

***New Phytologist* Supporting Information**

Article title: Endophytism and Endolichenism in Pezizomycetes: the exception or the rule?
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The following Supporting Information is available for this article:

Fig. S1 Flow chart outlining the basic steps for assembling data on Pezizomycetes endophytes and endolichenics.

Fig. S2 Phylogeny of endophytic fungi in Pezizomycetes based on 28S sequences analyzed with Maximum Likelihood. This figure is an expanded, linear version of Figure 1 that includes more detailed annotation.

Fig. S3 Phylogeny based on ITS sequences of Ascobolaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood.

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Fig. S29 Phylogeny based on ITS sequences of Rhizinaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S30 Phylogeny based on ITS sequences of Sarcoscyphaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S31 Phylogeny based on ITS sequences of Sarcosmataceae (*Donadinia*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S32 Phylogeny based on ITS sequences of Sarcosmataceae (*Galiella*, *Plectania*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S33 Phylogeny based on ITS sequences of Sarcosmataceae (*Pseudoplectania*, *Sarcosoma*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S34 Phylogeny based on ITS sequences of Sarcosmataceae (*Urnula*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S35 Phylogeny based on ITS sequences of Tarzettaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S36 Phylogeny based on ITS sequences of Tuberaceae analyzed with Maximum Likelihood.

Fig. S37 Phylogeny based on ITS sequences of Geomoriaceae and an undetermined lineage of related endophytic and endolichenic fungi analyzed with Maximum Likelihood.

Fig. S1 Flow chart outlining the basic steps for assembling data on Pezizomycete endophytes and endolichens. The ITS and 28S workflows are similar except that iterative BLAST searches based on ITS reference sequences from voucher specimens (black circular arrows) were used extensively to identify endophytes and endolichens whereas this process was not done for 28S because relatively few 28S sequences were available for endophytes and endolichens outside of those from the University of Arizona (UA) collection. Note that the ITS and 28S datasets were compared and verified during the phylogeny-building portion of the workflow. During the final steps of the ITS workflow we used the ITS phylogenies to compile conservative tree-based OTU estimates which were secondarily compared with OTU estimates based on a 97% similarity sequence-clustering approach (see Supporting Information Notes S1 for details).

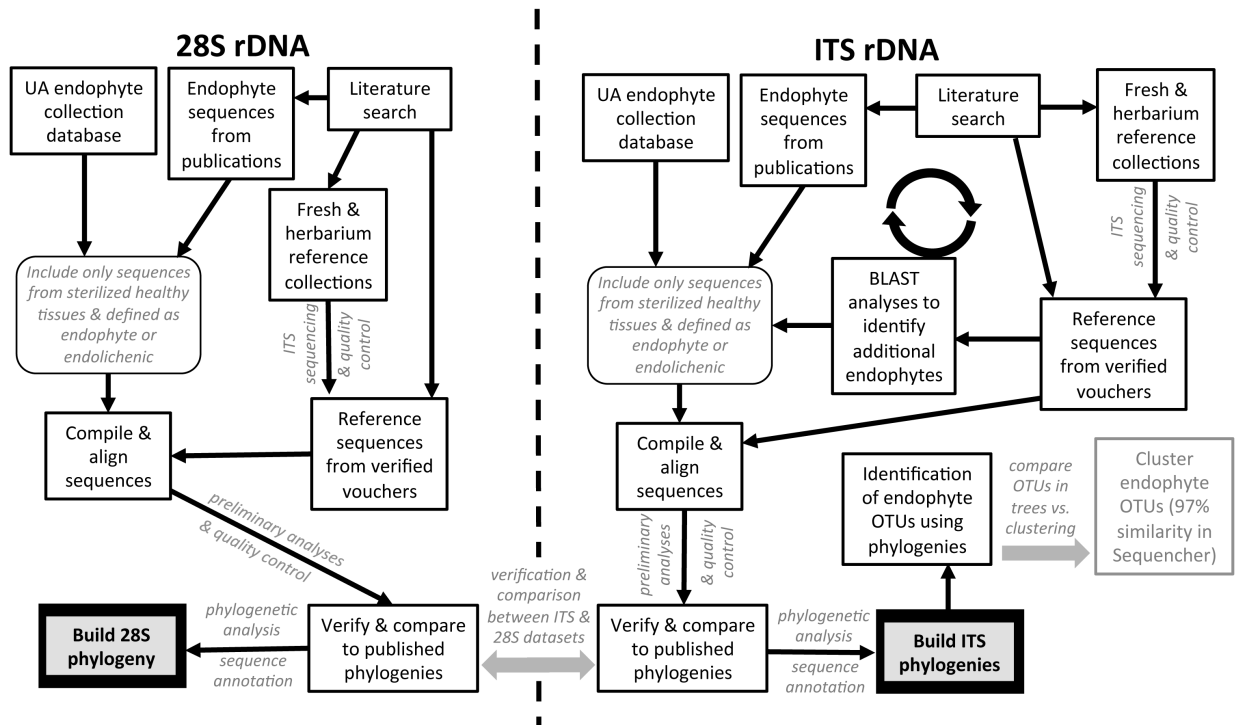
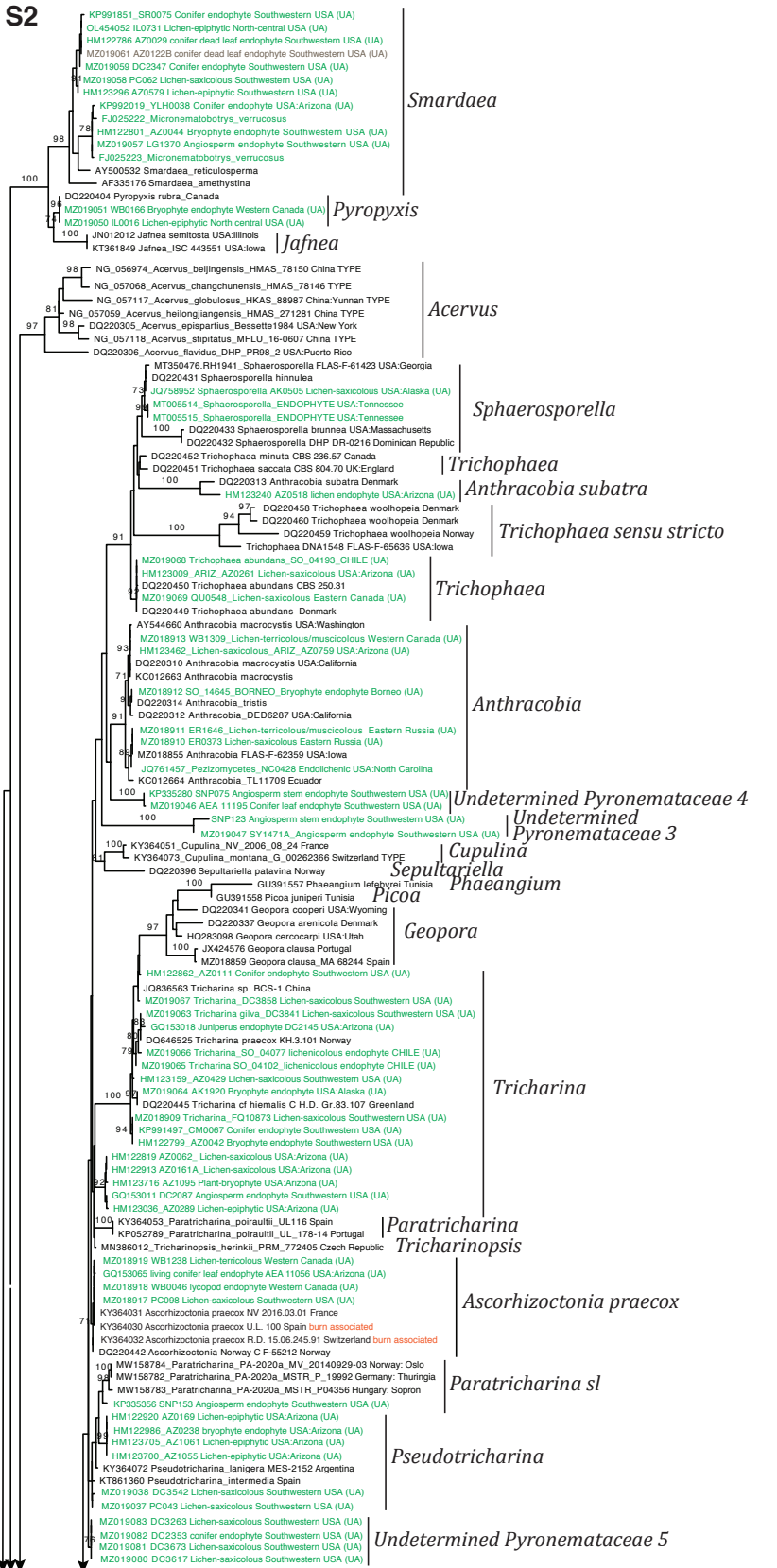


Fig. S2 Phylogeny of endophytic fungi in Pezizomycetes based on 28S sequences analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with support based on 1000 bootstrap replicates and taxa in the Orbiliomyceetes used as the outgroup. Bootstrap support $\geq 70\%$ is shown above each node. Green asterisk beside *Mattiolomyces* and *Tuber* species refers to documented endophyte associations although 28S rDNA sequences were not available from endophytes for these taxa. Known genera and families are demarcated with larger bold text and vertical bars. An undetermined lineage related to Tuberaceae and Geomoriaceae is also highlighted. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE" and sequences from ectomycorrhizas are designated with the abbreviation "ECM" preceded by host name if available. The abbreviation "sl" is used for "*sensu lato*" and "ss" is used for "*sensu stricto*." Terminals are color coded by their sequence source with (fruitbody, black; asexual sporemat, blue; endophytic or endolichenic, green), and substrates for fruitbody are color coded if they were collected on a burnt substrate (orange) or on dung (yellow-brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S2



Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Isolate from dead leaf
- Asexual spore mat
- Fruitbody on burned site

Figure S2
(Cont.)

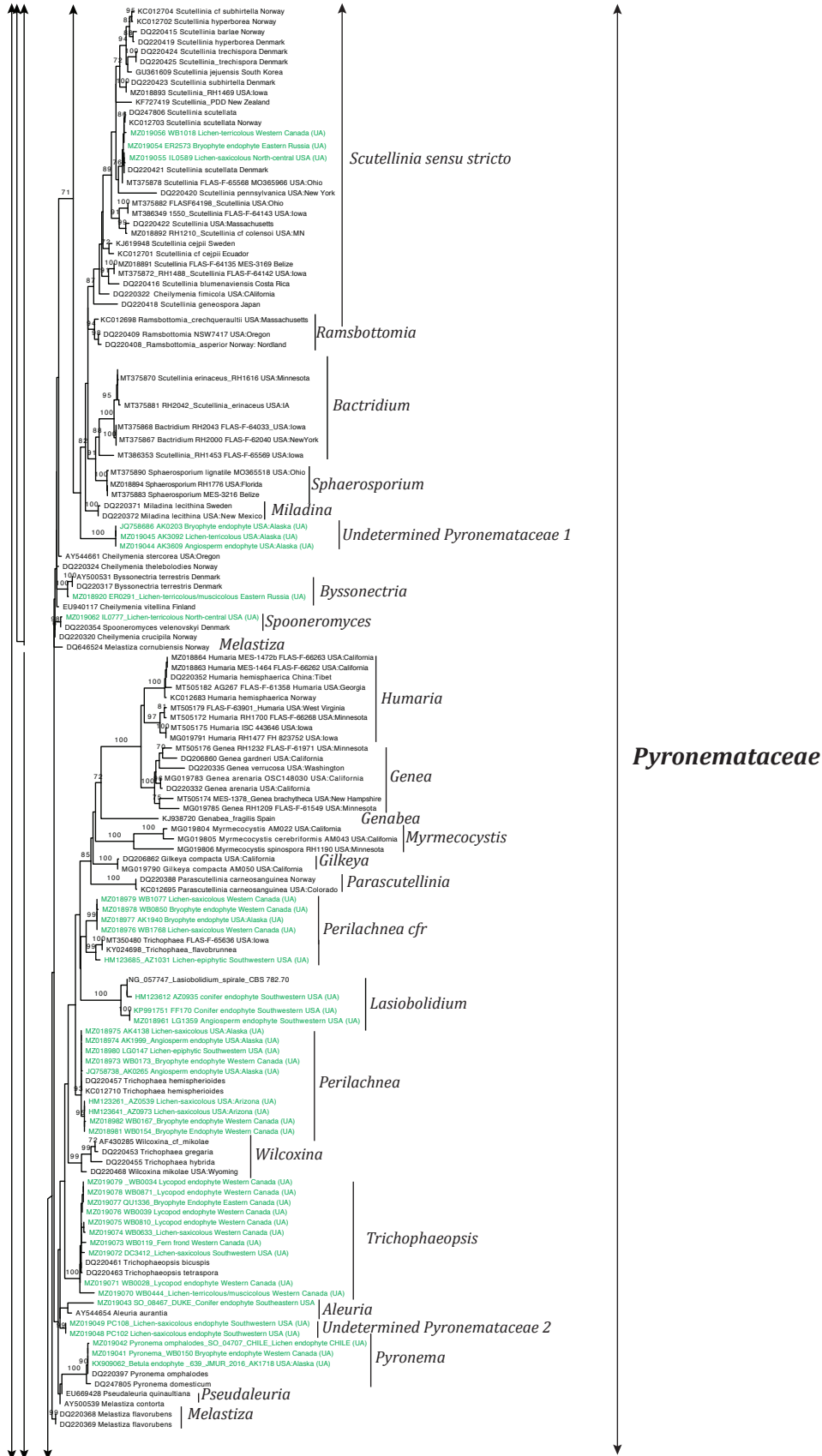


Figure S2
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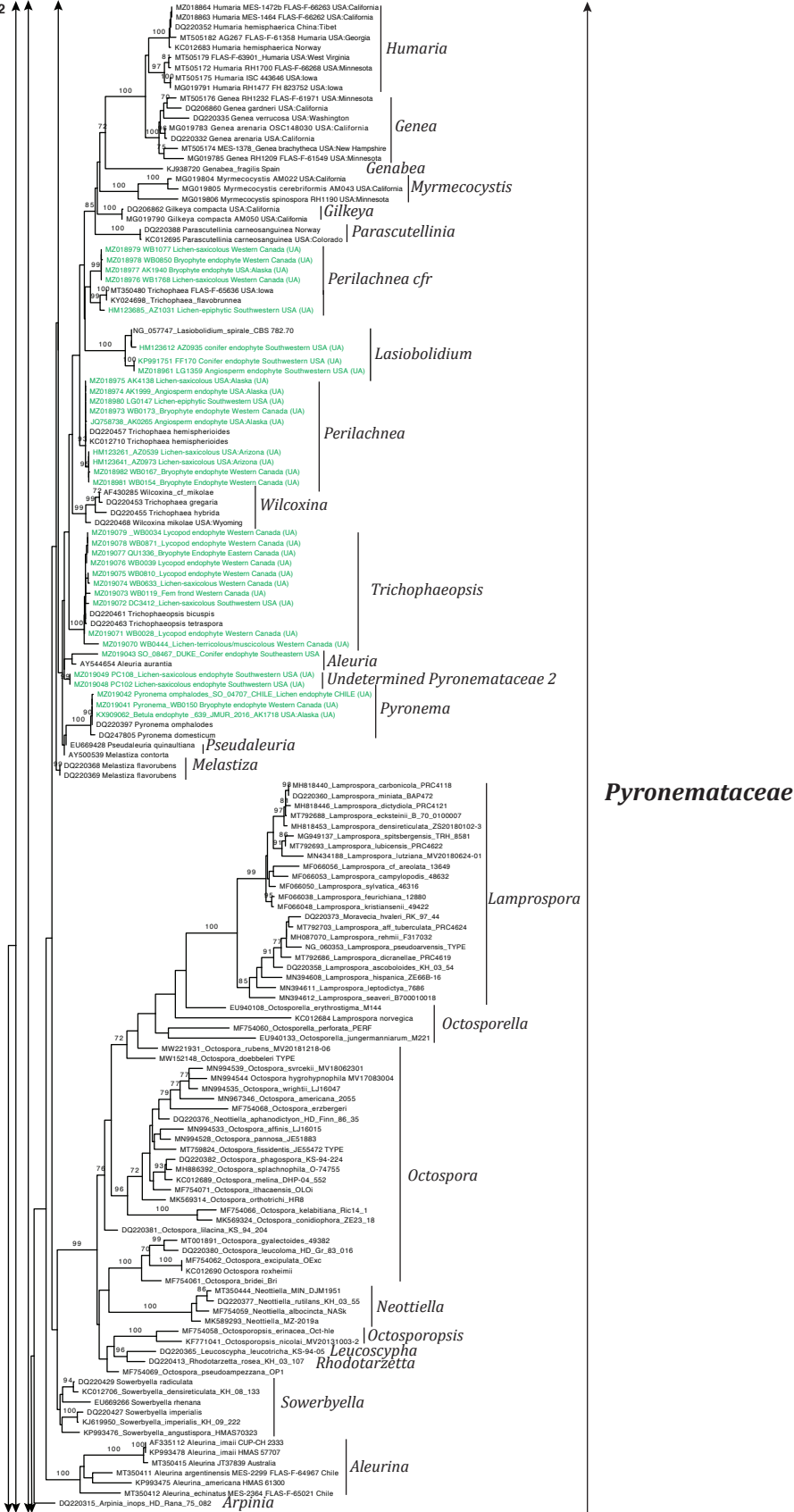


Figure S2
(Cont.)

