Antarctica were identified based on sequences similarity and phylogenetic analysis of ITS rDNA region supported by morphological data. Both species were repeatedly collected from different parts of James Ross Island, which indicates their distribution across the deglaciated part of Ulu Peninsula.

References

Ambrožová, K., Láska, K. (2016): The air temperature change on James Ross Island within the context of the Antarctic Peninsula. *In*: A. Nováček (ed.): *Sborník příspěvků z výroční konference ČGS, 5-7 September 2016,* Jihočeská Univerzita, České Budějovice, pp. 20–25. (In Czech).

Barták, M., Váczi, P., Stachoň, Z. and Kubešová, S. (2015): Vegetation mapping of moss dominated areas of northern part of James Ross Island (Antarctica) and a suggestion of protective measures. *Czech Polar Reports,* 5(1): 75-87.

Crous, P. W., Braun, U., Schubert, K. and Groenewald, J. Z. (2007): Delimiting *Cladosporium* from morphologically similar genera. *Studies in Mycology,* 58: 33-56.

Crous, P. W., Schumacher, R. K., Akulov, A., Thangavel, R., Hernández-Restrepo, M., Carnegie, A. J., Cheewangkoon, R., Wingfield, M. J., Summerell, B. A., Quaedvlieg, W., Coutinho, T. A., Roux, J., Wood, A. R., Giraldo, A. and Groenewald, J. Z. (2019): New and Interesting Fungi. 2. *Fungal Systematics and Evolution,* 3: 57-134.

De Hoog, S., Zalar, P., Urzì, C., De Leo, F., Yurlova, N. and Sterflinger, K. (1999): Relationships of dothideaceous black yeasts and meristematic fungi based on 5.8S and ITS2 rDNA sequence comparison. *Studies in Mycology,* 43: 31-37.

Egidi, E., De Hoog, G. S., Isola, D., Onofri, S., Quaedvlieg, W., De Vries, M., Verkley, G. J. M., Stielow, J. B., Zucconi, L. and Selbmann, L. (2014): Phylogeny and taxonomy of meristematic rock-inhabiting black fungi in the *Dothideomycetes* based on multilocus phylogenies. *Fungal Diversity,* 65: 127-165.

Felsenstein, J. (1985): Confidence limits on phylogenies: An approach using the bootstrap. *Evolution,* 39: 783-791.

Friedmann, E.I. (1982): Endolithic Microorganisms in the Antarctic Cold Desert. *Science,* 215: 1045-1053.

Gorbushina, A. (2007): Life on the rocks. *Environmental microbiology,* 9: 1613-1631.

Isola, D., Zucconi, L., Onofri, S., Caneva, G., De Hoog, G. S. and Selbmann, L. (2015): Extremotolerant rock inhabiting black fungi from Italian monumental sites. *Fungal Diversity,* 76: 75-96.

Jukes, T. H., Cantor, C. R. (1969): Evolution of protein molecules. *In*: H. N. Munro (ed.): Mammalian Protein Metabolism, Academic Press, New York, pp. 21–132.

Kumar, S., Stecher, G., Li, M., Knyaz, C. and Tamura, K. (2018): MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution,* 35: 1547-1549.

Marvanová, L., Laichmanová, M. (2014): *Campylospora leptosoma* sp. nov. and characteristics of *Campylospora* spp., based on morphology and on ITS sequences. *Mycosphere,* 5(2): 245-261.

Perini, L., Gostinčar, C., Anesio, A. M., Williamson, C., Tranter, M. and Gunde-Cimerman, N. (2019): Darkening of the Greenland Ice Sheet: Fungal Abundance and Diversity Are Associated With Algal Bloom. *Front Microbiology,* 10: 557. https://doi.org/10.3389/fmicb.2019.00557

Quaedvlieg, W., Binder, M., Groenewald, J. Z., Summerell, B. A., Carnegie, A. J., Burgess, T. I. and Crous, P. W. (2014): Introducing the Consolidated Species Concept to resolve species in the *Teratosphaeriaceae*. *Persoonia Molecular Phylogeny and Evolution of Fungi,* 33: 1-40.

Ruibal, C., Gueidan, C., Selbmann, L., Gorbushina, A. A., Crous, P. W., Groenewald, J. Z., Muggia, L., Grube, M., Isola, D., Schoch, C. L., Staley, J. T., Lutzoni, F. and De Hoog, G. S. (2009): Phylogeny of rock-inhabiting fungi related to *Dothideomycetes*. *Studies in Mycology,* 64: 123-133.

Ruibal, C., Platas, G. and Bills, G. F. (2008): High diversity and morphological convergence among melanised fungi from rock formations in the Central Mountain System of Spain. *Persoonia Molecular Phylogeny and Evolution of Fungi,* 21: 93-110.

