**Vondrák J., Svoboda S., Košnar J., Malíček J., Šoun J., Frolov I., Svensson M., Novotný P. & Palice Z. (2023) Martin7: a reference database of DNA barcodes for European epiphytic lichens and its taxonomic implications. – Preslia 95: 311–345.**

**Supplementary Data S1.** Comments to identities of sequences in Martin7.

### *Absconditella celata*

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Sarea* spp. with identities 83–85%. According to our data, *Absconditella sphagnorum* has closer ITS. Our mtSSU has the closest NCBI BLAST to *A. sphagnorum* (AY300872) with 85% identity.

### *Absconditella lignicola*

ITS and mtSSU adopted from Suija & van den Boom (2023).

### *Absconditella sphagnorum*

Our ITS has the closest NCBI BLAST to *Absconditella* sp. (KR017125) with identity 86%. (The single NCBI sequence of ITS named *A. sphagnorum* from China (JX298897) is not related to our ITS and probably belongs to another species.) Our mtSSU matches *A. sphagnorum* (AY300872; Lumbsch et al. 2004) with the identity over 99%.

### *Absconditella* sp. 1

Its ITS matches *Absconditella* sp. (KR017125; identity 87%) and *Sarea* spp. (identities up to 83%). The mtSSU has the closest NCBI BLAST to *A. sphagnorum* (identity 90%) and *Absconditella* sp. (identities 90–92%).

### *Absconditella* sp. 2

Only mtSSU sequenced. The closest NCBI BLAST matches are *A. sphagnorum* (identity 94%) and *Absconditella* sp. (identities 94–95%).

### *Absconditella pauxilla*

ITS and mtSSU adopted from Suija & van den Boom (2023).

### *Absconditonia rubra*

Our identical ITS sequences from two specimens are almost identical with *A. rubra* (van den Boom et al. 2015, as *Absconditella rubra*). Sequences of mtSSU absent from NCBI. Our single mtSSU has the closest NCBI BLAST to *Absconditonia sublignicola* (FJ904691) with 85% identity.

### *Absconditonia sublignicola*

Our ITS and mtSSU match the sequences of *A. sublignicola* with identities 98–99.5% (Suija & van den Boom 2023).

### *Acolium inquinans*

Our ITS matches *A. inquinans* in NCBI with identities 99–100%. Sequence of mtSSU adopted from Wedin et al. (2002).

***Acolium karelicum***

Our ITS matches *A. karelicum* in NCBI with identities 99–100%. Sequences mtSSU absent from NCBI and not obtained by us.

***Acolium sessile***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Acolium* and *Thelomma* with identities up to 86%. Sequences of mtSSU not obtained by us.

***Acrocordia cavata***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Anisomeridium guangdongensis* (Zhang et al. 2020; identity 81%); our mtSSU to *Acrocordia subglobosa* (GU327681, identity 96%). According to our results, *Acrocordia cavata* is related to *A. gemmata* with observed identity 92% in ITS and 94% in mtSSU.

***Acrocordia gemmata***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Anisomeridium guangdongensis* (Zhang et al. 2020; identity 81%); our mtSSU to *Acrocordia subglobosa* (GU327681, identity 96%).

***Agonimia allobata***

Our ITS matches *A. allobata* in NCBI with identities 99–100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Agonimia* spp. (identities 96–97%).

***Agonimia borysthenica***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to the sequence called *A. repleta* (JF509160) with the identity 99.5%. (JF509160 probably represents incorrectly named *A. borysthenica*.) The real *A. repleta* (JF509161) is 95% identical. Our mtSSU matches *A. repleta* (DQ328985) with the identity 97%.

***Agonimia flabelliformis***

Our sequences match *A. flabelliformis* in NCBI with identities 99–100% in ITS and mtSSU.

***Agonimia opuntiella***

Usually muscicolous on calcareus or base-rich siliceous rocks, but occassionally occurring on bark. ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Verrucariaceae* spp. with identities up to 87%. Our mtSSU has the closest NCBI BLAST to *A. tristicula* (AY300876) with the identity almost 99%.

***Agonimia repleta***

Our sequences match *A. repleta* in NCBI (identities over 99.5% in ITS and mtSSU).

***Agonimia tristicula***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *A. repleta* (JF509161) with the identity 86%. Our mtSSU matches *A. tristicula* (AY300876) with the identity 99%.

***Agyrium roseum* ined.**

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Agyrium rufum* with identities 90–92% in ITS and 98% in mtSSU.

***Agyrium rufum***

ITS and mtSSU adopted from NCBI.

***Agyrium* sp.**

Probably an undescribed species occurring on wood in maritime habitats influenced by salt spray. Its sequences are closest to *A. rufum*; ITS is 91.5–93.5% identical and mtSSU c. 99% identical.

***Alectoria sarmentosa***

ITS and mtSSU adopted from NCBI.

***Alloarthopyrenia italica* (= *Arthopyrenia cinereopruinosa* auct.)**

On the basis of identical mtSSU sequences, we consider *Alloarthopyrenia italica* and younger synonym to *A. cinereopruinosa* (morphology of both also appears to be identical, Brian Coppins, in litt.). ITS (of *Alloarthopyrenia*) adopted from Hyde et al. (2016). Our mtSSU is identical with *Alloarthopyrenia italica* in NCBI (Hyde et al. 2016). Similar mtSSU also has *Arthopyrenia fallaciosa* and *Trypetheliaceae* (identities up to 90%).

***Allocalicium adaequatum***

ITS and mtSSU adopted from Prieto & Wedin (2017).

***Alyxoria ochrocheila***

ITS absent from NCBI. Most of our attempts to obtain ITS ended up with sequences of basidiomycete contaminants *Kockovaella* / *Fellomyces*. The single obtained ITS is possible of the target lichen. It has the closest NCBI BLAST to *Lecanoromycetes* spp. with identities up to 90%, but with low covers up to 20%. It is almost 80% identical with our ITS of *A. varia*. Our sequences of mtSSU from two specimens are 96% identical and match *A. ochrocheila* in NCBI with identities 92–100%.

***Alyxoria varia***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Schismatomma pericleum* and *Enterographa divergens* with identities about 94% but with the cover of only 32%. Our almost identical mtSSU sequences from four specimens representing various morphotypes (with pruinose vs. non-pruinose apothecia; short vs. long apothecia) match *A. varia* in NCBI with identities 95–100%.

***Amandinea punctata***

Our two epiphytic specimens have 97% identical ITS and 100% identical mtSSU. ITS sequences match *A. punctata* in NCBI with identities 94–99%, mtSSU with 97–99%.

***Anaptychia ciliaris***

Our ITS matches *A. ciliaris* in NCBI with identities 90–99%; our mtSSU with identities over 99.5%.

***Anaptychia crinalis***

ITS sequences adopted from Lohtander et al. (2008) and Mark et al. (2016), and mtSSU from Lohtander et al. (2008).

***Andreiomyces obtusaticus***

Sterile crust containing at least traces of anthraquinones (similar TLC characters to those at *Arthonia vinosa*), obtusatic acid, barbatic acid and baeomycesic acid. Our two ITS sequences are more than 99.5% identical and match *A. obtusaticus* (AF517896) with 100% identity, but with only 30% coverage. The North American *Andreiomyces morozianus* (Hodkinson & Lendemer 2013) is closely related with identity c. 96.5% in ITS. Sequences of mtSSU absent from NCBI. Our almost identical mtSSU sequences from two specimens have the closest NCBI BLAST to *Melarthonis piceae* (89% identity) and *Galbinothrix caesiopruinosa* (also 89%).

***Anisomeridium biforme***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Anisomeridium guangdongensis* (Zhang et al. 2020; identity 89%). Our mtSSU has the closest BLAST to genera *Anisomeridium*, *Megalotremis* and *Trypetheliopsis* (*Monoblastiaceae*) with identities up to 92%.

***Anisomeridium polypori***

ITS and mtSSU absent from NCBI. Our ITS sequences from four specimens are c. 90% identical and have the closest NCBI BLAST to *Anisomeridium guttuliferum* (Zhang et al. 2020; identities 80–85%). Our single mtSSU matches *Anisomeridium* cf. *willeyanum* (JN887407) with the identity almost 98%. Other related sequences are from *Monoblastiaceae* with identities up to 90%.

***Anzina carneonivea***

Our ITS matches *A. carneonivea* in NCBI (AF274077; Lumbsch et al. 2001) with the identity over 98%. Sequence of mtSSU adopted from Schmitt et al. (2003).

***Aquacidia trachona* (= *Bacidia trachona*)**

Frequently saxicolous lichen, occassionally occurring also on bark in humid forests. Our ITS matches *B. trachona* in NCBI with identities 98–100%, mtSSU with 100%.

***Arctomia delicatula***

ITS absent from NCBI. Sequence of mtSSU adopted from Resl et al. (2015).

***Arthonia albopulverea***

ITS abd mtSSU absent from NCBI. Our ITS has the closest NCBI blast to *A. dispresa* and *A. radiata* with identities 89–90% and our mtSSU to *A. dispersa* and *A. punctiformis* with identities up to 94%.

***Arthonia apatetica***

Our sequences match *A. apatetica* in NCBI with 100% identity in ITS and 98–100% in mtSSU. It is a member of *Bryostigma* (cf. Frisch et al. 2014).

***Arthonia atra***

ITS absent from NCBI. Our mtSSU matches *A. atra* in NCBI with identities 97–100%.

***Arthonia biatoricola***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Bryostigma dokdoense* (identities 86–88%). Our mtSSU sequences are identical with *A. biatoricola* (KJ850990). It is a member of *Bryostigma* (cf. Frisch et al. 2014).

***Arthonia bueriana***

A little known, but morphologically well recognisable species (Redinger 1937) occurring in termophilous central European forests. ITS and mtSSU absent from NCBI. Our ITS is close to our sequence of *A. didyma* with the identiy 97% but with low cover (43%).

***Arthonia cinereopruinosa* (= *Leprantha cinereopruinosa*)**

ITS absent from NCBI. Sequence of mtSSU adopted from Ertz et al. (2018b).

***Arthonia didyma***

Our ITS, together with previously published sequence (Vondrák et al. 2022), has the closest NCBI BLAST to *Coniocarpon* spp. with identities 90%. Our mtSSU matches *A. didyma* (EU704047) with the identity 100%.

***Arthonia dispersa***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Coniocarpon* and *Arthonia sardoa*, in both cases with identities below 90%. Our mtSSU sequences match *A. dispersa* in NCBI with identities 99–100%.

***Arthonia faginea***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to members *Arthonia* and *Bryostigma*, always with identities below 90%. Our mtSSU has the closest NCBI BLAST to *Arthonia lapidicola* (identity 99%, cover 69%). *Arthonia faginea* differs from *A. lapidicola* by ecology (epiphyte on bark), and also morphologically, especially by 2-septate ascospores.

***Arthonia ilicina***

ITS absent from NCBI. Sequence of mtSSU adopted from Frisch et al. (2014).

***Arthonia incarnata***

ITS absent from NCBI and sequences obtained by us are not reliable. Our mtSSU matches *A. incarnata* in NCBI with identities 98–99%.

***Arthonia mediella***

ITS absent from NCBI. Our ITS represent three genotypes sharing c. 90% identity and all have the closest NCBI BLAST to *Chrysothrix* and *Andreiomyces* with identities about 95%. Sequences of mtSSU adopted from Frisch et al. (2014; KJ851014 and KJ851015). Probably more than one species included.

***Arthonia patellulata***

ITS adopted from Kelly et al. (2011). Sequences of mtSSU absent from NCBI.

### *Arthonia pinastri*

ITS absent from NCBI. Sequence of mtSSU adopted from Thiyagaraja et al. (2020, sub *Naevia pinastri*).

### *Arthonia* cf. *pinastri*

Our specimens from Rhodos match the description of *A. pinastri*, but the mtSSU sequence is quite distinct from that generated by Thiyagaraja et al. (2020). ITS has the closest NCBI blast to *A. dispersa* (96% identical) and mtSSU to *Arthothelium scandinavicum* (OQ646104; 93% identical).

### *Arthonia punctiformis*

ITS absent from NCBI. Our putative target ITS is not reliable, but is close to our *A. spadicea*. Our mtSSU sequences from three specimens represent two genotypes with 95% identity. One is identical with *A. punctiformis* in NCBI (KJ850973); the second is 95% identical with KJ850973. *Arthonia dispersa* is closely related to both genotypes, with the identity about 95%.

### *Arthonia radiata*

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Coniocarpon* spp. and *Arthonia sardoa*, in both cases with identities up to 90%. Our mtSSU is identical with sequences of *A. radiata* in NCBI.

### *Arthonia ruana*

ITS absent from NCBI and we failed to generate reliable sequences although repeatedly attempted. Our almost identical mtSSU sequences from three specimens match *A. ruana* in NCBI with identities 95–100%.

### *Arthonia sardoa*

ITS adopted from NCBI (Myllys et al. 1999, unpublished). Sequences of mtSSU absent from NCBI.

### *Arthonia spadicea* (= *Diarthonis spadicea*; see Cannon et al. 2020)

ITS and mtSSU absent from NCBI. Our ITS and mtSSU have the closest NCBI BLAST hits in *Acarosporaceae*, but with identities up to 80%. This result seems suspicious because the sequences do not resemble those from other *Arthoniomycetes*. However, we consider our repeated results reliable, especially mtSSU where identical sequences were obtained independently from six specimens.

### *Arthonia tenellula*

ITS and mtSSU absent from NCBI. Our mtSSU is closest to the sequence of *Arthonia* (= *Bryostigma*) *faginea* which is 95% identical. Reliable ITS sequence not obtained yet.

### *Arthonia thoriana*

ITS absent from NCBI and we failed to generate reliable sequences although repeatedly attempted. Our identical mtSSU sequences from five specimens match *A. thoriana* in NCBI with 100% identity.

### *Arthonia vinosa*

ITS and mtSSU absent from NCBI. Our repeated attempts to obtain ITS ended up in sequencing contaminations, e.g. *Kockovaella*/*Fellomyces*. Our mtSSU has the closest NCBI BLAST to *A. physcidiicola* (KF707646) with the identity 95%. Other *Arthoniaceae* have mtSSU identities up to 93%.

***Arthopyrenia analepta***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Alloarthopyrenia italica* (Hyde et al. 2016), which is a younger synonym to *Arthopyrenia cinereopruinosa* (see below). Our identical mtSSU sequences from three specimens have the closest BLAST to *A. fallaciosa* with identities 95–96% and with *Trypetheliaceae* with identities up to 90%.

***Arthopyrenia cerasi***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Trypethelium eluteriae* with identities up to 88%. Sequence of mtSSU adopted from Thiyagaraja et al. (2021; MZ221617, sub *Arthopyrenia* sp. in NCBI).

***Arthopyrenia fallaciosa***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Alloarthopyrenia italica* (= *Arthopyrenia cinereopruinosa*) with the identity 95%. Similar sequences have *Trypetheliaceae* (shared identities up to 90%). Our mtSSU matches *Arthopyrenia fallaciosa* in NCBI with 100% identities and *Trypetheliaceae* with identities up to 91%.

***Arthopyrenia salicis***

Our identical ITS sequences of three specimens match *A. salicis* sequences provided by Marthinsen et al. (2019) with 98–99% identities. Other relatives are *Capnodiales* spp. with identities up to 88%. Our mtSSU has the closest NCBI BLAST matches to *Capnodiales* spp. (e.g. *Mycospaerella* and *Racodium*) with identity up to 90%. According to our data, the morphologically similar *Naetrocymbe punctiformis* is related to *A. salicis*, with identities 85% in ITS and 91% in mtSSU.

***Arthopyrenia subcerasi***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST matches to *Cladosporiales* and *Capnodiales*. Its identity needs to be confirmed. Sequence of mtSSU not obtained.

***Arthothelium norvegicum***

ITS absent from NCBI. Sequence of mtSSU adopted from Frisch et al. (2014).

***Arthothelium orbilliferum***

ITS absent from NCBI. Sequence of mtSSU adopted from Frisch et al. (2017).

***Arthothelium scandinavicum***

ITS and mtSSU absent from NCBI. Our single ITS has the closest NCBI BLAST to *Arthonia didyma* (OL457936) with identity 80%, but with 50% cover. Our mtSSU has the closest NCBI BLAST to *Arthothelium puniceum* with 95% identity and *A. orbilliferum* with 92%.

***Arthothellium spectabile***

ITS absent from NCBI and not obtained by us. Our attempts ended up with sequences of contaminations, e.g. *Kockovaella*/*Fellomyces*. Our mtSSU matches *A. spectabile* in NCBI with identities 96.5–99%.

***Arthrosporum populorum* (= *Toninia populorum*)**

Sequences of ITS adopted from Ekman (2001) and Kistenich et al. (2018), mtSSU adopted from Kistenich et al. (2018).

***Aspicilia laevata***

Predominantly saxicolous lichen, with occassional occurrences on bark, usually on tree bases. Our ITS and mtSSU from and corticolous specimen match *A. laevata* in NCBI.

***Bacidia absistens***

ITS and mtSSU adopted from NCBI (Norwegian specimen; Kistenich et al. 2018). We also adopted NCBI sequence of ITS from Gerasimova (2021, unpublished). This sequence from Caucasus is rather distinct from the Norwegian (only 92.5% identical).

***Bacidia albogranulosa***

ITS and mtSSU adopted from Malíček et al. (2018c) and Vondrák et al. (2022).

***Bacidia arceutina***

Our ITS matches *B. arceutina* with identities 98–100%, mtSSU with 100%.

***Bacidia auerswaldii* (= *Scutula effusa*)**

ITS and mtSSU adopted from Vondrák et al. (2022).

***Bacidia biatorina***

Our ITS and mtSSU match *B. biatorina* in NCBI with 100% identities.

***Bacidia circumspecta* (= *Scutula circumspecta*)**

Our ITS sequences match *B. circumspecta* in NCBI with identities 94–100%. Our mtSSU is identical with *B. circumspecta* (MG929848).

***Bacidia fraxinea***

Our ITS match *B. fraxinea* with identities 99–100%. Sequences of *Bacidia rubella* are also very similar, with identities 98–99%. Our mtSSU are almost identical with sequences of both *B. fraxinea* and *B. rubella* in NCBI.

***Bacidia hyalina***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Bacidia iberica***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI blast to *B. rubella* and *B. fraxinea* with identities up to 96%. Sequences of mtSSU not obtained yet.

***Bacidia* cf. *igniarii***

ITS and mtSSU of *B. igniarii* absent from NCBI. Our ITS has the closest NCBI BLAST to *B. circumspecta* in NCBI with identities 90–92%. Our mtSSU has the closest BLAST to *B. circumspecta*, *B. auerswaldii* and *B. biatorina* – in all cases with identities 96–97%. Taxonomic identity of our specimen with *B. igniarii* is not clear.

***Bacidia incompta* (= *Bellicidia incompta*)**

Our ITS and mtSSU match *B. incompta* in NCBI with identities 100%.

***Bacidia inconspicua* ined.**

ITS and mtSSU adopted from Malíček et al. (2018c, as *Bacidia rubella*).

***Bacidia laurocerasi***

Our ITS matches *B. laurocerasi* in NCBI with identities 98–100%, mtSSU with 100%.

***Bacidia parathalassica***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI blast to *B. rubella* and *B. fraxinea* with identities up to 97%. Sequences of mtSSU not obtained yet.

***Bacidia polychroa***

Our ITS sequences match *B. polychroa* in NCBI with identities 98–100%, mtSSU with 100%.

***Bacidia rosella***

Our ITS and mtSSU match *B. rosella* in NCBI with identities 100% or close.

***Bacidia rubella***

Our ITS matches *B. rubella* in NCBI with identities 97–100%, mtSSU with identities over 99%.

***Bacidia subincompta***

See under *Toniniopsis dissimilis* and *T. separabilis*.

***Bacidia suffusa***

ITS and mtSSU adopted from NCBI (Gerasimova et al. 2021; unpublished).

***Bacidia vermifera* (= *Bibbya vermifera*)**

Our ITS matches *B. vermifera* in NCBI with identities 97–100%, mtSSU with 100%.

***Bacidina adastra***

Our ITS matches *B. adastra* (= *B. caligans* auct.) in NCBI with identities 99–100%. Sequences of mtSSU are absent from NCBI and not obtained by us.

***Bacidina arnoldiana***

Usually considered as saxicolous lichen, but it is common on tree bark in central European lowland forests. Our ITS matches *B. arnoldiana* in NCBI with identities 99–100%. Our mtSSU has the closest NCBI BLAST to *B. inundata* with identity 98% and *B. arnoldiana* with 97%. Possibly it is a close species to *B. inundata*, but *B. inundata* (single sequence in NCBI; AF282094) has the identity with our sequence only 96%.

***Bacidina brandii***

ITS adopted from Czarnota & Guzow-Krzemińska (2018). Sequences of mtSSU absent from NCBI.

**_Bacidina caerulea_**

ITS adopted from Ekman (2023). Sequences of mtSSU absent from NCBI.

**_Bacidina chloroticula_**

Intricate taxon involving more species. One of our ITS (Type1; s.str.) matches *B. chloroticula* (AF282098; Ekman 2001) with almost 100% identity; but our second ITS (Type2) has the closest NCBI BLAST to *Bacidina* spp. with identities up to 97%. Our single mtSSU (Type1) matches *B. chloroticula* (KJ766357; Miadlikowska et al. 2014) with 100% identity.

**_Bacidina delicata_**

ITS and mtSSU adopted from Sérusiaux et al. (2012).

**_Bacidina flavoleprosa_**

Our ITS matches *B. flavoleprosa* (JN972443) in NCBI with the identity 97%. Other *Bacidina* spp. are less than 96% identical. Sequences of mtSSU not obtained by us and absent from NCBI.

**_Bacidina lignicola_**

Our ITS sequences match the best *B. lignicola* in NCBI with identities >99.5% (OP256857; Ekman 2023). Sequences of mtSSU absent from NCBI. Our mtSSU is closest to *B. inundata* with identities about 98.5%.

**_Bacidina assulata_ (= _Bacidina mendax_)**

Our three ITS sequences, sharing 98% identity, match *B. mendax* in NCBI with identities 97–100%. Sequences of mtSSU absent from NCBI. Our single mtSSU has the closest NCBI BLAST to *B. inundata* with identity 98.5%. One of sequenced specimens was identified as *B. etayana* on the base of its morphology. Existence of *B. etayana*, as and separate species, is questionable.

**_Bacidina modesta_ (= _B. sulphurella_)**

ITS adopted from Czarnota & Guzow-Krzemińska (2012), mtSSU from Vondrák et al. (2022) and Malíček et al. (2023).

**_Bacidina neosquamulosa_**

ITS adopted from Ekman (2023), mtSSU from Sérusiaux et al. (2012).

**_Bacidina phacodes_**

Our ITS match *B. phacodes* in NCBI with identities 98–100%, mtSSU with 100%.

**_Bacidina piceae_**

Our ITS matches *B. piceae* in NCBI with the identity 99.5%. *B. friesiana* has also similar sequence sharing the identity 94%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Bacidina* spp. with identities up to 95%.

**_Bacidina populnea_**

ITS adopted from Ekman (2023). Sequences of mtSSU absent from NCBI.

***Bacidina pycnidiata***

ITS adopted from Czarnota & Guzow-Krzemińska (2018). Sequences of mtSSU absent from NCBI and not obtained by us.

***Bacidina violacea***

Our ITS matches *B. violacea* in NCBI with the identity over 98%. Other *Bacidina* spp. are less than 97% identical. Sequences of mtSSU absent from NCBI and not obtained by us.

***Bacidina* sp. 1 (sensu Vondrák et al. 2022) (= *Bacidina acerina* sp. nov.)**

Described here as *B. acerina*. The ITS sequences obtained from seven specimens are 97% identical and have the closest NCBI BLAST to *Bacidina varia* and *B. friesiana* with identities up to 93%. In the Bayesian tree, *B. acerina* belongs to and clade including *B. friesiana*, *B. phacodes* and *B. piceae*. The mtSSU sequences from the nine specimens are 99.5% identical, and the closest NCBI BLAST results to them are representatives of *Bibbya*, *Bacidina*, *Toniniopsis* and *Waynea* with the identities up to 95%. However, the position in the Bayesian mtSSU tree places *Bacidina acerina* in a common group with *B. phacodes* and *B. piceae*.

***Bacidina* sp. 2 (sensu Vondrák et al. 2022)**

Not specifically epiphytic, occurring on organic and anorganic substrates. Our ITS sequences match *Bacidina* sp. 2 with almost 100% identities. Sequences of mtSSU adopted from Vondrák et al. (2022).

***Bacidina* sp. 3 (sensu Vondrák et al. 2022)**

Not specifically epiphytic, occurring on organic and anorganic substrates. Our ITS sequences of an epiphytic specimen match saxicolous *Bacidina* sp. 3 in NCBI with identities 99%. Sequence of mtSSU adopted from Vondrák et al. (2022).

***Bacidina* sp. 4 (= *Bacidina paradoxa* sp. nov.)**

Described here as *B. paradoxa*. Identical ITS sequences obtained from three specimens have the closest NCBI relatives *Bacidina flavoleprosa* and *B. terricola* sharing about 97% identity with the new *B. paradoxa*. In the Bayesian tree, *B. paradoxa* stands in a common polytomy with many species of the genus. Identical mtSSU sequences from the three specimens have no close relatives in NCBI and BLAST to *Bacidina* spp. with identities up to 92%. In the mtSSU Bayesian tree, *B. paradoxa* stands in polytomy with e.g. *B. delicata* and *B. neosquamulosa*.

***Bacidina* sp. 5**

ITS not obtained. Our mtSSU has the closest NCBI BLAST to *B. terricola* with the identity 95%. Possibly and distant haplotype of *Bacidina* sp. 4, but the identity with other haplotypes is only 94%.

***Bacidina* sp. 6**

Epiphytic sterile sorediate crust from Caucasus. ITS not obtained. Our mtSSU has the closest NCBI BLAST to *B. sulphurella* with the identity 96%. Other *Bacidina* spp. are less than 95% identical.

***Bactrospora dryina***

ITS and mtSSU absent from NCBI. Our almost identical sequences from six specimens have the closest NCBI BLAST to *B. corticola* with identities 81–82%. Identical sequences of mtSSU from five specimens have no close relatives in NCBI; various *Lecanoromycetes* are identical up to 84%.

***Bactrospora corticola***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU absent from NCBI.

***Bactrospora homalotropa***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *B. corticola* in NCBI with identities about 84%. Our mtSSU sequence has no close relatives in NCBI; various *Ascomycetes* are identical up to 87%, and *B. dryina* is 81% identical.

***Bactrospora patellarioides* var. *patellarioides***

ITS and mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *B. dryina* (93% identity, but only 41% cover). Reliable ITS not sequenced yet.

***Baeomyces rufus***

Usually on anorganic substrata, but often occurring on bark and wood of root-plates. ITS adopted from Marthinsen et al. (2019), mtSSU from Miadlikowska et al. (2014).

***Belonia herculina* (= *Gyalecta herculina*)**

Our ITS matches *B. herculina* in NCBI with identities 98–99%. Sequence of mtSSU not obtained by us and only one short sequence is present in NCBI.

***Biatora aegrefaciens***

ITS adopted from Printzen (2014). Sequences of mtSSU absent from NCBI.