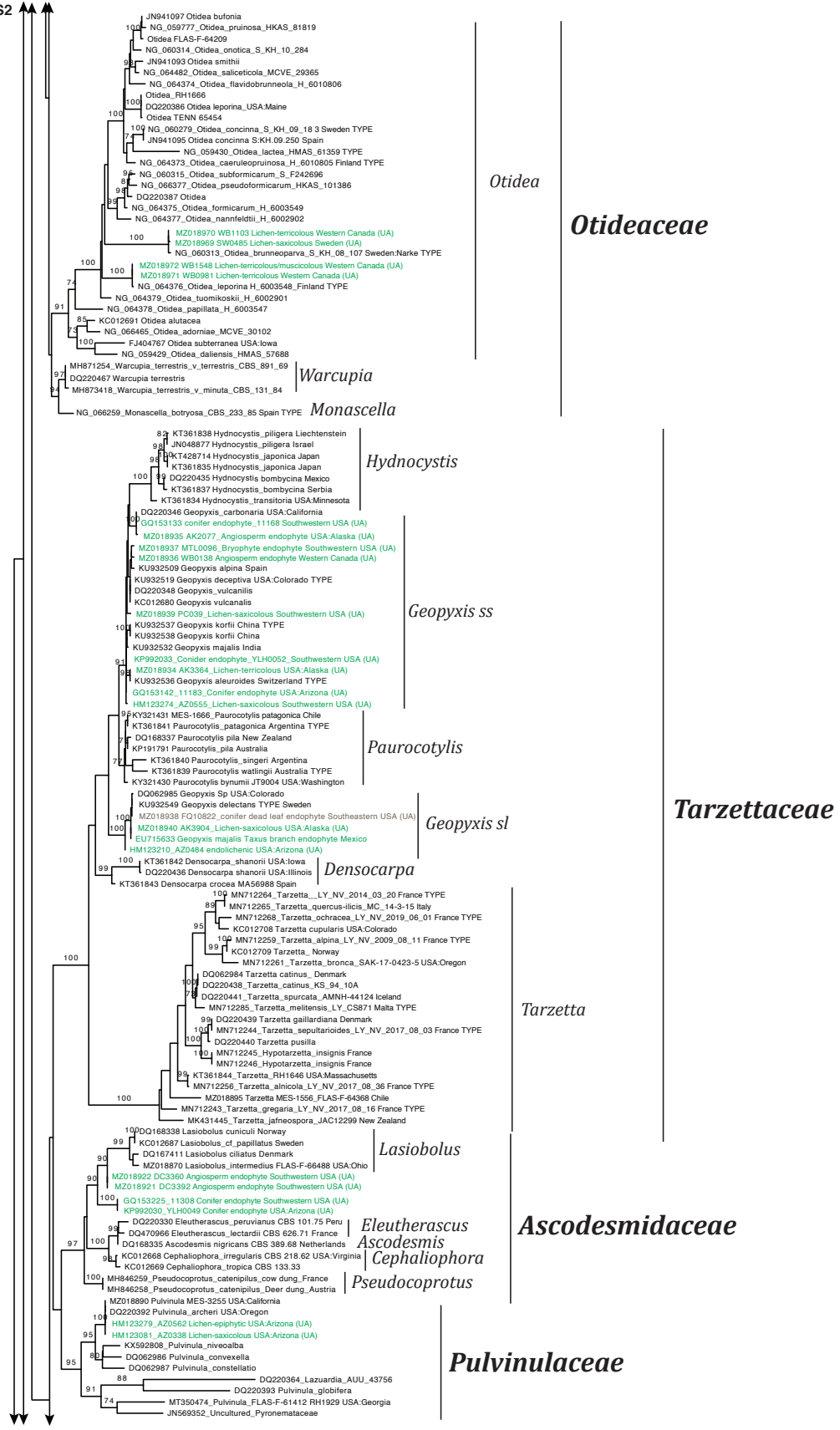


Figure S2
(Cont.)

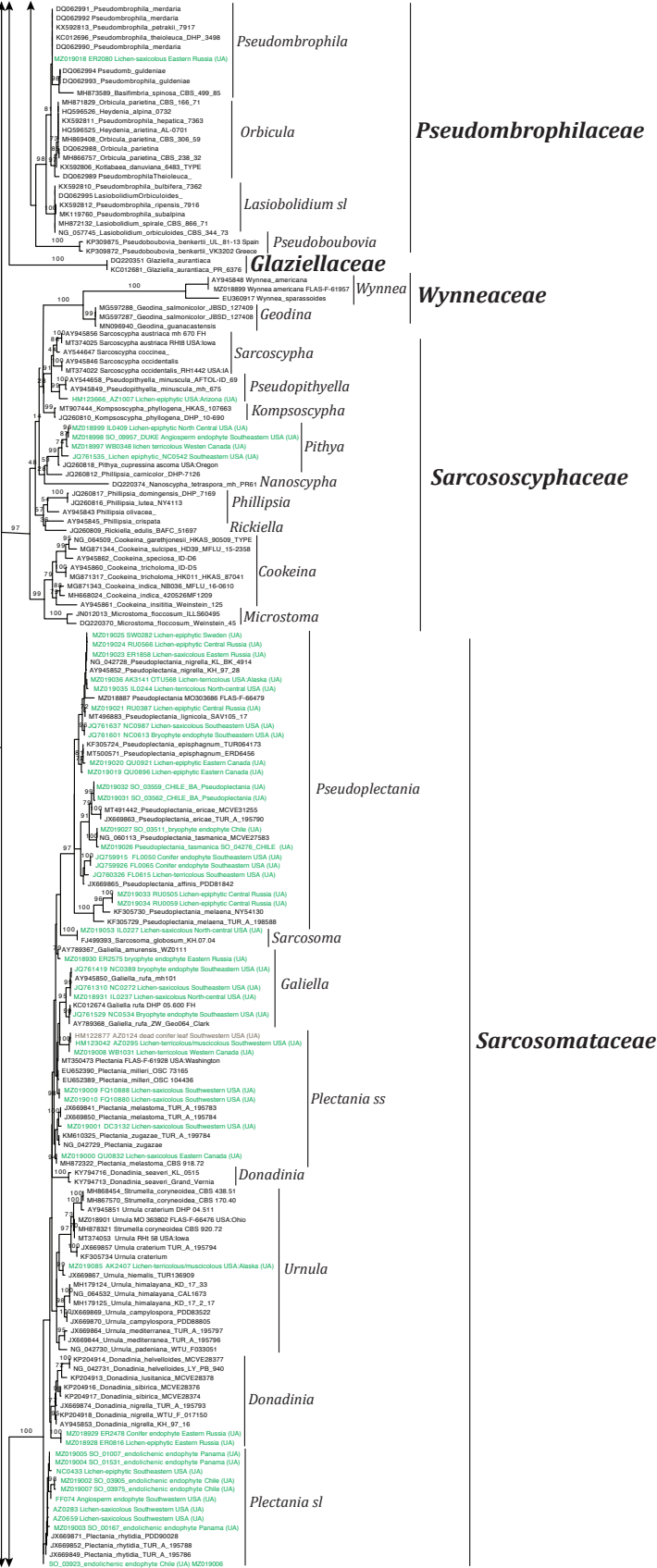


Figure S2
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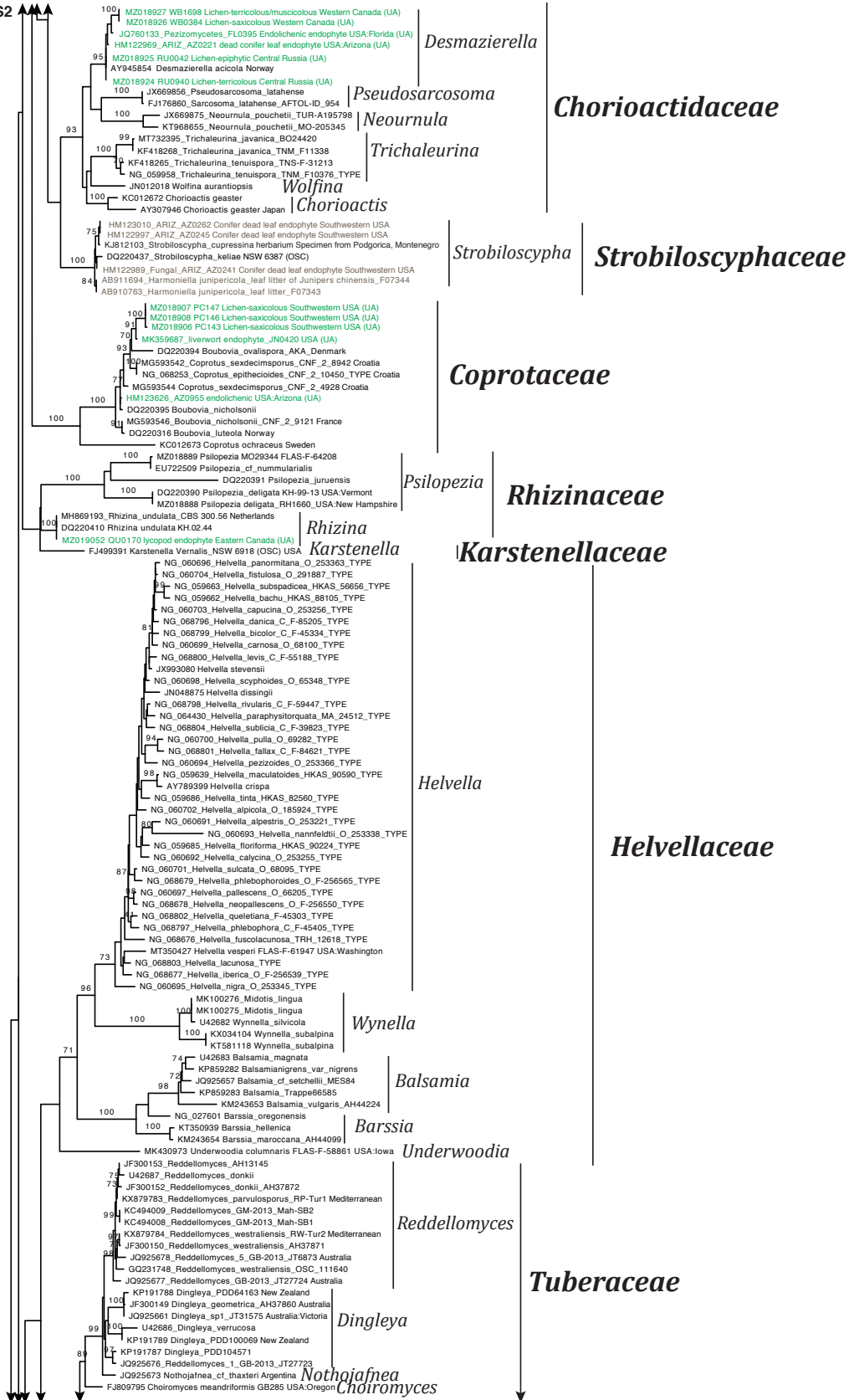


Figure S2
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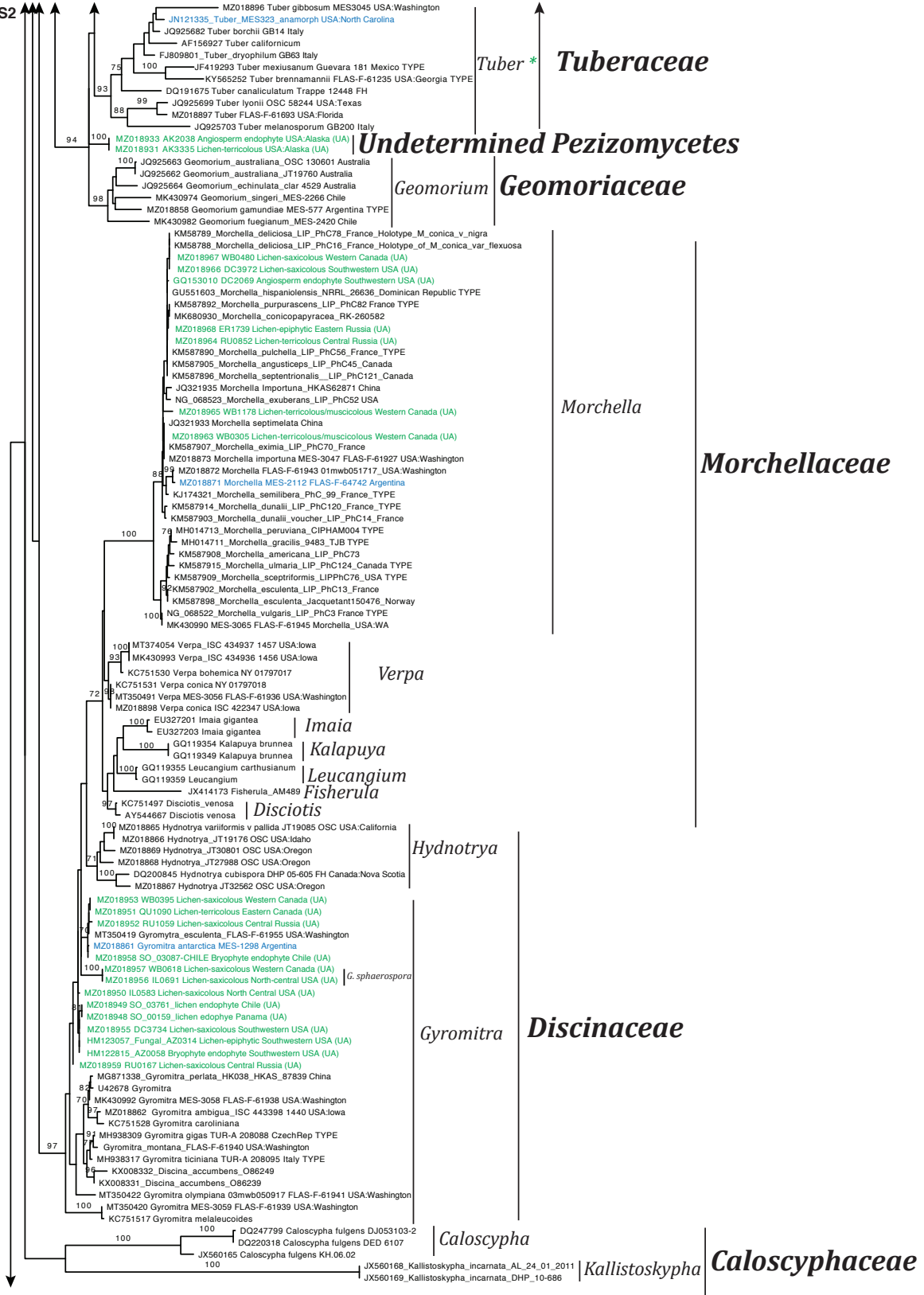


Figure S2
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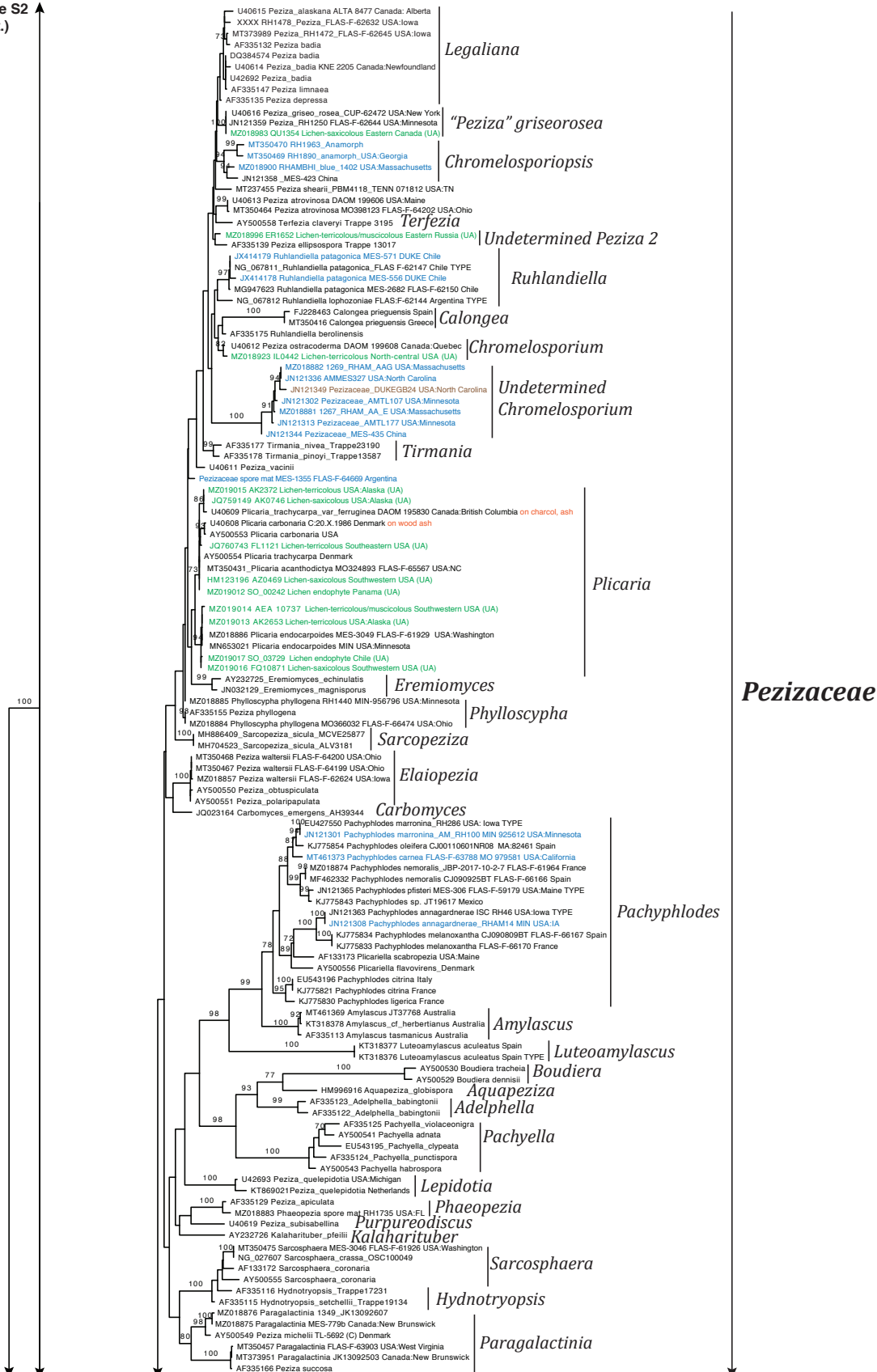