Ruibal, C., Platas, G. and Bills, G. (2005): Isolation and characterization of melanized fungi from limestone formation in Mallorca. *Mycological Progress,* 4: 23-38.

SELBMANN, L., DE HOOG, G. S., MAZZAGLIA, A., FRIEDMANN, E. I. and ONOFRI, S. (2005): Fungi at the edge of life: cryptoendolithic black fungi from Antarctic desert. *Studies in Mycology,* 51: 1-32.

SELBMANN, L., DE HOOG, G. S., ZUCCONI, L., ISOLA, D., RUISI, S., GERRITS VAN DEN ENDE, A. H., RUIBAL, C., DE LEO, F., URZÌ, C. and ONOFRI, S. (2008): Drought meets acid: three new genera in a dothidealean clade of extremotolerant fungi. *Studies in Mycology,* 61: 1-20.

SELBMANN, L., GRUBE, M., ONOFRI, S., ISOLA, D. and ZUCCONI, L. (2013): Antarctic Epilithic Lichens as Niches for Black Meristematic Fungi. *Biology,* 2: 784-797.

SELBMANN, L., ISOLA, D., EGIDI, E., ZUCCONI, L., GUEIDAN, C., DE HOOG, G.S. and ONOFRI, S. (2014): Mountain tips as reservoirs for new rock-fungal entities: *Saxomyces* gen. nov. and four new species from the Alps. *Fungal Diversity,* 65: 167-182.

SELBMANN, L., ISOLA, D., ZUCCONI, L. and ONOFRI, S. (2011): Resistance to UV-B induced DNA damage in extreme-tolerant cryptoendolithic Antarctic fungi: detection by PCR assays. *Fungal Biology,* 115: 937-944.

SERT, H. B., SÜMBÜL, H. and STERFLINGER, K. (2007): Microcolonial fungi from antique marbles in Perge/Side/Termessos (Antalya/Turkey). *Antonie Van Leeuwenhoek,* 91: 217-227.

STERFLINGER, K. (1998): Temperature and NaCl- tolerance of rock-inhabiting meristematic fungi. *Antonie Van Leeuwenhoek,* 74: 271-281.

STERFLINGER, K. (2006): Black Yeasts and Meristematic Fungi: Ecology, Diversity and Identification. *In*: G. Péter, C. A. Rosa (eds.): Biodiversity and Ecophysiology of Yeasts, The Yeast Handbook. Springer, Berlin, Heidelberg, pp. 501–514.

THOMPSON, J. D., HIGGINS, D. G. and GIBSON, T. J. (1994): CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position–specific gap penalties and weight matrix choice. *Nucleic Acids Research,* 22: 4673-4680.

URZÌ C., DE LEO F., DE HOOG S. and STERFLINGER, K. (2000): Recent Advances in the Molecular Biology and Ecophysiology of Meristematic Stone-Inhabiting Fungi. *In*: O. Ciferri, P. Tiano, G. Mastromei (eds): Of Microbes and Art. Springer, Boston, MA, pp. 17–22.

VILGALYS R., HESTER M. (1990): Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriolog,* 172: 4238-4246.

WOLLENZIEN, U., DE HOOG, G. S., KRUMBEIN, W. E. and URZÌ, C. (1995): On the isolation of microcolonial fungi occurring on and in marble and other calcareous rocks. *Science of the Total Environment,* 167: 287-294.

ZHANG, Z., SCHWARTZ, S., WAGNER, L. and MILLER, W. (2000): A greedy algorithm for aligning DNA sequences. *Journal of Computational Biology,* Feb-Apr; 7(1-2): 203-14. doi: 10.1089/10665270050081478. PMID: 10890397.

ZHDANOVA, N. N., ZAKHARCHENKO, V. A., VEMBER, V. V. and NAKONECHNAYA, L. T. (2000). Fungi from Chernobyl: Mycobiota of the inner regions of the containment structures of the damaged nuclear reactor. *Mycological Research,* 104: 1421-1426.

ZUCCONI, L., ONOFRI, S., CECCHINI, C., ISOLA, D., RIPA, C., FENICE, M., MA-DONNA, S., REBOLEIRO-RIVAS, P. and SELBMANN, L. (2014): Mapping the lithic colonization at the boundaries of life in Northern Victoria Land, Antarctica. *Polar Biology,* 39: 91-102.

Web sources / Other sources

[1] Czech Geological Survey, 2009. James Ross Island - northern part. Topographic map 1: 25 000. First edition. Praha, Czech Geological Survey. ISBN 978-80-7075-734-5.