***Biatora amylacea* ined.**

To be described soon by Palice and Printzen. Our ITS is identical with *B. amylacea* in NCBI (MK778585). Other *Biatora* spp. are identical less than 88%. Our identical mtSSU sequences from four specimens are also identical with *B. amylacea* in NCBI (MK778516). *B. radicicola* has similar sequences with identities 98%.

***Biatora bacidioides***

ITS and mtSSU adopted from Malíček et al. (2018a).

***Biatora beckhausii***

Our ITS matches *B. beckhausii* in NCBI with the identity 97% and mtSSU with 97–100%.

***Biatora chrysantha***

Our identical ITS from two specimens are identical with *B. chrysantha* in NCB. Sequences of mtSSU adopted from NCBI (ON226893).

***Biatora chrysanthoides***

ITS and mtSSU adopted from Printzen (2014).

***Biatora efflorescens***

Our ITS matches *B. efflorescens* in NCBI with identities 99–100% and mtSSU with 100%.

### *Biatora fallax*

Our ITS matches *B. fallax* in NCBI with identities 99–100% and mtSSU with 100%.

### *Biatora flavopunctata*

ITS and mtSSU adopted from Printzen (2014).

### *Biatora globulosa*

Our ITS sequences from two specimens match the single NCBI *B. globulosa* (AF282073) with identities 97.5% and our mtSSU matches *B. globulosa* (KF662414) with the identity 99.5%.

### *Biatora helvola*

Our ITS matches *B. helvola* in NCBI with identities 97–100% and mtSSU matches *B.* cf. *helvola* (KF662415) with 99.5%.

### *Biatora hemipolia*

Our ITS matches *B. hemipolia* (AF282072) with the identity almost 100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Biatora* spp. with identities up to 95%.

### *Biatora hypophaea*

ITS adopted from Printzen (2014). Sequences of mtSSU absent from NCBI.

### *Biatora ligni-mollis*

Our ITS and mtSSU match *B. ligni-mollis* in NCBI with 100% identities.

### *Biatora longispora*

ITS and mtSSU adopted from Malíček et al. (2018a) and Vondrák et al. (2018).

### *Biatora meiocarpa*

ITS and mtSSU adopted from Reese Næsborg et al. (2007).

### *Biatora mendax*

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Biatora* spp., but with low identities up to 88%. Sequences of mtSSU not obtained.

### *Biatora ocelliformis*

Our ITS sequences match *B. ocelliformis* in NCBI with identities 97–100%. Sequences of mtSSU absent from NCBI and not obtained by us.

### *Biatora pontica*

Our ITS and mtSSU match *B. pontica* in NCBI with 99–100% identities.

### *Biatora radicicola*

ITS and mtSSU adopted from Printzen et al. (2016).

### Biatora rufidula

ITS and mtSSU adopted from Printzen (2014).

***Biatora sphaeroidiza***

ITS adopted from Printzen (2014). Sequences of mtSSU absent from NCBI and not obtained by us.

***Biatora subduplex***

ITS and mtSSU adopted from Printzen (2014).

***Biatora troendelagica***

Our ITS is not *Biatora*, but *Lecidea turgidula* and *L. leprarioides* have close sequences with identities up to 93%. Sequences of mtSSU absent from NCBI and not obtained by us.

***Biatora vacciniicola***

ITS and mtSSU adopted from Palice et al. (2018).

***Biatora vernalis***

Our ITS matches *B. vernalis* in NCBI (AF282070; Ekman 2001) with the identity 100%. Sequence of mtSSU adopted from Bendiksby & Timdal (2013).

***Biatora veteranorum***

Our ITS and mtSSU match *B. veretanorum* in NCBI with 100% identities.

***Biatorella dryophila***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Myriospora* with identities up to 91%. Sequence of mtSSU not obtained.

***Biatorella flavella***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Sarea* spp. and *Candelariella* spp. with identities up to 83%. According to our data, *Thelocarpon epibolum* has even closer ITS, 87% identical. Sequences of mtSSU not obtained by us.

***Biatorella ligni-putridis* ined.**

This lignicolous species with tiny pale ochre apothecia will be possibly described by Palice. ITS not obtained. Our mtSSU sequences from two specimens, sharing 98% identity, have the closest NCBI BLAST to *Sarea*, *Pleopsidium* and *Myriospora* with identities about 90%. It is perhaps and member of *Lichinomycetes* sensu Díaz-Escandón et al. (2022).

***Biatoridium delitescens***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Sarea* with identities up to 82% and our mtSSU to *Myriospora* with identities up to 84%. Our sequences of *Biatorella ligni-putridis* are 92.5% identical and *Biatoridium monasteriense* about 90%.

***Biatoridium monasteriense***

ITS and mtSSU absent from NCBI. Our ITS sequences from two specimens are almost identical but differ in a long indel in ITS2 region. They have the closest NCBI BLAST to *Acarosporomycetidae* and *Lichinomycetes* (sensu Díaz-Escandón et al. 2022), but with low covers. Our identical mtSSU sequences from two specimens have the closest NCBI BLAST to *Sarea* with identities up to 86% and *Sarcosagium* (81%).

**_Bilimbia sabuletorum_**

Our ITS and mtSSU match *B. sabuletorum* in NCBI with identities above 99%.

**_Blastenia ammiospila_**

Usually muscicolous on ground or on stems of alpine shrubs, but occasionally on bark (especially in northern Europe). ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia coralliza_**

Our ITS matches *B. coralliza* in NCBI with up to 100% identities. Another ITS adopted from Arup & Åkelius (2009). Sequences of mtSSU absent from NCBI and our mtSSU has the closes NCBI blast to *Blastenia* spp. with identities up to 98.5%.

**_Blastenia ferruginea_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia furfuracea_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia herbidella_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia hungarica_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia lauri_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia monticola_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia palmae_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Blastenia relicta_**

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

***Blastenia subathallina***

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

***Blastenia xerothermica***

ITS adopted from Vondrák et al. (2020). Sequences of mtSSU absent from NCBI and not obtained by us.

***Bryobilimbia sanguineoatra***

Our ITS matches *B. sanguineoatra* in NCBI with the identity almost 100%. Sequence of mtSSU adopted from Ekman et al. (2008).

***Bryoria bicolor***

Our ITS matches *B. bicolor* in NCBI with the identity 100%. Sequences of mtSSU adopted from Myllys et al. (2011).

***Bryoria fuscescens* (including *B. capillaris* and *B. implexa*)**

Our ITS and mtSSU sequences match *B. fuscescens* in NCBI with identities 100% or close.

***Bryoria nadvornikiana***

Our ITS and mtSSU match *B. nadvornikiana* in NCBI with 100% identities.

***Bryostigma muscigenum***

ITS and mtSSU adopted from Vondrák et al. (2022). Our additional ITS is distinct from the NCBI sequence, sharing the identity 89%. Probably more species are hidden under the name *B. muscigenum*. According to our data, *Arthonia apatetica*, *A. biatoricola* and *A. faginea* belong to *Bryostigma*.

***Buellia arborea***

Our ITS matches the single *B. arborea* in NCBI with the identity almost 100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest BLAST to *Buellia* spp. with identities up to 91%.

***Buellia arnoldii***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU not available in NCBI.

***Buellia disciformis***

Our ITS sequences are generally of two genotypes that are 90% identical. One genotype apparently represents *B. disciformis* s.str. with inspersed hymenium and another represents a lichen with translucent hymenium. Both genotypes are also available in NCBI. The real *B. disciformis* is FR799136-40, MZ159559 and OK332941. Sequences of mtSSU adopted from Wedin et al. (2002).

***Buellia dives***

ITS and mtSSU absent from NCBI. Our sequences have the closest NCBI BLAST to *Buellia* spp.; 86% in ITS; 91% in mtSSU.

***Buellia erubescens***

Our ITS matches *B. erubescens* in NCBI with identities 95–98%. Sequences of mtSSU absent from NCBI. Our mtSSU matches *B. disciformis* (AY143401) with the identity over 99.5%.

***Buellia griseovirens***

Our specimens have ITS of two genotypes with 98.5% identity. Both match *B. griseovirens* with identities 98–100%. Identical mtSSU from six specimens match *B. griseovirens* (KC681811) with 100% identity.

***Buellia hyperbolica***

ITS and mtSSU absent from NCBI. Our ITS match *Buellia* spp. and *Dimelaena* spp. with identities up to 88%. Our mtSSU matches *B. dialyta* (DQ972982) with 100% identity and *B. centralis* (AY640586) with identity over 99%. Both latter species are non-European.

***Buellia schaereri***

Our ITS matches *B. schaereri* in NCBI with 92–99% identities, mtSSU with 98–99%.

***Buellia triseptata***

ITS adopted from Helms et al. (2003), mtSSU absent from NCBI.

***Bunodophoron melanocarpum***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU not included in Martin7.

***Byssoloma diederichii***

ITS and mtSSU sequences absent from NCBI. Our ITS has the closest NCBI BLAST to *Leimonis* and *Psilolechia* with identities about 87%. Our mtSSU has the closest NCBI BLAST to *Micarea doliiformis* and *M. substipitata* with identities up to 93%. According to our data, the closest known relative is *Fellhanera viridisorediata* with the identity 95% in ITS and 97% in mtSSU. *Byssoloma diederichii* is not related to members of the core of *Byssoloma*.

***Byssoloma leucoblepharum***

ITS adopted from Andersen & Ekman (2004) and mtSSU from Andersen & Ekman (2005).

***Byssoloma marginatum***

ITS adopted from Andersen & Ekman (2004) and mtSSU from Andersen & Ekman (2005).

***Byssoloma subdiscordans***

ITS adopted from Andersen & Ekman (2004) and mtSSU from Andersen & Ekman (2005).

***Calicium abietinum***

ITS adopted from NCBI (DQ789077; Tibell 2006). Our mtSSU matches *C. abietinum* in NCBI with identities 99–100%.

***Calicium adspersum***

Our ITS sequences from two specimens are 97.5% identical. They represent different ecotypes: ITS from a lichen on oak bark in a well-lit forest matches *C. adspersum* in NCBI with identities 99–100%.

ITS from a lichen on fir bark in shaded montane old-growth forest matches *C. adspersum* in NCBI with identities up to 97.5%. Sequences of mtSSU adopted from Prieto & Wedin (2017).

***Calicium denigratum***

ITS and mtSSU adopted from Prieto & Wedin (2017).

***Calicium episcalaris***

Our identical ITS from two specimens are also identical with the type sequence of *C. episcalaris*, KX228552 (Tibell & Knuttson 2016). Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *C. pinastri* with the identity 100%. *Calicium episcalaris* is similar to *C. montanum* and it was reported under this name from the Czech Republic (Šoun 2010; Vondrák et al. 2022). In contrast to its original diagnosis, it is not strictly lichenicolous on *Hypocenomyce scalaris*.

***Calicium glaucellum***

Our ITS sequences match *C. glaucellum* in NCBI with identities 94–100% and mtSSU matches the single NCBI sequence of *C. glaucellum* (KX512980) with 99.5%.

***Calicium hyperelloides***

ITS adopted from Tibell (2003), mtSSU absent from NCBI.

***Calicium lenticulare***

Our ITS matches *C. lenticulare* in NCBI with identities 90–93%. Sequences of mtSSU adopted from Prieto & Wedin (2017).

***Calicium lucidum* (= *Cyphelium lucidum*)**

ITS adopted from Tibell (2007). Sequences of mtSSU absent from NCBI.

***Calicium montanum***

ITS adopted from Tibell &Knutsson (2016). Our mtSSU is almost identical with our sequences of *C. episcalaris*, from which it differs in three nucleotide positions.

***Calicium notarisii* (= *Cyphelium notarisii*)**

ITS and mtSSU adopted from Prieto &Wedin (2017) and Tibell (2003).

***Calicium parvum***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *C. pinicola* in NCBI with identities 91–92%, our mtSSU with 96–97%.

***Calicium pinastri***

ITS adopted from Vondrák et al. (2022). Our mtSSU matches *C. pinastri* in NCBI (OL396696) with the identity almost 100%.

***Calicium pinicola***

ITS and mtSSU adopted from Prieto &Wedin (2017).

***Calicium quercinum***

ITS adopted from Prieto &Wedin (2017). Sequences of mtSSU absent from NCBI.

***Calicium salicinum***

The two specimens in Martin7 are 93% identical in ITS anf 98% in mtSSU. ITS (type1) matches *C. salicinum* in NCBI with identities 93–100%. ITS (type2) matches *Calicium* sp. (DQ789083, DQ789088) with identities 93%. Our mtSSU (type1) matches *C. lecideinum* (KX512961) with identity 97%, mtSSU (type2) matches *C. viride* with identity 96%. (The mtSSU in NCBI named *C. salicinum*, KX512982, is less similar to our sequences.)

***Calicium tigillare***

Our ITS matches *C. tigillare* in NCBI with identities 99–100%, mtSSU with 100%.

***Calicium trabinellum***

Our ITS matches *C. trabinellum* (AY450579; Prieto &Wedin 2017) with 100% identity. Sequences of mtSSU absent from NCBI and not obtained by us.

***Calicium trachylioides***

ITS and mtSSU adopted from Prieto & Wedin (2017).

***Calicium victorianum***

ITS adopted from Aguirre-Hudson et al. (2007), mtSSU absent from NCBI.

***Calicium viride***

Our ITS matches both *C. corynellum* and *C. viride* (cf. Yahr 2015) with identities over 98%. Our mtSSU matches with *C. corynellum* and *C. viride* in NCBI with identities over 99.5%.

***Caloplaca ahtii***

ITS adopted from Vondrák et al. (2019). Sequences of mtSSU absent from NCBI.

***Caloplaca alnetorum* (= *Athallia alnetorum*)**

ITS adopted from Arup et al. (2013). Sequences of mtSSU absent from NCBI and not obtained by us.

***Caloplaca alstrupii***

ITS and mtSSU absent from NCBI. Various species of *Caloplaca* (in the traditionally broad sense) have the closest NCBI BLAST to identities 88% in ITS and 97% in mtSSU. According to the current trends in taxonomy of *Caloplaca*, this species merits its own new genus.

***Caloplaca asserigena***

ITS and mtSSU sequences adopted from NCBI.

***Caloplaca* aff. *atroflava***

Sorediate crust with grey-green areoles and pale green flat soralia without anthraquinones. Overlooked lichen on tree bases of e.g. ashes and oaks in ravine forests and forest-steppes in low altitudes. Also occurring on nutrient-rich stones. Either a separate species or a sorediate morphotype of *C. atroflava* (saxicolous lichen, usually known without vegetative diaspores). Our ITS has the closest NCBI BLAST to *C. atroflava* with identities 97–100%; mtSSU with identities close to 100%.

***Caloplaca baltistanica***

ITS adopted from Vondrák et al. (2016a). Sequences of mtSSU absent from NCBI.

***Caloplaca borealis***

ITS adopted from Vondrák et al. (2019). Sequences of mtSSU absent from NCBI.

***Caloplaca caesiorufella***

ITS adopted from Spribille et al. (2020). Sequences of mtSSU absent from NCBI.

***Caloplaca cerina***

Our ITS sequence has the closest NCBI BLAST to *C. cerina* (HM538471; Šoun et al. 2011) with identity 98%. Our mtSSU has the closest NCBI BLAST to *Caloplaca* (s.str.) with identities 98–99%. It is a genetically variable species including numerous quite distant genotypes.

***Caloplaca cerinella* (= *Athallia cerinella*)**

ITS adopted from Vondrák et al. (2012). Sequences of mtSSU absent from NCBI and not obtained by us.

***Caloplaca cerinelloides* (= *Athallia cerinelloides*)**

ITS adopted from Vondrák et al. (2012) and mtSSU from Arup et al. (2013).

***Caloplaca chlorina***

Predominantly saxicolous lichen that occassionally overcomes to bark, especially to tree bases in humid sites. Our ITS matches *C. chlorina* in NCBI with identities 97–100% and our mtSSU with 100%.

***Caloplaca chrysodeta* (= *Leproplaca chrysodeta*)**

Usually saxicolous, but sometimes occurring on mossy bark of old trees, e.g. *Acer pseudoplatanus*. ITS and mtSSU adopted from Arup et al. (2013).

***Caloplaca chrysophthalma* (= *Solitaria chrysophthalma*)**

ITS and mtSSU sequences adopted from Arup et al. (2013).

***Caloplaca* aff. *chrysophthalma* (undescribed species)**

Lichen without vegetative diaspores forming orange pycnidia and apothecia on pale grey to pale yellow thallus. The similar species is *Caloplaca* (*Gyalolechia*) *flavorubescens*, or *Caloplaca* (*Athallia*) *alnetorum*, but the sorediate *Caloplaca* (*Solitaria*) *chrysophthalma* is the most closely related; identity in ITS about 94%, in mtSSU 98%. This undescribed species is so far only known from Podyjí region in Southern Moravia (Czech Republic). Sequences of ITS and mtSSU from two specimens are identical.

***Caloplaca epiphyta* (= *Gyalolechia epiphyta*)**

ITS adopted from Vondrák et al. (2016b; as *Gyalolechia epiphyta*). Sequences of mtSSU absent from NCBI.

***Caloplaca ferrugineoides* (= *Calogaya ferrugineoides*)**

ITS adopted from Vondrák et al. (2017; as *Calogaya ferrugineoides*). Sequences of mtSSU absent from NCBI.

***Caloplaca flavocitrina* (= *Flavoplaca flavocitrina*)**

Usually saxicolous, but occassionally on base-rich bark at trunk bases. Our ITS of epiphytic thalli have the closest NCBI BLAST to *C. flavocitrina* with identities 98–100%. Sequence of mtSSU adopted from Vondrák et al. (2022).

***Caloplaca flavorubescens* (= *Gyalolechia flavorubescens*)**

ITS and mtSSU adopted from Arup et al. (2013).

***Caloplaca haematites* (= *Sanguineodiscus haematites*)**

ITS and mtSSU adopted from Frolov et al. (2021).

***Caloplaca holocarpa* (= *Athallia holocarpa*)**

Usually saxicolous, but occassionally on tree bark and wood in nitrophilous communities. ITS adopted from Vondrák et al. (2012); sequence of mtSSU adopted from Arup et al. (2013).

***Caloplaca lobulata* (= *Calogaya lobulata*)**

Our ITS has the closest NCBI BLAST to *C. lobulata* with identities 97–100%. Our mtSSU has the closest NCBI BLAST to *C.* aff. *lobulata* with identities close to 100%.

***Caloplaca lucifuga***

Our ITS sequences have the closest NCBI BLAST to *C. lucifuga* with identities about 99%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Caloplaca* spp. (s.lat.) with identities up to 97%.

***Caloplaca luteoalba* (= *Cerothallia luteoalba*)**

ITS and mtSSU adopted from Arup et al. (2013).

***Caloplaca microphyllina***

ITS and mtSSU adopted from Søchting et al. (2021).

***Caloplaca monacensis***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Caloplaca obscurella***

Our ITS sequences match *C. obscurella* in NCBI with identities 98–100%. Sequences of mtSSU absent from NCBI. Our mtSSU has NCBI BLASTs up to 97.5% with various *Teloschistaceae*.

***Caloplaca* aff. *obscurella***

ITS adopted from Vondrák et al. (2018). Sequences of mtSSU absent from NCBI.

***Caloplaca phlogina* (= *Scythioria phlogina*)**

Our ITS has the closest NCBI BLAST to *C. phlogina* with identities 99–100%. Sequence of mtSSU adopted from Vondrák et al. (2022).

***Caloplaca pollinii***

ITS adopted from Bungartz et al. (2020). Sequences of mtSSU absent from NCBI.

***Caloplaca pyracea* (= *Athallia pyracea*)**

Sequence ITS adopted from Vondrák et al. (2022). Our mtSSU sequence has the closest NCBI BLAST to the single available *C. pyracea* with identity almost 100%.

***Caloplaca raesaenenii***

Our ITS has the closest NCBI BLAST to *C. raesaenenii* with identities 99–100%. Sequence of mtSSU adopted from Søchting et al. (2007).

***Caloplaca sorocarpa***

ITS adopted from Vondrák et al. (2018). Sequences of mtSSU absent from NCBI.

***Caloplaca stillicidiorum***

ITS adopted from Šoun et al. (2011). Sequence of mtSSU adopted from Gaya et al. (2015).

***Caloplaca subochracea* var. *luteococcinea* (sensu Sipman)**

Although this species, currently called *Gyalolechia luteococcinea*, is considered saxicolous, our sequences are from an abundant lichen on bark and wood on coastal dunes of Rhodos. Our ITS sequences are about 99.5% identical with MN172443 (*Caloplaca subochracea* var. *luteococcinea* sensu Sipman & Raus), mtSSU not sequenced yet.

***Caloplaca syvashica***

ITS adopted from Vondrák et al. (2012). Sequences of mtSSU absent from NCBI.

***Caloplaca substerilis***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Caloplaca turkuensis***

ITS adopted from Šoun et al. (2011), mtSSU from Urbanavichus et al. (2020).

***Caloplaca ulcerosa* (= *Coppinsiella ulcerosa*)**

Our ITS matches *C. ulcerosa* in NCBI with identities 98–99.5%. Other ITS and mtSSU adopted from Vondrák et al. (2022).

***Caloplaca* sp. (*Athallia* cf. *cerinelloides* sensu Sipman)**

A Mediterranean coastal species. Our ITS sequences match *Athallia* cf. *cerinelloides* sensu Sipman & Raus (MN989243, MN989244) with identities about 99%.

***Caloplaca* sp. (= *Athallia* sp.)**

A Mediterranean corticolous species resembling *Athallia holocarpa*. ITS adopted from Vondrák et al. (2012).

***Candelaria concolor***

Our ITS has the closest NCBI BLAST to *C. concolor* with 100% identities and our mtSSU with identities 86–100%. Huge variability in mtSSU sequences in NCBI is perhaps due to incorrectly edited sequences or incorrectly assigned sequences to species names.

***Candelaria pacifica***

ITS adopted from Westberg & Arup (2010); type sequence. Sequences of mtSSU absent from NCBI and not obtained by us.

***Candelariella antennaria***

ITS adopted from NCBI (Kocakaya & Halıcı 2017, unpublished). Sequences of mtSSU absent from NCBI.

***Candelariella aurella***

Usually saxicolous, rarelly on wood and bark. ITS and mtSSU sequences from an epiphytic specimen adopted from Vondrák et al. (2022).

***Candelariella blastidiata***

ITS and mtSSU adopted from Malíček et al. (2018a).

***Candelariella boleana***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Candelariella* spp. with identities up to 96%. Sequence of mtSSU not obtained by us.

***Candelariella efflorescens***

ITS and mtSSU absent from NCBI. Our ITS sequences have the closest NCBI BLAST to *Candelariella vitellina* with identities up to 96%. Our mtSSU has the closest NCBI BLAST to *Candelariella* spp. with identities up to 96%. Thallus morphology and the number of spores in asci resemble *C. xanthostigma*, but thalline granules are distinctly smaller in *C. efflorescens.* We have sequenced another sorediate *Candelariella*, with distinct soralia and even smaller vegetative propagules, and it likely represents another species that we call *Candelariella* sp. (specimen PRA-Vondrák26086; ITS: OQ717355; mtSSU: OQ682902).

***Candelariella faginea***

ITS and mtSSU adopted from Urbanavichus et al. (2020).

***Candelariella lutella***

Sequence ITS adopted from Westberg et al. (2007). Sequences of mtSSU absent from NCBI and not obtained by us.

***Candelariella reflexa***

Our ITS has the closest NCBI BLAST to the single available *C. reflexa* (EF535189) with 100% identity; mtSSU *C. reflexa* (DQ912272) with identity only 96%.

***Candelariella rubrisoli***

Our ITS sequences match *Candelariella rubrisoli* (sub *Candelariella* sp.; MG694273) with identities >98%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Candelariella* spp. with identities up to 96%. (This species is recognisable from *C. efflorescens* and other sorediate *Candelariella*, even in a sterile state, by squamulose thalli with marginal soralia; Liu et al. 2019).

***Candelariella subdeflexa***

ITS adopted from Yakovchenko et al. (2017). Sequences of mtSSU absent from NCBI and not obtained by us.

***Candelariella viae-lacteae***

ITS and mtSSU absent from NCBI. Our ITS matches *C. antennaria* in NCBI with identities 96.5–97.5%. Our mtSSU has the closest NCBI BLAST matches to *Candelariella* spp. with identities up to 93.5%.

***Candelariella xanthostigma***

Our ITS sequence has the closest NCBI BLAST to North American sequences of *C. xanthostigma* with identities only 95–96%. Sequences of mtSSU absent from NCBI and not obtained by us.

***Carbonicola anthracophila* (= *Hypocenomyce anthracophila*)**

ITS adopted from Bendiksby & Timdal (2013). Our mtSSU has the closest NCBI BLAST to *C. anthracophila* with identities 100%.

***Carbonicola myrmecina***

ITS and mtSSU adopted from Bendiksby & Timdal (2013).

***Carestiella socia***

ITS and mtSSU adopted from Wedin et al. (2006).

***Catillaria erysiboides***

ITS adopted from Schmull et al. (2011) and mtSSU from Miadlikowska et al. (2014).

***Catillaria fungoides***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *C. fungoides* (Vondrák et al. 2022) with almost 100% identity.

***Catillaria nigroclavata***

Our ITS has the closest NCBI BLAST to *C. nigroclavata* with almost 100% identities. Our mtSSU has the closest NCBI BLAST to the single available *C. nigroclavata* (OL396762; incorrectly under the name *C. nigroisidiata*) with identity 100%.

***Catinaria atropurpurea***

ITS absent from NCBI. Our ITS from two specimens represent genotypes identical from 89%. Both have the closest NCBI BLAST to *Catillaria* spp. with identities up to 92%. Our mtSSU sequences from three specimens represent three distinct genotypes, all have the closest NCBI BLAST to the single available sequence of *C. atropurpurea* (MG925865) with identities 93, 95 and 96%.

***Catinaria neuschildii***

ITS and mtSSU absent from NCBI. Our ITS is very close to sequences of *C. atropurpurea*, but differs from them in 20 unique nucleotide positions. Sequence of mtSSU not obtained by us.

***Celothelium ischnobelum***

ITS and mtSSU absent from NCBI. Our identical ITS sequences from two specimens have the closest NCBI BLAST to *Phaeomoniellales* spp. (*Chaetothyriomycetidae*) with identities up to 85%. Our identical mtSSU sequences from two specimens have the closest NCBI BLAST to *C. cinchonarum* with identities 90%.

***Cetraria sepincola***

Our ITS and mtSSU match *C. sepincola* with identities close or equal to 100%.

***Cetrelia cetrarioides***

Our ITS matches *C. cetrarioides* with identities 98–99%. Sequences of mtSSU adopted from Crespo et al. (2010).

***Cetrelia chicitae***

ITS adopted from Mark et al. (2019); mtSSU absent from NCBI and not obtained by us.

***Cetrelia monachorum***

Our ITS sequences have the closest NCBI BLAST to *C. monachorum* with identities 100%. Our mtSSU has the closest NCBI BLAST to *C. olivetorum* in NCBI, which apparently represents incorrectly assigned *C. monachorum*.

***Cetrelia olivetorum***

ITS adopted from Mark et al. (2019) and mtSSU from Crespo et al. (2010).

***Chaenotheca brachypoda***

Our ITS (only ITS2 region) has the closest NCBI BLAST to *C. brachypoda* (Tibell 2001) with identities 98–99%. Our mtSSU has the closest NCBI BLAST to the single available *C. brachypoda* (JX000122) with identity 98%.

