

## *Toniniopsis bartakii* - A new species of lichenised fungus from James Ross Island (Antarctic Peninsula)

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**Abstract:** The new lichen species *Toniniopsis bartakii* is described from James Ross Island, the North-East Antarctic Peninsula region. It is phylogenetically most closely related to *T. bagliettoana* but differs mainly in forming a more developed, squamulose thallus. It is morphologically more similar to *T. coelestina* but differs mainly in the pigmentation in the proper exciple. An identification key to the known species of *Toniniopsis* is also provided.

**Key words:** Antarctica, biodiversity, lichenized fungi, *Ramalinaceae*, mtSSU, nrITS

### 1. Introduction

James Ross Island belongs to the North-East Antarctic Peninsula region and has a special location in the transition zone between maritime and continental climate types (Bednarek-Ochyra et al., 2000). The island has a large area (2600 km<sup>2</sup>), and the deglaciated part (170 km<sup>2</sup>) has a vegetation cover which is dominated by lichens and mosses. There are no vascular plants on James Ross Island. As the deglaciated areas are large on James Ross Island, the lichen biodiversity is high (Halıcı et al., 2018). Our knowledge of the lichen biodiversity in Antarctica is still insufficient. For instance, Dodge (1973) reported 415 species from this continent while describing many species and claiming that the endemism rate is rather high in Antarctica. Castello and Nimis (1997), however, examined most of the types for the species described by Dodge and reported that only 20% of the species were valid. Because of these reasons, the first author began collecting lichens on James Ross Island in 2016 and studied them by the aid of molecular techniques (Halıcı et al., 2017; 2018, Halıcı and Bartak 2019).

One of the collections, M. G. Halıcı and M. Bartak ERCH JR 209, morphologically similar to a squamulose species of *Toninia* A. Massal. or *Toniniopsis* Frey, turned out to be genetically close to the cosmopolitan, crustose lichen *Toniniopsis bagliettoana* (A. Massal. & De Not.) Kistenich & Timdal. The genus *Toniniopsis* was resurrected from the synonymy of *Toninia* by Kistenich et al. (2018a), but the

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species, although they are shown to belong in *Toniniopsis* by Kistenich et al. (2018a; as *Bacidia bagliettoana* [A. Massal. & De Not.] Jatta), was only recently transferred to *Toniniopsis* in Cannon et al. (2021). This paper discusses the identity of the collection from James Ross Island.

### 2. Materials and methods

#### 2.1. Morphology and thin-layer chromatography

Lichen sample was collected from James Ross Island in Antarctica. The type specimen detailed below is deposited in Erciyes University Herbarium Kayseri, Turkey (ERCH). The specimen was examined by standard microscopic techniques. Hand-cut sections were studied in water, potassium hydroxide (KOH), and Lugol's solution (I). Measurements were made in water. Ascospores were measured from five different ascocmata for each species. The measurement results are given as minimum–maximum, from n = 30 measurements. Thin-layer chromatography (TLC) was carried out to determine compounds, using solvent system C (Orange et al., 2010).

#### 2.2. Molecular methods

##### 2.2.1. DNA isolation, polymerase chain reaction (PCR), and sequencing

Total DNA was extracted from apothecia by using the DNeasy Plant Mini Kit (Qiagen) according to the manufacturer's instructions. Polymerase chain reaction (PCR) was carried out in 50 µL reaction volumes using 4

$\mu\text{L}$  of  $10\times$  reaction buffer,  $4 \mu\text{L}$   $\text{MgCl}_2$  (50 mM),  $0.5 \mu\text{L}$  each primer (ITS1F and ITS4),  $2 \mu\text{L}$  dNTP (10 mM),  $0.2 \mu\text{L}$  Taq DNA polymerase,  $4 \mu\text{L}$  of template DNA and  $34.8 \mu\text{L}$   $\text{dH}_2\text{O}$  on a thermal cycler equipped with a heated lid. ITS4 (White et al., 1990) and ITS1-F (Gardes and Bruns, 1993) were used to amplify the ITS sequence. PCR amplification was performed under the following conditions: an initial denaturation for 7 min at  $95^\circ\text{C}$ ; six cycles for 1 min at  $94^\circ\text{C}$ , 1 min at  $56^\circ\text{C}$  and 1 min at  $72^\circ\text{C}$ ; and 30 cycles for 1 min at  $94^\circ\text{C}$ , 1 min at  $53^\circ\text{C}$ , and 2 min at  $72^\circ\text{C}$ . A final extension step of 10 min at  $72^\circ\text{C}$  was added, after which the samples were kept at  $4^\circ\text{C}$ . The PCR products were visualised on 1.2% agarose gel as a band of approximately 600 bp or 800 bp.

Sequence analyses of the lichen sample obtained from the PCR products was performed by the BM Labosis Laboratory (Ankara, Turkey).