Figure S2
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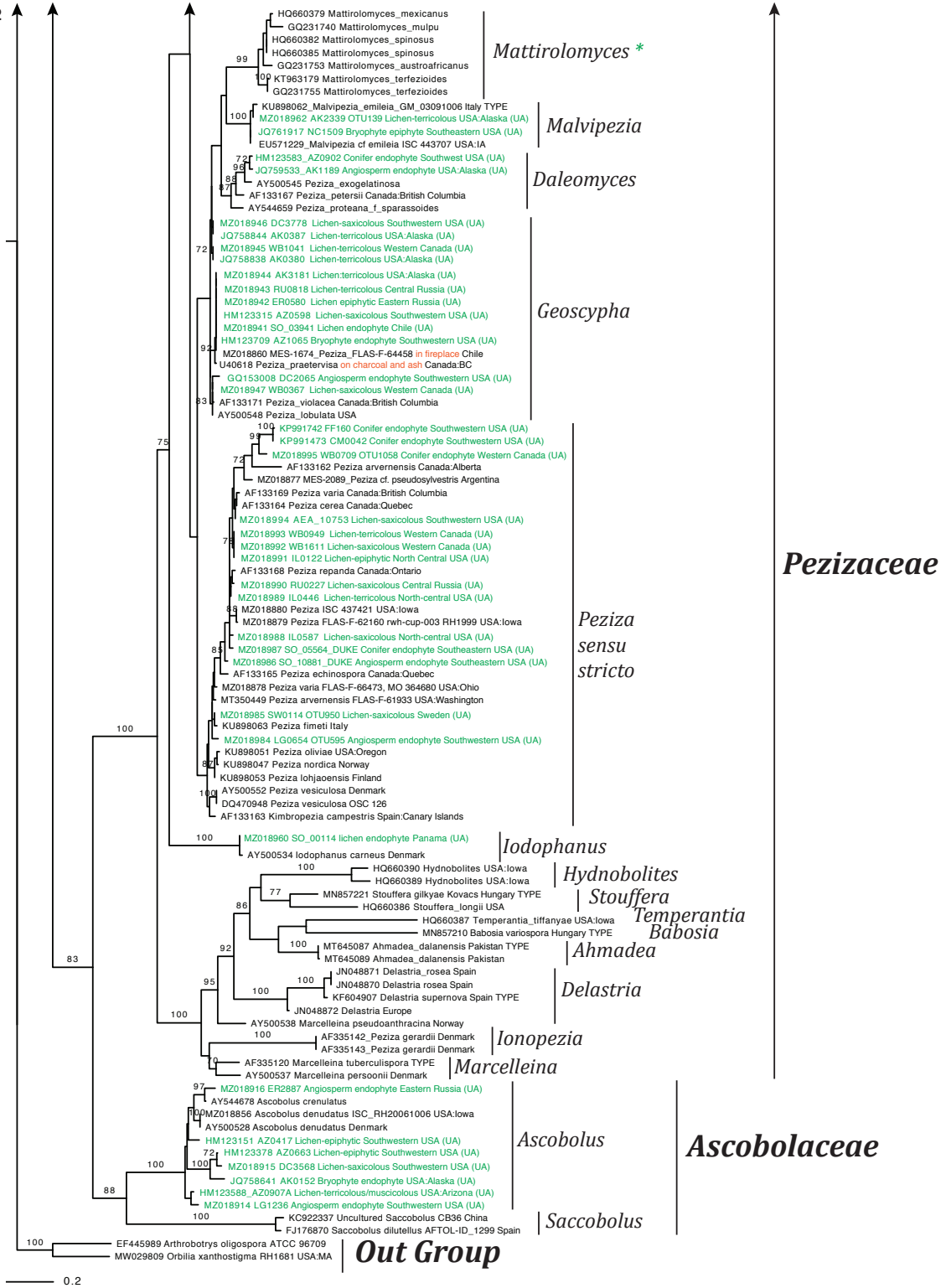
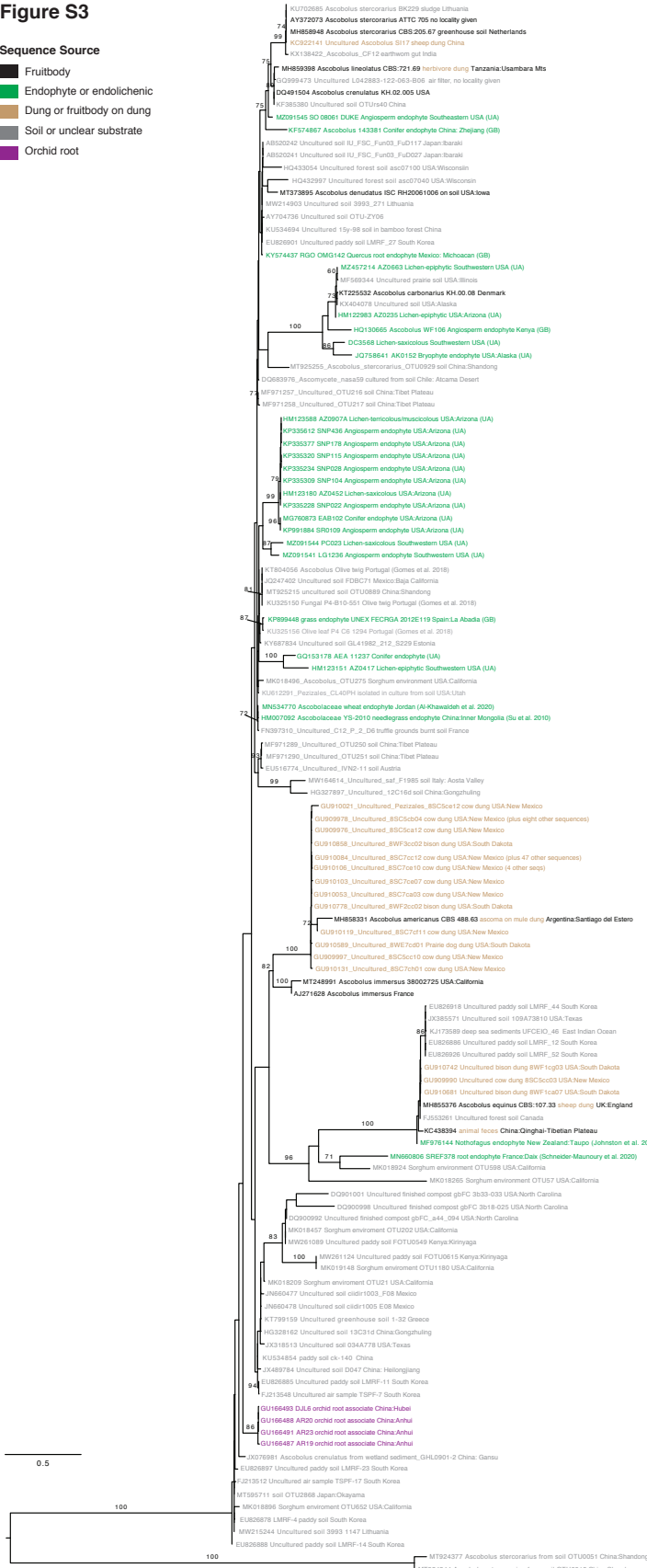


Fig. S3 Phylogeny based on ITS sequences of Ascobolaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; in orchid root, purple; soil, gray) and substrates for fruitbodies are color coded if they were collected on dung (yellow-brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with "GB" if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S3

Sequence Source
■ Fruitbody
■ Endophyte or endolichenic
■ Dung or fruitbody on dung
■ Soil or unclear substrate
■ Orchid root



Ascobolus stercorarius

Ascobolus lineolatus

Ascobolus crenulatus

Ascobolus denudatus

Ascobolus carbonarius

Ascobolus sp. 1

Ascobolus americanus

Ascobolus immersus

Ascobolus equinus

Ascobolus sp. 2

Fig. S4 Phylogeny based on ITS sequences of Ascodesmidaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mats, blue; orchid roots, purple; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange) or on dung (yellow-brown). Endophyte sequences originating from the University of Arizona are indicated with “UA”. Endophyte sequences that are not from the UA database include a reference to the publication or dissertation where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

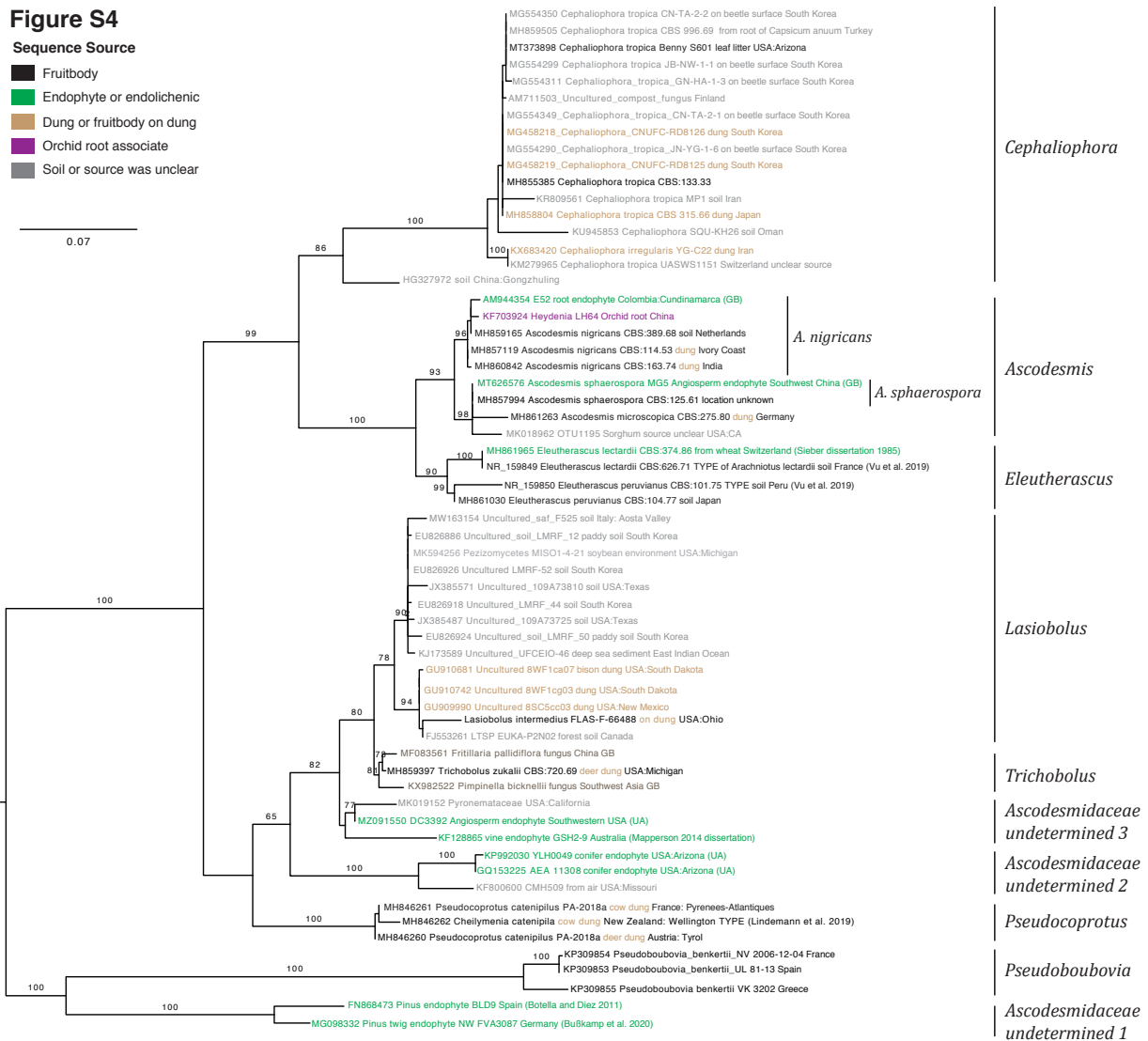
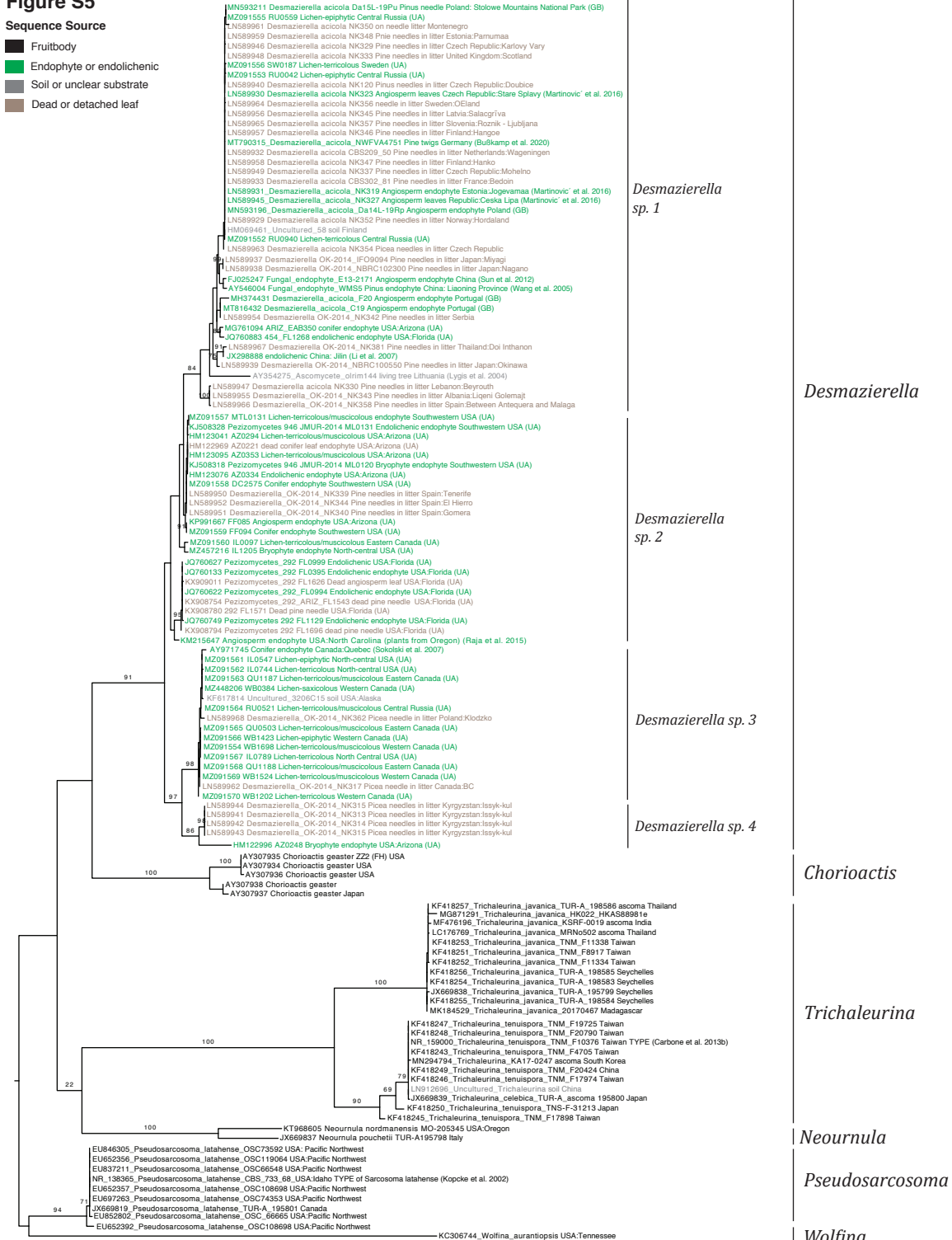


Fig. S5 Phylogeny based on ITS sequences of Chorioactidaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; dead leaf, gray brown; soil, gray). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S5

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Soil or unclear substrate
- Dead or detached leaf



0.2

Fig. S6 Phylogeny for Coprotaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; soil, gray) and substrates for fruitbodies are color coded if they were collected on dung (yellow-brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

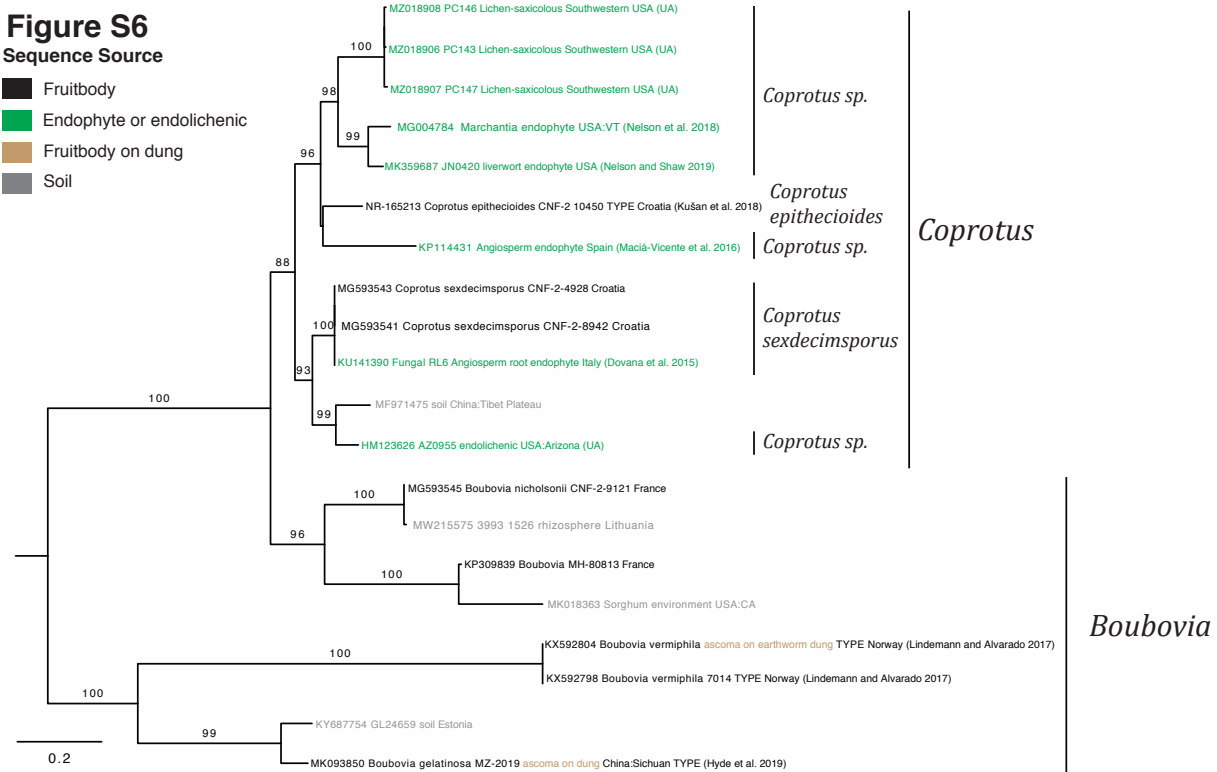


Fig. S7 Phylogeny based on ITS sequences of Discinaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE” and sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mats, blue; ectomycorrhiza reddish brown; orchid roots, purple; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange) or on dung (yellow-brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S7

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Ectomycorrhiza
- Orchid root
- Asexual spore mat
- Soil
- Fruitbody or asexual spore mat on burned site