***Chaenotheca brunneola***

Our ITS has the closest NCBI BLAST to *C. brunneola* with identities 98–100%. Sequences of mtSSU absent from NCBI. Our identical mtSSU from two specimens have the closest NCBI BLAST to *Chaenotheca* spp. with identities up to 92%.

***Chaenotheca chlorella***

Our ITS has the closest NCBI BLAST to *C. chlorella* with identities 99–100%. Our mtSSU has the closest NCBI BLAST to the single available *C. chlorella* (OK465561) with identity 100%.

***Chaenotheca chrysocephala***

Our ITS has the closest NCBI BLAST to *Chaenotheca* spp., including *C. chrysocephala*, with identities up to 90%. Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenotheca cinerea***

ITS adopted from Tibell (2001). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenotheca ferruginea***

Our ITS has the closest NCBI BLAST to *C. ferruginea* with identities 98–99%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Chaenotheca* spp. with identities up to 91%.

***Chaenotheca furfuracea***

Our ITS has the closest NCBI BLAST to *C. furfuracea* with identities 92–100%. Our mtSSU has the closest NCBI BLAST to the single available *C. furfuracea* with identity 100%.

***Chaenotheca gracillima***

Our ITS has the closest NCBI BLAST to *C. gracillima* with identities 92–100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Chaenotheca* spp. with identities up to 93%.

***Chaenotheca gracilenta***

ITS and mtSSU adopted from NCBI.

***Chaenotheca hygrophila***

Our ITS matches *C. hygrophila* in NCBI with identities 85–92.5%, Other *Chaenotheca* spp. are <85% identical. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Chaenotheca* spp. with identities up to 88.5%.

***Chaenotheca hispidula***

Our ITS has the closest NCBI BLAST to the single available *C. hispidula* (AF298128; India, Tibell 2001) with identity 90%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *C. chlorella* with identity 98%.

***Chaenotheca laevigata***

Our ITS has the closest NCBI BLAST to *C. laevigata* and *C. chlorella*, but with identities only 88–90%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *C. chlorella* with identity 96%.

***Chaenotheca nitidula***

ITS adopted from Tibell & Koffman (2002). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Chaenotheca phaeocephala_**

Our ITS has the closest NCBI BLAST to *C. phaeocephala* with identities 99–100%. Our mtSSU has the closest NCBI BLAST to the single available *C. phaeocephala* (OK465562) with identity 100%.

**_Chaenotheca sphaerocephala_**

Our ITS has the closest NCBI BLAST to *C. stemonea* with identities up to 89%. (The ITS of *C. sphaerocephala* in NCBI (AF298134; India, Tibell 2001) is 86% identical and perhaps represents a different species.) Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Chaenotheca* spp. with identities up to 90%.

**_Chaenotheca stemonea_**

Our almost identical ITS from four specimens has the closest NCBI BLAST to *C. stemonea* (KX133006) with identity 99%. Other two NCBI sequences of *C. stemonea* are quite distinct, with 93 and 83% identity. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Chaenotheca* spp. with identities up to 89%.

**_Chaenotheca subroscida_**

Our ITS has the closest NCBI BLAST to *C. subroscida* with identities close or equal to 100%. Another related species is *C. phaeocephala* (identity about 95%). Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *C. phaeocephala* (OK465562) with identity almost 99%.

**_Chaenotheca trichialis_**

Our ITS sequences have the closest NCBI BLAST to *C. trichialis* with identities 95–100% and mtSSU to the single available *C. trichialis* (JX000120) with identity almost 100%.

**_Chaenotheca xyloxena_**

Our identical ITS from three specimens have the closest NCBI BLAST to *C. xyloxena* with identities 97–99%. Sequences of mtSSU absent from NCBI and our 5 identical mtSSU sequences have the closest NCBI BLAST to *C. trichialis* (JX000120) with identity 97%.

**_Chaenothecopsis consociata_**

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Chaenothecopsis debilis_**

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Chaenothecopsis epithallina_**

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

**_Chaenothecopsis fennica_**

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis haematopus***

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis montana***

ITS adopted from Tuovila et al. (2012). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis nigra***

Our ITS has the closest NCBI BLAST to *Chaenothecopsis* sp. (JX119110) with identity 93%; mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis orientalis***

A species similar but unrelated to *C. savonica*. Our ITS has the closest NCBI BLAST to *C. orientalis* with identities 91–100%; our mtSSU to *C. viridialba* with identity 95%.

***Chaenothecopsis pusilla***

Our ITS has the closest NCBI BLAST to one of NCBI sequences of *C. pusilla* (AF243132) with identity 97%, but with identity <85% to another one (AY795866). Apparently, more species are named *C. pusilla*.

***Chaenothecopsis pusiola***

ITS adopted from Tibell & Vinuesa (2005) and Tuovila et al. (2012). Sequences of mtSSU absent from NCBI. Our sequence matches *Chaenothecopsis* spp. with identities up to 94%.

***Chaenothecopsis rubescens***

*Chaenothecopsis* with single-celled ascospores has strongly purple reaction of stipe with KOH and is lichenicolous on *Bactrospora dryina*. Our ITS has the closest NCBI BLAST to *C. kilimanjaroensis* (NR_173886) and *C. nana* (AY795862) with identities over 90%, but with low covers (about 30%). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis savonica***

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis* cf. *tasmanica***

Our ITS has the closest NCBI BLAST to *C. vainioana* with identity 91%; our mtSSU to *C. viridialba* with identity 91%.

***Chaenothecopsis vainioana***

ITS adopted from Tuovila et al. (2012). Sequences of mtSSU absent from NCBI and not obtained by us.

***Chaenothecopsis viridireagens***

ITS adopted from Tibell & Vinuesa (2005) and Tuovila et al. (2012). Sequences of mtSSU absent from NCBI and not obtained by us.

### *Chaenothecopsis* sp. 1

Apparently, a common species on wood of beech snags, in sites sheltered from rain. It is habitually similar to *Mycocalicium subtile*, but resembles anatomically *C. pusiola* (i.e. spores with pale septum, green stipe tissue reacts red with KOH). Our slightly variable ITS sequences from three specimens have the closest NCBI BLAST to *Chaenothecopsis* sp. (JX119110; Tuovila et al. 2012) with identities 93, 93 and 100%. Our mtSSU has the closest NCBI BLAST to *Mycocalicium subtile* with identities up to 95%.

### *Chaenothecopsis* sp. 2

Morphologically and ecologically resembling the previous species (sp. 1), but the reaction of stipe recalls *C. debilis* (N+ red-violet; Groner 2006). Our ITS has the closest NCBI BLAST to *Chaenothecopsis* sp. (JX119110) with identity 87%; mtSSU to *Sphinctrina turbinata* (FJ713611) with identity 95%.

### *Chaenothecopsis* sp. 3

Lichenicolous on *Chaenotheca brachypoda*. It has single-celled ascospores and olive pigment in stipes (KOH+ brown). Habitually similar to *C. savonica*, but not related. Our ITS sequences have the closest NCBI BLAST to *Mycocalicium subtile* and *Chaenothecopsis haematopus* with identities about 95%, but with low covers (30–40%). Our mtSSU has the closest NCBI BLAST to *Mycocalicium subtile* with identities 94%.

### *Chaenothecopsis* sp. 4

Characterised by sessile apothecia, similar to *C. subparoica*, but epiphytic and lichenicolous on unidentified crust. ITS has the closest NCBI BLAST to *C. subparoica*, but with low identity (88%). Our mtSSU has the closest NCBI BLAST to *Chaenothecopsis viridialba* (AY853317) with identity 92%.

### *Cheiromycina flabelliformis*

ITS sequences absent from NCBI and not obtained by us. Our almost identical mtSSU sequences from six specimens have the closest NCBI BLAST to *C. reimeri* in NCBI with identities about 97%. (NCBI sequence called *C. flabelliformis* (MF431799) probably represents *C. petri*.)

### *Cheiromycina petri* (= *Lecidea coriacea*)

No ITS sequences in the NCBI so far. Our single ITS is identical with our sequence of *Lecidea coriacea*. Similarly, our identical mtSSU sequences of three specimens, that match *C. petri* in NCBI with identities 96–100%, are identical with our *Lecidea coriacea* sequences. It means that *L. coriacea* is a fertile variant of sporodochial *Cheiromycina petri*. We have observed some specimens with both apothecia and sporodochia.

### *Cheiromycina reimeri*

ITS absent from NCBI. Sequence of mtSSU adopted from Muggia et al. (2017).

### *'Cheiromycina' simplex* ined.

Undescribed species of a tiny, questionably lichenized, sporodochiate fungus with a Cheiromycina-like appearance but with simple, unbranched cylindrical conidia, containing eight thick-walled cells. Our ITS has the closest NCBI BLAST to *Sarea* spp. with identities up to 86%. Our identical mtSSU sequences from two specimens have the closest NCBI BLAST to *Myriospora*, *Pycnora* and *Candelariella* (*Lichinomycetes* sensu Díaz-Escandón et al. 2022) with identities up to 88%.

***'Cheiromycina' splendida*** **ined.**

Undescribed species with Cheiromycina-like sporodochia, but with monilliform chains of conidia. Our ITS has no close NCBI relatives and our identical mtSSU sequences of four specimens have the closest NCBI BLAST to *Thrombium epigaeum* (AY607750) with the identity 85% and to other *Ostropomycetidae* spp. with identities up to 84%.

***Chrysothrix caesia***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Schoch et al. 2009 (as *Arthonia caesia*).

***Chrysothrix candelaris***

Our ITS sequence has the closest NCBI BLAST to members of *Andreiomyces* and *Chrysothrix* with identities up to 95%, but with low covers (c. 20–50%). Sequence of mtSSU adopted from Frisch et al. (2014).

***Chrysothrix chrysophthalma***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Frisch et al. (2014).

***Chrysothrix fagicola*** **ined. (described here)**

We obtained ITS sequences from five specimens which are >99.5% identical. The sister lineage consists of *Chrysothrix* sequences (*C. candelaris*, *C. xanthina* and *C.* sp.) which are 85–93% identical to *C. fagicola*. These species together with *Arthonia mediella* form a supported clade of *Chrysotrichaceae* which is sister to *Andreiomycetaceae*. The two almost identical mtSSU sequences from *C. fagicola* are 86.5% identical with *C. caesia*. Both species then form a sister group to the clade *C. candelaris* and *C. xanthina*, and all these species together with other members of *Chrysothrix* and with *Arthonia mediella* form a clade corresponding to *Chrysotrichaceae*, a sister group to *Andreiomycetaceae*.

***Chrysothrix flavovirens***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Frisch et al. (2014).

***Cladonia bacilliformis***

ITS adopted from Stenroos et al. (2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Cladonia botrytes***

ITS adopted from Stenroos et al. (2002). Sequences of mtSSU absent from NCBI and not obtained by us.

***Cladonia caespiticia***

Usually terricolous, but rarely on bark and wood. ITS and mtSSU sequences adopted from Vondrák et al. (2022).

***Cladonia carneola***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Cladonia cenotea***

ITS adopted from NCBI (MK812699; Marthinsen et al. 2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Cladonia coniocraea***

ITS adopted from NCBI (MK812138; Marthinsen et al. 2019), sequence of mtSSU adopted from Konoreva et al. (2019b).

***Cladonia cyanipes***

ITS adopted from NCBI (MN726352; Prokopiev et al. 2019; ms). Sequences of mtSSU absent from NCBI and not obtained by us.

***Cladonia digitata***

Our ITS has the closest NCBI BLAST to *C. digitata* with identities up to 100%. Other *Cladonia* species (especially *C. borealis*) have very close sequences, 98–99% identical, whereas some *C. digitata* sequences are only 97% identical (e.g. MN387051; Stenroos et al. 2019). Our mtSSU has the closest NCBI BLAST to *C. digitata* with 100% identities.

***Cladonia fimbriata***

Our ITS has the closest NCBI BLAST to *C. fimbriata* (MK179532) with identity close to 100%. Sequence of mtSSU adopted from Konoreva et al. (2019b).

***Cladonia floerkeana***

Our ITS has the closest NCBI BLAST to *C. macilenta* with identities up to 100%; our mtSSU with identities 100%. Our ITS from *C. macilenta* differs from our *C. florkeana*, but this does not exclude the possibility that both "species" are conspecific and indistinguishable by our barcodes after including all the variation at both loci.

***Cladonia glauca***

Usually terricolous, but occassionally on bark and wood. ITS and mtSSU absent from NCBI. Our ITS and mtSSU have the closest NCBI BLAST to *Cladonia* spp. with identities up to 99%.

***Cladonia grayi***

ITS adopted from Stenroos et al. (2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Cladonia incrassata***

Our ITS has the closest NCBI BLAST to *C. incrassata* with identities almost 100%, but with low cover (about 50%). Our mtSSU has the closest NCBI BLAST to *Cladonia* spp. with identities up to 99%.

***Cladonia macilenta***

ITS and mtSSU sequences adopted from Vondrák et al. (2022).

***Cladonia merochlorophaea***

Our ITS has the closest NCBI BLAST to *C. cryptochlorophaea* and *C. merochlorophaea* with identities over 99%. Both species are apparently closely related. Our mtSSU has the closest NCBI BLAST to *Cladonia* spp. with identities up to 99%.

***Cladonia norvegica***

ITS and mtSSU absent from NCBI. Our ITS and mtSSU have the closest NCBI BLAST to *Cladonia* spp. with identities up to 97%, respectively 99%.

***Cladonia ochrochlora***

Our identical ITS from two specimens have the closest NCBI BLAST to sequences of *C. coniocraea* with identities close to 100%. Our mtSSU has the closest NCBI BLAST to *Cladonia* spp. with identities up to 99%.

***Cladonia parasitica***

ITS adopted from Vondrák et al. (2022). Our mtSSU has the closest NCBI BLAST to *Cladonia* spp. with identities up to 99%.

***Cladonia polydactyla***

Our ITS has the closest NCBI BLAST to *C. bellidiflora* / *C. polydactyla* with identities close or equal to 100%. Our mtSSU has the closest NCBI BLAST to *Cladonia* spp., including *C. polydactyla* (cf. Seinová et al. 2022), with identities close to 100%.

***Cladonia pyxidata***

Our ITS has the closest NCBI BLAST to *Cladonia* spp. including *C. pyxidata* with identities up to 99%. Sequence of mtSSU not obtained by us.

***Cladonia ramulosa***

Usually terricolous, but rarely on bark and wood. Our ITS and mtSSU adopted from Vondrák et al. (2022).

***Cladonia squamosa***

ITS adopted from Marthinsen et al. (2019). Our mtSSU has the closest NCBI BLAST to *Cladonia* spp. with identities up to 99%.

***Cladonia subulata***

Our ITS has the closest NCBI BLAST to *C. subulata* with 100% identities. Sequence of mtSSU adopted from NCBI.

***Cladonia sulphurina***

Our ITS has the closest NCBI BLAST to *C. sulphurina* (KY266846) with almost 100% identity. Our mtSSU has the closest NCBI BLAST to *Cladonia* spp. with identities up to 99.5%.

***Cliostomum corrugatum***

Our ITS has the closest NCBI BLAST to *Cliostomum corrugatum* with identity 99.5–100%. Our mtSSU has the closest NCBI BLAST to *Ramalina* spp. with identities up to 98.5% and to *Cliostomum griffithii* with identity 98%.

***Cliostomum flavidulum***

ITS and mtSSU absent from NCBI. Our ITS and mtSSU match *Cliostomum griffithii* in NCBI with the identities 94–94.5% and 98%, respectively.

***Cliostomum griffithii***

Our ITS has the closest NCBI BLAST to *C. griffithii* with 100% identities. Sequence of mtSSU adopted from Sérusiaux et al. (2010).

***Cliostomum haematommatis***

ITS and mtSSU adopted from Dietrich & Malíček (2019).

***Coenogonium luteum***

Our ITS has the closest NCBI BLAST matches to *C. isidiatum* with identities 84–87%. The only NCBI entry of *C. luteum* (HQ650710; Schmull et al. 2011) is 82% identical, but it is demonstrated that *C. luteum* has considerable internal variability in both ITS and mtSSU and perhaps comprises of two or more species (Malíček et al. 2023). Our mtSSU has also the closest hits to *C. isidiatum* in NCBI with identities about 92%. The only mtSSU sequence of *C. luteum* in NCBI (AY584699; Lutzoni et al. 2004) is only 90% identical.

***Coenogonium nimisii***

ITS and mtSSU adopted from Malíček et al. (2023).

***Coenogonium pineti***

Our ITS sequences belong to two genotypes 83% identical. Both genotypes have the closest NCBI BLAST to *Coenogonium isidiatum*, with identities 83–86%. One of our genotypes is 89% identical with the only NCBI *C. pineti* (KT695346). Our mtSSU sequences are 94% identical. They have the closest NCBI BLAST to *C. pineti* (AY300884, KR017337) with identities 92–100%.

***Coenogonium tavaresianum***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST match to *C. isidiatum* with identities c. 85%, but with low cover (42%). Our mtSSU has the closest NCBI BLAST match to *C. pineti* and *C. isidiatum* with identities up to 90%.

***Collema flaccidum***

ITS not available in NCBI and not sequenced by us. Sequence of mtSSU adopted from Otálora et al. (2010).

***Collema furfuraceum***

ITS not available in NCBI. Sequence of mtSSU adopted from Miadlikowska et al. (2014).

***Collema nigrescens***

Sequence of mtSSU adopted from Otálora et al. (2008). ITS absent in NCBI and not obtained by us.

***Collema subnigrescens***

ITS not available in NCBI. Sequence of mtSSU adopted from Wiklund & Wedin (2003).

***Coniocarpon cinnabarinum***

ITS and mtSSU adopted from Frisch et al. (2020).

***Coniocarpon fallax***

ITS and mtSSU adopted from Frisch et al. (2020).

***Cresponea premnea***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Roccellaceae* spp. that are up to 92% identical (but with low coverage; <50%). Our mtSSU is also closest to *Roccellaceae* spp., but with identities up to 85%.

***Crutarndina petractoides***

ITS absent from NCBI, mtSSU adopted from Rivas Plata et al. (2013).

***Cryptodiscus foveolaris***

Sequence ITS adopted from Baloch et al. (2009). Our mtSSU has the closest NCBI BLAST to *C. foveolaris* with identities 99–100%.

***Cryptodiscus incolor***

ITS and mtSSU adopted from Baloch et al. (2009).

***Cryptodiscus gloeocapsa***

Usually muscicolous on soil, but rarely also on moist wood and bark. Our sequences have the closest NCBI BLAST to *C. gloeocapsa* in NCBI (Baloch et al. 2009) with identity 88% in ITS, 90% in mtSSU.

***Cryptodiscus muriformis***

ITS and mtSSU adopted from Fernández-Brime et al. (2018).

***Cryptodiscus neglectus* ined.**

Our ITS has the closest NCBI BLAST to *C. epicladonia* (NR_154847) with the identity about 92%, our mtSSU with the identity 92.5%.

***Cryptodiscus pallidus***

Our ITS has the closest NCBI BLAST to *C. pallidus* with identities 99–100% and mtSSU with identities 98–100%.

***Cryptodiscus pini***

ITS and mtSSU adopted from Baloch et al. (2010).

***Cryptodiscus tabularum***

Our ITS has the closest NCBI BLAST to *C. tabularum* with identities 100% and mtSSU with identities 98–100%.

***Dendriscosticta wrightii***

ITS and mtSSU adopted from Spribille et al. (2020).

***Dendrographa decolorans***

Our two identical ITS sequence have the closest NCBI BLAST to *D. decolorans* (AY548808) with identity 97%. Our mtSSU sequence have the closest NCBI BLAST to *D. decolorans* with identities almost 100%.

***Dichoporis taylorii* (= *Strigula taylorii*)**

ITS and mtSSU absent from NCBI. We only sequenced mtSSU which has the closest NCBI BLAST to *Cyphellophora laciniata* (FJ225737) of *Chaetothyriomycetidae* with the identity 92%. The sequence needs confirmation.

***Dictyocatenulata alba***

ITS adopted from An et al. (2012). These sequences have the closest NCBI BLAST to *Sarea* with identities up to 83%, but according to our data, they are closer to *Thelenella* with identities over 90%. Sequences of mtSSU absent in NCBI. We obtained mtSSU sequences from six specimens 91% identical. The major genotype has the closest NCBI BLAST to *Thelenella muscorum* with identities up to 95% and the minor sequence is 98% identical with *T. vezdae*. *Dictyocatenulata* is a sporodochial member of *Thelenella*.

***Diploschistes muscorum***

ITS and mtSSU adopted from Fernández-Brime et al. (2013).

***Diplotomma alboatrum***

Epiphytic occurrences of *D. alboatrum* are rare and, in Central Europe, restricted to old-growth ravine forests and forest-steppes. Our ITS from an epiphytic specimen has the closest NCBI BLAST to *D. alboatrum* with identities 94–100%, mtSSU with identities 99–100%.

***Diplotomma pharcidium***

ITS adopted from Kelly et al. (2011). Sequences of mtSSU absent from NCBI and not obtained by us.

***Diplotomma* sp. 1**

Known from Rhodos, occurring on bark in shrub communities influenced by salt spray. ITS matches *Diplotomma* spp. with identities up to 93%. Sequences of mtSSU not obtained.

***Diplotomma* sp. 2**

Known from Rhodos, occurring on wood in shrub communities influenced by salt spray. ITS matches *Diplotomma* spp. with identities up to 96%; mtSSU matches *D. venustum* in NCBI (ON166685, KX512968) with identities over 99.5%. Our specimens are distinct from the saxicolous *D. venustum* and other *Diplotomma* species, especially by an inapparent thallus (*Buellia* appearance).

***Dirina ceratoniae***

ITS adopted from Tehler et al. (2013). Sequences of mtSSU absent from NCBI.

***Elixia cretica***

ITS absent from NCBI. Sequence of mtSSU adopted from Spribille & Lumbsch (2010).

***Elixia flexella***

Our ITS has the closest NCBI BLAST to *E. flexella* (KF360373) with identity 98% and mtSSU has the closest NCBI BLAST to *E. flexella* with identities close to 100%.

***Enchylium conglomeratum* (= *Collema conglomeratum*)**

Sequence of mtSSU adopted from Otálora et al. (2008). ITS absent in NCBI and not obtained by us.

***Enterographa crassa***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Ertz et al. (2009).

***Enterographa hutchinsiae***

Epiphytic occurrences are rare, restricted to humid microsites. ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *E. divergens* with identities about 96%. Our mtSSU has the closest NCBI BLAST to *E. hutchinsiae* with identities 99–100%.

***Enterographa zonata***

Epiphytic occurrences are rare, restricted to ravine forests or rocky sites. ITS absent from NCBI and not obtained by us. Our mtSSU has the closest NCBI BLAST to *E. zonata* with identities close to 100%.

***Eopyrenula avellanae***

We obtained sequences from both anamorph and teleomorph which have identical ITS and mtSSU. Our ITS sequences have the closest NCBI BLAST to *E. leucoplaca* (MK811948) with identity 91%. Other close sequences are from *Stictis* and *Conotrema* from *Ostropales* (identities 83–86%). Sequences of mtSSU absent from NCBI and our mtSSU have the closest NCBI BLAST to *Ostropales* spp. with identities up to 86%. Our mtSSU of *E. leucoplaca* is 89% identical.

***Eopyrenula leucoplaca***

Our ITS sequences have the closest NCBI BLAST to *E. leucoplaca* (MK811948) with identity close to 100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Ostropales* spp. with identities up to 87%. Our mtSSU of *E. avellanae* is 89% identical.

***Epigloea soleiformis***

ITS and mtSSU adopted from Pino-Bodas et al. (2017).

***Evernia divaricata***

Our ITS has the closest NCBI BLAST to *E. divaricata* with identities close to 100%. Sequence of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Evernia* spp. with identities close to 100%.

***Evernia mesomorpha***

Our ITS has the closest NCBI BLAST to *E. mesomorpha* with identities close to 100%. Sequences of mtSSU adopted from Crespo et al. (2007) and Miadlikowska et al. (2014).

***Evernia prunastri***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *E. prunastri* with identities close or equal to 100%.

***Exarmidium inclusum***

Usually treated as non-lichenised, but we consider it a semilichen (sensu Vondrák et al. 2022). Our ITS has the closest NCBI BLAST to *Cryptodiscus* and *Xylographa* with identities up to 83% and mtSSU with identities up to 90%.

***Felipes leucopellaeus***

ITS absent from NCBI. Our ITS sequences from two specimens are 99% identical. They have the closest NCBI BLAST to *Lecanoromycetes* spp. and *Leotiomycetes* spp. with identities up to 95%, but with low covers, 37%, so the BLAST results are hardly relevant. Our mtSSU has the closest NCBI BLAST to *F. leucopellaeus* (KJ850984) with 100% identity.

***Fellhanera bouteillei***

Our ITS has the closest NCBI BLAST to *F. bouteillei* z NCBI with identities 91–100%, mtSSU with identities 93–100%.

***Fellhanera* cf. *christiansenii***

Perhaps an undescribed species resembling *F. christiansenii*, but its brown hypothecium is not K+ purple and the ascospores are usually 7-septate. Our ITS has the closest NCBI BLAST to *F. microdiscus* (MK946978) with the identity 91.5%. Sequence of mtSSU not obtained.

***Fellhanera gyrophorica***

Our ITS has the closest NCBI BLAST to *F. gyrophorica* with identities 99–100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Fellhanera* sp. with identities up to 93%.

***Fellhanera subtilis***

ITS adopted from Andersen & Ekman (2004). Our mtSSU has the closest NCBI BLAST hit to *F. bouteillei* (KJ766392; Miadlikowska et al. 2014) with the identity 94%.

***Fellhanera viridisorediata***

ITS and mtSSU absent from NCBI. Our ITS sequences from two specimens (three independent isolations) are 98% identical and have no close sequences in NCBI (*Lecanoromycetes* spp. with identities up to 85%). Our mtSSU has the closest NCBI BLAST to *Micareaceae* and *Psoraceae* with identities up to 91%.

***Fellhaneropsis almquistiorum***

ITS and mtSSU absent from NCBI. Our ITS sequence has the closest NCBI BLAST to *F. myrtillicola* with identity 88%. Our mtSSU has the closest NCBI BLAST to *Micarea substipitata* with identities about 92%.

***Fellhaneropsis myrtillicola***

Our ITS has the closest NCBI BLAST to *F. myrtillicola* (AY756466) with identity 96%. Our mtSSU is 92–93% identical with *Micarea substipitata*.

***Fellhaneropsis vezdae***

ITS and mtSSU absent from NCBI. Our ITS sequence has the closest NCBI BLAST to *F. myrtillicola* with identity 87%. Our mtSSU is about 91% identical with *M. contexta* / *M. doliiformis* / *Micarea substipitata*.

***Flavoparmelia caperata***

ITS and mtSSU adopted from Blanco et al. (2005).

***Flavoparmelia soredians***

Our ITS and mtSSU has the closest NCBI BLAST to *F. soredians* with identities close to 100%.

***Flavopunctelia flaventior***

Our ITS and mtSSU has the closest NCBI BLAST to *F. flaventior* with identities 99–100%.

***Flavopunctelia soredica***

ITS and mtSSU adopted from Divakar et al. (2015).

***Francisrosea bicolor***

ITS absent from NCBI. Sequence of mtSSU adopted from Ertz et al. (2021).