### 2.2.2. Additional sequences

40 ITS and 20 mtSSU DNA sequences were downloaded from GenBank, representing a selection of 22 taxa in the former, broad circumscription of the genus *Toninia* (i.e., the current genera *Bibbya* J.H. Willis, *Kiliasia* Hafellner, *Thalloidima* A. Massal., *Toninia* s. str., and *Toniniopsis*; cfr. Kistenich et al. (2018a) and the outgroup genus *Bellicidia* Kistenich et al. in press; Table 1).

### 2.2.3. Sequence alignment and phylogenetic analysis

Sequence editing was performed with the software Geneious R9 (Kearse et al., 2012). The mtSSU and ITS sequences were aligned separately using the MAFFT-plugin (Kato and Standley, 2013) in Geneious. The E-INS-i algorithm was applied to our sequence datasets, setting the nucleotide scoring matrix to 1PAM / $\kappa=2$  and the gap open penalty to the default value of 1.53. We trimmed the 5'-end of the mtSSU alignment slightly to reduce the amount of missing data and trimmed the ITS alignment to comprise only the ITS-region, i.e. deleting the residual 18S and 28S sequence information. Each alignment was analysed by IQ-TREE v.1.6.7 (Nguyen et al., 2015) to find the best-fitting nucleotide substitution models and partitioning schemes (Chernomor et al., 2016; Kalyanamoorthy et al., 2017) among models implemented in MrBayes (i.e., 1-, 2-, and 6-rate models) and to infer a maximum likelihood tree with 1000 standard nonparametric bootstrap repetitions. We defined one subset for mtSSU and three subsets for ITS corresponding to the ITS1, 5.8S, and ITS2 regions, and analysed each dataset with the TESTMERGE function resembling PartitionFinder2. In addition, MrBayes v.3.2.6 (Altekar et al., 2004; Ronquist and Huelsenbeck, 2003) was used on each dataset as described in Kistenich et al. (2018b). The tree length  $\alpha/\beta$  was set to 1 for mtSSU and 0.32 for ITS. We set the temperature increment parameter to 0.1 for both analyses. We projected the bootstrap support (BS) values from the IQ-TREE analysis onto the

MrBayes consensus tree with posterior probabilities (PP) and collapsed branches with  $\text{BS} < 50$  and  $\text{PP} < 0.8$ . The resulting trees were edited in TreeGraph2 (Stöver and Müller, 2010).

## 3. Results

### 3.1 Sequence alignment and phylogenetic analysis

The mtSSU alignment comprised 21 accessions (Table 1) with a length of 814 bp. The ITS alignment consisted of 41 accessions with a length of 605 bp. *Bellicidia incompta* (Borrer) Kistenich et al. was used for rooting of all generated trees. Both alignments are available at TreeBase (study no. 27456). The software IQ-TREE suggested the following nucleotide substitution models for the predefined subsets: HKY+I+ $\Gamma$  for mtSSU, GTR+ $\Gamma$  for the combined ITS1 and ITS2 and K2P+I for 5.8S.

The Bayesian phylogenetic analyses halted automatically after  $2\times 10^6$  generations for mtSSU and  $4\times 10^6$  for ITS, respectively, when the ASDSF in the last 50% of each run had fallen below 0.01. Following a burnin of 50%, we used 1,001 trees of the mtSSU analysis and 2001 trees of the ITS analysis for each of the final Bayesian majority-rule consensus gene trees. The phylogenetic topologies generated by IQ-TREE vs. MrBayes of each marker showed no strongly supported (i.e.,  $\text{BS} > 70$  and  $\text{PP} > 0.9$ ) incongruences. The mtSSU extended majority rule consensus tree (Figure 1) showed good overall resolution, while the ITS extended majority rule consensus tree (Figure 2) showed poor resolution in the backbone but good resolution in more terminal groups. Both trees resolve the new species as sister to *Toniniopsis bagliettoana*. In the mtSSU tree (Figure 1), the genus *Toniniopsis* was resolved in a paraphyly with *Toninia*. In the ITS tree (Figure 2), *Toniniopsis* was resolved by forming three separate clades.

### 3.2. Taxonomy

*Toniniopsis bartakii* Halıcı, Kahraman, Kistenich & Timdal sp. nov. (Figure 3)

MycoBank No.: MB 838845

*Type*: Antarctic Peninsula, James Ross Island: Southern east part of Johnson Mesa,  $63^\circ 49' 46.2''\text{S}$ ,  $57^\circ 54' 21.6''\text{W}$ , alt. 292 m, 14 January 2017, ERCH JR 0.209 (ERCH—holotype).