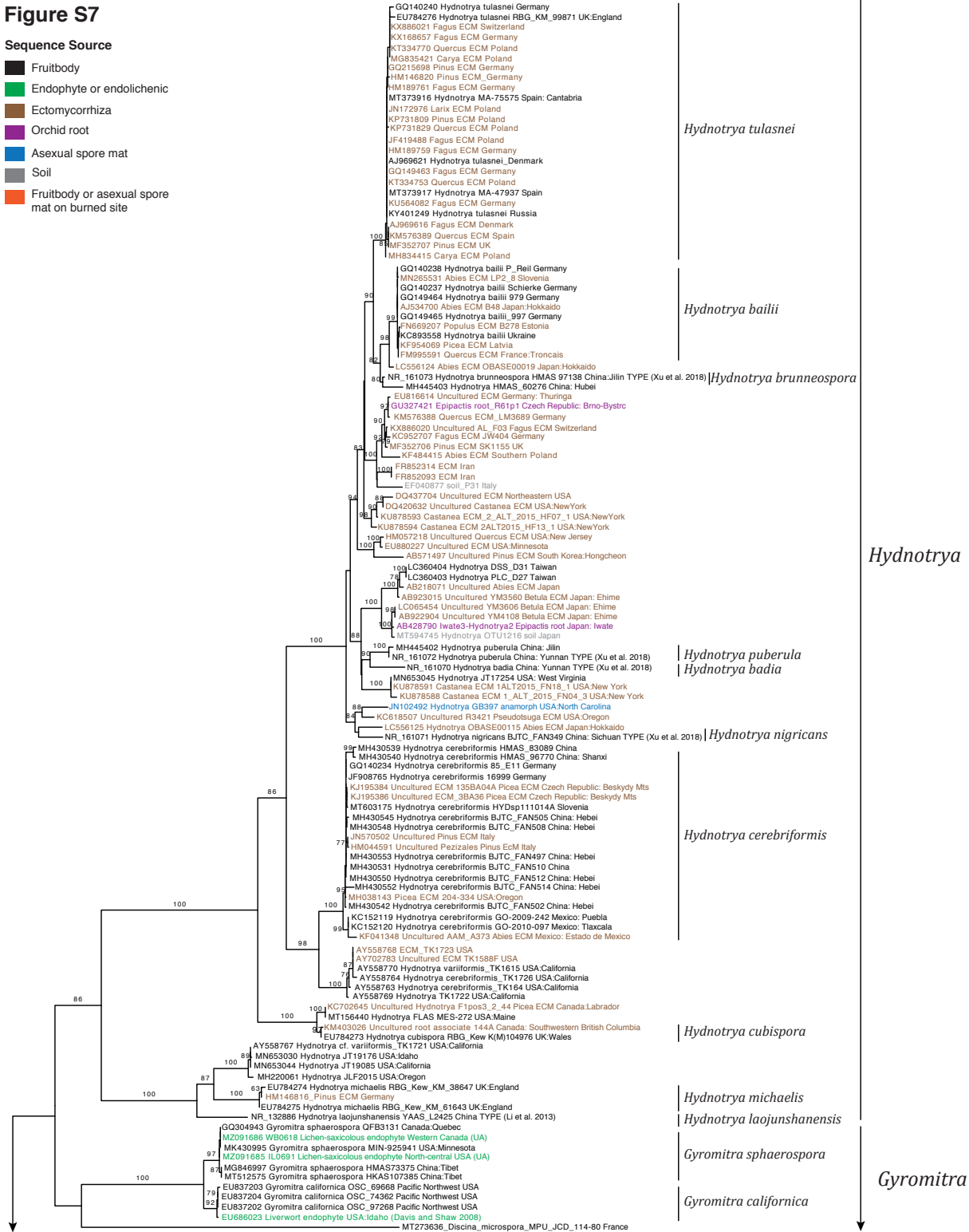
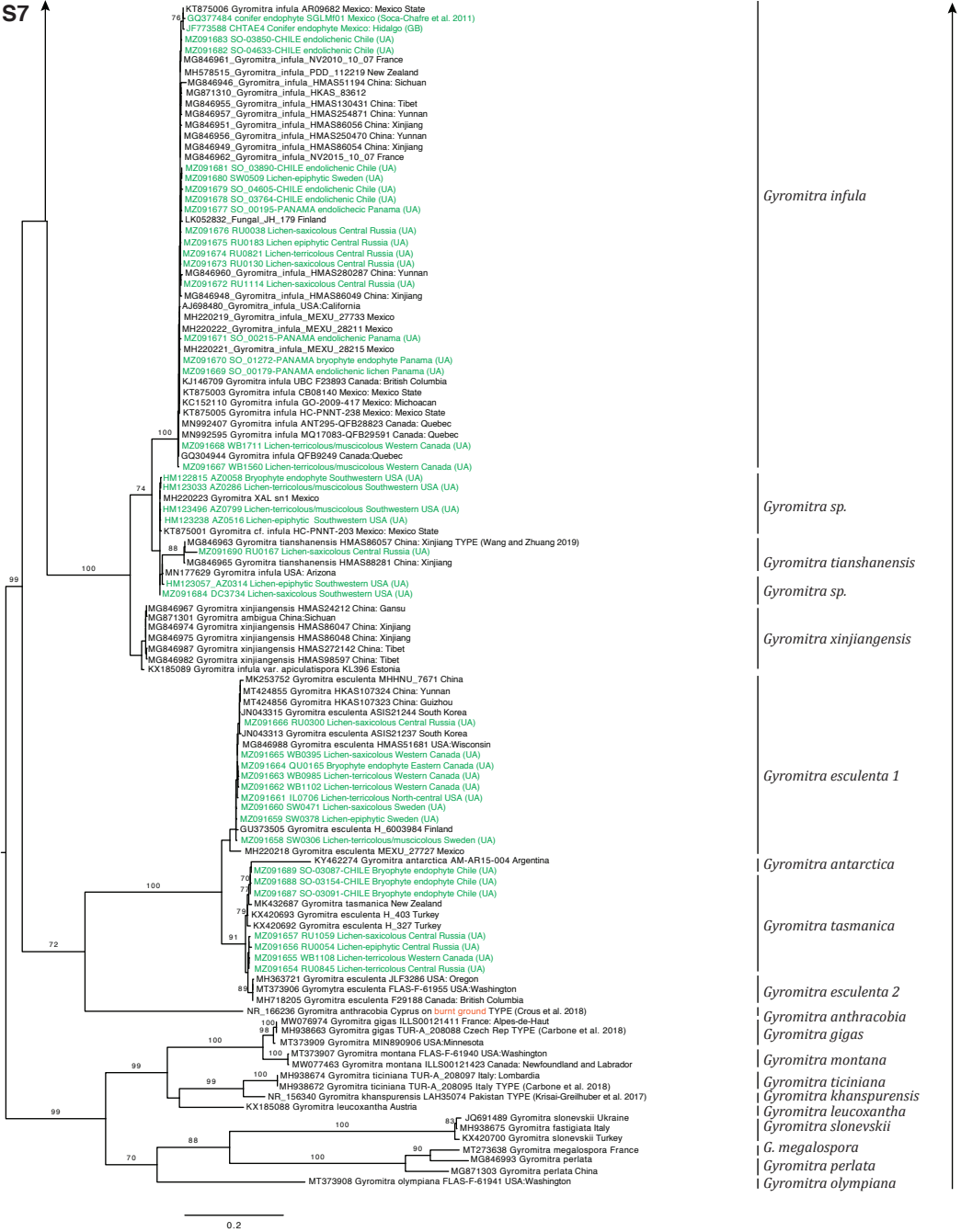


Figure S7
(Cont.)



0.2

Fig. S8 Phylogeny based on ITS sequences of Morchellaceae (pro parte) and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; orchid roots, purple). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S8

Sequence Source

- Fruitbody
- Endophyte
- Orchid root

0.05

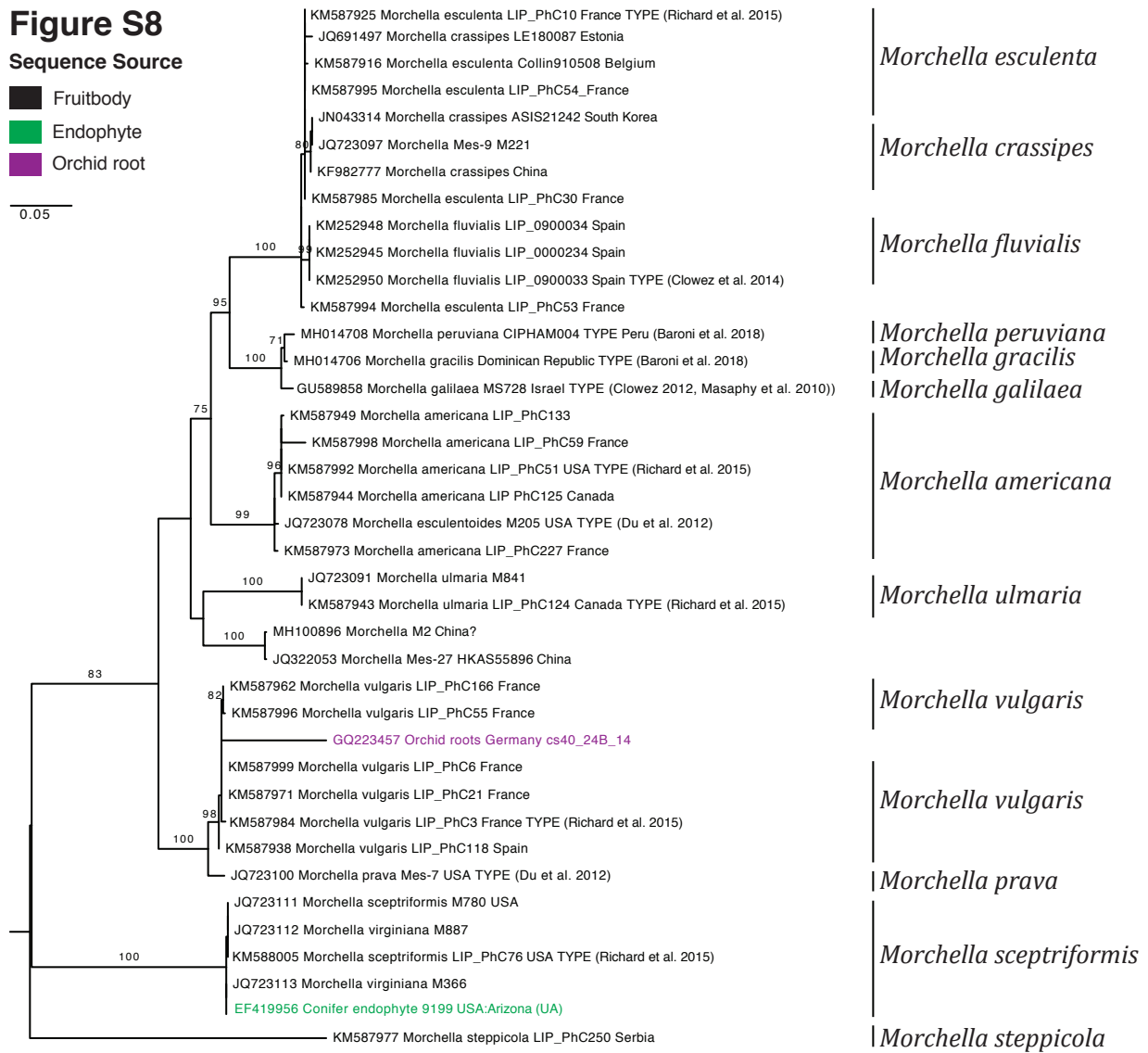


Fig. S9 Phylogeny based on ITS sequences of Morchellaceae (pro parte) and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mats, blue) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S9

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Asexual spore mat
- Fruitbody or asexual spore mat on burned site

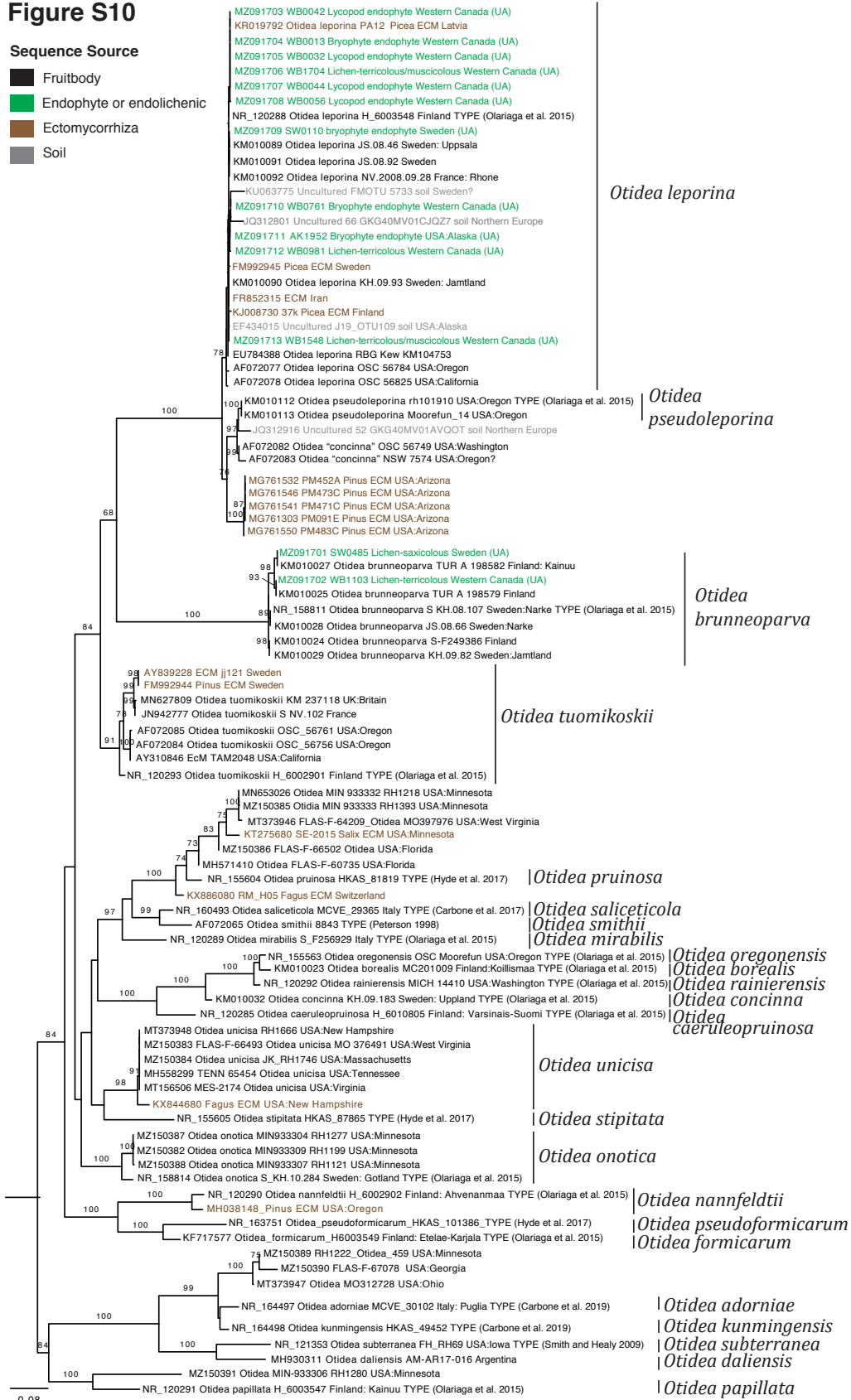


Fig. S10 Phylogeny based on ITS sequences of Otideaceae and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE” and sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish brown; soil, gray). All endophyte and endolichenic sequences originated from the University of Arizona and are indicated with “UA”. Sequences from type specimens include the reference for the sequence.

Figure S10

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Ectomycorrhiza
- Soil



0.08

Fig. S11 Phylogeny based on ITS sequences of Pezizaceae (*Calongea*, *Cazia*, *Chromelosporiopsis*, *Chromelosporium*, *Legaliana*, *Mycoclelandia*, *Ruhlandiella*, *Terfezia*, *Tirmania*) and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE” and sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mats, blue; ectomycorrhiza reddish brown; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

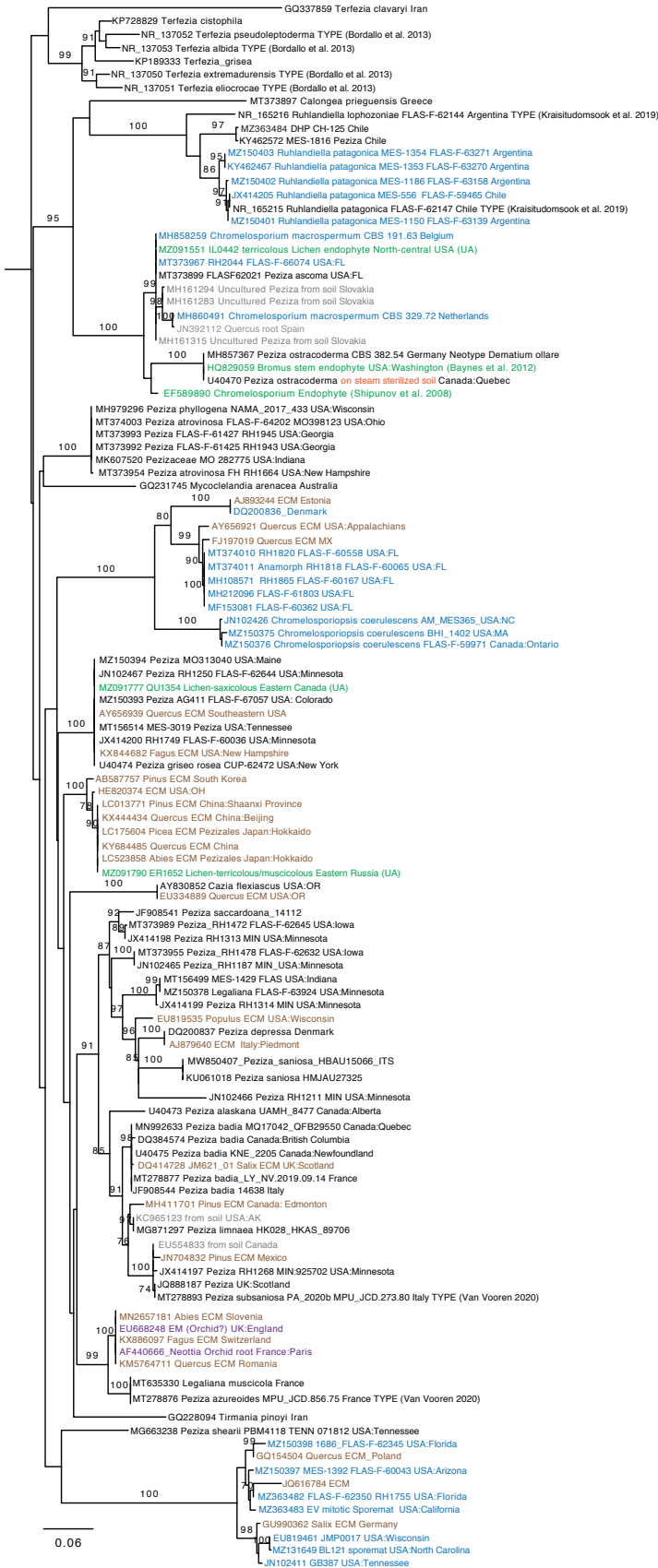


Figure S11

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Ectomycorrhiza
- Asexual spore mat
- Soil
- Fruitbody on burned or steamed site
- Orchid root

Terfezia

Calongea

Ruhlandiella

Chromelosporium macrospermum

"Peziza" ostracoderma

Undetermined *Chromelosporium*

Peziza atrovinosa

Mycocyaleandia

Chromelosporiopsis

"Peziza" griseorosea

Pezizaceae undetermined 1

Cazia flexiascus

Legaliana

Galactinia

Tirmania pinoyi

Pezizaceae undetermined 3

0.06

Fig. S12 Phylogeny based on ITS sequences of Pezizaceae (*Daleomyces*, *Malvipezia*) and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; dead leaf, gray brown; orchid root, purple). All endophyte and endolichenic sequences originated from the University of Arizona and are indicated with “UA”. Sequences from type specimens include the reference for the sequence.