***Frutidella furfuracea* (= *Lecidea pullata*)**

Our ITS sequences have the closest NCBI BLAST to *Lecidea pullata* with identities close to 100%. Sequence of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *F. caesioatra* (MG925872) with identity 97%.

***Fuscidea arboricola***

Our ITS has the closest NCBI BLAST to *F. pusilla* with identities about 92%. Our mtSSU has the closest NCBI BLAST to *F. pusilla* with identities about 98%.

***Fuscidea cyathoides***

ITS and mtSSU from an epiphytic sample adopted from Zahradníková et al. (2017).

***Fuscidea lightfootii***

ITS and mtSSU adopted from Zahradníková et al. (2018).

***Fuscidea pusilla***

Our ITS and mtSSU have the closest NCBI BLAST to *Fuscidea pusilla* with identities close to 100%.

***Fuscopannaria ahlneri***

ITS and mtSSU adopted from Carlsen et al. (2012).

***Fuscopannaria confusa***

ITS and mtSSU adopted from Carlsen et al. (2012).

***Fuscopannaria ignobilis***

ITS and mtSSU adopted from Ekman et al. (2014).

***Fuscopannaria leucosticta***

ITS adopted from Greenwood et al. (2016); mtSSU not considered.

***Fuscopannaria mediterranea***

ITS adopted from Carlsen et al. (2012) and Marthinsen et al. (2019); mtSSU from Carlsen et al. (2012).

***Fuscopannaria olivacea***

ITS and mtSSU adopted from Ekman et al. (2014).

***Fuscopannaria sampiana***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Carlsen et al. (2012).

***Gabura fascicularis***

ITS absent from NCBI. Sequence of mtSSU adopted from Otálora & Wedin (2013).

***Gassicurtia vernicoma***

Sequenced from Caucasus. Our mtSSU has the closest NCBI BLAST to *Buellia* spp. with identities up to 94%. ITS not obtained by us and absent from NCBI.

***Glyphis cicatricosa***

ITS adopted from NCBI (Dal Forno 2020; unpublished), mtSSU from Karthik et al. (2018, unpublished).

***Gomphillus calycioides***

ITS adopted from Keepers et al. (2019). Sequences of mtSSU absent from NCBI.

***Graphis librata***

ITS absent from NCBI. Sequence of mtSSU adopted from Rivas Plata et al. (2011).

***Graphis scripta***

Taxon with substantial genotype and morphological variability and probably more species are involved (Neuwirth & Aptroot 2011, Kraichak et al. 2015). Our four sequenced specimens represent four distinct genotypes: (1) a morphotype with white thallus has the closest NCBI BLAST to *G. scripta* with identities up to 90%. (2) a type with the closest NCBI BLAST to „*Graphis betulina*“ (MN387113) with almost 100% identity. (3) a type with the closest NCBI BLAST to *Graphis* sp. 2 sensu Singh et al. (2019). (4) a type with the closest NCBI BLAST to *G. scripta* (MK092086) with identity 96.5%. Our single mtSSU sequence has the closest NCBI BLAST to *Graphis scripta* with identities 93–100%.

***Gyalecta carneola***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *G. fagicola* (OL457941) with identity 92%. Our mtSSU has the closest NCBI BLAST to the single available *G. carneola* (MT831489) with identity 99.5%.

***Gyalecta carneolutea***

ITS absent from NCBI. Sequence of mtSSU adopted from Lücking et al. (2019).

***Gyalecta derivata***

ITS and mtSSU absent from NCBI. Our ITS sequences have the closest NCBI BLAST to *Gyalecta* spp. with identities up to 90%. Our mtSSU has the closest NCBI BLAST to *G. truncigena* (HM244743) with identity close to 98%.

***Gyalecta fagicola***

ITS adopted from Vondrák et al. (2022). Our mtSSU matches *G. fagicola* in NCBI with identities 99–100%.

***Gyalecta flotowii***

Our ITS sequences have the closest NCBI BLAST to *G. flotowii* with identities 100%. Sequence of mtSSU adopted from Baloch et al. (2010).

***Gyalecta friesii***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Fernández-Brime et al. (2011).

***Gyalecta geoica***

Although mostly known from bryophytes on calcareous substrata, *G. geoica* also occurs on mossy bark of old trees in virgin forests. ITS adopted from Marthinsen et al. (2019). Our mtSSU matches *G. geoica* in NCBI (HM244741; Baloch et al. 2010) with the identity 100%.

***Gyalecta herculina***

See under *Belonia herculina*.

***Gyalecta ophiospora***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *G. fagicola* (OL457941) with identity 81%. Our mtSSU has the closest NCBI BLAST to *G. fagicola* with identities 97–98%.

***Gyalecta truncigena***

ITS absent from NCBI. Our identical ITS from five specimens have the closest NCBI BLAST to *Gyalecta* spp. with identities up to 86%. Our identical mtSSU from four specimens have the closest NCBI BLAST to the single available *Gyalecta truncigena* (HM244743) with identity 99.5%.

***Gyalecta ulmi***

Our ITS has the closest NCBI BLAST to *G. ulmi* with identities 99–100%. Sequence of mtSSU adopted from Lumbsch et al. (2004).

***Gyalidea cylindrica***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Gomphillus* spp. with identities up to 96% but with low cover (about 30%). The species is related to *Gyalidea* sp. (the species below) and both do not belong to *Gyalidea* s.str.

***Gyalidea* sp.**

Probably undescribed species, related to *G. cylindrica*, but distinct by ascospore characters and by ecology (not muscicolous). The ITS sequence is 92% identical with ITS of *G. cylindrica*. The species is not *Gyalidea* s.str.

***Gyalidea minuta***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Gyalidea* spp. with identities up to 97%. Sequences of mtSSU not obtained.

***Gyalideopsis helvetica***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Gomphillus americanus* (KY381580) with the identity 97%, but with the cover only 41%. Our mtSSU has the closest NCBI BLAST to *Gyalectidium* spp. with identities up to 92%.

***Gyalideopsis muscicola***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Gomphillus calycioides* (MK092335) with the identity 81%. Sequence of mtSSU not obtained.

***Gyalideopsis piceicola***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Gomphillus americanus* (KY381580) with the identity 85%. Sequence of mtSSU not obtained.

***Haematomma ochroleucum***

Saxicolous in Central Europe, but numerous western European occurrences are epiphytic. ITS and mtSSU adopted from Kalb et al. (2008).

***Halecania viridescens***

ITS and mtSSU absent from NCBI. Our identical ITS from three specimens have the closest NCBI BLAST to *Catillaria* spp. with identities up to 87%. Our identical mtSSU from two specimens have the closest NCBI BLAST to *Catillaria* spp. with identities up to 95%.

***Haloplaca suaedae***

ITS and mtSSU adopted from Arup et al. (2013).

***Haloplaca* sp. 1**

Our ITS sequences match “*Haloplaca suaedae*” HM582200 from Turkish Black Sea coast with identities about 99.5%, however the type sequence of *H. suaedae* is only 88% identical. Sequences of mtSSU not obtained yet.

***Haloplaca* sp. 2**

Our ITS sequences match *Haloplaca* spp. in NCBI with identities up to 90%. Sequences of mtSSU not obtained yet.

***Hazslinszkya gibberulosa***

ITS and mtSSU absent from NCBI. Our identical ITS sequence from four specimens have no close NCBI BLAST results (highest identities below 80%).

***Hertelidea botryosa***

Our ITS has the closest NCBI BLAST to *H. botryosa* with identities 97–100%, our mtSSU to the single available *H. botryosa* (KJ766403) with identity 99%.

***Heterodermia obscurata***

ITS and mtSSU adopted from NCBI (Figueras et al. 2009, unpublished).

***Heterodermia speciosa***

Our ITS and mtSSU have the closest NCBI BLAST to *H. speciosa* with identities close to 99–100%.

***Hyperphyscia adglutinata***

ITS and mtSSU adopted from NCBI.

***Hypocenomyce scalaris***

Our ITS and mtSSU have the closest NCBI BLAST to *H. scalaris* with identities close to 100%.

***Hypogymnia austerodes***

ITS adopted from Marthinsen et al. (2019) and Divakar et al. (2019), mtSSU from Divakar et al. (2019).

***Hypogymnia bitteri***

ITS adopted from Marthinsen et al. (2019), mtSSU from Divakar et al. (2019).

***Hypogymnia farinacea***

Our ITS has the closest NCBI BLAST to *H. farinacea* with identities close to 100%. Our mtSSU has the closest NCBI BLAST to *H. farinacea* with identities over 99%.

***Hypogymnia hultenii***

ITS adopted from Marthinsen et al. (2019), mtSSU from Divakar et al. (2015) and Miadlikowska et al. (2014).

***Hypogymnia incurvoides***

ITS adopted from Marthinsen et al. (2019), mtSSU from Divakar et al. (2019).

***Hypogymnia physodes***

Our ITS has the closest NCBI BLAST to *H. physodes* with identities up to 100%. Our mtSSU has the closest NCBI BLAST to *H. farinacea* with identities over 99%.

**_Hypogymnia tubulosa_**

Our ITS has the closest NCBI BLAST to *H. tubulosa* with identities close to 100%. Sequence of mtSSU adopted from NCBI.

**_Hypogymnia vittata_**

Our ITS and mtSSU have the closest NCBI BLAST to *H. vittata* with identities 100% or close to 100%.

**_Hypotrachyna afrorevoluta_**

Our ITS sequences have the closest NCBI BLAST to *H. afrorevoluta* with identities 98–100%, mtSSU with identities close to 100%.

**_Hypotrachyna britannica_**

ITS and mtSSU adopted from Divakar et al. (2010).

**_Hypotrachyna lividescens_**

ITS and mtSSU adopted from Šoun et al. (2017).

**_Hypotrachyna minarum_**

ITS and mtSSU adopted from Blanco et al. (2004).

**_Hypotrachyna revoluta_**

Our ITS and mtSSU have the closest NCBI BLAST to *H. revoluta* with identities 100% or close to 100%.

**_Hypotrachyna sinuosa_**

ITS adopted from Marthinsen et al. (2019) and Divakar et al. (2006). Sequence of mtSSU adopted from Divakar et al. (2006).

**_Icmadophila ericetorum_**

Our ITS sequences have the closest NCBI BLAST to *I. ericetorum* with identities over 99%. Sequence of mtSSU adopted from Miadlikowska et al. (2014).

**_Ikaeria serusiauxii_**

ITS adopted from Sipman & Aptroot (2020). Sequences of mtSSU absent from NCBI.

**_Ikaeria aurantiellina_**

Our ITS from a Greek specimen is distinct from NCBI sequences from Macaronesia (only about 92% identical). Other ITS adopted from Sipman & Aptroot (2020). Sequences of mtSSU absent from NCBI.

**_Imshaughia aleurites_**

Our ITS has the closest NCBI BLAST to *I. aleurites* with identities 98.5–100% and our mtSSU with identities over 99%.

**_Inoderma byssaceum_**

ITS sequences absent from NCBI. Numerous attempts to obtain ITS ended up in a single target ITS, with the closest NCBI BLAST to *Cryptothecia subnidulans* (LC516425) with identity 83%. Our identical mtSSU from three specimens have the closest NCBI BLAST to *B. byssaceum* with identities close to 100%.

***Inoderma sorediatum***

ITS absent from NCBI and not obtained by us (despite of numerous attempts). Our identical mtSSU from three specimens have the closest NCBI BLAST to *B. sorediatum* with identities 100% or close to 100%.

***Inoderma subabietinum***

ITS absent from NCBI. Sequence of mtSSU adopted from Frisch et al. (2015).

***Jamesiella anastomosans***

ITS absent from NCBI. Our identical ITS from two specimens have the closest NCBI BLAST to *Gomphillus calycioides* (MK092335) with identity 97%, but the cover only 30%. Our mtSSU has the closest NCBI BLAST to the single available *J. anastomosans* (MZ827304) with identity 100%.

***Japewia aliphatica***

Our ITS sequence matches *J. aliphatica* with identities over 98.5% and our mtSSU with identities close to 100%.

***Japewia gyrophorica* ined. (here described)**

On the basis of ITS and mtSSU data, *Japewia* represents and well-defined genus within *Lecanorales* (Malíček et al. 2020). ITS sequences from four *Japewia gyrophorica* specimens are >99.5% identical and form a supported sister clade to *J. subaurifera* and *J. tornoensis*. Identical mtSSU sequences from three *Japewia gyrophorica* specimens are simultaneously more than 99.5% identical with sequences of *J. tornoensis*, and the two species are not distinguished in the Bayesian tree. The other two species, *J. aliphatica* and *J. subaurifera*, are distinct in mtSSU.

***Japewia subaurifera***

Our ITS sequences have the closest NCBI BLAST to *J. subaurifera* with identities 96–99%. Sequences of mtSSU sequences absent from NCBI. Our mtSSU sequences have the closest NCBI BLAST to *J. tornoensis* with identities about 99%.

***Japewia tornoensis***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Schmull et al. (2011).

***Karschia cezannei***

ITS absent from NCBI. Sequence of mtSSU adopted from Ertz & Diederich (2015).

***Karstenia idaei***

ITS and mtSSU adopted from Vondrák et al. (2022). Records from the Czech Republic under the name *Ramonia chrysophaea* belong here.

***Karstenia rhopaloides***

ITS and mtSSU adopted from Baloch et al. (2009).

***Karstenia* sp.**

Probably an undescribed species characterised by large grey discs immersed in weathered bark of old oaks. Only mtSSU sequenced and the sequence matches *Karstenia* spp. with identities above 95%.

***Lambiella fuscosora***

ITS and mtSSU adopted from Resl et al. (2015).

***Lecanactis abietina***

Our ITS sequences have the closest NCBI BLAST to *Lecanactis abietina* with identities more than 99%. Our mtSSU has the closest NCBI BLAST to the single available *L. abietina* (AY548813) with identities close or equal to 100%.

***Lecania chlorotiza***

ITS and mtSSU adopted from Reese Næsborg et al. (2007).

***Lecania croatica***

Our sequences represent two genotypes 94% identical in ITS and 98.5% in mtSSU. The sequences match *L. croatica* in NCBI with 94–95% in ITS and 98% in mtSSU.

***Lecania dubitans***

ITS and mtSSU adopted from Reese Næsborg et al. (2007).

***Lecania falcata***

ITS adopted from Sérusiaux et al. (2012). Our mtSSU has the closest NCBI BLAST to *L. falcata* (JQ796840) with 99% identity.

***Lecania fuscella***

ITS and mtSSU adopted from Reese Næsborg et al. (2007).

***Lecania naegelii***

ITS adopted from Reese Næsborg et al. (2007) and Kelly et al. (2011). Our mtSSU is identical with *L. naegelii* (AM292741; Reese Næsborg et al. 2007).

***Lecania prasinoides***

Our ITS sequences have the closest NCBI BLAST to sequences of *L. prasinoides* with identities 98–100%. Sequences of mtSSU absent from NCBI and our mtSSU has the closest NCBI BLAST to *L. sambucina* (AM292744) with identity 98.5%.

***Lecania sambucina***

Our ITS has the closest NCBI BLAST to two short NCBI sequences of *L. sambucina* with identities over 99%. Our mtSSU has the closest NCBI BLAST to the single available *L. sambucina* (AM292744) with identity 100%.

***Lecania* sp.**

A common species on bark and wood in maritime shrub habitats of Rhodos. ITS not sequenced yet. The sequence of mtSSU has the closest NCBI BLAST to the saxicolous *L. nylanderiana* (MG925878) with 97.5% identity.

***Lecanographa amylacea***

Our ITS and mtSSU from both morphotypes sensu Ertz et al. (2018a, i.e. including *Buellia violaceofusca*) have the closest NCBI BLAST to *L. amylacea* with 100% identities.

***Lecanographa lyncea***

ITS absent from NCBI. Our ITS is 97% identical to *L. amylacea*, but the closest NCBI BLAST result is *Milospium graphideorum* (NR_132925; identity 99.5%). This BLAST is either caused by misidentification of the host (*Lecanographa*) for its parasite (*Milospium*), or *M. graphideorum* is in fact a sporodochial morphotype of *Lecanographa lyncea*. Our mtSSU has the closest NCBI BLAST to *L. amylacea* with identities about 99%. (The single available mtSSU sequence of *L. lyncea* (MT873944) is 97% identical with our mtSSU.) Morphologically, our sequenced specimen represents a typical richly fertile *L. lyncea*.

***Lecanora aitema***

Our ITS has the closest NCBI BLAST to the single available *L. aitema* (GU480092; Pérez-Ortega et al. 2010) with identity 100%. Sequences of mtSSU absent from NCBI and not obtained by us.

***Lecanora albella***

Our ITS sequces include two genotypes 95% identical. One has the closest NCBI BLAST to *L. albella* with identities 97–99%, the second with identities 93–95%. Our mtSSU sequences from three specimens are almost identical and have the closest NCBI BLAST to *L. albella* with identities close to 100%.

***Lecanora albellula***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *L. albellula* with identities 100% or close to 100%.

***Lecanora allophana***

Our ITS has the closest NCBI BLAST to *L. allophana* with identities 97–99.5%. Sequences of mtSSU adopted from Malíček et al. (2017, 2023).

***Lecanora anopta***

ITS adopted from Ivanovich et al. (2021) and Pérez-Ortega et al. (2010). Our mtSSU sequence has the closest NCBI BLAST to one of *L. anopta* in NCBI (MT939156; Ivanovich et al. 2021) with identity close to 100%. Other two mtSSU sequences of *L. anopta* in NCBI are not closely related.

***Lecanora arachnoidea* ined. (described here)**

ITS sequences from two specimens (type & JV25905) sharing >99.5% identity, and identical mtSSU sequences from the same two specimens were obtained. Short identical mtSSU sequences (of 380 BP length) with 100% match to the type sequence were also generated from the three Ukrainian specimens (JV13908, 13946, 13988). The closest NCBI BLAST matches are to *Lecanorales* spp. with identities up to 84% (ITS) and 95% (mtSSU). Bayesian trees, including the closest known species in the NCBI, show the indistinct relationships of the newly described species with members of *Lecanorales* for both ITS and mtSSU loci.

***Lecanora argentata***

Our ITS sequences match *L. argentata* in NCBI with identities over 99.5%. Sequence of mtSSU adopted from NCBI (MK778529).

***Lecanora barkmaniana***

Our ITS matches *L. barkmaniana* in NCBI with identities 97–100%, our mtSSU with identities 98–100%.

***Lecanora cadubriae***

ITS absent from NCBI. Our two specimens have ITS sequences that are 98.5% identical and they have the closest NCBI BLAST to *Miriquidica gyrizans* with identities up to 87%. Our two mtSSU sekvences are >99% identical and they match the single *L. cadubriae* in NCBI (MZ409497) with the identity about 99%.

***Lecanora caledonica***

ITS and mtSSU adopted from Arup et al. (2023).

***Lecanora carpinea***

Our ITS sequences have the closest NCBI BLAST to *L. carpinea* with identities 90–100%. Our mtSSU sequence has the closest NCBI BLAST to *L. carpinea* with identities over 99%.

***Lecanora cateilea***

ITS adopted from Grube et al. (2004). Sequences of mtSSU absent from NCBI.

***Lecanora cinereofusca***

Our ITS sequences have the closest NCBI BLAST to *L. cinereofusca* with identities 98–99.5%; our mtSSU with identities close or equal to 100%.

***Lecanora circumborealis***

ITS and mtSSU absent from NCBI. Our ITS sequnces are c. 99% identical with our sequences of *L. pulicaris*. Sequences of mtSSU are indistinguishable from *L. pulicaris*.

***Lecanora compallens***

Our ITS sequences have the closest NCBI BLAST to *L. compallens* with identities 99.5–100%. Sequences of mtSSU absent from NCBI. Our mtSSU sekvences have the closest NCBI BLAST to *L. orosthea* and *L. sublivescens* with identities up to 99%.

***Lecanora confusa***

ITS adopted from Pérez-Ortega et al. (2010). Sequences of mtSSU absent from NCBI.

***Lecanora conizaeoides***

ITS and mtSSU adopted from Ivanovich et al. (2021).

***Lecanora excludens***

ITS and mtSSU adopted from Brodo et al. (2019).

***Lecanora expallens***

Our ITS sequences have the closest NCBI BLAST to *L. expallens* with identities 97.5–100%. Our identical mtSSU sequences from two specimens have the closest NCBI BLAST to the single available *L. expallens* (OK465587; Vondrák et al. 2022) with identities 98%.

***Lecanora exspersa***

Our ITS sequences have the closest NCBI BLAST to *L. expersa* with identities 97–99.5%, mtSSU with identities over 99%.

***Lecanora farinaria***

Our ITS and mtSSU sequences adopted from Malíček et al. (2017).

***Lecanora flavoleprosa***

Usually terricolous or saxicolous, rarely on wood or bark. Our ITS and mtSSU sequences adopted from Malíček et al. (2021).

***Lecanora glabrata***

Our ITS has the closest NCBI BLAST to *L. glabrata* with identities 98.5–100%, mtSSU with identities 100%.

***Lecanora glabrescens* ined.**

Undescribed species similar to *L. glabrata*. ITS and mtSSU absent from NCBI. Our sequences have the closest NCBI BLAST to *L. horiza* with identities 91–92% (ITS) and 97–98% (mtSSU).

***Lecanora horiza***

Our ITS has the closest NCBI BLAST to *L. horiza* with identities 98.5–99%. Sequences of mtSSU absent in NCBI. Our mtSSU has the closest NCBI BLAST to *L. allophana* with identities about 99%.

***Lecanora hybocarpa***

ITS and mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *L. pulicaris* with identities up to 98%. ITS not obtained by us.

***Lecanora hypoptoides***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Lecidea turgidula* and *L. leprarioides* with identities 91–92%. Our mtSSU has the closest NCBI BLAST to *Lecanorales* spp. with identities up to 95%.

***Lecanora chlarotera***

Our ITS sequences have the closest NCBI BLAST to *L. chlarotera* with identities 93–100%, our mtSSU with identities 100%.

***Lecanora impudens***

Sequences ITS and mtSSU adopted from Vondrák et al. (2022).

***Lecanora intumescens***

Our identical ITS sequence from two specimens have the closest NCBI BLAST to *L. intumescens* with identities over 99%. Our almost identical mtSSU from two specimens have the closest NCBI BLAST to *L. intumescens* with identities 96–100%.

***Lecanora leptyrodes***

Our ITS sequences have the closest NCBI BLAST to sequences called *L. carpinea* in NCBI with identities up to 100%. The closest NCBI sequences, however, belong to *L. leptyrodes* in fact (Malíček, in litt.). Our mtSSU has the closest NCBI BLAST to *L. leptyrodes* with identities 98.5–100%.

***Lecanora lividocinerea***

Our ITS matches *L. lividocinerea* in NCBI with identities 99.5–100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Lecanora* sect. *subfusca* spp. with identities up to 96%.

***Lecanora mughicola***

ITS adopted from Ivanovich et al. (2021). Our mtSSU has the closest NCBI BLAST to sequences *L. mughicola* with identities close to 100%.

***Lecanora mughosphagneti***

ITS and mtSSU absent from NCBI. Our ITS sequences have the closest NCBI BLAST to *L. albella* with identities 91–92%. According to our data, *L. norvegica* is closely related.

***Lecanora norvegica***

ITS and mtSSU absent from NCBI. Our ITS sequences from three specimens have the closest NCBI BLAST to *L. albella* with identities 91–92%. According to our data, *L. mugosphagneti* is closely related. Sequences of mtSSU not obtained by us.

***Lecanora phaeostigma***

Our ITS sequences from four specimens represent two diverging genotypes, c. 92% identical. Two ITS are identical with *L. phaeostigma* (OK332975) and other two are 91–92% identical with OK332975. Sequences of mtSSU absent from NCBI. Our mtSSU sequences represent two genotypes 99% identical. Both have the closest NCBI BLAST to *Umbilicariomycetidae*, with identities up to 91%.

***Lecanora populicola***

ITS adopted from Kelly et al. (2011). Sequences of mtSSU absent from NCBI and not obtained by us.

***Lecanora praesistens***

ITS adopted from Mark et al. (2016). Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *L. pulicaris* with identities close to 99%.

***Lecanora pulicaris***

Our ITS has the closest NCBI BLAST to *L. pulicaris* with identities over 99% and mtSSU with identities close to 100%.

***Lecanora rubicunda***

ITS and mtSSU absent from NCBI. Our ITS sequences have the closest NCBI BLAST to *Lecanora* sect. *subfusca* spp. with identities up to 87%, mtSSU with identities up to 97.5%.

***Lecanora salicicola***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *L. cenisia* and *L. exspersa* with identities about 92%. Our mtSSU has the closest NCBI BLAST to *L. cenisia* with identities about 99%.

***Lecanora saligna***

Our ITS and mtSSU adopted from Vondrák et al. (2022).

***Lecanora sarcopidoides***

Our ITS sequences have the closest NCBI BLAST to *L. sarcopidoides* with identities 99–100%, our mtSSU with identities close or equal to 100%.

***Lecanora sinuosa***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *L. praesistens* (KX132991; Mark et al. 2016) with identity 95.5%. Our mtSSU has the closest NCBI BLAST to *L. pulicaris* with identities up to 99%.

***Lecanora stanislai***

Sequence ITS adopted from Singh et al. (2019), mtSSU adopted from Vondrák et al. (2018) and Hofmeister et al. (2022).

***Lecanora strobilina***

ITS adopted from Pérez-Ortega & Kantvilas (2018) and mtSSU from Hofmeister et al. (2022).

***Lecanora subcarpinea***

ITS adopted from Grube et al. (2004). Our mtSSU has the closest NCBI BLAST to sequences called *L. carpinea* with identities up to 100%.

***Lecanora subintricata***

ITS and mtSSU adopted from Ivanovich et al. (2021).

***Lecanora sublivescens***

ITS and mtSSU adopted from NCBI (Weber et al.; unpublished).

***Lecanora subravida***

ITS and mtSSU adopted from Ivanovich et al. (2021).

***Lecanora subsaligna***

Our ITS has the closest NCBI BLAST to *L. subsaligna* with identities about 99%, mtSSU with identities close to 100%.

***Lecanora substerilis***

Our ITS has the closest NCBI BLAST to *L. substerilis* (KY548037) with identity over 99%. Sequence of mtSSU adopted from Malíček et al. (2017).

***Lecanora symmicta***

Our ITS sequences match *L. symmicta* in NCBI with identities 97–99%, our mtSSU with identities 100%.

***Lecanora thysanophora***

Our two ITS sequences represent two diverging genotypes, one has the closest NCBI BLAST to *L. thysanophora* with identities 98–99%, the second with identities 93–95%. Our almost identical mtSSU sequences from four specimens have the closest NCBI BLAST to *L. thysanophora* with identities close or equal to 100%.

***Lecanora varia***

Our ITS matches numerous NCBI sequences of *L. varia* with identities about 97%. Reliable sequences of mtSSU absent from NCBI and not sequenced by us.

***Lecanora variolascens***

ITS and mtSSU adopted from Malíček et al. (2017).

***Lecanorales* sp.**

This lichen is from mossy bark of *Pinus mugo* in subalpine zone of Ukrainian Carpathians. It resembles *Bilimbia*, *Bryobilimbia* or *Biatora*, but its ITS has no close relatives in NCBI. The closest NCBI BLAST is to *Lecanorales* (e.g. *Micarea*, *Japewia*, etc.), but with identities only up to 90%. Sequences of mtSSU not obtained by us.