*Diagnosis*: Similar to *Toniniopsis coelestina* (Anzi) Kistenich et al. but with smaller apothecia, which have a pale to colourless (not dark brown) inner part of the proper exciple. Differs from the phylogenetic sister species *T. bagliettoana* by having thicker, granulose to squamulose, and darker grey to brownish thallus; apothecial disc that apparently remains flat, and apothecial margin which is thicker and more persistent.

*Etymology*: Named in honour of Prof. Dr. Miloš Barták (Masaryk University Brno, Czech Republic), who conducted research on Antarctic terrestrial vegetation for

**Table 1.** mtSSU and ITS sequences used in the analyses.

Species		Authorship	Country	Year	Voucher	mtSSU	ITS
<i>Bellicidia incompta</i>		(Borrer) Kistenich et al.	Sweden	1997	Ekman 3144 (BG)	MG925849	AF282092
<i>Bibbya albomarginata</i>		(H. Kiliyas & Gotth. Schneid.) Kistenich et al.	Peru	2006	Timdal 10481 (O)	MG925927	MG926024
<i>Bibbya bullata</i>	I	(Meyen & Flot.) Kistenich et al.	New Zealand	2002	Bannister s.n. (O)	MG925928	MG926025
<i>Bibbya bullata</i>	II	(Meyen & Flot.) Kistenich et al.	Australia	1994	Elix & Streimann 40393 (O)	MG925929	MG926026
<i>Bibbya ruginosa</i>		(Tuck.) Kistenich et al.	Greenland	2005	Timdal 10087 (O)	MG925937	MG926033
<i>Bibbya vermifera</i>		(Nyl.) Kistenich et al.	Sweden	1998	Johansson 1619 (BG)	MG925852	AF282109
<i>Kiliasia athallina</i>		(Hepp) Hafellner	Austria	1994	Poelt, Pittoni & Köckinger (GZU)	-	MG926023
<i>Kiliasia philippea</i>		(Mont.) Hafellner	Norway	1994	Haugan & Timdal H3750 (O)	-	AF282112
<i>Kiliasia sculpturata</i>		(H. Magn.) Kistenich et al.	Russia	1992	Haugan & Timdal YAK17/30 (O)	MG925938	MG926034
<i>Thalloidima candidum</i>	I	(Weber) A. Massal.	Norway	2012	Hofton 12366 (O)	MG925931	MG926028
<i>Thalloidima candidum</i>	II	(Weber) A. Massal.	Norway	1997	Bratli & Timdal 8733 (O)	MG925932	AF282117
<i>Thalloidima physaroides</i>	I	(Opiz) Kistenich et al.	Norway	2013	Bendiksby et al. 12969 (O)	MG925935	MG926031
<i>Thalloidima physaroides</i>	II	(Opiz) Kistenich et al.	Norway	1995	Haugan & Timdal 8121 (O)	MG925936	MG926032
<i>Thalloidima toninianum</i>		(A. Massal.) A. Massal.	Spain	2015	Timdal 13773 (O)	MG925942	MG926036
<i>Toninia cinereovirens</i>		(Schaer.) A. Massal.	Norway	1994	Haugan & Timdal 7953 (O)	AY567724	AF282104
<i>Toninia populorum</i>		(A. Massal.) Kistenich et al.	Austria	1998	Ekman 3392 (BG)	MG925843	MG925950
<i>Toninia sp.</i>			Svalbard	2013	Zhang ZT2013191	-	KP314433
<i>Toninia squalida</i>		(Ach.) A. Massal.	Norway	1996	Haugan 4970 (O)	MG925940	AF282103
<i>Toninia talparum</i>		Timdal	USA	1998	Timdal SON120/01 (O)	-	AF282108
<i>Toninia tristis</i>		(Th. Fr.) Th. Fr.	Norway	1995	Haugan & Timdal 8109 (O)	-	AF282105
<i>Toniniopsis aromatica</i>	I	(Sm.) Kistenich et al.	Norway	1995	Haugan & Timdal 4819 (O)	MG925926	AF282126
<i>Toniniopsis aromatica</i>	II	(Sm.) Kistenich et al.	Norway	2009	Klepsland JK09-L101 (O)	-	MG838184
<i>Toniniopsis aromatica</i>	III	(Sm.) Kistenich et al.	Norway	2011	Haugan 10465 (O)	-	MG838161
<i>Toniniopsis aromatica</i>	IV	(Sm.) Kistenich et al.	Norway	2014	Klepsland JK14-L451 (O)	-	MG838189
<i>Toniniopsis bagliettoana</i>	I	(A. Massal. & De Not.) Kistenich & Timdal	Sweden	1997	Ekman 3150 (BG)	MG925847	AF282123

Table 1. (Continued).