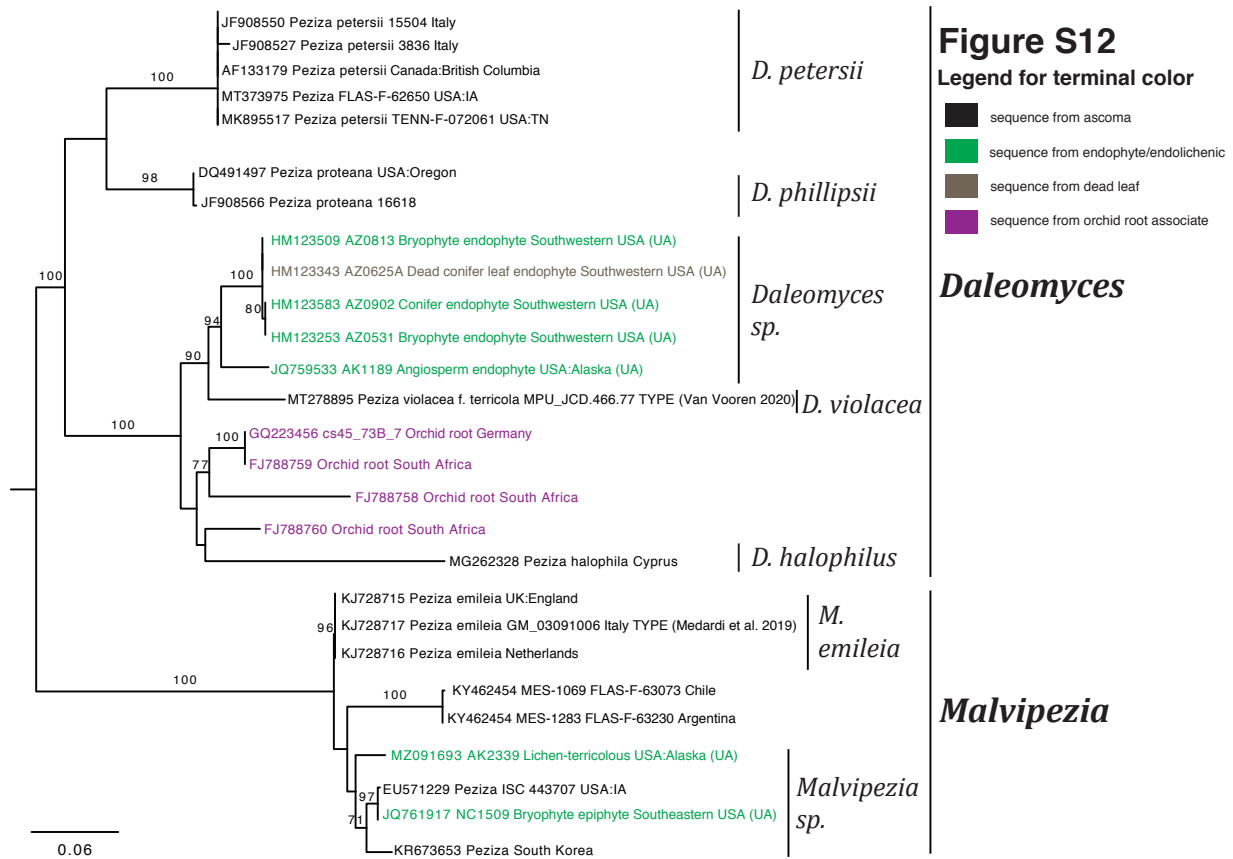
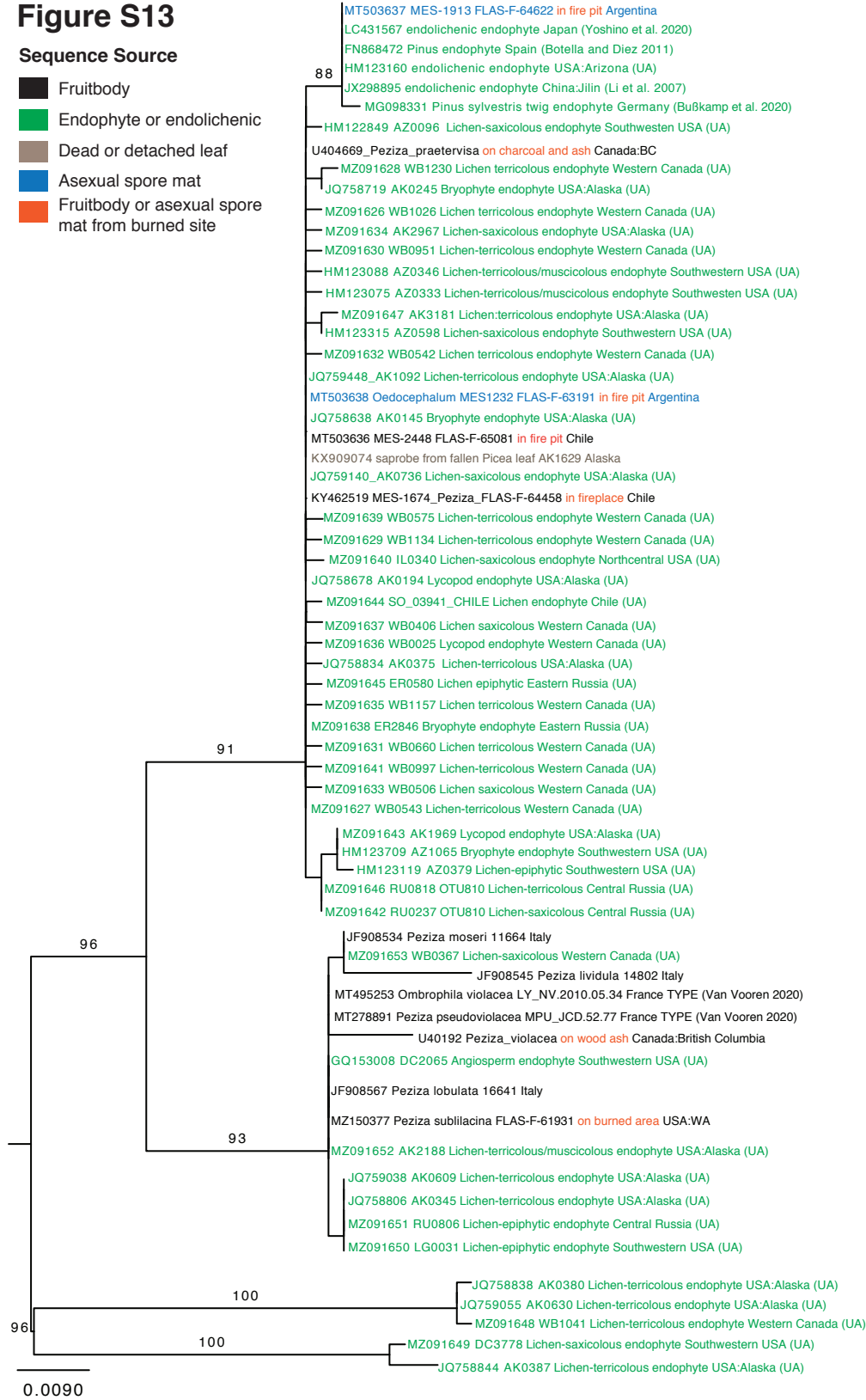


Fig. S13 Phylogeny based on ITS sequences of Pezizaceae (*Geoscypha*) and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; dead leaf, gray brown; asexual sporemat, blue) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S13

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Dead or detached leaf
- Asexual spore mat
- Fruitbody or asexual spore mat from burned site



Geoscypha tenacella

Geoscypha violacea

Geoscypha sp. 1

Geoscypha sp. 2

0.0090

Fig. S14 Phylogeny based on ITS sequences of Pezizaceae (*Iodophanus*) and related endophytic or endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; orchid root, purple; environmental such as air, dust, soil, or water, gray) and substrates for fruitbodies are color coded if they were collected on dung (yellow brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S14

Sequence Source

- Fruitbody or culture from fruitbody
- Endophyte or endolichenic
- Air, dust, soil, or water
- Orchid root
- Fruitbody on dung

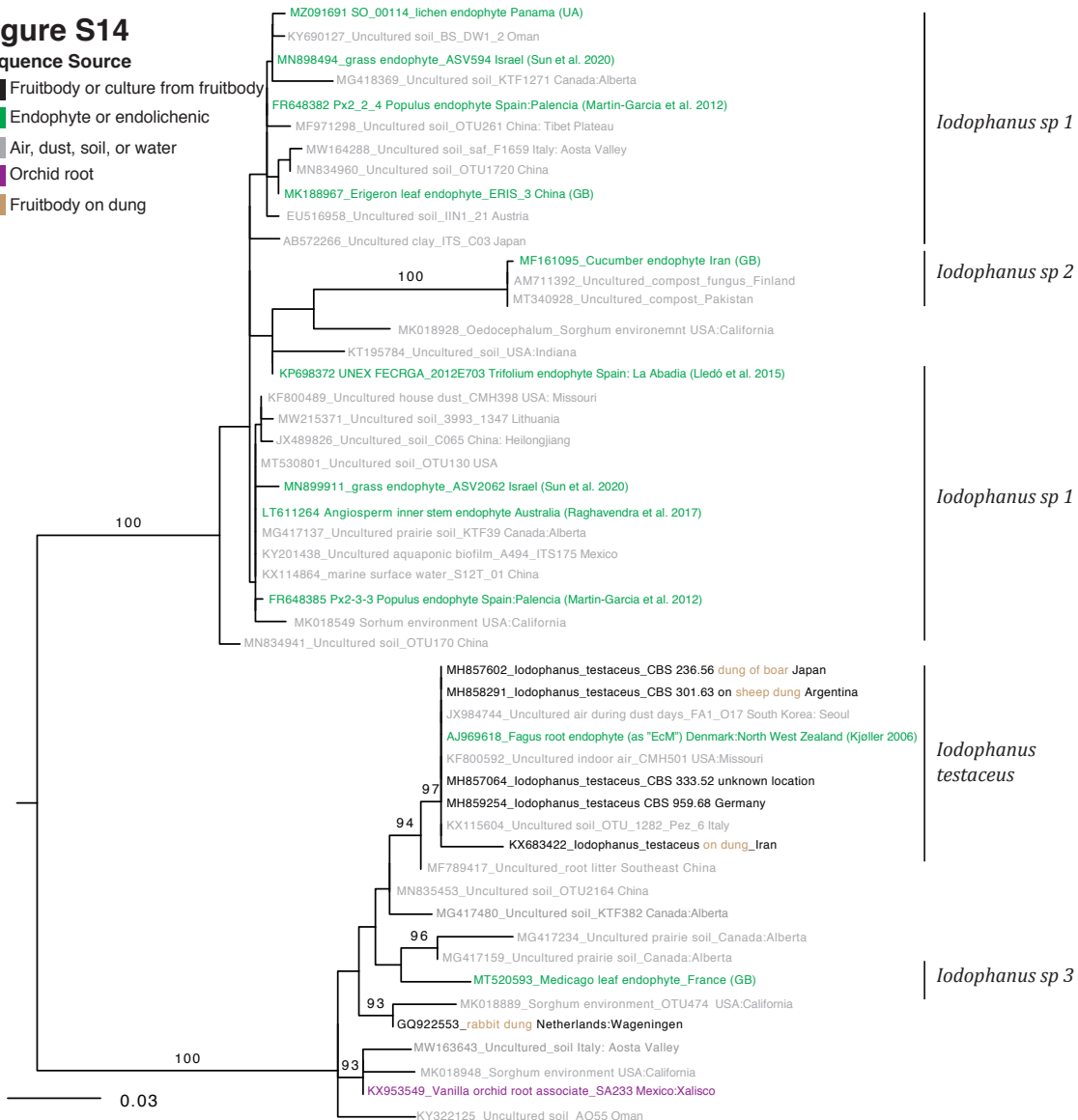


Fig. S15 Phylogeny based on ITS sequences of Pezizaceae (*Lepidotia*) and related endophyte analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green). The endophyte sequence includes a reference to the publication where it was obtained. Sequences from type specimens include the reference for the sequence.



Fig. S16 Phylogeny based on ITS sequences of Pezizaceae (*Mattiolomyces*, *Elderia*) and related endophytes analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information. Terminals are color coded by their sequence source (fruitbody, black; endophyte, green). Endophyte sequences include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

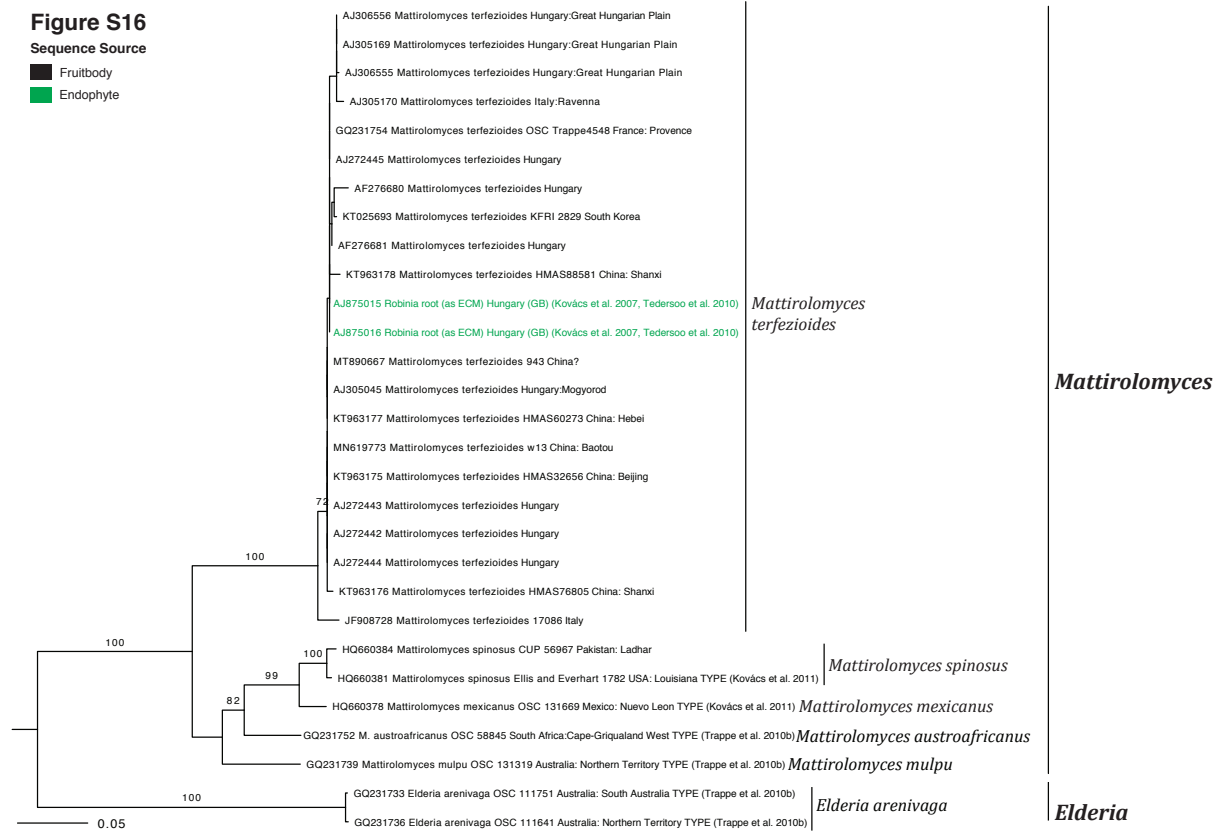


Fig. S17 Phylogeny based on ITS sequences of Pezizaceae (*Peziza sensu stricto*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; orchid root, purple; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange) or on dung (yellow brown). All endophyte and endolichenic sequences originated from the University of Arizona and are indicated with "UA". Sequences from type specimens include the reference for the sequence.