***Lecidea albofuscescens***

ITS and mtSSU absent from NCBI. Our identical ITS sequences of two specimens have no close relatives in NCBI (*Lecanorales* spp. with identities up to 84%). Our mtSSU has the closest NCBI BLAST to *Lecanorales* spp. with identities up to 88%. According to our data, our mtSSU are close to some *Malmideaceae* with identities above 90%.

***Lecidea albohyalina***

We have sequenced a richly fertile specimen as well as a specimen with numerous pycnidia only and both have ITS and mtSSU sequences close to identical. Our sequences BLAST to the only *L. albohyalina* in NCBI (Printzen 2014), with identities 98.5–100% in ITS and 100% in mtSSU.

***Lecidea apochroeella***

ITS and mtSSU absent from NCBI. We obtained only mtSSU and it has the closest NCBI BLAST to *L. hypopta* with the identity about 91%. The taxonomic identity of our specimen is not confirmed.

***Lecidea betulicola***

ITS and mtSSU absent from NCBI. Our ITS and mtSSU are close to our sequences of *L. coriacea* (= *Cheiromycina coriacea/C. petri*) with the identity 95% in ITS and c. 98.5% in mtSSU.

**_Lecidea erythrophaea_**

ITS and mtSSU absent from NCBI. Our ITS sequences have the closest NCBI BLAST to *Lecidea plebeja* with identities about 85%. Sequence of mtSSU not obtained by us.

**_Lecidea huxariensis_**

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Lecanorales* spp. with identities up to 90.5%, our mtSSU with identities up to 91%.

**_Lecidea hypopta_**

ITS absent from NCBI. We obtained only mtSSU and our two sequences have the closest NCBI BLAST to the only NCBI sequence of *L. hypopta* (FJ644537, Stenroos et al. 2009).

**_Lecidea leprarioides_**

No mtSSU sequences in NCBI so far. Our ITS has the closest NCBI BLAST to the single *L. leprarioides* (HQ650666) sharing identity 100%. Our mtSSU has the closest NCBI BLAST to the related species, *L. turgidula* (KJ766424), sharing identity 96%.

**_Lecidea malmeana_**

ITS absent from NCBI. Sequence of mtSSU adopted from Spribille et al. (2020).

**_Lecidea_ cf. _myriocarpella_**

ITS and mtSSU absent from NCBI. We obtained only ITS and our sequence BLASTs to various *Lecanorales* with identities up to 90%. The taxonomic identity of our specimen is not confirmed.

**_Lecidea nylanderi_**

Our ITS sequences BLAST with the single reliable *L. nylanderi* in NCBI (HQ650667; Schmull et al. 2011) with identities above 99%. Our identical mtSSU sequences from two specimens match *L. nylanderi* (HQ660572, Schmull et al. 2011) with the identity over 99%, but HQ660572 lacks several short indels and possibly is distorted by internal cutouts.

**_Lecidea plebeja_**

ITS and mtSSU sequences adopted from Vondrák et al. (2022).

**_Lecidea roseotincta_**

ITS and mtSSU sequences adopted from Schmull et al. (2011).

**_Lecidea sphaerella_**

Our ITS sequence matches *L. sphaerella* in NCBI with identities close to 100% and our mtSSU with the identity 100%.

**_Lecidea strasseri_**

ITS and mtSSU absent from NCBI. Our ITS sequences blast with *L. berengeriana* in NCBI with identities 91–100%. Our two identical mtSSU sequences have the closest NCBI BLAST to *L. berengeriana* (HQ660562) with the identity 90%.

***Lecidea turficola***

ITS and mtSSU absent from NCBI. Our ITS and mtSSU have the closest NCBI BLAST to *Lecidoma demissum* (HQ650630; Schmull et al. 2011) with the identity 92.3%; our mtSSU to *Lecidoma demissum* (DQ986881; Miadlikowska et al. 2006) with the identity 92.3%.

***Lecidea turgidula***

Our ITS sequences are represented by two genotypes. Both have the closest NCBI BLAST to *L. turgidula* (FR799212; Kelly et al. 2011) with identities 99.5% and respectively 96%. Our mtSSU matches *L. turgidula* (KJ766424; Miadlikowska et al. 2014) with the identity 99.5%.

***Lecidella achristotera***

Morphological recognition of this species from *L. elaeochroma* based on an inspersed hymenium is supported by ITS and mtSSU data. Our two identical ITS are less than 97% identical with our *L. elaeochroma* sequences and our three almost identical mtSSU are about 99% identical with *L. elaeochroma*.

***Lecidella albida***

Our ITS and mtSSU match NCBI sequences (Vondrák et al. 2022) with identities 97% and 100% respectively.

***Lecidella* cf. *subviridis***

The sequenced specimen, matching *L. subviridis* by its morphology and TLC data, is in fact not related to other *Lecidella* and has no closest relatives in NCBI. Its ITS sequence has closest NCBI BLAST results with various *Lecanorales* with identities up to 90%. Sequences of mtSSU not obtained.

***Lecidella elaeochroma* f. *sorediata***

ITS and mtSSU absent from NCBI. We obtained only mtSSU which is identical with our sequences of *L. achristotera*. It is not clear, if *L. elaeochroma* s.str. produces sorediate morphotypes as well.

***Lecidella elaeochroma* var. *flavicans***

ITS and mtSSU absent from NCBI. Our ITS matches *L. elaeochroma* s.lat. sequences with identities up to 97.5%. Sequences of mtSSU not obtained.

***Lecidella elaeochroma***

Our sequences represent two genotypes sharing about 98% identity in ITS and 99% in mtSSU. The ITS sequences have the closest NCBI BLAST to *L. elaeochroma* sharing identities 91–100%. Our mtSSU has the closest NCBI BLAST to *Lecidella* spp. with identities up to 98.5%.

***Lecidella flavosorediata***

Our ITS and mtSSU match NCBI sequences (Vondrák et al. 2022) with identities 99–100% and 100% respectively.

***Lecidella scabra***

ITS adopted from Mark et al. (2016). Sequences of mtSSU not available in NCBI.

***Lecidella* sp.**

Known from Rhodos, occurring on bark in shrub communities influenced by salt spray. ITS matches *L. elaeochroma* s.lat. sequences with identities up to 96%, mtSSU with identities up to 99%. It differs from *L. elaeochroma* in an indistinct thallus.

***Lepra albescens***

Our ITS matches *P. albescens* in NCBI with identities over 95%, our mtSSU with identities 100% or close.

***Lepra amara***

Our ITS sequences match *P. amara* in NCBI with identities 99–100%. Our mtSSU has the closest NCBI BLAST to *P. mammosa* (AY212854) with the identity 99.5%; available sequences of *P. amara* are less than 97.5% identical.

***Lepra amara* var. *isidiata***

Our ITS and mtSSU are identical or almost identical with our sequences of *P. amara*. Formation of isidia is probably a character triggered in *P. amara* in xeric conditions.

***Lepra multipuncta***

ITS and mtSSU adopted from Park et al. (2017).

***Lepra ophthalmiza***

Reliable ITS absent from NCBI. (KU894636 and KU894637 named *P. ophthalmiza* are apparently *P. multipuncta*.) Our identical ITS from two different extractions of a single specimen have close NCBI BLAST results to various *Ostropomycetidae*, but not *Pertusariales*. Although the BLAST result is suspicious, we consider the sequence obtained by repeated Sanger sequencing of independent extractions to be reliable. Our mtSSU sequences from two different extractions of a single specimen were 98% identical (i.e. differ in substitutions at 17 nucleotide positions). It suggests intragenomic variability in mtSSU. Both sequences have the closest NCBI BLAST match to *Pertusaria panyrga* (AY567994, Schmitt & Lumbsch 2004) with identity 97–98%. The second closest BLAST is *P. ophthalmiza* (AY567993) with identity 94–95%. As the morphology of our specimen matches *P. ophthalmiza*, we did not identify it with ecologically and morphologically different *P. panyrga*.

***Lepra trachythallina***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *P. corallina* with identities 96.5%. Sequence of mtSSU not obtained.

***Lepra waghornei***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *P. submultipuncta* from the Far East with identities 98%. Sequence of mtSSU not obtained.

***Lepraria eburnea***

Sequence ITS adopted from Ekman & Tønsberg (2002), mtSSU sequence adopted from Lendemer & Hodkinson (2013).

***Lepraria elobata***

Our ITS matches *L. elobata* in NCBI with identities 97–99.5%. Sequence of mtSSU adopted from Lendemer & Hodkinson (2013).

***Lepraria finkii***

Our ITS match *L. finkii* in NCBI with identities 90–100%. The large variability in sequences suggests more species being identified as *L. finkii*. Sequences of mtSSU adopted from the NCBI.

***Lepraria incana***

Our ITS matches *L. incana* in NCBI with identities 98–100%. Sequence of mtSSU adopted from Miadlikowska et al. (2006).

***Lepraria jackii***

Our ITS sequences have the closest NCBI BLAST to *L. jackii* with identities over 99%. Reliable mtSSU sequences absent from NCBI. Our mtSSU has the closest NCBI BLAST to *L. caesioalba* with identities 99.5%.

***Lepraria rigidula***

ITS adopted from Weckesser et al. (2021) and mtSSU from Lendemer & Hodkinson (2013).

***Lepraria umbricola***

Our ITS match *L. umbricola* with identities over 99.5%. Reliable mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Lepraria* spp. with identities up to 99%.

***Lepraria vouauxii***

ITS adopted from Ekman & Tønsberg (2002) and mtSSU from Lendemer & Hodkinson (2013).

***Leprocaulon microscopicum* (= *Leprocaulon quisquiliare*)**

Usually saxicolous, but epiphytic occurrences (often on tree bases) are not rare in sparse forests near rocky outcrops. ITS adopted from Vondrák et al. (2022), mtSSU from Miadlikowska et al. (2014).

***Leprocaulon nicholsiae***

Usually saxicolous, but epiphytic occurrences (often on tree bases) are not rare in sparse forests near rocky outcrops. Our ITS match *L. nicholsiae* in NCBI with identities 95–100%. Sequence of mtSSU adopted from Tripp & Lendemer (2019).

***Leptogium brebissonii***

Sequences of ITS absent from NCBI. mtSSU adopted from Otálora et al. (2010).

***Leptogium burnetiae***

Sequences of ITS absent from NCBI. mtSSU adopted from Otálora et al. (2010).

***Leptogium cochleatum***

ITS adopted from Marthinsen et al. (2019). Reliable mtSSU absent from NCBI. (mtSSU from a Thayland, KT947100, probably belongs to a different species.)

***Leptogium corticola***

Sequences of ITS absent from NCBI. Sequences of mtSSU adopted from Otálora et al. (2010).

***Leptogium cyanescens***

ITS adopted from Otálora et al. (2010), mtSSU from Jayalal et al. (2014).

***Leptogium hibernicum***

ITS and mtSSU adopted from Bjelland et al. (2017).

***Leptogium juressianum***

ITS and mtSSU adopted from Kaasalainen et al. (2021).

***Leptogium saturninum***

ITS adopted from Marthinsen et al. (2019), mtSSU from Schultz (HBG-Schultz08809; unpublished).

***Leptorhaphis atomaria***

Sequences of ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST with *Xenocylindrosporium margaritatum* (*Phaeomoniellales*) with identities about 98%. Our mtSSU sequence has the closest NCBI BLAST to *Chaetothyriomycetes* spp.

***Leptorhaphis epidermidis***

Sequences of ITS and mtSSU absent from NCBI. We only sequenced a part of ITS (ITS2 region), which is more than 90% identical with other *Leptorhaphis* sequences.

***Leptorhaphis maggiana***

Sequences of ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST with *Xenocylindrosporium* sp. (*Phaeomoniellales*) with identities about 98%, but with low cover (c. 50%). Our mtSSU sequence has the closest NCBI BLAST to *Chaetothyriomycetes* spp.

***Letharia vulpina***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Lichenomphalia umbellifera***

ITS adopted from Vondrák et al. (2022). Sequences of mtSSU absent from NCBI and not sequenced by us.

***Lithothelium hyalosporum***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Lithothelium* spp. and *Pyrenula* spp. with identities up to 84%. Our mtSSU has the closest NCBI BLAST to *Lithothelium* and *Serusiauxia inexpectata*. The closest is *L. septemseptatum* with the identity 95%.

***Lithothelium phaeosporum***

ITS adopted from Vondrák et al. (2022) and our mtSSU match *L. phaeosporum* in NCBI (Vondrák et al. 2022) with identities over 99%.

***Lithothelium septemseptatum***

Our ITS and mtSSU sequences match the previously published sequences in Vondrák et al (2022) with almost 100% identities.

***Lobaria immixta***

ITS and mtSSU adopted from Cornejo & Scheidegger (2010).

***Lobaria pulmonaria***

Our ITS and mtSSU match *L. pulmonaria* in NCBI with identities 99–100%.

***Lobarina scrobiculata***

ITS adopted from Marthinsen et al. (2019), mtSSU from Lutzoni et al. (2004).

***Lopadium disciforme***

ITS absent from NCBI. Our ITS sequence has no close relatives in NCBI, the closest sequences with identities up to 93% belong to *Ramalinaceae*, but have low coverage, up to 24%. Our almost identical mtSSU sequences from two specimens match *L. disciforme* in NCBI (AY756373; Ekman et al. 2008) with 100% identity.

***Loxospora cismonica***

Our ITS matches the only *L. cismonica* sequence in NCBI (Schmull et al. 2011) with the identity 95%. Our mtSSU matches *L. cismonica* (DQ986899; Miadlikowska et al. 2006) with the identity 99%.

***Loxospora cristinae***

Our ITS and mtSSU sequences match *L. cristinae* in NCBI with identities over 99%.

***Loxospora elatina***

Our ITS matches *L. elatina* in NCBI with identities over 99.5%, our mtSSU matches the only available *L. elatina* (KR017350; Resl et al. 2015) with 100% identity.

***Macentina abscondita***

ITS sequences absent from NCBI. Our ITS sequences from two specimens are 97% identical and have the closest NCBI match to *Psoroglaena stigonemoides* (MZ159334) with the identities 97 and 98%, but with the cover 37% only. Our mtSSU from two specimens are almost 99% identical and BLAST with various *Verrucariaceae* in NCBI with identities up to 85%. Muggia et al. (2010) provided one short mtSSU of *M. abscondita* (GU121614; 523BP), which is only below 90% identical with our sequences.

***Maronea constans***

ITS adopted from NCBI (Thor et al., unpublished) and mtSSU from Zahradníková et al. (2018).

***Megalaria grossa***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Ekman et al. (2008).

***Megalaria laureri***

ITS not available in NCBI. Sequence of mtSSU adopted from Spribille et al. (2020).

***Megalaria pulverea***

Our ITS sequences match *M. pulverea* in NCBI with identities over 99.5%. Sequences of mtSSU not available in NCBI and not obtained by us.

***Megalospora porphyritis***

ITS and mtSSU adopted from Urbanavichus et al. (2020).

***Megalospora tuberculosa***

ITS and mtSSU adopted from NCBI (Bogomazova & Yahr 2018, unpublished).

***Megaspora rimisorediata***

ITS adopted from NCBI (Ismayil 2015; unpublished). Sequences of mtSSU absent from NCBI.

***Megaspora verrucosa***

ITS adopted from Ivanova & Hafellner (2002) and mtSSU from Nordin et al. (2010).

***Melanelixia epilosa***

Our ITS and mtSSU match *M. epilosa* in the sense of Leawitt et al. (2016) with 100% identity or close.

***Melanelixia glabra***

ITS and mtSSU sequences adopted from Leawitt et al. (2016).

***Melanelixia glabratula***

Our ITS matches *M. glabratula* in NCBI with identities over 99.5%. Our mtSSU match sequences named *M. fuliginosa* (i.e. either *M. fuliginosa* s.str. or the closely related *M. glabratula*) with identities 100% or close.

***Melanelixia subargentifera***

Our ITS and mtSSU match *M. subargentifera* in NCBI with identities over 99.5%.

***Melanelixia subaurifera***

Our ITS and mtSSU match *M. subaurifera* in NCBI with identities over 99.5%.

***Melanohalea elegantula***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Melanohalea exasperata***

Our ITS and mtSSU match *M. exasperata* in NCBI with identities 98–99.5% and 99–99.5% respectively.

***Melanohalea exasperatula***

ITS and mtSSU sequences adopted from Leawitt et al. (2016).

***Melanohalea laciniatula***

ITS adopted from Kelly et al. (2011) and mtSSU from Leawitt et al. (2016).

***Melanohalea olivacea***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Miadlikowska et al. (2014).

***Melanohalea septentrionalis***

ITS adopted from Marthinsen et al. (2019), mtSSU from Blanco et al. (2004).

***Melaspilea bagliettoana***

ITS and mtSSU absent from NCBI. Our identical ITS sequences from two specimens have the closest NCBI BLAST to *Morenoina* (*Dothideomycetes*) with identities 85%. Our mtSSU has the closest NCBI BLAST to *Petrophila* spp. and *Lichenothelia* spp. (*Dothideomycetes*) with identities up to 91%.

***Melaspileella proximella***

Our ITS and mtSSU adopted from Vondrák et al. (2018).

***Menegazzia subsimilis***

ITS adopted from Marthinsen et al. (2019). Sequence of mtSSU not available in NCBI.

***Menegazzia terebrata***

Our ITS match *M. terebrata* in NCBI with identities 99–100%. Sequence of mtSSU adopted from Arup et al. (2007).

***Micarea adnata***

Our ITS has the closest NCBI BLAST to the single available *M. adnata* (AY756468) with identity close to 100% and our mtSSU has the closest NCBI BLAST to the single available *M. adnata* (KX459344) with identity 100%. Other *Micarea* species are less than 90% identical.

***Micarea botryoides***

Muscicolous species usually occurring on damp rocks, but rarely also on wood and bark. (The similar epiphytic species with shorter pycnidia and occurring on bases of spruce trunks, earlier called *M. botryoides*, is here recognised as *Micarea* sp. 7.) ITS sequences adopted from Marthinsen et al. (2019) and Andersen & Ekman (2004). Sequence of mtSSU adopted from Andersen & Ekman (2005).

***Micarea byssacea***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *M. byssacea* with identities over 99%.

***Micarea cinerea***

ITS adopted from Andersen & Ekman (2004), mtSSU from Andersen & Ekman (2005).

***Micarea contexta***

Reliable ITS and mtSSU absent from NCBI. We only obtained mtSSU which is close to *M. substipitata* in NCBI and to *M. contexta* from the Far East (MN166047; Konoreva et al. 2019a) with identities 92–93%.

***Micarea coppinsii***

ITS absent from NCBI. Our ITS sequence has the closest NCBI BLAST to *M. cinerea* and *M. peliocarpa* with identities about 90%. Sequence of mtSSU adopted from Vondrák et al. (2022).

***Micarea czarnotae***

Our ITS sequences have the closest NCBI BLAST to the sequence of *M. czarnotae* (MG521557) with identity close to 100%. Our mtSSU has the closest NCBI BLAST to *M. czarnotae* with identities over 99%.

***Micarea deminuta***

ITS adopted from Andersen & Ekman (2004), mtSSU from Andersen & Ekman (2005).

***Micarea denigrata***

Our mtSSU sequences represent two genotypes 95–96% identical. Both have the closest NCBI BLAST to *M. denigrata* with identities 95–100%. Our single ITS has the closest NCBI BLAST to *M. denigrata* with identities 96–100%.

***Micarea doliiformis***

ITS adopted from Schmull et al. (2011), mtSSU from Sérusiaux et al. (2010).

***Micarea elachista***

Our ITS has the closest NCBI BLAST to *M. elachista* (MG521548) with identity over 99%, mtSSU to *M. elachista* with identities 100%.

***Micarea eximia***

ITS and mtSSU adopted from Kantelinen et al. (2021).

***Micarea fallax***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *M. fallax* with identities over 99%.

***Micarea fennica***

ITS and mtSSU adopted from Launis & Myllys (2019).

***Micarea flavoleprosa***

Sequence of mtSSU adopted from Launis et al. (2019a). ITS absent from NCBI and not obtained by us.

***Micarea globulosella* TYPE1**

Type1 usually occurs on bark in montane forests. ITS adopted from Launis et al. (2019a). Our mtSSU sequences represent two genotypes and both have the closest NCBI BLAST to *M. globulosella* with identities either almost 100% or 95–96%.

***Micarea globulosella* TYPE2**

Type2 is known from wood in low altitudes. Our ITS has the closest NCBI BLAST to *M. globulosella* (OK332999; Vondrák et al. 2022) with identity over 99%. TYPE1 is <90% identical and probably represents a separate species. Sequence of mtSSU not obtained by us.

***Micarea hedlundii***

ITS adopted from Launis et al. (2019a). Our mtSSU has the closest NCBI BLAST to *M. hedlundii* with identities 98–100%.

***Micarea herbarum***

ITS sequences not available in NCBI and not sequenced by us. Sequences of mtSSU sequences adopted from Malíček (2022b), van den Boom et al. (2017) and Czarnota & Guzow-Krzemińska (2010; as *Micarea nowakii*). Variability in 27 nucleotide positions was detected in the three sequences.

***Micarea hypoviolascens***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *M. denigrata* with identities 83–84% and our mtSSU to *M. contexta* with the identity 91.5%.

***Micarea isidioprasina***

Our ITS sequence represent two diverging genotypes and both have the closest NCBI BLAST to *M. isidioprasina* with identities about 99%, respectively 94–95%. Sequence of mtSSU adopted from Guzow-Krzemińska et al. (2019).

***Micarea laeta***

ITS and mtSSU sequences adopted from Launis et al. (2019b).

***Micarea lignaria***

ITS adopted from van den Boom et al. (2017). Our mtSSU matches *M. lignaria* in NCBI with 100% identities.

***Micarea melaena***

Reliable ITS absent from NCBI. The single available sequence (AY756483) is a fungal contaminant. Our mtSSU is identical with the NCBI sequence called *M. contexta* from the Far East (MN166047; Konoreva et al. 2019a) which probably represents *M. melaena*. (The single NCBI sequence named *M. melaena* (AY567743) is not related to ours and has the closest NCBI BLAST to *Micarea myriocarpa* with the identity 94%.)

***Micarea melaeniza***

Reliable ITS and mtSSU absent from NCBI. The single ITS under this name (AY756484) is *Lepraria*. Our ITS sequences are close to our sequences of *M. nigella* and mtSSU is even identical with *M. nigella*. The closest NCBI BLAST match is *M. deminuta* with identities up to 90% (ITS) and 97% (mtSSU).

***Micarea melanobola***

ITS and mtSSU sequences adopted from Launis et al. (2019a).

***Micarea microareolata***

ITS adopted from Launis et al. (2019b). Our mtSSU has the closest NCBI BLAST to *M. microareolata* with identities 94–100%.

***Micarea micrococca***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *M. micrococca* with identities close or equal to 100%.

***Micarea microsorediata***

ITS adopted from Guzow-Krzemińska et al. (2019). Our mtSSU sequence has the closest NCBI BLAST to *M. microsorediata* with identities close or equal to 100%.

***Micarea misella***

Our ITS sequence has the closest NCBI BLAST to *M. misella* with identities 97–98%, mtSSU with identities close or equal to 100%.

***Micarea nigella***

Reliable ITS and mtSSU absent from NCBI. The single ITS under this name (AY756488) is a fungal contamination. Our ITS sequences are close to our sequences of *M. melaeniza* and mtSSU is even identical with *M. melaeniza*. The closest NCBI BLAST match is *M. deminuta* with identities up to 93% (ITS) and 97% (mtSSU).

***Micarea nitschkeana***

Reliable ITS absent from NCBI. The single ITS under this name (AY756489) is a fungal contamination. Our ITS sequence has the closest NCBI BLAST to *M. denigrata* with identities 86–87%. Our mtSSU has the closest NCBI BLAST to *M. nitschkeana* (EF453685) with 100% identity.

***Micarea nowakii***

ITS absent from NCBI. Our ITS sequences represent two diverging genotypes 95% identical and both have the closest NCBI BLAST to *M. melanobola* with identities up to 92%. Our mtSSU represent two diverging genotypes 98% identical. One has the closest NCBI BLAST to most NCBI sequences of *M. nowakii* with identities over 99%, the second is identical to *M. nowakii* (EF453665), but only 97% identical with other NCBI sequences of *M. nowakii*.

***Micarea pauli***

ITS and mtSSU sequences adopted from Guzow-Krzemińska et al. (2019).

***Micarea peliocarpa***

Our ITS has the closest NCBI BLAST to *M. peliocarpa* with identities 94–100%, our mtSSU with identities over 99%.

***Micarea perparvula***

Sequence of mtSSU adopted from Malíček (2022a). ITS absent from NCBI and not obtained by us.

***Micarea prasina***

Our ITS and mtSSU represent two diverging genotypes. All genotypes have the closest NCBI BLAST to *M. prasina* with identities 95 and 100% in ITS and 98 and 100% in mtSSU.

***Micarea pseudomicrococca***

ITS and mtSSU sequences adopted from Launis et al. (2019b).

***Micarea pusilla***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Micarea pycnidiophora***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Micarea* spp. with identities up to 90%. Our mtSSU je identical to the single available *M. pycnidiophora* (KX459364).

***Micarea soralifera***

ITS adopted from Guzow-Krzeminska et al. (2016). Our mtSSU sequences have the closest NCBI BLAST to *M. soralifera* with identities over 98%.

***Micarea* sp. 1**

Only mtSSU sequenced with the closest NCBI BLAST to *Micarea meridionalis* and *M. soralifera* with identities about 96.5%. Possibly a diverging genotype of *M. soralifera*.

***Micarea* sp. 2**

Only mtSSU sequenced with the closest NCBI BLAST to *Micarea prasina* agg. with identities up to 93.5%.

***Micarea* sp. 3**

Only mtSSU sequenced. The closest match is to our *Micarea* sp. 1 which is 95.5% identical. The closest NCBI BLAST match is *M. soralifera* with identities about 96.5%.

***Micarea* sp. 4**

Only mtSSU sequenced with the closest NCBI BLAST to *M. microareolata* with identities 94.5–95.5%. Possibly a diverging genotype of *M. microareolata*.

***Micarea* sp. 5**

Only ITS sequenced with the closest NCBI BLAST to *M. isidioprasina* with identities 92–93%. Possibly a diverging genotype of *M. isidioprasina*.

***Micarea* sp. 6**

A lichen with delicately coralloid thallus similar to *Bacidia squamellosa*. Only ITS sequenced with the closest NCBI BLAST to *M. micrococca* agg. with identities up to 92%.

***Micarea* sp. 7**

A common species on trunk bases of young spruces in managed forests with shortly stipitate pycnidia resembling young pycnidia of *M. botryoides*. Our sequences have the closest NCBI BLAST to *M. deminuta* with identities 90% (ITS) and 97% (mtSSU).

***Micarea* sp. 8**

A lichen from Scotland identified as *M. eximia* by B. Coppins. Sequences of *M. eximia* in NCBI are not similar (Kantelinen et al. 2021). Our mtSSU has the closest NCBI BLAST to *M. contexta* and *M. substipitata* with identities up to 93%. ITS not obtained.

***Micarea stipitata***

ITS sequence not available in NCBI and not sequenced by us. Sequence of mtSSU adopted from van den Boom et al. (2017).