<i>Toniniopsis bagliettoana</i>	II	(A. Massal. & De Not.) Kistenich & Timdal	Norway	2009	Haugan 8688 (O)	-	MG838180
<i>Toniniopsis bagliettoana</i>	III	(A. Massal. & De Not.) Kistenich & Timdal	Norway	2009	Klepsland JK09-L370 (O)	-	MG838178
<i>Toniniopsis coelestina</i>	I	(Anzi) Kistenich et al.	Norway	1997	Haugan 5985 (O)	MG925933	AF282127
<i>Toniniopsis coelestina</i>	II	(Anzi) Kistenich et al.	Norway	2010	Klepsland JK10-L342 (O)	-	MG838190
<i>Toniniopsis obscura</i>		Frey	Canada	1999	Westberg TNW2182 (UPS)	MG925943	MG926037
<i>Toniniopsis bartakii</i>			James Ross Island	2017	Halıcı & Bartak (ERCH ANT 209)	MW621866	MW620999
<i>Toniniopsis subincompta</i>	I	(Nyl.) Kistenich et al.	Sweden	1998	Ekman 3413 (BG)	MG925851	AF282125
<i>Toniniopsis subincompta</i>	II	(Nyl.) Kistenich et al.	Switzerland		WSL:DF231	-	KX098342
<i>Toniniopsis subincompta</i>	III	(Nyl.) Kistenich et al.	Norway	2014	Klepsland JK14-L020 (O)	-	MG838175
<i>Toniniopsis subincompta</i>	IV	(Nyl.) Kistenich et al.	Norway	2015	Klepsland JK15-L773 (O)	-	MG838176
<i>Toniniopsis subincompta</i>	V	(Nyl.) Kistenich et al.	Norway	2001	Løfall bpl-L7932 (O)	-	MG838165
<i>Toniniopsis subincompta</i>	VI	(Nyl.) Kistenich et al.	Norway	2013	Klepsland JK13-L056 (O)	-	MG838186
<i>Toniniopsis subincompta</i>	VII	(Nyl.) Kistenich et al.	Norway	2011	Timdal 12123 (O)	-	MG838157
<i>Toniniopsis verrucarioides</i>	I	(Nyl.) Kistenich, Timdal, Bendiksby & S. Ekman	Norway	1997	Bratli & Timdal 8709 (O)	-	AF282128
<i>Toniniopsis verrucarioides</i>	II	(Nyl.) Kistenich, Timdal, Bendiksby & S. Ekman	Norway	2013	Bendiksby et al. 12976 (O)	-	MG838167
<i>Toniniopsis verrucarioides</i>	III	(Nyl.) Kistenich, Timdal, Bendiksby & S. Ekman	Norway	2011	Klepsland JK11-L557a (O)	-	MG838179

decades and helped the first author in the field excursions on James Ross Island.

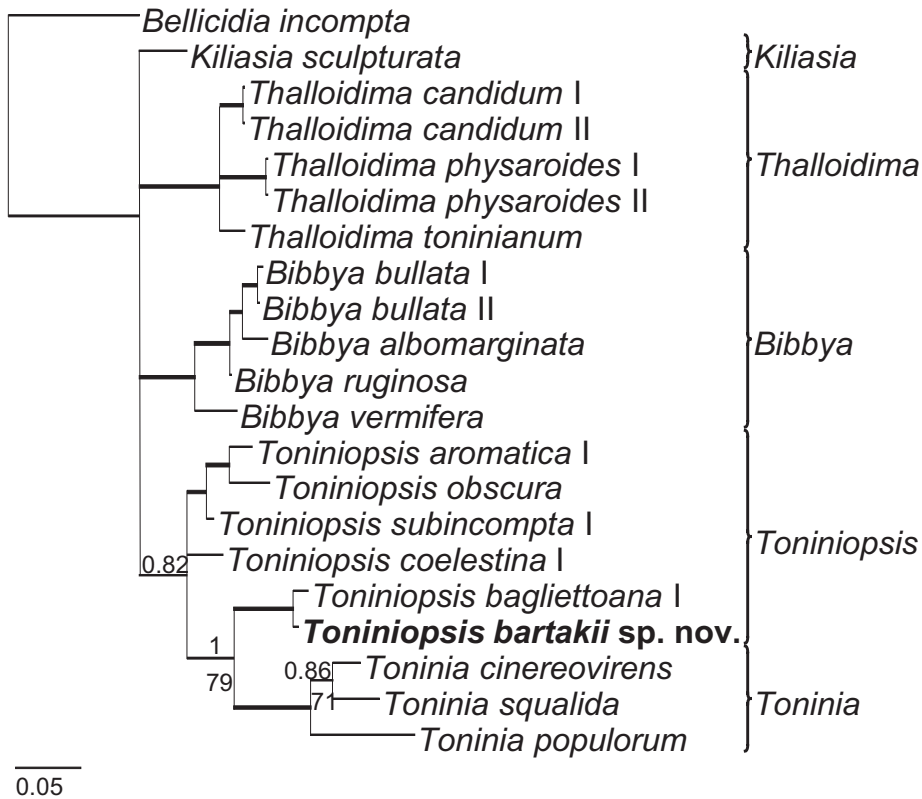
Description: Thallus granulose to squamulose; granules/squamules up to 1 mm in diam., contiguous, irregular, flat to weakly convex; upper surface ash grey to bluish grey, slightly pruinose, dull, lacking soredia, isidia, pores, pseudocyphellae and maculae; margin concolorous with upper side; upper cortex dark grey, 50–60 µm thick, lacking a well-defined epinecral layer, without crystals; algal layer green, 30–60 µm, containing trebouxoid, isodiametric algae up to 12 µm in diam.; medulla lacking crystals; lower cortex not well developed or almost excluded.