Figure S17

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Orchid root
- Soil
- Fruitbody on burned site
- Fruitbody on dung

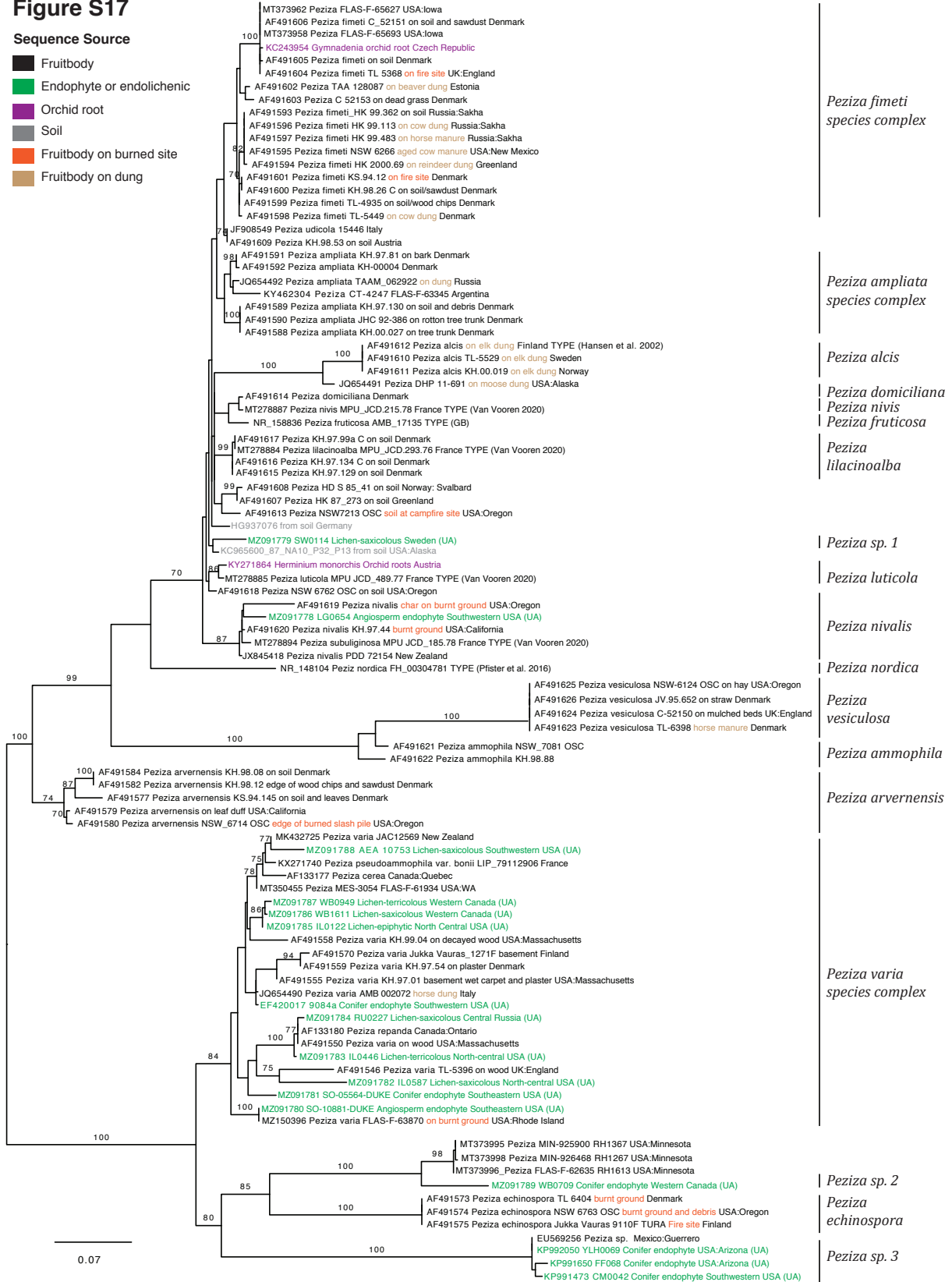


Fig. S18 Phylogeny based on ITS sequences of Pezizaceae (*Plicaria*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mat, blue; dead leaf, dull brown; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences labeled with “GB” were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S18

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Asexual spore mat
- Dead or detached leaf
- Soil
- Fruitbody or asexual spore mat on burned site

0.02

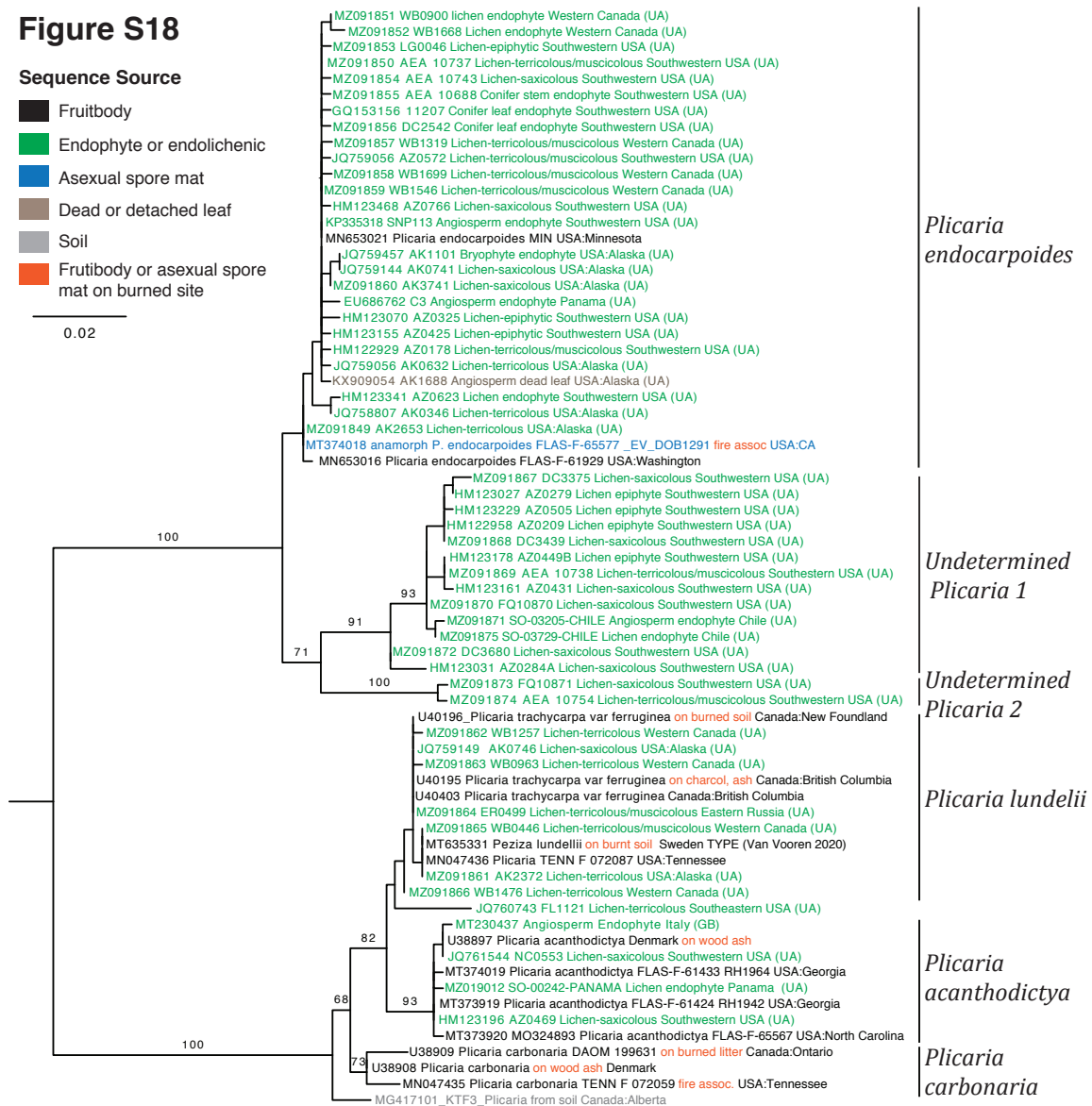


Fig. S19 Phylogeny based on ITS sequences of Pseudombrophilaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual sporemat, blue; orchid root, purple; soil, gray) and substrates for fruitbodies are color coded if they were collected on dung (yellow brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with "GB" if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S19

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Asexual spore mat
- Orchid root
- Fruitbody on dung
- Soil, dust, wood, water

0.02

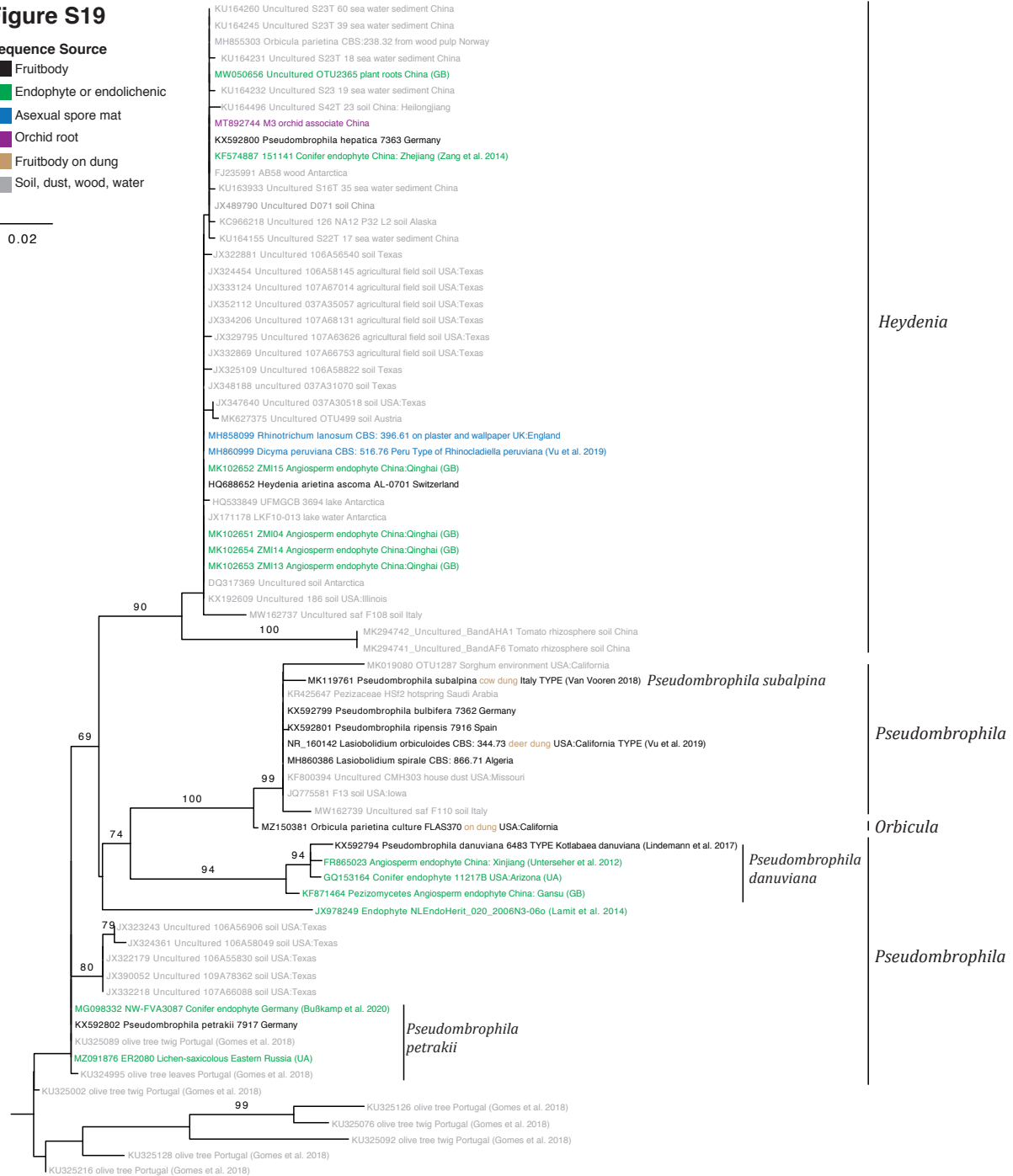


Fig. S20 Phylogeny based on ITS sequences of Pulvinulaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish-brown; soil or unidentified source, gray). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the dissertation where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S20

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Ectomycorrhiza
- Soil or unidentified source

— 0.2

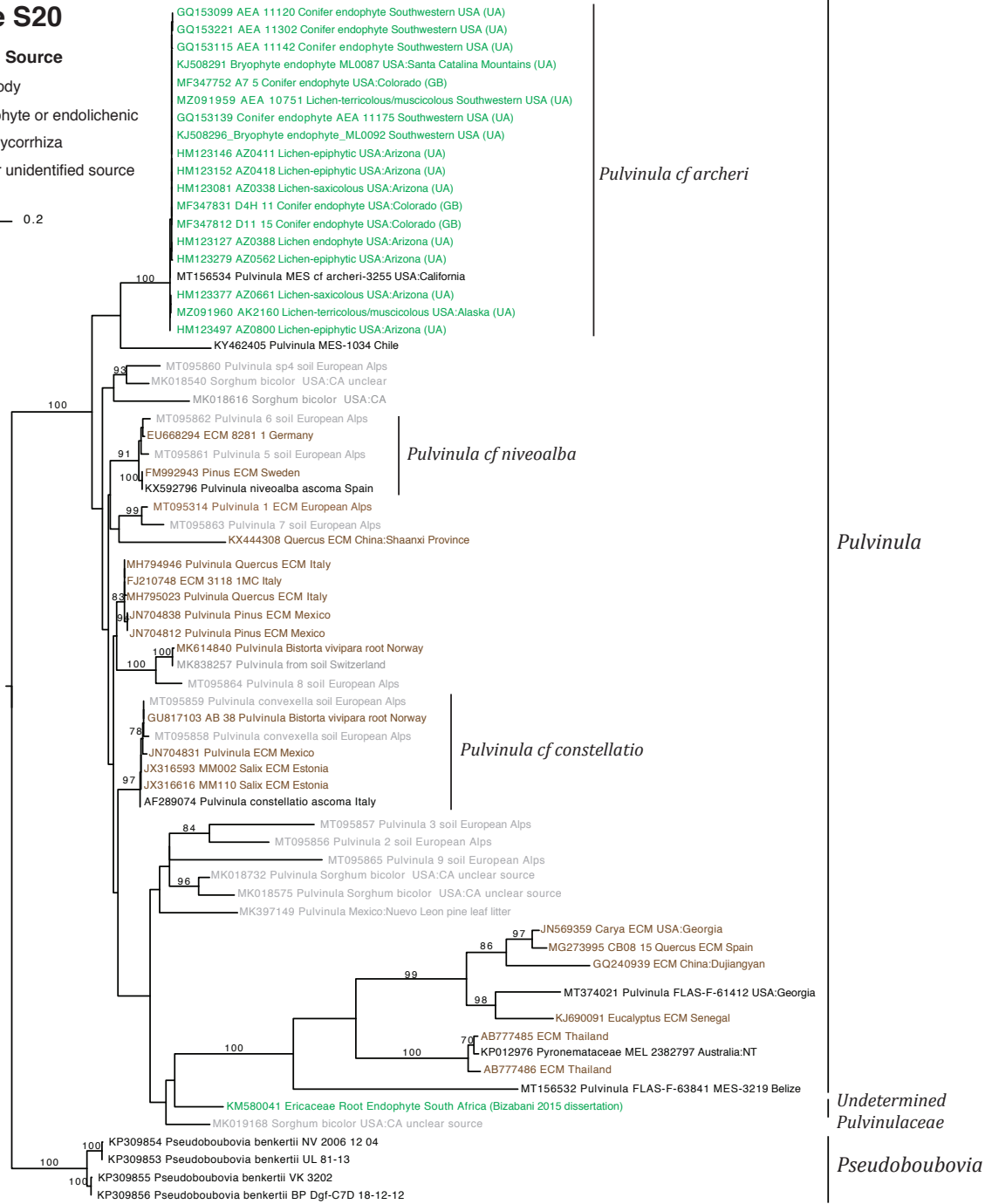


Fig. S21 Phylogeny based on ITS sequences of Pyronemataceae (*Byssonectria*, *Chaetothiersia*, *Cheilymenia*, *Parascutellinia*, *Pseudaleuria*, *Pyronema*, *Spooneromyces*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; dead leaf, gray brown; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange) or dung (yellow brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication or dissertation where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S21

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Soil
- Dead leaf
- Fruitbody from burned site
- Fruitbody on dung

0.2

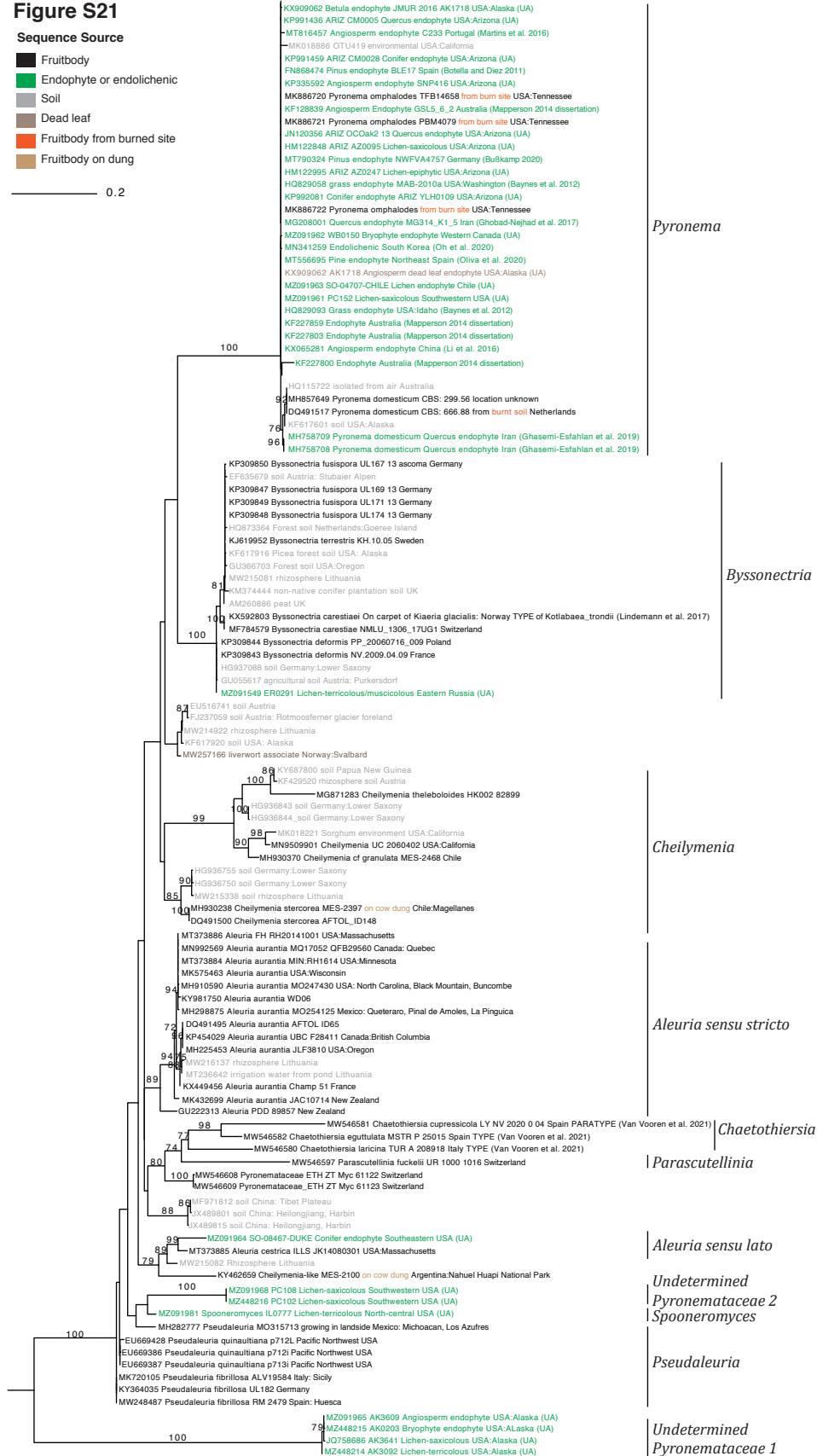
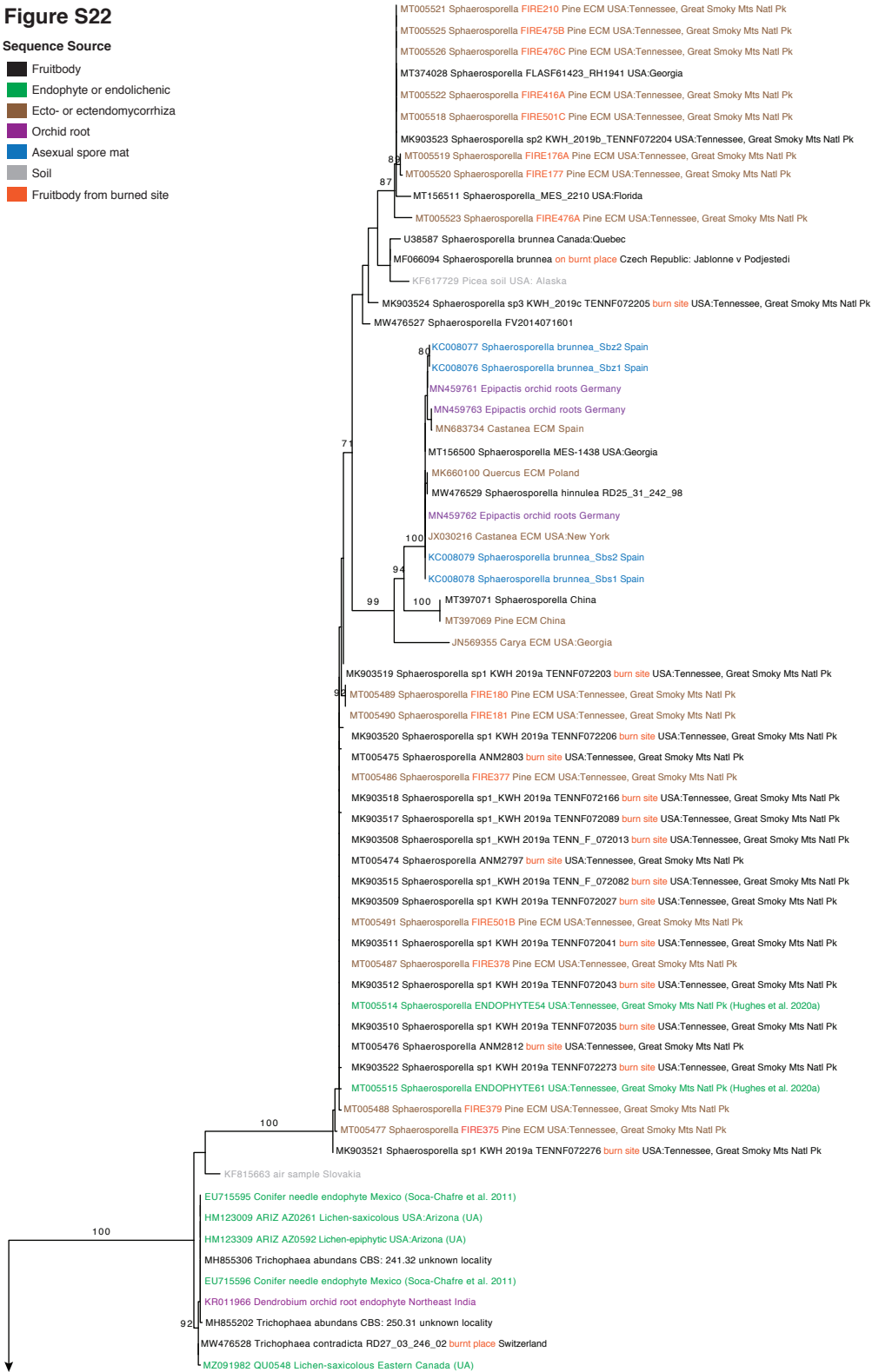