***Micarea substipitata***

Our ITS sequence has the closest NCBI BLAST to *M. substipitata* with identities over 98%. Sequence of mtSSU adopted from Vondrák et al. (2022).

***Micarea synotheoides***

ITS adopted from Andersen & Ekman (2004), mtSSU from Andersen & Ekman (2005).

***Micarea tomentosa***

Sequence of mtSSU adopted from Vondrák et al. (2022). ITS absent from NCBI and not obtained by us.

***Micarea viridileprosa***

ITS adopted from Vondrák et al. (2022). Our mtSSU has the closest NCBI BLAST to *M. viridileprosa* with identities close or equal to 100%.

***Micarea xanthonica***

Reliable ITS absent from NCBI. (KX132957, named *M. xanthonica* by Mark et al. 2016, refers to *M. viridileprosa*.) Sequence of mtSSU adopted from Andersen & Ekman (2005).

***Microcalicium ahlneri***

Sequence of mtSSU adopted from Vondrák et al. (2022). ITS absent from NCBI and not obtained by us.

***Microcalicium arenarium***

ITS adopted from Prieto et al. (2013). Sequence of mtSSU adopted from Vondrák et al. (2022).

***Microcalicium disseminatum***

Our ITS has the closest NCBI BLAST to *M. disseminatum* with identities close or equal to 100%, mtSSU with identities 100%.

***Microcalicium loraasii***

ITS (OK332872) and mtSSU (OK465491) adopted from Vondrák et al. (2022).

***Microcalicium minutum***

ITS (MZ969000) and mtSSU (OK019731) adopted from Vondrák et al. (2022).

***Miriquidica* cf. *majae***

ITS and mtSSU absent from NCBI. Only mtSSU obtained and our sequence has the closest NCBI BLAST to *Miriquidica* spp., *Protoparmelia* spp. and *Lecanora* spp. with identities up to 97%.

***Multiclavula mucida***

ITS sequence adopted from NCBI. mtSSU absent from NCBI and not obtained by us.

***Mycobilimbia carneoalbida***

Our ITS has the closest NCBI BLAST to *M. carneoalbida* with identities 98.5–100%, mtSSU with identities close or equal to 100%.

***Mycobilimbia epixanthoides***

Our ITS sequences represent two genotypes 92% identical. One of them has the closest NCBI BLAST to *M. epixanthoides* with identities 98–100% and the second with 92–93%. Our mtSSU sequences also represent two genotypes 98% identical. One has the closest NCBI BLAST to *M. epixanthoides* with identities 98–100% and the second with 96–97%.

***Mycobilimbia pilularis***

Our ITS matches with *M. pilularis* in NCBI with identities 100%. Sequence of mtSSU adopted from Printzen (2014).

***Mycobilimbia tetramera***

Our ITS and mtSSU sequences match *M. tetramera* in NCBI with identities over 99%.

***Mycoblastus affinis***

Our ITS has the closest NCBI BLAST to *M. affinis* with identities close to 100%. Our mtSSU has the closest NCBI BLAST to *Mycoblastus affinis* (DQ899307) with identity close to 100%.

***Mycoblastus alpinus***

Our ITS sequence has the closest NCBI BLAST to *M. affinis* and *M. alpinus* with identities over 99%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *M. affinis* (DQ899307) with identity 99.5%.

***Mycoblastus caesius***

ITS and mtSSU absent from NCBI. Our ITS sequences represent three genotypes 94% identical. Our mtSSU represent two genotypes 97% identical. *Mycoblastus caesius* does not belong to *Mycoblastus* s.str. (*Mycoblastaceae*). We have obtained ITS and mtSSU sequences from a number of specimens and it appears that *M. caesius* is placed in *Lecanorales*, but its family affiliation is not clear. Its highest NCBI BLAST hits are only around 86% in both mtSSU and ITS with e.g. *Pilocarpaceae*, *Psoraceae* and *Ramalinaceae*, but these results are rather irrelevant.

***Mycoblastus sanguinarius***

Sequences from one of our specimens (PRA-Vondrák23794) match *M. sanguinarius* in NCBI with identities 97–100% (ITS) and 99–100% (mtSSU). The specimen from the Caucasus (Herb. Malíček10999; MT784067 and MK778625) represents a diverging genotype that has the closest NCBI BLAST to *M. sanguinarius* with identities up to 93% (ITS) and 97% (mtSSU).

***Mycocalicium* sp.**

Species occurring on bark and wood of old oaks in lowland forests; probably undescribed. Its sequences are 96% (ITS) and 99% (mtSSU) identical with *M. subtile* (typically on wood of conifers).

***Mycocalicium subtile***

Our ITS has the closest NCBI BLAST to *M. subtile* with identities 93–100% and mtSSU with identities over 99%.

**_Mycomicrothelia confusa_**

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Marcelaria* (*Trypetheliaceae*) with identities 95.5%. Our mtSSU has the closest NCBI BLAST to *Mycomicrothelia* (*Trypetheliaceae*) with identities up to 95%.

**_Mycomicrothelia wallrothii_**

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Bathelium* (*Trypetheliaceae*) with identities up to 90%. Sequences of mtSSU absent from NCBI and not obtained by us.

**_Mycoporum antecellens_**

ITS and mtSSU absent from NCBI. We obtained nearly identical mtSSU sequences from two samples and these have the closest NCBI BLAST matches to *Capnodiales* (up to 88% identity). Our data indicated a close relationship to *Naetrocymbe punctiformis*, whose sequences have c. 92% identity with *M. antecellens*. It is still not clear if other *Mycoporum* species are related to *M. antecellens*. ITS not obtained by us.

**_Myelochroa aurulenta_**

ITS adopted from Nuñez-Zapata et al. (2017).

**_Myelochroa metarevoluta_**

ITS and mtSSU adopted from Nuñez-Zapata et al. (2017).

**_Myochroidea porphyrospoda_**

ITS and mtSSU absent from NCBI. Only mtSSU sequenced with the closest NCBI BLAST to *Lecanora cadubriae* (MZ409497 and our sequence) with identities about 98.5%. Our sequence of *Miriquidica* cf. *majae* is also close, with identity 95%.

**_Myriolecis hagenii_**

Our ITS matches *L. hagenii* (MK499339) with almost 100% identity. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *L. crenulata* with identities about 99%.

**_Myriolecis persimilis_**

Reliable ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Myriolecis* spp. with identities up to 95%. (Sequence of *L. persimilis* (ON116031) probably belongs to another species.) Our mtSSU has the closest NCBI BLAST to *L. crenulata* (OL604095) with the identity 99%. *Myriolecis persimilis* and *M. sambuci* are closely related and only distinguishable in ITS (mtSSU is identical).

**_Myriolecis sambuci_**

Our ITS has the closest NCBI BLAST to the single available sequence of *L. sambuci* (KT695378) with the identity 98.5%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *L. crenulata* with identities over 99%. *Myriolecis persimilis* and *M. sambuci* are closely related and only distinguishable in ITS (mtSSU is identical).

***Myrionora albidula***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Biatora ligni-mollis* with identity 96%. Our mtSSU has the closest NCBI BLAST to *M. albidula* (MG925886; Kistenich et al. 2018) with identity 100%. The second closest mtSSU BLAST result is *Biatora ligni-mollis* with identities up to 97%.

***Naetrocymbe punctiformis***

ITS and mtSSU absent from NCBI. Our identical ITS sequences from two specimens have the closest NCBI BLAST to *Capnodiales* spp. with identities up to 89%. Our identical mtSSU from three specimens have the closest NCBI BLAST to *Cystocoleus ebeneus* (*Capnodiales*) with identities 93–94%.

***Nephroma bellum***

Our ITS has the closest NCBI BLAST to *N. bellum* with identities over 99% and mtSSU with identities close or equal to 100%.

***Nephroma helveticum***

ITS and mtSSU adopted from Timdal et al. (2021).

***Nephroma laevigatum***

ITS and mtSSU adopted from Sérusiaux et al. (2011).

***Nephroma parile***

ITS adopted from Timdal et al. (2020) and mtSSU from Lohtander et al. (2002).

***Nephroma resupinatum***

Our ITS matches *N. resupinatum* in NCBI with identities 95–100%. Sequence of mtSSU adopted from Lohtander et al. (2002).

***Nephroma tangeriense***

ITS and mtSSU adopted from Lohtander et al. (2002).

***Nephroma tropicum***

ITS and mtSSU adopted from Timdal et al. (2021).

***Nephromopsis laureri***

Our ITS matches *N. laureri* in NCBI with identities 99.5%. Our mtSSU matches *Parmeliaceae* spp. (e.g. *Flavocetraria*, *Nephromopsis* and *Tuckermannopsis*) with identities about 99.5%.

***Normandina* aff. *acroglypta***

Our ITS sequences match *N. acroglypta* in NCBI with identities 90–95%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *N. pulchella* with identities about 96%. We sequenced richly fertile and non-sorediate specimen from Scotland and a sterile, richly sorediate specimen from Carpathians (typical for Central Europe), and both represented distinct genotypes, with 11 distinct BP in mtSSU and 57 in ITS. Our sequences do not match the newly described *N. chlorococca*.

***Normandina chlorococca***

ITS and mtSSU adopted from Orange (2022).

***Normandina pulchella***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Frisch & Ohmura (2015).

***Ocellomma picconianum***

ITS adopted from Kantvilas et al. (2020). Sequences of mtSSU absent from NCBI.

***Ochrolechia alboflavescens***

Our ITS matches *O. alboflavescens* in NCBI (MK812244; Marthinsen et al. 2019). Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *Ochrolechia* spp. with identities up to 93%.

***Ochrolechia androgyna***

Our ITS and mtSSU match *O. androgyna* in NCBI with identities 100% or close.

***Ochrolechia arborea***

ITS and mtSSU absent from NCBI. Our ITS matches *Ochrolechia* spp. with identities up to 87%, our mtSSU with 93%.

***Ochrolechia bahusiensis***

Our identical ITS sequences of three specimens match *O. bahusiensis* in NCBI with identities 99.5–100%. Sequences of mtSSU absent from NCBI. Sequences of mtSSU absent from NCBI. Our identical mtSSU of two specimens have the closest NCBI BLAST to *O. oregonensis* with the identity 96%. (AY567982, named *O. turneri*, is almost 100% identical, and we suspect it is incorrectly identified *O. bahusiensis*.)

***Ochrolechia mahluensis***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST result to *O. tartarea* and *O. frigida* with identities about 95%. Our mtSSU has the closest BLAST with *O. frigida* in NCBI with identities 98.5–99%.

***Ochrolechia microstictoides***

Our ITS sequences match *O. microstictoides* in NCBI with identities over 99.5%. Sequences of mtSSU absent from NCBI and our mtSSU has the closest BLAST to *Ochrolechia* spp. with identities up to 93%.

***Ochrolechia pallescens***

ITS and mtSSU adopted from Urbanavichus (2020).

***Ochrolechia subviridis***

Our ITS matches *O. subviridis* in NCBI with identities 98–100%. Sequences of mtSSU absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Schmitt & Lumbsch (2004).

***Ochrolechia szatalaensis***

Our ITS matches *O. szatalaensis* in NCBI with identities over 99.5%. Sequence of mtSSU adopted from Schmitt & Lumbsch (2004).

***Ochrolechia trochophora***

ITS and mtSSU adopted from Urbanavichus (2020).

***Ochrolechia turneri***

Our ITS and mtSSU match *O. turneri* (OK333002, OK465619) with identities 100% or close.

***Opegrapha celtidicola***

ITS absent in NCBI. Sequence of mtSSU adopted from Ertz et al. (2009). Our ITS from a specimen matching description of *O. celtidicola* (from coastal shrub communities in Rhodos) is rather distinct, only 89% identical with the sequence published by Ertz et al. (2009). Both are probably distinct species.

***Opegrapha niveoatra***

ITS absent from NCBI. Our ITS sequences include two genotypes about 90% identical. Both have the closest NCBI BLAST to *Schizopelte*/*Hubbsia* and *Combea* (*Opegraphaceae*) with identities up to 90%. Our mtSSU sequences from six specimens represent two genotypes 96% identical. One has the closest NCBI BLAST to *O. niveoatra* with identities 100%, the second with 96%.

***Opegrapha trochodes***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Syncesia* and *Enterographa* (*Roccellaceae*) with identities over 90%. The sequence of mtSSU has the closest NCBI BLAST to *Dirina*, *Schismatomma* and *Roccella* (*Roccellaceae*) with identities about 85%. It is not closely related to *Opegrapha* s.str. and probably belongs to *Roccellaceae*, not *Opegraphaceae*.

***Opegrapha vermicellifera***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Schizopelte*/*Hubbsia* and *Combea* (*Opegraphaceae*) with identities up to 90%. Our mtSSU is identical to *O. vermicellifera* (EU704077).

***Opegrapha vulgata***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Schizopelte*/*Hubbsia* and *Combea* (*Opegraphaceae*) with identities up to 90%. Sequences of mtSSU not obtained by us.

***Opegrapha* sp.**

Conspicuous pink leprose crust containing *Trentepohlia*. Probably undescribed *Opegrapha* common at low altitudes in western Caucasus. Our ITS has the closest NCBI BLAST to *Schizopelte*/*Hubbsia* and *Combea* (*Opegraphaceae*) with identity up to 90%.

***Pachnolepia pruinata***

Sequence of mtSSU adopted from Frisch et al. (2014). ITS absent from NCBI and not obtained by us.

***Palicella filamentosa* (= *Lecanora filamentosa*)**

Our ITS has the closest NCBI BLAST to *L. filamentosa* with identities 98–99%. Our mtSSU has the closest NCBI BLAST to the single available *L. filamentosa* (KJ152468) with identity 100%.

***Pannaria conoplea***

ITS adopted from Marthinsen et al. (2019) and Kelly et al. (2011) and mtSSU from Hurtado et al. (2020).

***Pannaria rubiginosa***

ITS adopted from Marthinsen et al. (2019) and mtSSU from Magain & Sérusiaux (2014).

***Parmelia barrenoae***

Our ITS matches *P. barrenoae* in NCBI with identities 99–100% and our mtSSU with 100% or close.

***Parmelia encryptata***

Our ITS matches *P. encryptata* sequences with >99.5% identities. Sequences of mtSSU absent from NCBI. Our mtSSU is more than 99.5% identical with sequences of *P. sulcata*.

***Parmelia ernstiae***

Our ITS sequences match *P. ernstiae* in NCBI with identities 99.5–100%, our mtSSU with 100%.

***Parmelia saxatilis***

Our ITS matches *P. saxatilis* in NCBI with identities over 98.5%, our mtSSU with 99.5–100%.

***Parmelia serrana***

Our ITS matches *P. serrana* in NCBI with identities 98.5–100%, our mtSSU with 100%.

***Parmelia submontana***

ITS adopted from NCBI (Thell & Persson 2016, unpublished), mtSSU from Urbanavichus et al. (2020).

***Parmelia sulcata***

Our ITS matches *P. sulcata* in NCBI with identities 97.5–100%, our mtSSU with 99–100%.

***Parmeliella parvula***

ITS adopted from Marthinsen et al. (2019), mtSSU from Carlsen et al. (2012).

***Parmeliella triptophylla***

Our ITS sequences match *P. triptophila* in NCBI with identities 99–100%, our mtSSU with 100%.

***Parmelina carporrhizans***

ITS adopted from Alors et al. (2014) and mtSSU from Nuñez-Zapata et al. (2017) and Blanco et al. (2004).

***Parmelina pastillifera***

Our ITS and mtSSU sequences match *P. pastillifera* in NCBI with identities 99–100%.

***Parmelina quercina***

ITS adopted from Argüello et al. (2007), mtSSU from Nuñez-Zapata et al. (2017).

***Parmelina tiliacea***

Our ITS matches *P. tiliacea* in NCBI with identities 98.5–100%, our mtSSU with 99–100%.

***Parmeliopsis ambigua***

Our ITS match *P. ambigua* with identities 97.5–100%, our mtSSU with 100%.

***Parmeliopsis hyperopta***

Our ITS match *P. hyperopta* with identities 99.5–100%, our mtSSU with 100%.

***Parmotrema arnoldii***

ITS adopted from NCBI - the single available sequence, KM250229 (Jang et al. 2014, unpublished). Sequences of mtSSU not available in NCBI.

***Parmotrema crinitum***

ITS adopted from Stelate et al. (2022), mtSSU from Miadlikowska et al. (2014).

***Parmotrema perlatum***

Our ITS matches *P. perlatum* in NCBI with identities 99–100%. Our mtSSU BLASTs to *Parmotrema* spp. with identities 98–99%.

***Parmotrema pseudoreticulatum***

ITS and mtSSU adopted from Divakar et al. (2005).

***Parmotrema reticulatum***

ITS and mtSSU adopted from Divakar et al. (2005).

***Parvoplaca nigroblastidiata***

Our ITS matches *P. nigroblastidiata* in NCBI with identities 97–99.5%, our mtSSU matches *Parvoplaca* spp. with identities 98–99.75%.

***Parvoplaca servitiana***

ITS and mtSSU adopted from Urbanavichus et al. (2020).

***Parvoplaca suspiciosa***

ITS adopted from Arup et al. (2013, 2015), mtSSU from Arup (ms., ined.).

***Parvoplaca tiroliensis***

ITS adopted from Arup et al. (2013) and Urbanavichus et al. (2020), mtSSU from Arup et al. (2013).

***Patellaria atrata***

Our ITS matches *P. atrata* in NCBI with identities 99–100%. Sequence of mtSSU adopted from Boehm et al. (2015).

***Pectenia atlantica***

ITS adopted from Otálora et al. (2017), mtSSU not considered.

***Pectenia plumbea***

ITS adopted from Otálora et al. (2017), mtSSU not considered.

***Peltigera collina***

Our ITS matches *P. collina* in NCBI with identities over 99.5%. Sequence of mtSSU adopted from Kistenich et al. (2019b).

***Peltigera degenii***

Our ITS matches *P. degenii* in NCBI with identities 95.5–100%. Sequence of mtSSU adopted from Lutzoni et al. (2004).

***Peltigera horizontalis***

Our ITS sequences match *P. horizontalis* in NCBI with identities 96–99.5%. Sequence of mtSSU adopted from Lohtander et al. (2002).

***Peltigera neckeri***

Usually terricolous, occasionally epiphytic. ITS adopted from Marthinsen et al. (2019), mtSSU absent from NCBI.

***Peltigera neocanina* ined.**

Our ITS sequences match *P. neocanina* ined. in NCBI with identities 92–100%. Our identical mtSSU from three specimens match *P. neocanina* (OK465624, Vondrák et al. 2022) with 100% identity.

***Peltigera polydactylon***

Our ITS sequences match *P. polydactylon* in NCBI with identities 99–100%, our mtSSU BLASTs to *Peltigera* spp. with identities up to 99.5%. Sequences of mtSSU from *P. polydactylon* are absent from NCBI.

***Peltigera praetextata***

Our ITS matches *P. praetextata* in NCBI with identities 99.5–100%. Sequence of mtSSU adopted from Lohtander et al. (2002).

***Pertusaria alpina***

Our ITS matches *P. alpina* in NCBI with identities over 99.5%. We also sequnced ITS of a specimen identified by morphology as *P. constricta* and its sequence was identical with the one of *P. alpina*. Possibly, *P. alpina* and *P. constricta* are conspecific. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *P. leioplaca* (AY300903) with the identity 99.3%.

***Pertusaria carneopallida***

ITS adopted from Marthinsen et al. (2019), mtSSU absent from NCBI.

### *Pertusaria coccodes*

Our ITS matches *P. coccodes* in NCBI with identities 98–100%. Sequence of mtSSU adopted from Schmitt & Lumbsch (2004).

### *Pertusaria constricta*

Our specimen identified as *P. constricta* has >99.5 identical ITS with sequences of *P. alpina*. Sequence of mtSSU not available.

### *Pertusaria coronata*

ITS sequences absent from NCBI. Our attempts to sequence ITS ended up in *Tremellaceae* in two cases. Our identical mtSSU sequences from two specimens match *Pertusaria* spp. in NCBI (including *P. coronata*) with identities about 99.5%.

### *Pertusaria flavida*

Our ITS matches *P. flavida* in NCBI with identities 100%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *P. hymenea* (AY567988) with 99% identity.

### *Pertusaria hymenea*

ITS absent from NCBI. Our almost identical ITS sequences from two specimens have the closest BLAST to *Pertusaria pertusa* (JN943618) with the identity about 99.5%. Our mtSSU sequences match *P. hymenea* (AY567988) with identities over 99.5%.

### *Pertusaria leioplaca*

Our ITS matches *P. leioplaca* in NCBI with identities 99.5–100% and our mtSSU with 100%.

### *Pertusaria macounii*

Our ITS match *P. pertusa* (MK812037, Marthinsen et al. 2019) with the 95% identity, but some *P. pertusa* in NCBI (AF332126, AF332127) are over 99% identical. Our mtSSU is almost identical with *P. pertusa* in NCBI. It is not clear, if lichens with pigmented ascospores (*P. macounii*) represent and species distinct from *P. pertusa*.

### *Pertusaria pertusa*

ITS adopted from Marthinsen et al. (2019) and mtSSU from Ivanova & Hafellner (2002).

### *Pertusaria pupillaris*

ITS not available in NCBI. Our identical ITS sequences from three specimens have an uncertain position according to the NCBI BLAST; their closest relative is *Ochrolechia parella* with identities 82–83%. Our mtSSU sequences match *P. pupillaris* in NCBI with 99–99.5% identities. One ITS sequence of *P. pupillaris* (PRA-JV25447) was quite distinct from others (93% identical) but its mtSSU was 99% identical with others. It suggests substantial variability in ITS within *P. pupillaris*.

### *Pertusaria* **aff.** *pupillaris*

Distinct from *P. pupillaris* by containing atranorin as an additional substance. ITS matches our *P. pupillaris* sequences with identities 90 and 94.5%. Sequence of mtSSU not obtained.

***Pertusaria pustulata***

ITS absent from NCBI. Sequence of mtSSU adopted from Schmitt et al. (2006).

***Pertusaria sommerfeltii***

ITS and mtSSU not available in NCBI. Our ITS has the closest NCBI BLAST to *P. leioplaca* with identities 88–89%, our mtSSU with the identity 97%.

***Phaeocalicium interruptum***

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI.

***Phaeocalicium populneum***

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI.

***Phaeocalicium praecedens***

ITS adopted from Tuovila et al. (2014). Sequences of mtSSU absent from NCBI and not obtained by us.

***Phaeographis dendritica***

ITS adopted from NCBI (Gaya et al. 2021, unpublished), mtSSU adopted from Rivas Plata et al. (2013).

***Phaeophyscia ciliata***

Our ITS and mtSSU sequences match both *P. ciliata* and *P. orbicularis* with 99–99.5%; *P. ciliata* and *P. orbicularis* are indistinguishable with the use of both barcodes.

***Phaeophyscia endophoenicea***

Our ITS is 96–99% identical with NCBI sequences of *P. endophoenicea*. As the species is variable in ITS, we also adopted sequences from Grube & Arup (2001), Helms et al. (2003) and Lohtander et al. (2000). Sequences of mtSSU not available in NCBI. Our mtSSU is up to 98.5% identical with sequences of *Phaeophyscia* spp.

***Phaeophyscia chloantha***

Our ITS matches *P. chloantha* and *P. melanchra* in NCBI with identities 98.5–99%. Our mtSSU matches *P. chloantha* in NCBI with identities over 99%.

***Phaeophyscia kairamoi***

Usually saxicolous, but rarely also on bark. ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Phaeophyscia nigricans***

ITS adopted from Lohtander et al. (2000) and mtSSU from Lohtander et al. (2008).

***Phaeophyscia orbicularis***

Our ITS and mtSSU sequences match both *P. ciliata* and *P. orbicularis* with 99–100%; *P. ciliata* and *P. orbicularis* are indistinguishable with the use of both ITS and mtSSU.

**_Phaeophyscia poeltii_**

ITS adopted from Mark et al. (2016), mtSSU absent in NCBI.

**_Phaeophyscia pusilloides_**

Reliable ITS and mtSSU absent from NCBI. Our almost identical ITS sequences of three specimens have the closest NCBI BLAST to *P. ciliata* with identities about 96.5%. (GU247170, named *P. pusilloides*, is identical or almost identical with sequences of *P. orbicularis* and probably represents this species.) Our almost identical mtSSU sequences of two specimens have the closest NCBI BLAST to *Phaeophyscia* spp. with identities up to 98%. (GU247203, named *P. pusilloides*, is identical with our *P. orbicularis* and probably represents this species.)

**_Phaeophyscia rubropulchra_**

Our ITS matches *P. rubropulchra* in NCBI with identities 99.5–100%. Sequences of mtSSU absent from NCBI and our mtSSU has the closest BLAST to *Phaeophyscia* spp. with identities up to 98%.

**_Phlyctis agelaea_**

Our ITS matches the only *P. agelaea* in NCBI (MK812009, Marthinsen et al. 2019) with the identity 100%. *Phlyctis argena* sequences are distinct sharing identities up to 92.5%. Our mtSSU is identical with both *P. argena* and *P. agelaea* in NCBI.

**_Phlyctis argena_**

Our ITS matches *P. argena* in NCBI with identities 98.5–100%. Our mtSSU is identical with both *P. argena* and *P. agelaea* in NCBI.

**_Phyllopsora rosei_**

ITS and mtSSU adopted from Kistenich et al. (2019a).

**_Physcia adscendens_**

Our ITS sequences match *P. adscendens* in NCBI with identities 97.5–99.5%, but the regions ITS1 and ITS2 are invariable; the variability is restricted to the intron of c. 280 BP lenght in front of ITS1. Our mtSSU sequences match *Physcia* spp. with identities 99.5–100%.

**_Physcia aipolia_**

Our ITS matches *P. aipolia* in NCBI with identities 98.5–100%, but the regions ITS1 and ITS2 are invariable; the variability is restricted to the intron of cca 280 BP lenght in front of ITS1. Our mtSSU sequences match *Physcia* spp. with identities 99.5–100%.

**_Physcia biziana_**

ITS and mtSSU adopted from NCBI, Figueras et al. (2009, unpublished).

**_Physcia dubia_**

Our ITS matches *P. dubia* in NCBI with identities over 99.5%. Our mtSSU sequences match *Physcia* spp. with identities 99.5–100%.

***Physcia leptalea***

ITS sequences adopted from Lohtander et al. (2000) and mtSSU from NCBI, Figueras et al. (2009, unpublished).

***Physcia stellaris***

Our ITS matches *P. stellaris* in NCBI with identities over 97.5–99.5%, but the variability is almost restricted to the intron of cca 280 BP lenght in front of ITS1. Our mtSSU sequences match *Physcia* spp. with identities 99.5–100%.

***Physcia tenella***

ITS sequences adopted from NCBI (Brunauer 2008, unpublished; Gaya et al. 2021, unpublished). Sequences of mtSSU adpoted from Lohtander et al. (2008) and Prieto & Wedin (2017).

***Physcia tribacia***

Saxicolous occurrences prevail in central Europe, but this species also occasionally grows on bark. ITS adopted from Helms et al. (2003). Sequences of mtSSU absent from NCBI.

***Physcia vitii***

Little known species with ITS data only available from Pakistan (Firdous et al. 2022). Sequences of mtSSU absent from NCBI.

***Physconia detersa***

ITS adopted from Lohtander et al. (2008) and Starosta & Svoboda (2020); mtSSU from Lohtander et al. (2008).