Apothecia single or aggregated, black, epruinose or weakly pruinose, up to 0.5 mm diam.; disc plane or weakly concave; margin persistent, concolorous with the disc, epruinose, becomes thicker when mature; proper

exciple greenish black in the rim, pale to colourless in inner part, without crystals (polarized light!); epithecium greenish black, 40–110 µm, K– and N–, without crystals; hypothecium brown, 20–30 µm; hymenium hyaline except upper part brownish, 70–90 µm, K– and N+ violet-red, without crystals. Asci 8-spored, 45–60 × 7–12 µm. Ascospores bacilliform to acicular, hyaline, 3(–6)-septate, (17–) 24.5–31–37.5 (–41) × (1.5–) 2–2.5–3 (–5) µm, length/width ratio: (4–) 8–12–16 (–26.5) (n=30). Conidiomata not observed. Thallus and medulla K– and KI–. No lichen substances were detected in TLC.

#### 4. Discussion

The new species differs from the phylogenetic sister species *T. bagliettoana* mainly in the development of the thallus. In *T. bagliettoana*, the thallus is crustose, forming a thin



**Figure 1.** mtSSU molecular phylogenetic tree. Extended majority-rule consensus tree resulting from the IQ-TREE analysis of the mtSSU alignment with Bayesian PP  $\geq 0.8$  and/or IQ-TREE maximum likelihood BS  $\geq 50$  and branch lengths. Strongly supported branches (PP  $\geq 0.95$  and BS  $\geq 80$ ) are marked in bold; for other branches, support values are indicated. The new species is marked in bold. *Bellicidia incompta* was used for rooting.

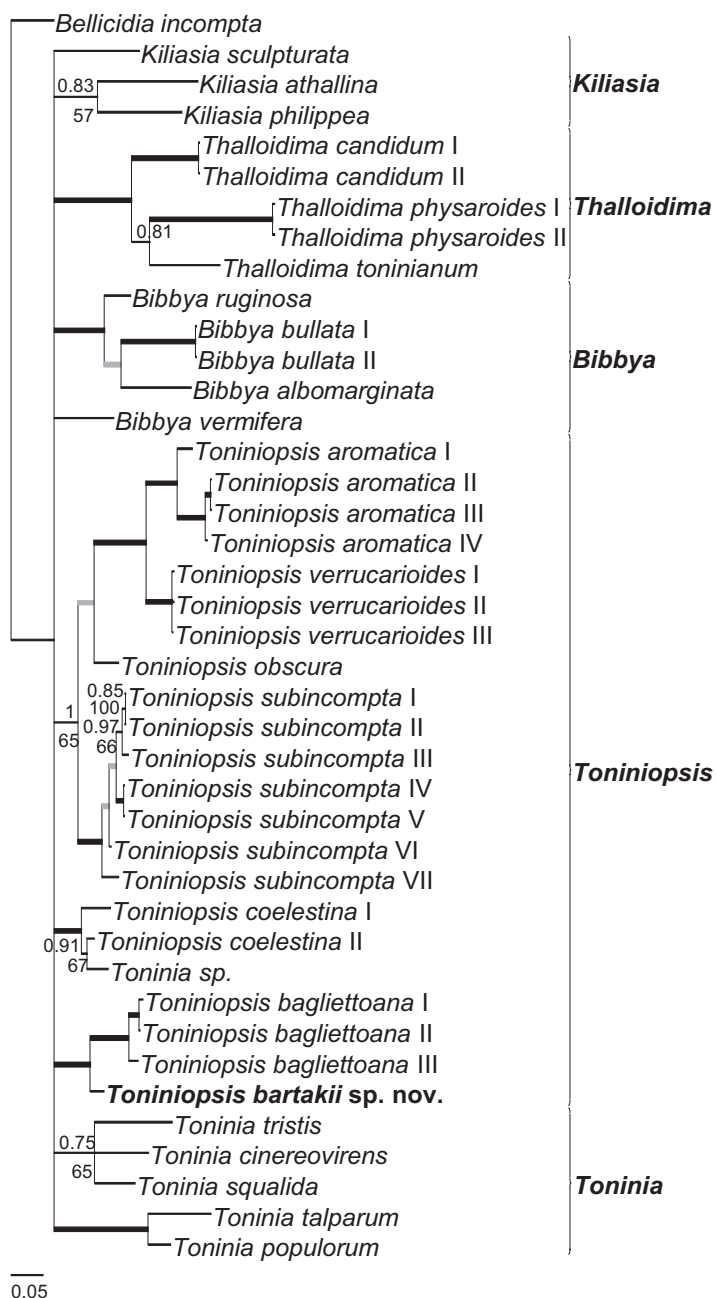
greyish white crust over bryophytes, plant debris, and soil, whereas, in *T. bartakii*, the thallus is thicker, granulose to squamulose, and darker grey to brownish. The apothecial disc of *T. bagliettoana* is flat and thinly marginate when young, and later becomes convex with an excluded margin; in *T. bartakii* the disc apparently remains flat and has a thicker, more persistent margin (although this observation is based on the holotype, only). The thallus of *T. bartakii* actually resembles more that of the European species *T. coelestina*, a species that is recovered more distantly in our phylogenies (Figures 1–2). The apothecia of *T. coelestina* are larger (up to 1.6 mm) and have a dark brown inner part of the exciple (Timdal, 1992; as *Toninia coelestina*). The main differences of the related species are given in Table 2.