Fig. S22 Phylogeny based on ITS sequences of Pyronemataceae (*Anthracobia*, *Parawilcoxina*, *Sphaerosporella*, *Trichophaea* pro parte¹, *Trichophaeopsis*, and two undetermined Pyronemataceae lineages) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish-brown; orchid root, purple; asexual spore mat, blue; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Sequences originating from the University of Arizona are indicated as (UA). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication or dissertation where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence. ¹“*Trichophaea* pro parte” refers to the fact that *Trichophaea* is currently paraphyletic. *Trichophaea woolhopeia* is the lectotype of the genus, but is not included in this phylogenetic treatment.

Figure S22

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Ecto- or ectendomycorrhiza
- Orchid root
- Asexual spore mat
- Soil
- Fruitbody from burned site



Sphaerosporella

*Trichophaea
abundans
Trichophaea
contradicta*

Figure S22
(Cont.)

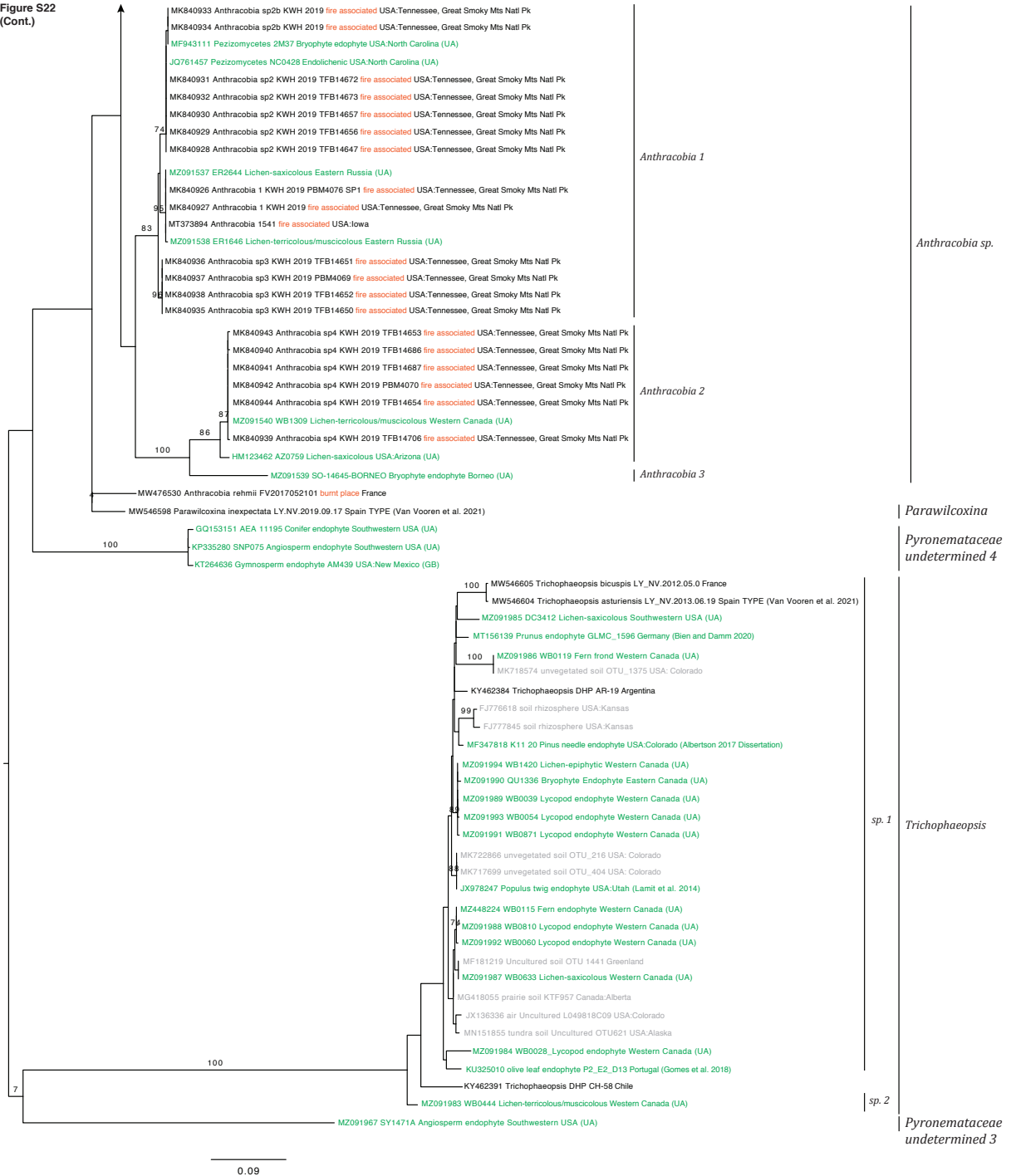


Fig. S23 Phylogeny based on ITS sequences of Pyronemataceae (*Ascorhizoctonia*, *Cupulina*, *Geopora*, *Lasiocupulina*, *Paratricharina*, *Pseudotracharina*, *Sepultariella*, *Tricharina*, *Tricharinopsis*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Sequences from ectomycorrhizas are designated with the abbreviation "ECM" preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish-brown; dead leaf, gray brown; orchid root, purple; soil, water, or insect, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication or thesis where they were obtained or are labeled with "GB" if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S23

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Dead leaf
- Ectomycorrhiza
- Orchid root
- Soil, water or insect
- Fruitbody from burned site

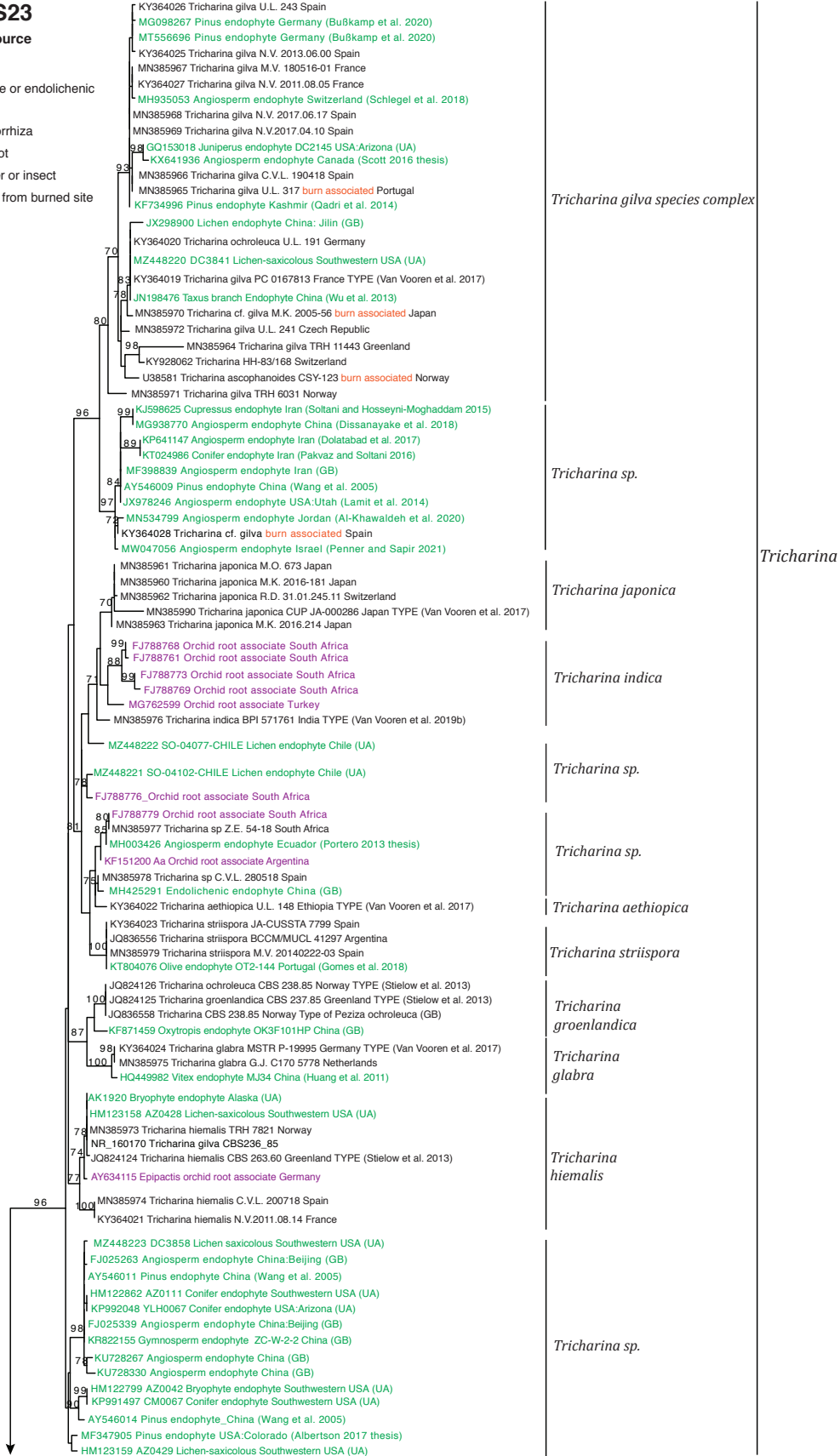


Figure S23
(Cont.)

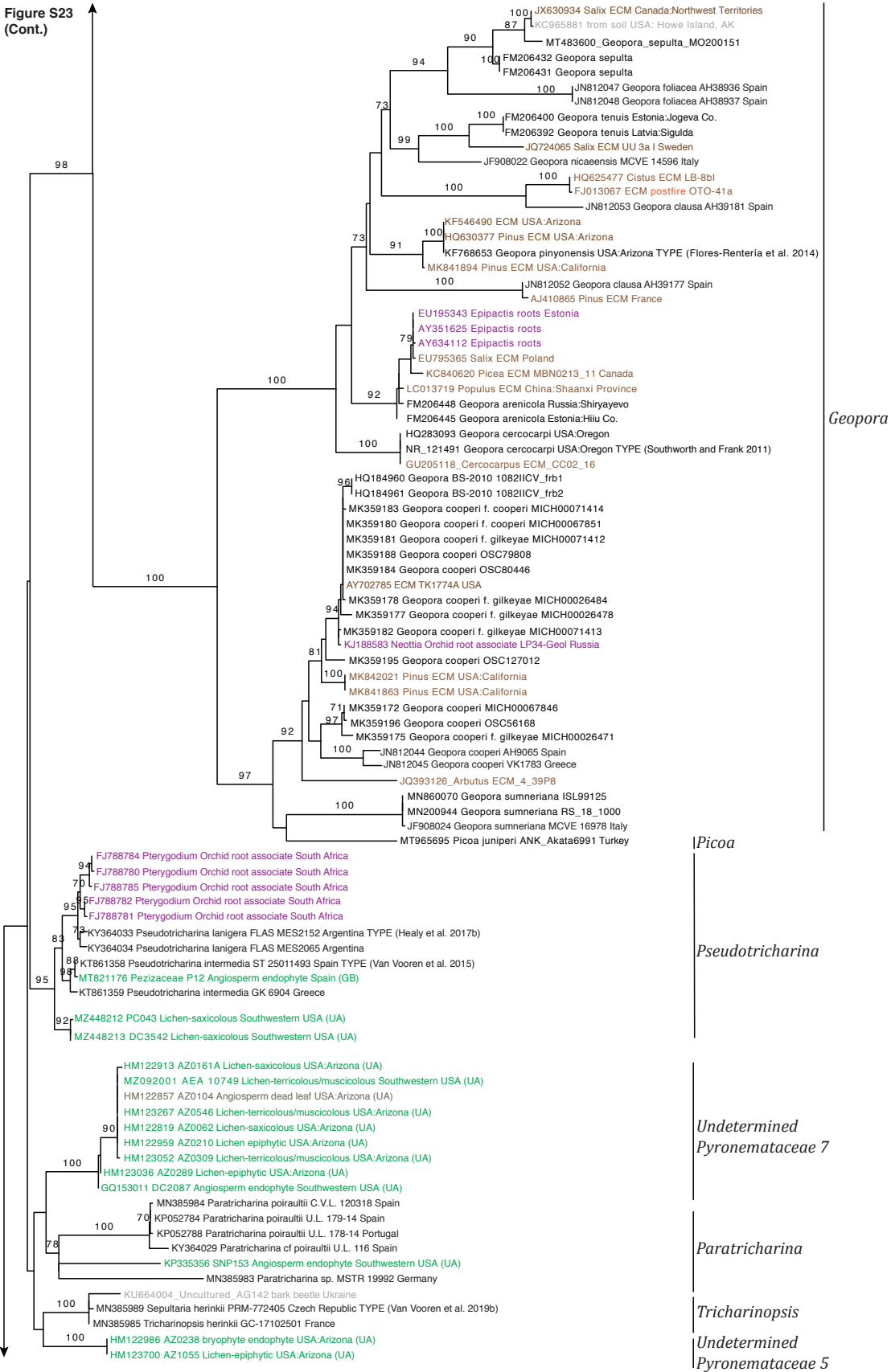


Figure S23
(Cont.)

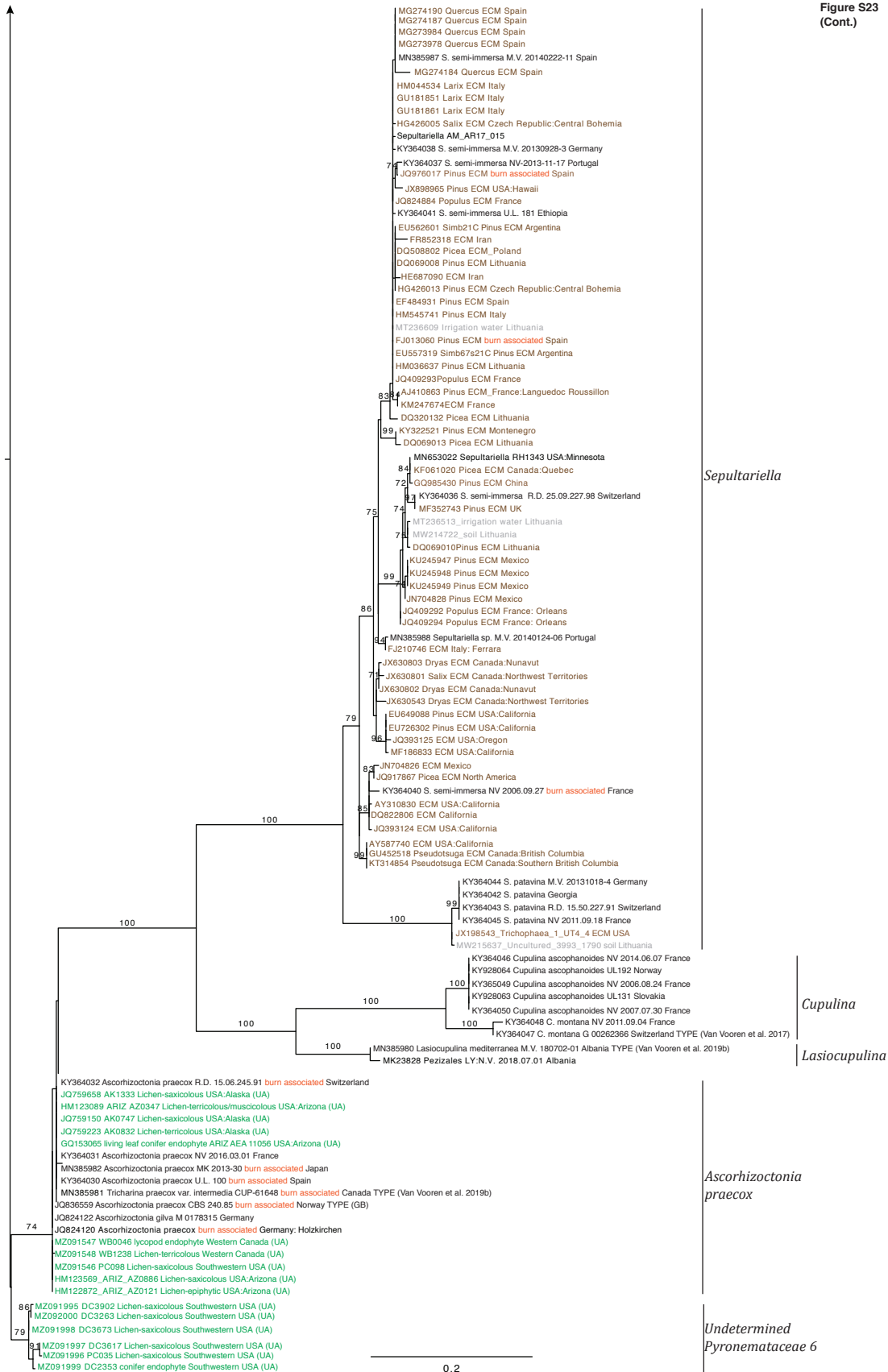


Fig. S24 Phylogeny based on ITS sequences of Pyronemataceae (*Lasiobolidium* pro parte¹) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. Taxa detected as endophytes are highlighted in green and the legend for other colors is shown in the upper lefthand corner. Details such as GenBank accession numbers, sources of sequences, locality data and type status are noted on each terminal. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic and endolichenic, green; soil, gray). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

¹“*Lasiobolidium* pro parte” refers to the fact that *Lasiobolidium* is currently paraphyletic. The *Lasiobolidium* represented in this tree is correctly named because it contains the type species as demonstrated by a sequence from the type specimen. Another entity named “*Lasiobolidium*” is treated in the Pseudombrophilaceae.