***Physconia distorta***

Sequences of mtSSU absent from NCBI. Out ITS matches *P. distorta* in NCBI with identities 99.5–100%. Our mtSSU has the closest NCBI BLAST to *Physconia* spp. with identities 99–100%.

***Physconia enteroxantha***

ITS adopted from Vondrák et al. (2022) and Starosta & Svoboda (2020); mtSSU from Vondrák et al. (2022).

***Physconia grisea***

ITS adopted from Lohtander et al. (2008) and Starosta & Svoboda (2020); mtSSU from Lohtander et al. (2008).

***Physconia perisidiosa***

Our ITS match *P. perisidiosa* in NCBI with identities 95–99.5% and our mtSSU with about 99.5%.

***Physconia servitii***

ITS adopted from Lohtander et al. (2008), mtSSU absent in NCBI.

***Physconia subpulverulenta***

ITS adopted from Divakar et al. (2007), mtSSU absent in NCBI.

***Physconia thorstenii***

ITS adopted from Divakar et al. (2007), mtSSU absent in NCBI.

***Physconia venusta***

ITS adopted from Lohtander et al. (2008) and Starosta & Svoboda (2020); mtSSU from Lohtander et al. (2008). This species repesents the fertile, non-sorediate counterpart of *P. perisidiosa* and both species are indistinguishable by ITS neither mtSSU.

***Piccolia ochrophora***

ITS and mtSSU absent from NCBI. Our ITS sequences from three specimens are more than 96% identical and they have no relative sequences in NCBI with the cover over 45%. Our mtSSU has the closest NCBI BLAST results with various *Lichinomycetes* and *Acarosporomycetidae* with identities up to 85%.

***Placynthiella dasaea***

Our ITS matches *P. dasaea* in NCBI (KX132967) with 99% identity. Sequences of *P. icmalea* are more distinct, sharing identities 98–98.5%. Sequences of mtSSU absent from NCBI. Our mtSSU matches our sequences of *P. icmalea* with identities 99.5–100%.

***Placynthiella icmalea***

Our ITS sequences from three specimens are slightly variable, with the identity 96.5%. They all have closest match either to *P. dasaea* or *P. icmalea* in NCBI with identities above 97%. Our mtSSU sequences match *P. icmalea* in NCBI with identities over 99%.

***Placynthiella uliginosa***

Our ITS has the closest NCBI BLAST to *P. oligotropha* with identities 96.5%. (The only NCBI *P. uliginosa*, HQ650633, is only 93.5% identical.) Our mtSSU matches *P. oligotropha* and *P. uliginosa* in NCBI with identities about 98.5%.

***Platismatia glauca***

Our ITS matches with *P. glauca* in NCBI with identities 97–99.5%, our mtSSU with identities 98–98.5%.

***Pleurosticta acetabulum***

Our ITS and mtSSU have the closest NCBI BLAST to *P. acetabulum* with identities 99.5–100%.

***Polycauliona* spp.**

See below *Xanthoria*.

***Polychidium dendriscum***

ITS and mtSSU adopted from Spribille et al. (2020).

***Porina aenea***

ITS not available in NCBI. Our ITS sequence has the closest BLAST to *P. chlorotica* with identities about 90%. Our mtSSU sequences match *P. aenea* in NCBI with identities 97–100%.

***Porina borreri***

ITS not available in NCBI. Sequence of mtSSU adopted from Ertz & Diederich (2022).

***Porina byssophila***

Epiphytic occurrences of this species are rather common, especially in lower altitudes. Morphologically it differs from *P. aenea* by less glossy and pale grey thallus and perithecia c. 2/3 immersed in thallus. It rather resembles e.g. *Strigula jamesii*. Our ITS sequences from two specimens match *P. byssophila* in NCBI with identities 95–100% and our single mtSSU with identities over 99%.

***Porina collina***

Our ITS matches *P. collina* in NCBI with identities 97.5–98.5%. Sequences of mtSSU adopted from Orange et al. (2020).

***Porina leptalea***

Our ITS sequence matches *Porina* spp. (including and single available *P. leptalea*, MN687942) with identities up to 85%. Our identical mtSSU sequences from two samples match *Porina aenea* and *P. chlorotica* with identities 96–99%. The single available mtSSU of *P. leptalea* (OK058494 from Mauritius; Ertz & Diederich 2022) is only 85% identical.

***Porina multipuncta***

ITS and mtSSU adopted from Orange et al. (2020).

***Porina pseudohibernica***

ITS and mtSSU not available in NCBI. Our sequences have the closest NCBI BLAST to *P. collina* with identities 92.5–93.5% (ITS) and 88–93% (mtSSU).

***Porina rosei***

Our ITS is identical with sequences of *P. rosei* provided by Malíček et al. (2023). Sequences of mtSSU adopted from Malíček et al. (2023).

***Protopannaria pezizoides***

ITS adopted from Marthinsen et al. (2019), mtSSU from Ekman et al. (2014).

***Protoparmelia hypotremella***

ITS and mtSSU sequences adopted from Vondrák et al. (2022).

***Protoparmelia oleagina***

ITS and mtSSU adopted from Singh et al. (2017).

***Pseudevernia furfuracea***

Our ITS matches *P. furfuracea* in NCBI with identities 98–100%, our mtSSU with 100%.

***Pseudocyphellaria intricata***

ITS and mtSSU adopted from NCBI (Bogomazova & Yahr 2018, ms.).

***Pseudocyphellaria lacerata***

ITS and mtSSU adopted from NCBI (Bogomazova & Yahr 2018, ms.).

***Pseudocyphellaria norvegica***

ITS and mtSSU adopted from NCBI (Bogomazova & Yahr 2018, ms.).

***Pseudocyphellaria crocata***

ITS adopted from Moncada et al. (2014); mtSSU not considered.

***Pseudocyphellaria aurata***

ITS adopted from Moncada et al. (2014); mtSSU not considered.

***Pseudographis elatina***

Our ITS matches the single *P. elatina* in NCBI (MK751794) with 100% identity and our mtSSU matches the single NCBI sequence (MK751717) with almost 100%.

***Pseudoschismatomma rufescens***

ITS not available in NCBI. Our almost identical ITS from two samples have the closest NCBI BLAST to *Schismatomma*/*Ocellomma*/*Roccella* with identities about 80%. Our mtSSU sequences match *P. rufescens* with identities over 99.5%.

***Pseudothelomma ocellatum***

Our ITS matches *T. ocellatum* in NCBI with identities 99–100%, our mtSSU with 100%.

***Psilolechia clavulifera***

Our ITS matches *P. clavulifera* in NCBI with identities 96–97%. Sequences of mtSSU not available in NCBI and our sequence has the closest BLAST to *P. lucida* (KJ766473) with the identity 97%.

***Psilolechia tori* ined.**

Undescribed species on rotten wood. Only ITS sequenced and has the closest NCBI BLAST to *P. leprosa* with identities 86–87%.

***Psilolechia* sp.**

Strile crust on wood usually covered by mold-like conidiophore coat. ITS matches *Psilolechia clavulifera* with 90% identity, mtSSU with 97% identity.

***Psoroglaena dictyospora***

ITS and mtSSU absent from NCBI. Our ITS has the closest match with *Psoroglaena* sp. (JF939053) with the identity 93%. Our mtSSU matches various *Verrucariaceae* with identities up to 86%.

***Psoroglaena stigonemoides***

ITS and mtSSU absent from NCBI. Our ITS has the closest match with *Psoroglaena* sp. (JF939053) with the identity 93%. Our mtSSU matches *Psoroglaena* spp. with identities up to 89%.

***Psoroma hypnorum***

ITS adopted from Marthinsen et al. (2019), mtSSU from Ekman et al. (2014).

***Ptychographa xylographoides***

ITS and mtSSU adopted from Spribille et al. (2014).

***Punctelia borreri***

Our ITS matches *P. borreri* in NCBI with identities 98–100% and mtSSU with the identity 100%.

***Punctelia jeckeri***

Our ITS matches *P. jeckeri* in NCBI with identities 97.5–100%. Sequences of mtSSU absent from NCBI and our mtSSU has the closest NCBI BLAST to *P. castanea* (KR024492) with the identity 99%.

***Punctelia perreticulata***

ITS and mtSSU adopted from Crespo et al. (2004).

***Punctelia reddenda***

ITS and mtSSU adopted from Crespo et al. (2004).

***Punctelia subrudecta***

Our ITS matches *P. subrudecta* in NCBI with identities 99–100% and our mtSSU with 99.5–100%.

***Puttea caesia***

ITS and mtSSU absent from NCBI. Our ITS has no close relatives in NCBI, but it is 94.5% identical with our sequences of *P. margaritella*. Sequences of mtSSU not obtained by us.

***Puttea exsequens***

ITS and mtSSU absent from NCBI. ITS not obtained by us, but our mtSSU has the closest NCBI BLAST to *Malmideaceae* (*Cheiromycina petri* and *Lecidea hypopta*) with identities 91–92%. It is more closely related to our mtSSU of *P. margaritella* with the identity 95%.

***Puttea margaritella***

ITS and mtSSU absent from NCBI. Our identical ITS sequences of three specimens have no close relatives in NCBI, but they are 94.5% identical with our sequence of *P. caesia*. Our identical mtSSU sequences of three specimens have the closest NCBI BLAST to *Malmideaceae* (*Lecidea hypopta* and *L. malmeana*) with identities 91–92%. They are more closely related to our mtSSU of *P. exsequens* with the identity 95%.

***Pycnora praestabilis***

ITS sequences absent from NCBI. Our ITS matches our *P. sorophora* sequences with identities 99–100%, mtSSU with 100%. (The only available mtSSU from *P. praestabilis*, KJ766478, is only 98.5% identical with our sequence.)

***Pycnora sorophora***

Our ITS and mtSSU sequences match *P. sorophora* in NCBI with identities 99.5–100%.

***Pycnora xanthococca***

ITS and mtSSU adopted from Bendiksby & Timdal (2013).

***Pyrenula chlorospila***

Our ITS and mtSSU sequences have the closest NCBI BLAST to *P. chlorospila* (JQ927452; Weerakoon et al. 2012) with identities 100%.

***Pyrenula coryli***

ITS and mtSSU sequences absent from NCBI. Our ITS has the closest NCBI BLAST to *Pyrenula* spp. with identities up to 89%. Sequences of mtSSU not obtained by us.

***Pyrenula dermatodes***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Pyrenula* spp. and *Anthracothecium* spp. (*Pyrenulaceae*) with identities up to 87%. Sequences of mtSSU absent from NCBI and not obtained by us.

***Pyrenula laevigata***

Our ITS matches *P. laevigata* in NCBI with identities 99–99.5%. Our mtSSU sequences represent two distinct genotypes. One is identical with the only *P. laevigata* in NCBI (AY568029) and the other one is only 92% identical with AY568029.

***Pyrenula macrospora***

ITS and mtSSU adopted from Weerakoon et al. (2012).

***Pyrenula nitida***

Our ITS matches *P. nitida* in NCBI with identities over 99.5%, our mtSSU sequences with identities over 99%.

***Pyrenula nitidella***

ITS and mtSSU sequences adopted from Vondrák et al. (2022).

***Pyrenula occidentalis***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU absent from NCBI and not sequenced by us.

***Pyrenula subelliptica***

Originally a tropical lichen that also occurs in Europe (Caucasus). ITS adopted from Gueidan et al. (2016). Our mtSSU matches *P. subelliptica* in NCBI (KT808534) with the identity close to 100%.

***Pyrgidium montellicum***

ITS and mtSSU adopted from Thiyagaraja et al. (2022).

***Pyrrhospora quernea***

Our ITS is identical with *P. quernea* (AF517930; Ekman & Tønsberg 2002). Sequence of mtSSU adopted from Andersen & Ekman (2005).

***Pyxine sorediata***

ITS and mtSSU adopted from Prieto & Wedin (2017).

***Ramalina calicaris***

ITS adopted from Sipman & Raus (2020). Sequences of mtSSU absent from NCBI and our mtSSU is not reliable.

***Ramalina canariensis***

ITS adopted from Sipman & Raus (2020). Sequences of mtSSU absent from NCBI. Our mtSSU matches *Ramalina* spp. with identities up to 99%.

***Ramalina dilacerata***

ITS and mtSSU adopted from Spribille et al. (2020).

***Ramalina europaea***

Our ITS sequences match *R. europaea* in NCBI with identities 97–100%. The type ITS of *R. pollinaria* is 99% identical with our sequences. Our mtSSU sequences are identical with *R. europaea* in NCBI.

***Ramalina farinacea***

Our ITS and mtSSU sequences match *R. farinacea* in NCBI with identities over 99.5%.

***Ramalina fastigiata***

Our ITS matches *R. fastigiata* in NCBI with identities 98–99.5%. Our mtSSU has the closest NCBI BLAST to *Ramalina* spp. with identities up to 100%.

***Ramalina fraxinea***

Our ITS matches *R. fraxinea* in NCBI with identities 99.5–100%. Sequence of mtSSU adopted from Kistenich et al. (2018).

***Ramalina obtusata***

Our ITS and mtSSU match the only *R. obtusata* in NCBI (OK333014, OK465639; Vondrák et al. 2022) with identities about 99.8%.

***Ramalina panizzei***

ITS adopted from Urbanavichus et al. (2020). Sequences of mtSSU absent from NCBI.

***Ramalina roesleri***

ITS adopted from LaGreca et al. (2020). Sequences of mtSSU in NCBI are short, not included in the database.

***Ramalina pollinaria***

ITS adopted from Gasparyan et al. (2017). Sequences of mtSSU absent from NCBI.

***Ramalina sinensis***

ITS and mtSSU adopted from Kistenich et al. (2018).

***Ramalina thrausta***

Our ITS matches with *R. chondrina* and *R. thrausta* in NCBI with identities 100% or close. Sequence of mtSSU adopted from the NCBI. Our mtSSU has the closest NCBI BLAST to *Ramalina* spp. with identities up to 100%.

***Ramboldia cinnabarina***

ITS adopted from Resl et al. (2015). Sequences of mtSSU absent from NCBI.

***Ramboldia elabens***

ITS adopted from Marthinsen et al. (2019), mtSSU from Miadlikowska et al. (2014).

***Ramboldia russula***

ITS and mtSSU adopted from Kalb et al. (2008).

***Ramonia chrysophaea***

See under *Karstenia idaei.*

***Ramonia luteola***

ITS and mtSSU absent from NCBI. ITS not obtained by us. Our mtSSU has the closest NCBI BLAST to *Francisrosea* (*Gyalectaceae*) with the identities about 88%.

***Reichlingia anombrophila***

ITS absent from NCBI. Sequence of mtSSU adopted from Ertz et al. (2020).

***Reichlingia leopoldii***

ITS absent from NCBI. Our identical sequences of two specimens have the closest NCBI BLAST to *Coniocarpon*, but with low cover (about 90% identitiy, 20% cover). Our mtSSU sequences match *R. leopoldii* with identities 100% or close.

***Reichlingia zwackhii***

ITS absent from NCBI. Our identical sequences of two specimens have the closest NCBI BLAST to *Coniocarpon*, but with low cover (about 95% identitiy, 11% cover). Our mtSSU matches *R. zwackhii* (KF707652) with the identity 99.9%.

***Rhaphidicyrtis trichosporella***

ITS and mtSSU absent from NCBI. Our identical ITS sequences from three specimens have the closest NCBI BLAST to *Paraphaeomoniella capensis* (*Phaeomoniellales*) with identities up to 92%. Sequences of mtSSU not obtained.

***Ricasolia amplissima***

ITS sequence adopted from NCBI. Our mtSSU has the closest NCBI BLAST to *R. amplissima* with identities 100%.

***Ricasolia virens***

ITS and mtSSU adopted from Simon et al. (2020).

***Rinodina albana***

Our ITS matches *R. albana* in NCBI (GU553297; Nadyeina et al. 2010) with the identity 99%. Sequences of mtSSU absent from NCBI. Our mtSSU has closest BLAST results to various *Rinodina* spp. with identities up to 95%.

***Rinodina anomala***

ITS adopted from Sipman & Aptroot (2020). Sequences of mtSSU absent from NCBI.

***Rinodina archaea***

ITS sequences absent from NCBI. Sequence of mtSSU adopted from Vondrák et al. (2022). The sequence is identical with our sequences of *R. orculata* and *R. trevisanii* (all sequenced specimens identified by Helmut Mayrhofer).

***Rinodina capensis***

Our ITS matches *R. capensis* in NCBI (GU553293; Nadyeina et al. 2010) with the identity over 99%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI BLAST to *R. subpariata* with identities up to 99%.

***Rinodina colobina***

ITS and mtSSU absent from NCBI. Our ITS sequences BLAST with various *Physciaceae* with identities up to 89%, our mtSSU with identities up to 96%. There are no closely related taxa in our dataset either.

***Rinodina dalmatica***

ITS and mtSSU absent from NCBI. Our ITS matches *Physciaceae* spp. with identities up to 88%, mtSSU with identities up to 95%.

***Rinodina efflorescens***

Our ITS sequences match *R. efflorescens* in NCBI with identities 100% or close. Sequences of mtSSU absent from NCBI and not obtained by us.

***Rinodina excrescens***

ITS and mtSSU absent from NCBI. Our ITS sequences match *R. efflorescens* with identities 94–95%, our mtSSU BLAST with numerous *Rinodina* spp. with identities up to 96%.

***Rinodina exigua***

Our ITS match *R. exigua* in NCBI (GU553294; Nadyeina et al. 2010) with identities 100% or close. Sequences of mtSSU absent from NCBI. Our mtSSU BLAST with numerous *Physciaceae* with identities up to 96%.

***Rinodina freyi***

Our ITS sequences match *R. septentrionalis* in NCBI (GU553303; Nadyeina et al. 2010; possibly *R. freyi*) with identities over 98%. Our mtSSU sequences match *R. freyi* (KX015701; Resl et al. 2016) with 99% identities.

**_Rinodina furfuracea_**

ITS and mtSSU absent from NCBI. Our ITS matches *R. nimisii* (AJ544184) with 97% identity. Sequences of mtSSU not obtained yet. Our sequenced specimen has ascospore morphology of *R. furfuracea*, but the size of vegetative diaspores fit *R. nimisii*.

**_Rinodina griseosoralifera_**

Sequences of ITS absent from NCBI. Our ITS is up to 90% identical with various *Physciaceae*. Our mtSSU sequences match *R. griseosoralifera* in NCBI (MK778573; Urbanavichus et al. 2020) with identities over 99%.

**_Rinodina isidioides_**

ITS and mtSSU absent from NCBI. Our ITS BLAST with various *Physciaceae* with identities up to 88%. According to our data, its sequence is close to *R. griseosoralifera* with identities over 95%. Our mtSSU has the closest NCBI match to *R. griseosoralifera* in NCBI (MK778573; Urbanavichus et al. 2020) with the identity 97%.

**_Rinodina malangica_**

Sequences of ITS absent from NCBI. Our ITS BLAST with various *Physciaceae* with identities up to 91%. Our mtSSU sequences match *R. malangica* in NCBI (MK778574; Urbanavichus et al. 2020) with the identity over 99%.

**_Rinodina nimisii_**

ITS adopted from Helms et al. (2003). Sequences of mtSSU absent from NCBI.

**_Rinodina oleae_**

ITS and mtSSU sequences adopted from Nadyeina et al. (2010).

**_Rinodina orculata_**

ITS and mtSSU absent from NCBI. Our ITS is identical with our sequence of *R. trevisanii*. Our mtSSU is identical with our sequences of *R. archaea* and *R. trevisanii* (all sequenced specimens identified by Helmut Mayrhofer).

**_Rinodina pityrea_**

ITS and mtSSU absent from NCBI. Our ITS sequences BLAST with various *Physciaceae* with identities up to 90% and our mtSSU with identities up to 95%.

**_Rinodina plana_**

ITS adopted from Grube & Arup (2001), mtSSU from Wedin et al. (2002).

**_Rinodina poeltiana_**

Our ITS and mtSSU sequences match *R. poeltiana* in NCBI (OK333023, OK465651; Vondrák et al. 2022) with identities over 99%.

**_Rinodina pyrina_**

Sequences of mtSSU absent from NCBI. Our ITS matches *R. pyrina* in NCBI with identities 98–99.5%. Our mtSSU matches various *Physciaceae* with identities up to 96.5%.

**_Rinodina roboris_**

Our ITS matches *R. roboris* in NCBI (MK811851) with the identity 99%. Sequences of mtSSU absent from NCBI and our mtSSU has the closest NCBI BLAST match to *R. subpariata* (KX015698) with the identity c. 97.5%.

**_Rinodina sheardii_**

ITS and mtSSU sequences adopted from Urbanavichus et al. (2020; sub *Rinodina* sp.).

**_Rinodina sophodes_**

Our ITS matches *R. sophodes* in NCBI (GU553304; Nadyeina et al. 2010) with the identity 97%. Our mtSSU matches *R. sophodes* (AY143426; Wedin et al. 2002) with the identity 98.5%.

**_Rinodina subpariata_**

Our ITS sequences match *R. subpariata* in NCBI with identities 96–99.5% and our mtSSU with identities 99–99.5%.

**_Rinodina tenuis_**

ITS and mtSSU absent from NCBI. Our sequences (both ITS and mtSSU) are more than 99% identical with our sequenced *R. willeyi*. Both species (*R. willeyi* sorediate and *R. tenuis* non-sorediate) are closely related.

**_Rinodina trevisanii_**

No reliable ITS and mtSSU sequences in NCBI. The only available ITS sequence (KX015684) is of poor quality with ambiguousity in numerous nucleotide positions. Our ITS is identical with our sequence of *R. orculata*. Our mtSSU is identical with our sequences of *R. archaea* and *R. orculata* (all sequenced specimens identified by Helmut Mayrhofer).

**_Rinodina willeyi_**

ITS and mtSSU absent from NCBI. Our sequences (both ITS and mtSSU) are more than 99% identical with our sequenced *R. tenuis*.

**_Ropalospora viridis_**

Our ITS from five specimens represent two genotypes 99% identical. They have the closest NCBI BLAST to *R. viridis* (LC516200) with identities 99–100%. Our sequences of mtSSU from five specimens are identical and have the closest NCBI BLAST to *Ropalospora phaeoplaca* (EF659768) with the identity 97%.

**_Rostania occultata_**

Our mtSSU has the closest NCBI BLAST to *C. occultatum* with identities 99–100%. ITS absent in NCBI and not obtained by us.

**_Rostania effusa_**

ITS not available in NCBI. Sequence of mtSSU adopted from Košuthová et al. (2019).

**_Rostania pallida_**

ITS not available in NCBI. Sequence of mtSSU adopted from Košuthová et al. (2019).

***Rostania populina***

ITS not available in NCBI. Sequence of mtSSU adopted from Košuthová et al. (2019).

***Sarcosagium campestre***

Sequences of ITS absent from NCBI. Our ITS sequences are not reliable. They BLAST to various *Helotiales* (*Leotiomycetidae*) with identities up to 90%.

***Sarea coeloplata***

Our ITS matches *S. coeloplata* (type 2, sensu Mitchell et al. 2021) with identities 98.5–100%. MtSSU adopted from Vondrák et al. (2022).

***Sarea difformis***

ITS and mtSSU sequences adopted from Mitchell et al. (2021).

***Sarea resinae***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Schaereria corticola***

ITS sequences absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Urbanavichus et al. (2020).

***Schismatomma pericleum***

Our sequences match *S. pericleum* in NCBI with identities over 98% (ITS) and 99.5% (mtSSU).

***Schizotrema quercicola***

ITS absent from NCBI. Sequence of mtSSU adopted from Ertz et al. (2019).

***Schizoxylon albescens***

ITS and mtSSU adopted from Wedin et al. (2006).

***Schizoxylon berkeleyanum***

ITS and mtSSU adopted from Fernández-Brime et al. (2018).

***Schizoxylon gilenstamii***

ITS and mtSSU adopted from Fernández-Brime et al. (2018).

***Sclerophora amabilis***

ITS and mtSSU not available in NCBI. Our identical sequences from two specimens match the sequence named “*S. pallida*” (FR799287; Kelly et al. 2011) with the 100% identity, but this sequence probably belongs to *S. amabilis*. Other *Sclerophora* species BLAST with identities up to 88%. Our mtSSU has the closest NCBI BLAST to *Chaenotheca* spp. and *Sclerophora* spp. with identities up to 92%.

***Sclerophora coniophaea***

ITS not available in NCBI. Our ITS has the closest NCBI match to *Chaenotheca cinerea* (identities 83–85%) and *S. farinacea* (identity 83%). Our mtSSU matches *S. coniophaea* in NCBI (JX000131; Prieto et al. 2013) with 100% identity.

***Sclerophora farinacea***

Our ITS matches *S. farinacea* in NCBI with identities 89.5–90%. Such low identities are suspicious and not clear to us yet. Our mtSSU matches *S. farinacea* in NCBI (JX000130; Prieto et al. 2013) with 99.5% identity.

***Sclerophora pallida***

ITS and mtSSU not available in NCBI. ITS sequence not obtained by us even after numerous attempts. (ITS sequences in NCBI, named *S. pallida*, FR799287 and FR799288 (Kelly et al. 2011), are identical to our sequences of *S. amabilis*.) Our mtSSU sequences are only about 91% identical with our *S. amabilis* sequence.

***Sclerophora peronella***

Our ITS matches *S. peronella* in NCBI with identities about 99.5%. Sequences of mtSSU absent from NCBI. Our mtSSU has the closest NCBI match to *S. farinacea* in NCBI (JX000130; Prieto et al. 2013) with the identity 95%.

***Scoliciosporum chlorococcum***

Our ITS represent two distinct genotypes sharing identity below 90%. One matches *S. chlorococcum* (FR799323) with the identity 99.6%, the other has the closest NCBI BLAST to *S. umbrinum* with identities 86.5–87.5%. Two different genotypes are also represented in mtSSU. One has the closest NCBI BLAST to *S. fabisporum* (MT611934) with the identity 94%, the other to *S. umbrinum* with identities 95–96%. Both genotypes probably represent two distinct species.

***Scoliciosporum curvatum***

ITS and mtSSU absent from NCBI. Our identical ITS sequences of two specimens have no close relatives in NCBI; the closest matches are to *Lecanorales* spp. with identities up to 91%, but with low cover, up to 50%. Our mtSSU sequences have the closest NCBI BLAST to *S. umbrinum* and *Lecanorales* spp. with identities up to 86%.

***Scoliciosporum gallurae***

Our specimen identified morphologically as *S. gallurae* has identical ITS with sequences of *S. sarothamni*. Sequences of mtSSU not available.

***Scoliciosporum sarothamni***

ITS and mtSSU absent from NCBI. Our two identical ITS sequences have the closest NCBI matches to *S. umbrinum* with identities 93–94%. (KX133008, named *S. umbrinum*, is identical to our sequences and probably represents *S. sarothamni*.) Our two mtSSU sequences from a single specimen are 98.5% identical and both have the closest NCBI match to *S. fabisporum* (MT611934) with identities 94% and respectively 92%.

**_Scoliciosporum schadeanum_**

ITS absent from NCBI. Our identical sequences from three specimens have the closest NCBI BLAST to *Biatora* spp., especially to *B. pallens* with the identity 90%. Our mtSSU sequences match *S. schadeanum* (KJ766492) with the identity 99.7%.