The two gene trees presented in this study (Figures 1–2) do not recover *Toninia* and *Toniniopsis* as two monophyletic genera but either rather unresolved (ITS) or *Toninia* paraphyletic with *Toniniopsis* nested within (mtSSU). Only a few individuals were used for the mtSSU tree (Figure 1), though. The split of *Toninia* s. lat. into five genera, including *Toninia* s. str. and *Toniniopsis*, was discussed in detail by Kistenich et al. (2018a) based on a five-marker phylogenetic analysis. Kistenich et al. (2018a) showed that

several genetic markers are necessary for resolving *Toninia* as a monophyletic genus. On the other hand, they could not resolve *Toniniopsis* as a monophyletic genus using five genetic markers indicating that the taxonomy within this group might still not be fully resolved and understood.

An identification key to the species of *Toniniopsis*

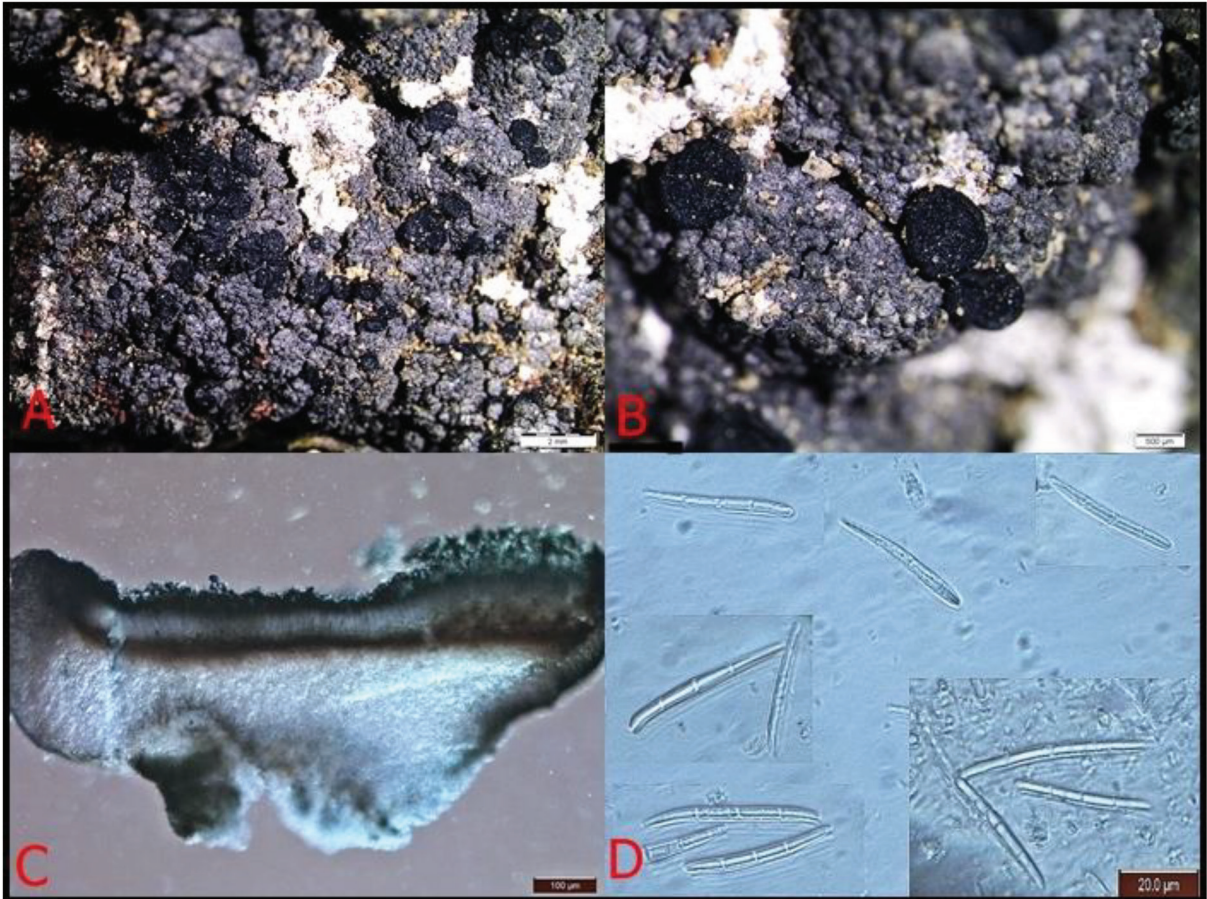
1. Ascospores narrowly ellipsoid to bacilliform, 1- to 3-septate ..... 2
1. Ascospores bacilliform to acicular, 3- to 7-septate .. 5
2. Thallus crustose ..... 3
2. Thallus squamulose ..... 4
3. On inland limestone; thallus finely warted to granular ..... *T. coprodes* (Körb.) S. Ekman & Coppins
3. On coastal rocks; thallus rimose to areolate, not granular . *T. mesoidea* (Nyl.) Timdal.
4. Epithecium brown, N- ..... *T. verrucarioides* (Nyl.) Kistenich, Timdal, Bendiksby & S. Ekman.
4. Epithecium green, N+ violet ..... *T. aromatica* complex (including *T. fusispora*)
- ..... *T. aromatica* complex (including *T. fusispora*)
5. Thallus forming a thin crust ..... 6
5. Thallus granulose to squamulose ..... 9
6. On acidic rock; ascospores 11-19  $\mu\text{m}$  long, 3 (-) septate at maturity .. *T. inornata* (Nyl.) S. Ekman & Coppins



**Figure 2.** ITS molecular phylogenetic tree. Extended majority-rule consensus tree resulting from the IQ-TREE analysis of the ITS alignment with Bayesian PP  $\geq 0.7$  and/or IQ-TREE maximum likelihood BS  $\geq 50$  and branch lengths. Strongly supported branches (PP  $\geq 0.95$  and BS  $\geq 80$ ) are marked in bold black; bold grey branches show PP  $\geq 0.9$  or BS  $\geq 70$ ; for other branches, support values are indicated. The new species is marked in bold. *Bellicidia incompta* was used for rooting.

- 6. On bark, soil, or plant debris; ascospores  $> 20 \mu\text{m}$  long, 3- to 7-septate ..... 7
- 7. On bark of tree trunks ..... 7
- T. subincompta* Kistenich, Timdal, Bendiksby & S. Ekman.
- 7. On soil or plant debris ..... 8
- 8. Hypothecium dark brown, at least in upper part; apothecia epruinose ..... 8

- T. bagliettoana* (A. Massal. & De Not.) Kistenich & Timdal
- 8. Hypothecium pale brown to colourless; young apothecia often pruinose ..... 8
- T. illudens* (Nyl.) Kistenich, Timdal, Bendiksby & S. Ekman.
- 9. Thallus containing a series of terpenoids; on limestone in the eastern Mediterranean region ..... 9
- ..... *T. cretica* (Timdal) Timdal.



**Figure 3.** *Toniniopsis bartakii* sp. nov. A–B: Thallus with apothecia. C: Section through apothecium. D: Ascospores. Photos: M. G. Halıcı, M. Kahraman.

**Table 2.** Main taxonomical differences of *T. bartakii* from the morphologically related species.

Taxonomical character	<i>T. bagliettoana</i>	<i>T. bartakii</i>	<i>T. coelestina</i>
Growth form	crustose	granulose to squamulose	granulose to squamulose
Apothecia, in diam.	up 1.4 mm	up to 0.5 mm	up to 1.6 mm
Inner part of proper exciple	pale brown to colourless	pale brown to colourless	dark brown
Ascospores, length	25–45 µm	24.5–37.5 µm	20–40 µm
Chemistry	No lichen substances	No lichen substances	No lichen substances

9. Thallus lacking lichen substances ..... 10

10. Inner part of proper exciple dark brown, confluent with hypothecium; apothecia up to 1.6 mm diam.; European montane to alpine region .....