**_Scoliciosporum umbrinum_**

We expect at least three species being named *S. umbrinum*. The relationship between saxicolous and epiphytic populations is not clear yet. Our ITS matches *S. umbrinum* in NCBI with identities 92.5–95.5%. Sequence of mtSSU adopted from Andersen & Ekman (2005).

**_Scytinium aragonii_**

Our ITS matches *S. aragonii* with identities 97.5–99.5%. Sequences of mtSSU absent from NCBI. Our almost identical mtSSU of two specimens have the closest NCBI BLAST to *Scytinium* spp. with identities up to 98.5%.

**_Scytinium fragrans_**

ITS absent from NCBI. Sequences of mtSSU adopted from Otálora et al. (2010, 2013), but are almost or entirely identical with sequences of *Scytinium magnussonii*, thus we cannot recognise between these species on the basis of current data.

**_Scytinium gelatinosum_**

Usually muscicolous on rocks and soil, occasionally epiphytic. ITS adopted from Otálora et al. (2008), mtSSU not included.

**_Scytinium lichenoides_**

ITS sequences adopted from Otálora et al. (2008) and Schmull et al. (2011). Our mtSSU sequences match *S. lichenoides* with identities over 99.5%.

**_Scytinium magnussonii_**

ITS adopted from Vondrák et al. (2022; OL396660, sub *L. lichenoides*). Our mtSSU match *S. magnussonii* in NCBI with 100% identities.

**_Scytinium subtile_**

Our sequences from specimens from soil crust and from tree bark are distinct; specimens are 88% identical in ITS and 97.5% in mtSSU. Our ITS from the epiphyte has the closest NCBI BLAST to *Scytinium* spp. with identities up to 91%. (KU529976, MZ243573, named *S. subtile*, are not closely related.) Our mtSSU sequences from epiphytes have the closest BLAST to *Scytinium* spp. with identities up to 98.5%. (JX992969 and JX992970, named *S. subtile*, are about 98% identical.)

**_Scytinium teretiusculum_**

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *S. lichenoides* with identities 89–93%; our mtSSU sequences BLAST to *S. lichenoides* and *S. magnussonii* with identities about 98%.

**_Snippocia nivea_**

ITS absent from NCBI. Sequence of mtSSU adopted from Ertz et al. (2018b).

***Sphaeronema truncatum***

This wood-dwelling coelomycete from *Ostropomycetidae* is a little-known but common European semilichen. ITS and mtSSU absent from NCBI. Our ITS sequences from seven specimens are more than 99.5% identical and they have the closest NCBI BLAST to *Mulderomyces* (c. 87% identity) and *Elongaticonidia* (c. 86.5% identity); both *Ostropales*. Our mtSSU has the closest BLAST to lichens from *Ostropales* (*Thrombium*) and *Trapeliales* (*Rimularia*) with identities up to 87.5%.

***Sphaerophorus globosus***

Our ITS matches *S. globosus* in NCBI with identities over 99%, our mtSSU with 100%.

***Sphinctrina anglica***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *S. leucopoda* (AY795875) with the identity 93.5%. Our mtSSU has the closest BLAST to *S. turbinata* (FJ713611) with the identity 99%.

***Sphinctria leucopoda***

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI and not obtained by us.

***Sphinctrina tubaeformis***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Sphinctrina* spp. with identities up to 88%. Our mtSSU has the closest NCBI BLAST to *S. turbinata* (FJ713611) with the identity 98%.

***Sphinctrina turbinata***

Our ITS matches *S. turbinata* in NCBI with identities 98.5–99%, our mtSSU with 100%.

***Sporodophoron cretaceum***

ITS absent from NCBI. Sequence of mtSSU adopted from Frisch et al. (2015).

***Sporodophoron* aff. *cretaceum***

Trentepohlioid lichen with white pruinose apothecia, 4-septate ascospores with an enlarged upper cell and without sporodochia. Related species are without apothecia and with sporodochia (Frisch et al. 2015). Our ITS sequence is close to *Coniocarpon* (*Arthoniaceae*) in NCBI. According to our ITS data, *Sporodophoron* is more close to *Inoderma*, which fits mtSSU phylogeny. Our mtSSU sequence is 97–99% identical with *S. cretaceum* and the same identity shows *S. primorskiense*. Both species are morphologically distinct.

***Staurolemma omphalarioides***

ITS adopted from Bendiksby et al. (2014) and mtSSU from Bendiksby et al. (2014) and Otálora et al. (2008).

***Steinia geophana***

ITS absent from NCBI. Our ITS sequences from three specimens are 92% identical. They have the closest NCBI BLAST to *Dothideomycetes* spp. and *Lecanoromycetes* spp. with identities up to 85%. Sequence of mtSSU adopted from Printzen et al. (2012).

***Stenocybe major***

ITS and mtSSU absent from NCBI. Our ITS sequences have the closest NCBI BLAST to *S. pullatula* (AY795878) with the identity 90%. Our mtSSU has the closest BLAST to *Mycocalicium subtile* with identities 96–97%.

***Stenocybe pullatula***

ITS adopted from Tibell & Vinuesa (2005). Sequences of mtSSU absent from NCBI. Our mtSSU has the closest BLAST to *Mycocalicium subtile* with identities 95–96%.

***Sticta atlantica***

ITS and mtSSU adopted from Magain & Sérusiaux (2015).

***Sticta canariensis***

ITS and mtSSU adopted from Magain & Sérusiaux (2015).

***Sticta ciliata***

ITS and mtSSU adopted from Magain & Sérusiaux (2015).

***Sticta fuliginoides***

Our ITS matches *S. fuliginoides* in NCBI with identities over 99%. Sequence of mtSSU adopted from Magain & Sérusiaux (2015).

***Sticta fuliginosa***

ITS and mtSSU adopted from Magain & Sérusiaux (2015).

***Sticta limbata***

ITS and mtSSU adopted from Magain & Sérusiaux (2015).

***Sticta sylvatica***

ITS and mtSSU adopted from Magain & Sérusiaux (2015).

***Stictis brunnescens***

ITS and mtSSU adopted from Wedin et al. (2005).

***Stictis confusum***

ITS and mtSSU adopted from Wedin et al. (2006).

***Stictis mollis***

ITS and mtSSU adopted from Wedin et al. (2004).

***Stictis populorum***

ITS and mtSSU adopted from Wedin et al. (2004).

***Stictis radiata***

ITS and mtSSU adopted from Wedin et al. (2004).

***Stictis urceolatum***

ITS and mtSSU adopted from Schmull et al. (2011).

***Strangospora moriformis***

Our identical ITS sequences of three specimens have the closest NCBI BLAST to *Sarea* spp. with identities up to 88%. Our mtSSU matches the only available sequence of *Strangospora* (KJ766500; Miadlikowska et al. 2014; sub *S. pinicola*) with identities 99.5%. Other relatives are *Acarosporomycetidae* with identities up to 90%.

***Strangospora pinicola***

Our ITS differs from our *S. moriformis* sequences; both are about 96% identical. The closest NCBI BLAST is to *Sarea* spp. with identities up to 89.5%. Our mtSSU matches the only available sequence of *Strangospora* (KJ766500; Miadlikowska et al. 2014; sub *S. pinicola*) with the identity 97%. Other relatives are *Acarosporomycetidae* with identities up to 92%.

***'Strigula' inconspicua* ined.**

Tiny semilichen with translucent perithecia and 1-septate ascospores. ITS not obtained. Our mtSSU has the closest NCBI BLAST to *Dothideomycetes* spp. (up to 82% identities) and *Ostropomycetidae* spp. (up to 80% identities).

***'Strigula'* sp. 2 (sensu Vondrák et al. 2022)**

Mentioned in the section "known-unknowns" in Vondrák et al. (2022). Only mtSSU sequenced in two specimens. Our almost identical sequences have the closest NCBI BLAST to *Trichomeriaceae* (*Chaetothyriomycetidae*) with the identitities up to 99%. Assignment of sequences needs confirmation.

***Swinscowia glabra* (= *Strigula glabra*)**

ITS and mtSSU absent from NCBI. Our identical ITS sequences from two specimens have the closest NCBI BLAST to *S. jamesii* (OL453195) with the identity 88%. Sequences of mtSSU absent from NCBI and not obtained by us.

***Swinscowia jamesii* (= *Strigula jamesii*)**

Our ITS sequences represent two distinct genotypes. One matches *S. jamesii* in NCBI (OL453195) with the identity over 99.5%, the other with identity 86%. Our mtSSU matches *S. jamesii* (OK465657) with 100% identity.

***Swinscowia stigmatella* (= *Strigula stigmatella*)**

ITS absent from NCBI. Our identical ITS sequences from two specimens have the closest NCBI BLAST to *S. jamesii* (OL453195) with the identity 80%. Our identical mtSSU sequences from two specimens match the single *S. stigmatella* in NCBI (AY607748) with the identity 91%.

***Syncesia myrticola***

ITS adopted from Ertz et al. (2018c). Sequences of mtSSU absent from NCBI.

***Synarthonia astroidestera***

Sequence of mtSSU adopted from Ertz et al. (2020). Sequence ITS absent from NCBI and not obtained by us.

***Synarthonia ochracea***

ITS and mtSSU adopted from Van den Broeck et al. (2018).

***Szczawinskia leucopoda***

ITS not available in NCBI. Sequence of mtSSU adopted from Andersen & Ekman (2005).

***Szczawinskia tsugae***

ITS adopted from Andersen & Ekman (2004), mtSSU from Andersen & Ekman (2005).

***Teloschistes chrysophthalmus***

ITS adopted from Martin & Winka (2000), mtSSU from Miadlikowska et al. (2014).

***Tetramelas chloroleucus***

ITS adopted from Marthinsen et al. (2019). Sequences of mtSSU absent from NCBI and not obtained by us.

***Tetramelas* sp.**

Our ITS has the closest NCBI BLAST to *Tetramelas* spp. with identities up to 93% and our mtSSU to *Buellia* spp. with identities up to 95%.

***Tetramelas triphragmioides***

ITS adopted from Helms et al. (2003). Sequences of mtSSU absent from NCBI and not obtained by us.

***Thelenella modesta***

ITS and mtSSU absent from NCBI. Our ITS has the closest NCBI BLAST to *Dictyocatenulata alba* with identities 82–86%. Our mtSSU has the closest NCBI BLAST to *Thelenella muscorum* (AY607743) with the identity 92%.

***Thelenella muscorum* var. *muscorum***

Our ITS sequences have the closest NCBI BLAST to *Dictyocatenulata alba* with identities 79–80%. Our mtSSU sequences match *T. muscorum* (AY607743) with the identity over 99.5%.

***Thelenella vezdae***

Our ITS sequences have the closest NCBI BLAST to *Dictyocatenulata alba* with identities 80–81.5%. Our mtSSU sequences have the closest NCBI BLAST to *Thelenella muscorum* (AY607743) with the identity 91%.

***Thelocarpon epibolum***

ITS adopted from NCBI (Eberhard & Krause 2019, unpublished) and its identity is suspicuous. Sequences of mtSSU absent from NCBI and our mtSSU has the closest BLAST to *T. impressellum* (JN206651) with the identity 94%.

***Thelocarpon impressellum***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Lumbsch et al. (2009).

***Thelocarpon intermediellum***

ITS and mtSSU absent from NCBI. Our ITS sequences of three specimens have the closest NCBI BLAST to *Acarosporaceae* and *Sarea* with identities up to 85%, our mtSSU sequences to *Thelocarpon laureri* (KT232226) with identities about 95%.

***Thelocarpon lichenicola***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Lumbsch et al. (2009).

***Thelopsis rubella***

ITS absent from NCBI. Our ITS has the closest NCBI BLAST to *Gyalectaceae* spp. with identities up to 90%. Sequence of mtSSU adopted from Ertz et al. (2021).

***Thelotrema lepadinum***

Our ITS and mtSSU sequences match *T. lepadinum* in NCBI with identities 99.5–100%.

***Thelotrema macrosporum***

ITS adopted from Marthinsen et al. (2019), mtSSU from Parnmen et al. (2012).

***Thelotrema suecicum***

Our ITS and mtSSU sequences match *T. suecicum* in NCBI with identities 99.5–100%.

***Tholurna dissimilis***

ITS adopted from Marthinsen et al. (2019), mtSSU from Wedin et al. (2002).

***Toensbergia leucococca***

Our ITS matches *T. leucococca* in NCBI with identities 98–99.5%, our mtSSU with 100%.

***Toniniopsis separabilis* (= *Bacidia subincompta* p.p.)**

Our ITS sequences from two specimens differ in 2% of nucleotide positions. Both have the closest NCBI BLAST to *T. separabilis* with identities 98–100%. Our two identical mtSSU have the closest NCBI BLAST to *T. separabilis* with identities 100%.

***Toniniopsis dissimilis* (= *Bacidia subincompta* p.p.)**

ITS and mtSSU adopted from Gerasimova et al. (2021).

***Toniniopsis* sp.**

Epiphytic *Bacidia* (s.lat.) with typically white pruinose apothecial margin. Our ITS has the closest NCBI BLAST to *Toniniopsis*, but with identities only up to 87%. Sequences of mtSSU not obtained.

***Tornabea scutellifera***

ITS and mtSSU adopted from Prieto & Wedin (2017).

***Trapelia corticola***

Our ITS matches *T. corticola* in NCBI with identities about 98%, our mtSSU with identities about 99%.

***Trapeliopsis flexuosa***

Our ITS matches *T. flexuosa* in NCBI with identities 97–99%, our mtSSU with identities 95–100%.

***Trapeliopsis gelatinosa***

Usually occurs on soil, but has occassional epiphytic occurrences. ITS and mtSSU adopted from Resl et al. (2015).

***Trapeliopsis glaucolepidea***

Our ITS matches *T. glaucolepidea* in NCBI (haplotypes H1 and H2 sensu Palice & Printzen 2004) with identities 100% and close. Additional ITS adopted from Palice & Printzen (2004; haplotype H07). Sequence of mtSSU adopted from Schmitt et al. (2003).

***Trapeliopsis granulosa***

Our ITS matches *T. granulosa* in NCBI with 97.5–100% identities, our mtSSU with 99–100%.

***Trapeliopsis pseudogranulosa***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Trapeliopsis viridescens***

Our ITS matches *T. viridescens* in NCBI with identities over 99.5%, our mtSSU with 99.5%.

***Tuckermannopsis chlorophylla***

Our ITS and mtSSU sequences match *T. chlorophylla* in NCBI with identities 99–100%.

***Tylophoron hibernicum***

ITS absent from NCBI and not obtained by us. Sequence of mtSSU adopted from Frisch et al. (2014).

***Usnea articulata***

ITS adopted from Kelly et al. (2011). Sequences of mtSSU absent from NCBI.

***Usnea barbata***

Sequences of mtSSU absent from NCBI. Our ITS sequences are close to those of *U. intermedia* and differ in only two nucleotide positions. Our mtSSU sequences of *U. barbata* and *U. substerilis* are identical and differ from most others in two indel positions only.

***Usnea ceratina***

ITS adopted from Mark et al. (2016). No mtSSU sequences in NCBI and not obtained by us.

***Usnea cornuta***

ITS adopted from Kelly et al. (2011). No mtSSU sequences in NCBI and not obtained by us.

**Usnea dasopoga**

Sequences of mtSSU absent from NCBI. Our ITS matches *U. dasopoga* in NCBI with identities close to 100%. Our mtSSU is the most distinct from other *Usnea* sequences. It has eleven unique nucleotide positions.

**Usnea flammea**

ITS adopted from Marthinsen et al. (2019). No mtSSU sequences in NCBI and not obtained by us.

**Usnea flavocardia**

ITS sequences adopted from Kelly et al. (2011) and Lücking et al. (2020). No mtSSU sequences in NCBI and not obtained by us.

**Usnea florida**

ITS adopted from Saag et al. (2011). No mtSSU sequences in NCBI and not obtained by us.

**Usnea fulvoreagens**

Our ITS sequence matches with *U. fulvoreagens* in NCBI (AB051638; Ohmura 2002) with 100% identity. No mtSSU sequences in NCBI and not obtained by us either.

**Usnea glabrata**

Sequences of mtSSU absent from NCBI. Our ITS has the closest NCBI match to *U. glabrata* (KJ406281; Millanes et al. 2014) with identity 98.5%. Our mtSSU sequences of *U. glabrata*, *U. hirta* and *U. viktoriana* are identical and differ from most others in two indel positions only.

**Usnea glabrescens**

Our ITS sequences match *U. glabrescens* (051639; Ohmura 2002) with identities 98.5–99.5%. No mtSSU sequences in NCB and not obtained by us.

**Usnea hirta**

Sequences of mtSSU absent from NCBI. Our ITS matches *U. hirta* in NCBI with identities over 99%. Our mtSSU sequences of *U. glabrata*, *U. hirta* and *U. viktoriana* are identical and differ from most others in two indel positions only.

**Usnea intermedia**

Our ITS sequences are close to those of *U. barbata* and differ in only two nucleotide positions. No mtSSU sequences in NCBI and not obtained by us.

**Usnea longissima**

ITS adopted from Ohmura (2002), mtSSU from Arup et al. (2007).

**Usnea perplexans**

ITS adopted from Mark et al. (2016). No mtSSU sequences in NCBI and not obtained by us.

**Usnea rubicunda**

ITS adopted from Marthinsen et al. (2019). No mtSSU sequences in NCBI and not obtained by us.

***Usnea subfloridana***

Sequences of mtSSU absent from NCBI. Our ITS has closest NCBI matches to *U. subfloridana* and *U. florida* with identities 98.5–100%. Our mtSSU differs from other *Usnea* sequences in only two nucleotide positions.

***Usnea substerilis***

ITS adopted from Saag et al. (2011). Our mtSSU sequences of *U. barbata* and *U. substerilis* are identical and differ from most others in two indel positions only. Sequences of mtSSU absent from NCBI.

***Usnea viktoriana***

Our ITS is identical with *Usnea viktoriana* in NCBI (KU352663; sub *U. praetervisa*, Clerc & Otte 2018). Sequences of mtSSU absent from NCBI and our mtSSU sequence is identical to those of *U. glabrata* and *U. hirta* and differ from most *Usnea* spp. in two indel positions only.

***Usnea wasmuthii***

Our ITS sequences match *U. wasmuthii* in NCBI with identities 99.5–100%. No mtSSU sequences in NCBI and not obtained by us either.

***Usnea* sp.**

It is usually identified as *U. wasmuthii*, but it is rich in isidiomorphs and has quite distinct ITS that has closest NCBI match with "*U. wasmuthii*" (AB051675; Ohmura 2002), but other ITS of *U. wasmuthii* are distinct.

***Usnocetraria oakesiana***

ITS and mtSSU adopted from the NCBI (KC990141; EU435375).

***Vahliella saubinetii***

ITS absent from NCBI. Sequence of mtSSU adopted from Wedin et al. (2011).

***Varicellaria hemisphaerica***

Our ITS matches *V. hemisphaerica* in NCBI (HQ650676; Schmull 2011) with the identity 98.5%. Our mtSSU matches *V. hemisphaerica* in NCBI with identities 99.5–100%.

***Varicellaria rhodocarpa***

Epiphytic occurrences are rare, in coniferous forests at timberline. Our ITS and mtSSU match with *V. rhodocarpa* in NCBI with identities 94–100%.

***Varicellaria velata***

ITS adopted from Prieto et al. (2013) and mtSSU from Schmitt et al. (2010).

***Verrucaria breussii***

ITS sequences absent in NCBI and not sequenced by us. Our mtSSU adopted from Vondrák et al. (2022).

***Verrucaria bryoctona***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Verrucaria hegetschweileri***

ITS and mtSSU adopted from Vondrák et al. (2022).

***Verrucaria lapidicola***

Usually epilithic, but occassionally on bases of tree trunks. Our ITS matches *V. lapidicola* in NCBI with 95.5–99%. Sequences mtSSU absent from NCBI and not sequenced by us.

***Verrucaria phloeophila***

Our ITS sequences have the closest NCBI BLAST to *V. hydrophila* sharing identities 94–95%. Our mtSSU sequences have closest BLAST to *V. dolosa* with identities 97–98%.

***Verrucaria teyrzowensis***

Sequences of mtSSU absent from NCBI. Our ITS sequences from epiphytic lichens match *V. teyrzowensis* in NCBI (MZ969005; Vondrák et al. 2022) with 100% identities.

***Verrucaria trabalis***

Our ITS sequences match *Agonimia allobata* (JF509162) with 100% identity, but this NCBI sequence in fact does not belong to *Agonimia*. Other NCBI matches are *Verrucaria* spp. with identities up to 90%. Our mtSSU has the closest NCBI match to *Agonimia* spp. and *Verrucaria viridigrana* with identities up to 96.5%.

***Verrucaria viridigrana***

Species closely related to *V. bryoctona*. ITS and mtSSU partly adopted from Vondrák et al. (2022). Whereas our mtSSU sequences are almost identical, we revealed two distinct genotypes in ITS sharing 95–98% identities.

***Verrucaria* sp. (*Verrucaria* cf. *phloeophila*)**

Our ITS matches numerous *Verrucaria* spp. with identities up to 91%. Our mtSSU sequences match "*V. phloeophila*" in NCBI (DQ329013; Del Prado et al. 2006) with 98.5–99% identities, but they are only about 93% identical with *V. phloeophila* in our understanding.

***Vezdaea aestivalis***

ITS and mtSSU absent from NCBI. Our identical ITS sequences of three specimens have the closest NCBI BLAST to *Candelariomycetidae* spp. and *Acarosporomycetidae* spp., but with low covers, up to 40%. Our almost identical mtSSU sequences of four specimens have no close relatives in NCBI. Closest matches are to various *Ascomycota* with identities up to 78%.

***Vezdaea retigera***

ITS and mtSSU sequences absent from NCBI. Our ITS is short, including only the ITS2 region, which is 91% identical with our sequence of *V. rheocarpa*. Our short mtSSU sequence (221 BP) has the closest NCBI BLAST to members of following classes: *Dothideomycetes*, *Eurotiomycetes*, *Lecanoromycetes*, *Lichinomycetes* and *Sareomycetes*. Identity of mtSSU needs confirmation.

***Vezdaea rheocarpa***

ITS and mtSSU sequences absent from NCBI. Our ITS has the closest NCBI match to *Sarea* spp. with identities up to 84%. Our short mtSSU sequences (both 231 BP) have the closest NCBI BLAST to members of following classes: *Dothideomycetes*, *Eurotiomycetes*, *Lecanoromycetes*, *Lichinomycetes* and *Sareomycetes*. Identity of mtSSU sequences need confirmation.

***Violella fucata***

Sequences of mtSSU absent from NCBI. Our ITS sequences include two genotypes. One is identical with *V. fucata* (JN009733, JN009732, KX132968) and another is close to KX132980. Both genotypes are about 91% identical. MtSSU not sequenced.

***Vulpicida pinastri***

ITS adopted from Marthinsen et al. (2019). Our mtSSU matches *V. pinastri* in NCBI with identities 100% or close.

***Wadeana dendrographa***

ITS and mtSSU sequences absent from NCBI. Our ITS has the closest NCBI BLAST to *Acarosporaceae* spp. with identities up to c. 85%. Sequence of mtSSU not obtained.

***Xanthomendoza fallax* (incl. *Xanthomendoza huculica*)**

Our ITS match *X. fallax* in NCBI with identities 97–100%; our mtSSU is identical with *X. fallax* (MH156652; Malíček et al. 2018b). Morphological distinguishing from *X. huculica* is dubious and Lindblom et al. (2019) consider both species synonymous. Our sequences of specimens identified as *X. huculica* are almost identical with those identified as *X. fallax* (>99% identity in ITS) and we also consider both synonymous.

***Xanthomendoza fulva***

ITS adopted from Marthinsen et al. (2019). Our mtSSU is identical with *X. fulva* in NCBI (Fedorenko et al. 2009).

***Xanthomendoza huculica***

Recognition from *X. fallax* is questionable and needs further studies. We consider it a synonym to *X. fallax*. ITS of both species is about 99% identical in ITS and 100% in mtSSU. Additional sequences adopted from Fedorenko et al. (2012) and Malíček et al. (2018b).

***Xanthomendoza oregana***

ITS adopted from Lindblom & Blom (2014). Sequences of mtSSU not included in Martin7.

***Xanthomendoza ulophyllodes***

The species is more common in eastern Europe where it grows as epiphyte, but also on stones and soil. Our ITS sequences of epiphytic populations match *X. ulophyllodes* in NCBI with identities 99–100% and our mtSSU with 100%. It is closely related to *X. fallax*.

***Xanthoria candelaria***

Our sequences match *X. candelaria* in NCBI with identities 98–99% in ITS and over 99% in mtSSU. Hardly recognisable from *X. polycarpa* by mtSSU, where both species differ in only three nucleotide positions.

***Xanthoria parietina***

Our ITS and mtSSU sequences match *X. parietina* in NCBI with identities over 99%.

***Xanthoria polycarpa***

Our ITS and mtSSU sequences match *X. polycarpa* in NCBI with identities over 99%. Hardly recognisable from *X. candelaria* by mtSSU, where both species differ in only three nucleotide positions.

***Xyleborus* sp.**

No ITS and mtSSU sequences to *Xyleborus* spp. in NCBI. We obtained only mtSSU which is close to alleged *Malmideaceae* (e.g. *Cheiromycina* spp., *Lecidea hypopta* and *L. malmeana*) with identities up to 93%.

***Xylographa pallens***

ITS and mtSSU sequences adopted from Spribille et al. (2014).

***Xylographa parallela***

Our ITS matches *X. paralella* in NCBI with identities 97.5–100%. MtSSU adopted from Urbanavichus et al. (2020).

***Xylographa rubescens***

Our ITS matches *X. rubescens* in NCBI with identities over 99% and our mtSSU with identities close to 100%. It is hardly distinguishable by mtSSU sequences from related species (e.g. *X. paralella*).

***Xylographa soralifera***

ITS and mtSSU sequences adopted from Spribille et al. (2014).

***Xylographa trunciseda***

Our ITS sequences match *X. trunciseda* in NCBI with identities 96.5–99.5% and our mtSSU with identities over 98%.

***Xylographa vitiligo***

Our ITS matches *X. vitiligo* in NCBI with identities 98.5–100% and our mtSSU with identities about 99%.

***Xylopsora caradocensis***

Sequences of mtSSU absent from NCBI. Our ITS matches *X. caradocensis* in NCBI (KF360385; Bendiksby & Timdal 2013) with the identity 99.5%. Our mtSSU sequences have the closest NCBI BLAST to *X. friesii* and *X. canopeorum* with identities almost 99%.

### *Xylopsora friesii*

Our ITS sequences match *X. friesii* in NCBI with identities 95–100% and our mtSSU with identities over 99%. Two genotypes observed in ITS sharing about 96% identity.

### *Xylopsora* sp. 1

Sorediate lichen closely related to *X. friesii* (type1), but with 10 distinct nucleotide positions. It is indistinguishable from *X. friesii* in mtSSU and possibly represents sorediate morphotype of this species.

### *Zwackhia sorediifera*

ITS absent from NCBI. Sequence of mtSSU adopted from Frisch et al. (2014).

### *Zwackhia viridis*

ITS absent from NCBI. Our almost identical sequences from two specimens have no close relatives in NCBI; their closest BLAST results are *Acarosporomycetes* spp. and *Lecanoromycetes* spp. with very low cover (about 20%). Our mtSSU sequences match *Z. viridis* in NCBI with identities 100% or close.

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