*T. coelestina* (Anzi) Kistenich, Timdal, Bendiksby & S. Ekman

10. Inner part of proper exciple pale brown to colourless, contrasting the dark brown hypothecium; apothecia up to 0.5 mm in diam.; Antarctic .... *Toniniopsis bartakii* sp. nova

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## References

- Altekar G, Dwarkadas S, Huelsenbeck JP, Ronquist F (2004). Parallel metropolis coupled Markov chain Monte Carlo for Bayesian phylogenetic inference. *Bioinformatics* 20: 407-415. doi: 10.1093/bioinformatics/btg427
- Bednarek-Ochyra H, Váňa J, Ochyra R, Lewis-Smith RI (2000). The liverwort flora of Antarctica. Cracow, Poland: W. Szafer Institute of Botany, Polish Academy of Sciences.
- Cannon P, Ekman S, Kistenich S, LaGreca S, Printzen C et al. (2021). *Lecanorales: Ramalinaceae*, including the genera *Bacidia*, *Bacidina*, *Bellicidia*, *Biatora*, *Bibbya*, *Bilimbia*, *Cliostomum*, *Kiliasia*, *Lecania*, *Megalaria*, *Mycobilimbia*, *Phyllopsora*, *Ramalina*, *Scutula*, *Thalloidima*, *Toninia*, *Toniniopsis* and *Tylothallia*. *Revisions of British and Irish Lichens* 11: 1-82.
- Castello M, Nimis PL (1997). *Diversity of lichens in Antarctica*. In: Valencia J, Walton DWH, Battaglia B (editors). *Antarctic Communities Species, Structure and Survival*. London, UK: Cambridge University Press, pp. 15-21.
- Chernomor O, von Haeseler A, Minh BQ (2016). Terrace aware data structure for phylogenomic inference from supermatrices. *Systematic Biology* 65: 997-1008. doi:10.1093/sysbio/syw037
- Dodge CW (1973). *Lichen flora of the Antarctic continent and adjacent islands*. Canaan, New Hampshire: Phoenix Publishing.
- Gardes M, Bruns TD (1993). ITS primers with enhanced specificity for basidiomycetes-application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2: 113-118. doi: 10.1111/j.1365-294x
- Halıcı MG, Barták M (2019). *Sphaerellothecium reticulatum* (Zopf) Etayo, a new lichenicolous fungus for Antarctica. *Czech Polar Reports* 9 (1): 13-19. doi: 10.5817/CPR2019-1-2
- Halıcı MG, Bartak M, Güllü M (2018). Identification of some lichenised fungi from James Ross Island (Antarctic Peninsula) using nrITS markers. *New Zealand Journal of Botany* 56 (3): 276-290. doi: 10.1080/0028825x.
- Halıcı MG, Güllü M, Barták M (2017). First record of a common endolithic lichenized fungus species *Catenarina desolata* Sochting, Sgaard & Elvebakk. from James Ross Island (Antarctic Peninsula). *Czech Polar Reports* 7 (1): 11-17. doi: 10.5817/CPR2017-1-2
- Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermini LS (2017). ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14: 587. doi:10.1038/nmeth.4285
- Katoh K, Standley DM (2013). MAFFT Multiple Sequence Alignment Software Version 7: Improvements in performance and usability. *Molecular Biology and Evolution* 30: 772-780. doi: 10.1093/molbev/mst010
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M et al. (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* 28: 1647-1649. doi: 10.1093/bioinformatics/bts199
- Kistenich S, Rikkinen J, Thüs H, Vairappan C, Wolseley PA et al. (2018b). Three new species of *Krogia* (*Ramalinaceae*, lichenized Ascomycota) from the Paleotropics. *MycKeys* 40: 69-88. doi:10.3897/mycokeys.40.26025
- Kistenich S, Timdal E, Bendiksby M, Ekman S (2018a). Molecular systematics and character evolution in the lichen family *Ramalinaceae* (Ascomycota: *Lecanorales*) *Taxon* 67: 871-904. doi: 10.12705/675.1
- Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* 32: 268-274. doi:10.1093/molbev/msu300
- Orange A, James PW, White FJ (2010). *Microchemical methods for the identification of lichens*. London: British Lichen Society.
- Ronquist F, Huelsenbeck JP (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572-1574. doi: 10.1093/bioinformatics/btg180
- Stöver BC, Müller KF (2010). TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses. *BMC Bioinformatics* 11: 7. doi:10.1186/1471-2105-11-7.
- Timdal E (1992). A monograph of the genus *Toninia* (*Lecideaceae*, Ascomycetes). *Opera botanica* 110: 1-137.
- White TJ, Bruns T, Lee S, Taylor J (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (editors.). *PCR protocols: A Guide to Methods and Applications*. New York, NY, USA: Academic Press, pp. 315-322.