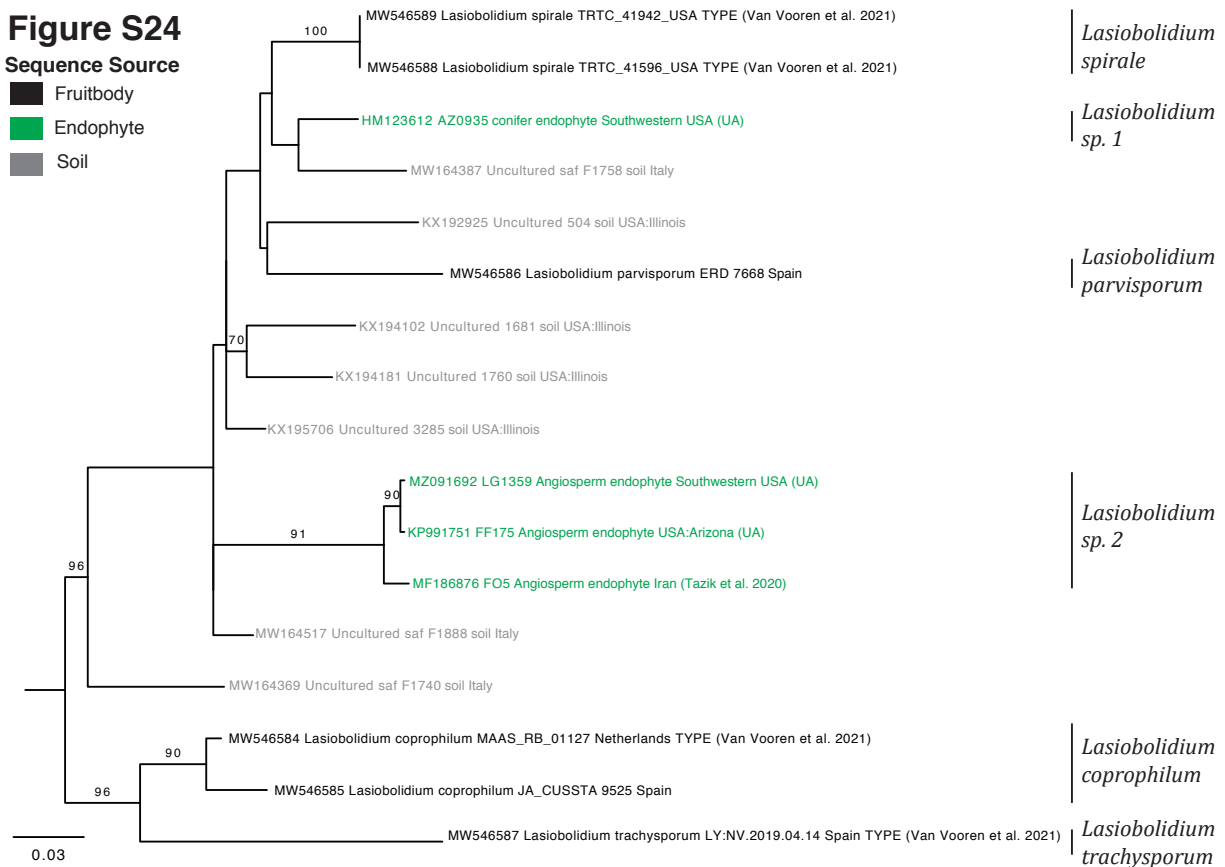


Fig. S25 Phylogeny based on ITS sequences of Pyronemataceae (*Perilachnea*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic and endolichenic, green; dead leaf, gray brown), and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S25

Sequence Source

- Fruitbody
- Endophyte or endolithic
- Dead leaf
- Fruitbody from burned site



Fig. S26 Phylogeny based on ITS sequences of Pyronemataceae (*Jafnea*, *Pyropyxis*, *Smardaea*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; dead leaf, gray brown; undetermined environmental source, gray). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication or dissertation where they were obtained. Sequences from type specimens include the reference for the sequence.

Figure S26

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Dead leaf
- Unclear

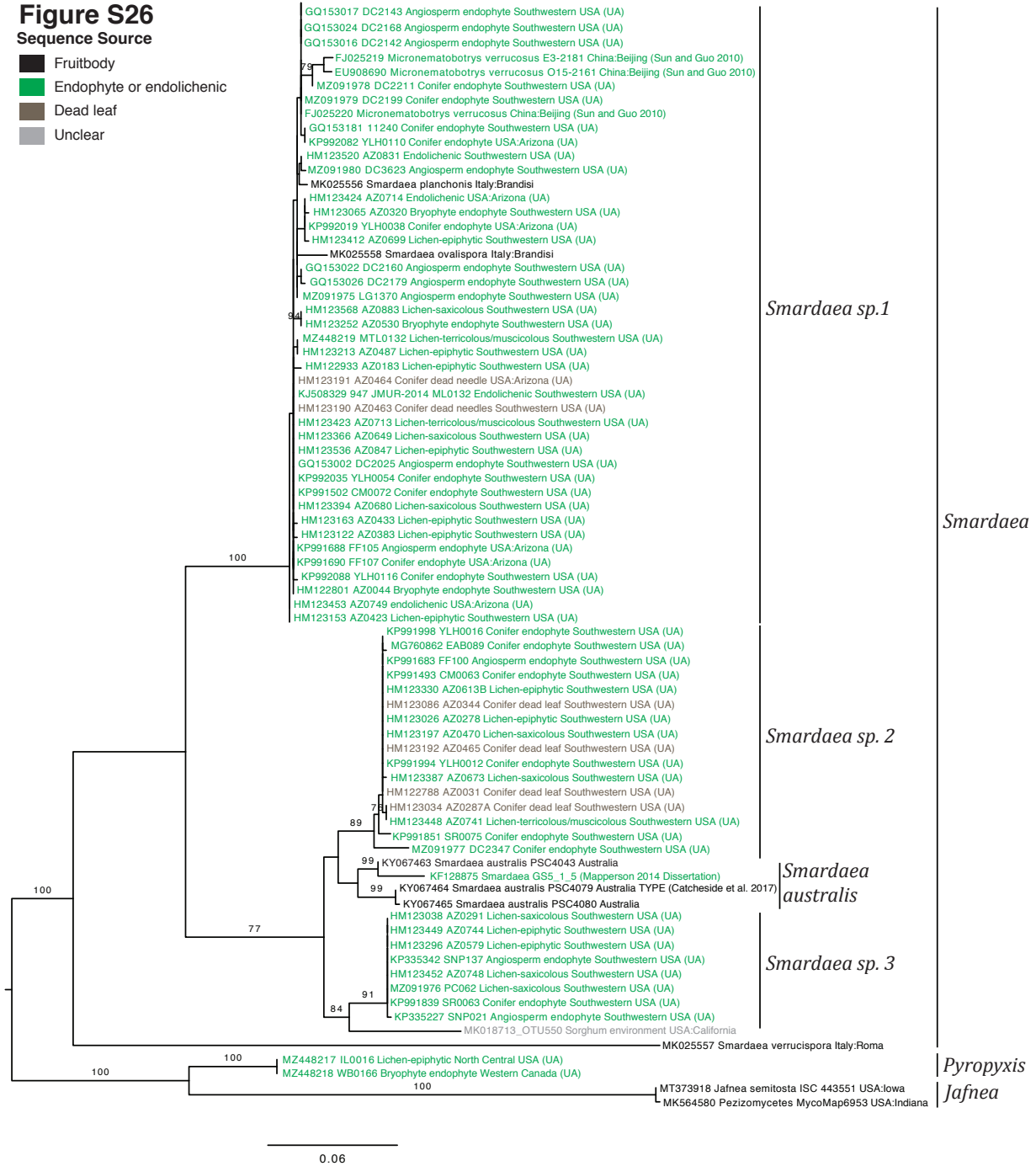


Fig. S27 Phylogeny based on ITS sequences of Pyronemataceae (*Bactridium*, *Miladina*, *Ramsbottomia*, *Scutellinia*, *Sphaerosporium*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mat, blue; soil, gray) and substrates for spore mats are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained.

Figure S27
Sequence Source

- Fruitbody
- Endophyte or endolicheric
- Asexual spore mat
- Soil
- Asexual spore mat on burnt substrate

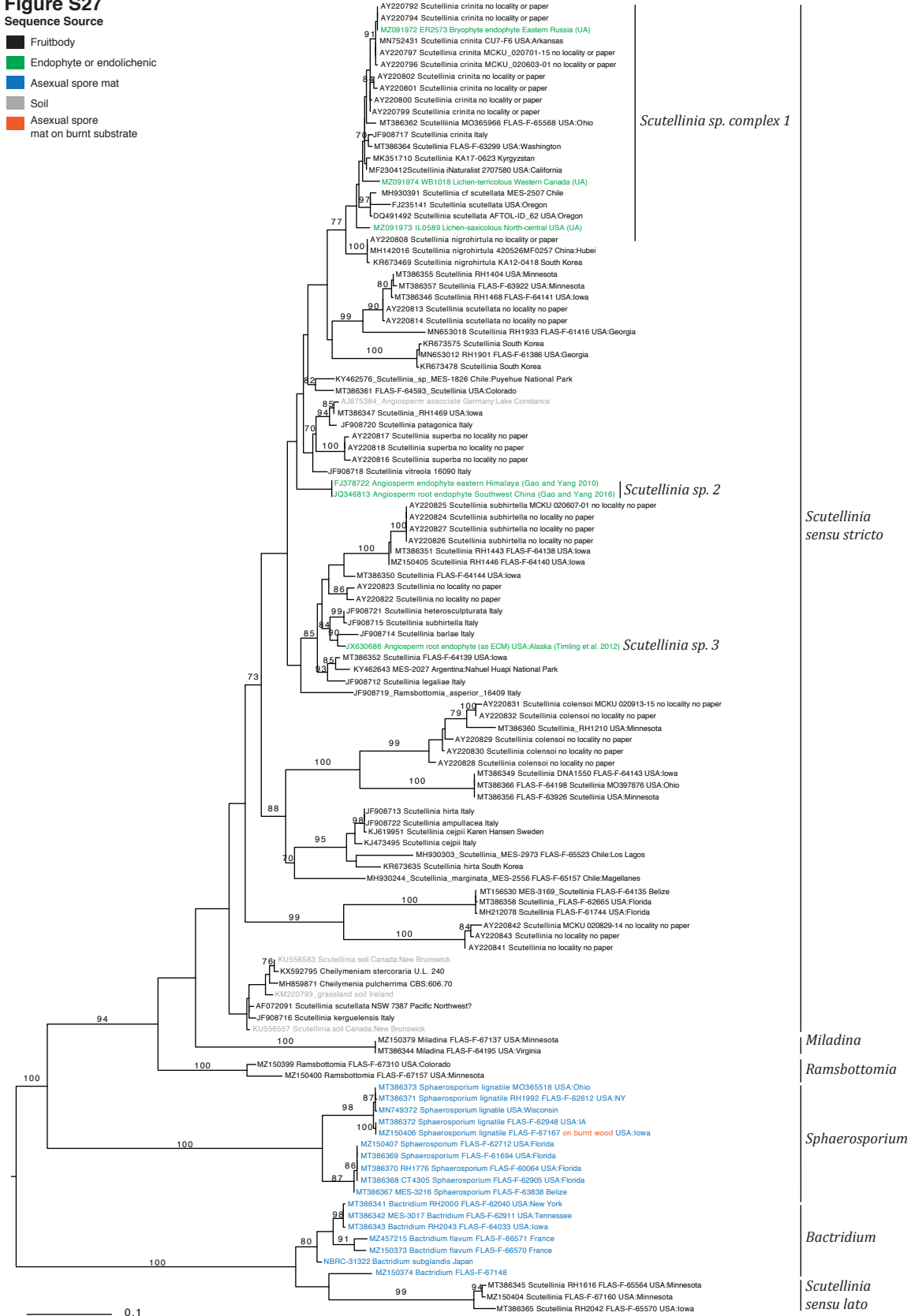


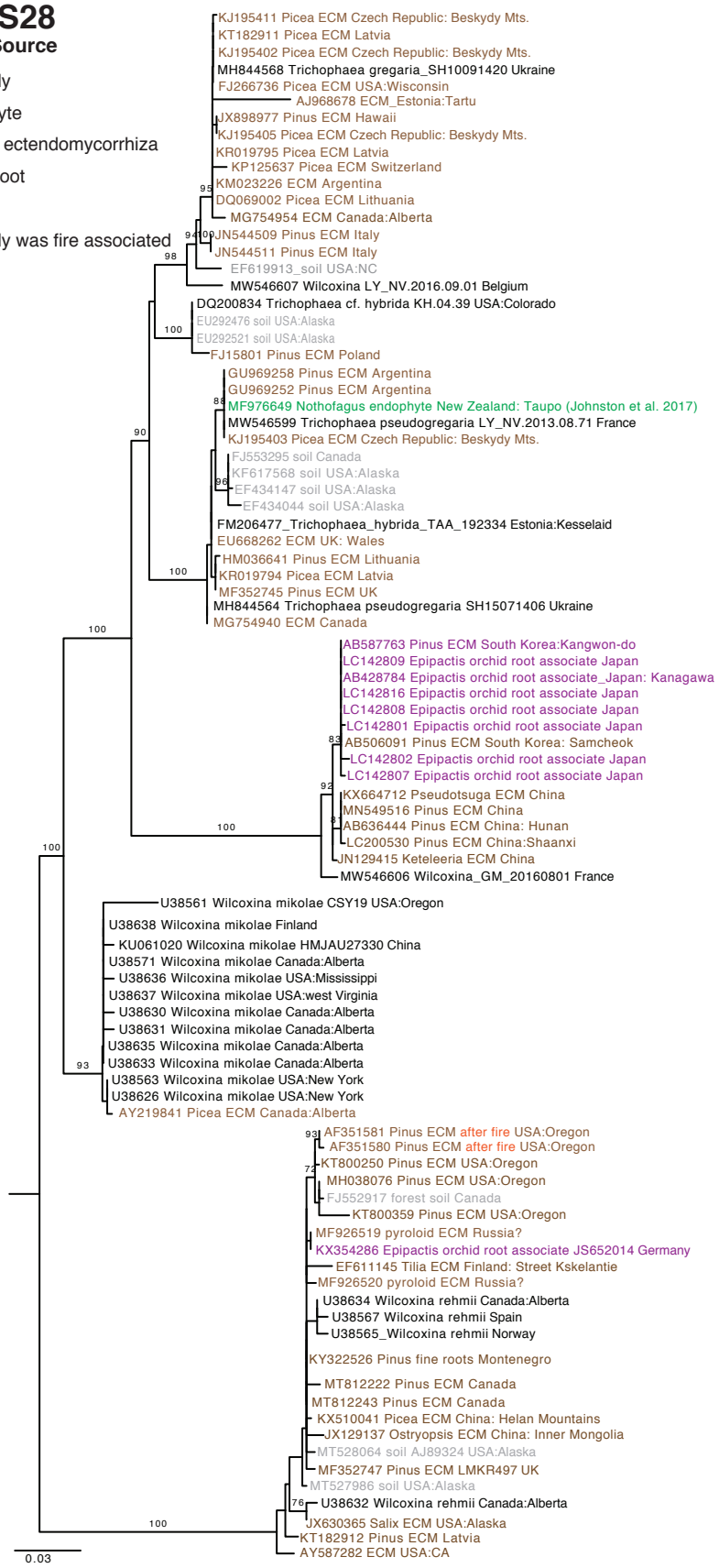
Fig. S28 Phylogeny based on ITS sequences of Pyronemataceae (*Trichophaea* pro parte¹, *Wilcoxina*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish-brown; orchid root, purple; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte sequence includes a reference to the publication where it was obtained.

¹“*Trichophaea* pro parte” refers to the fact that *Trichophaea* is currently paraphyletic.

Trichophaea woolhopeia is the lectotype of the genus, and is not included in the *Trichophaea* clades represented in this tree.

Figure S28
Sequence Source

- Fruitbody
- Endophyte
- Ecto- or ectendomycorrhiza
- Orchid root
- Soil
- Fruitbody was fire associated



Trichophaea gregaria?

Trichophaea hybrida?

Trichophaea pseudogregaria

Wilcoxina sp.

Wilcoxina mikolae

Wilcoxina rehmlii

Fig. S29 Phylogeny based on ITS sequences of Rhiziniaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mat, blue) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). All endophyte and endolichenic sequences originated from the University of Arizona and are indicated with “UA”. Sequences from type specimens include the reference for the sequence.

Figure S29

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- From asexual spore mat or culture
- Fruitbody from burned site

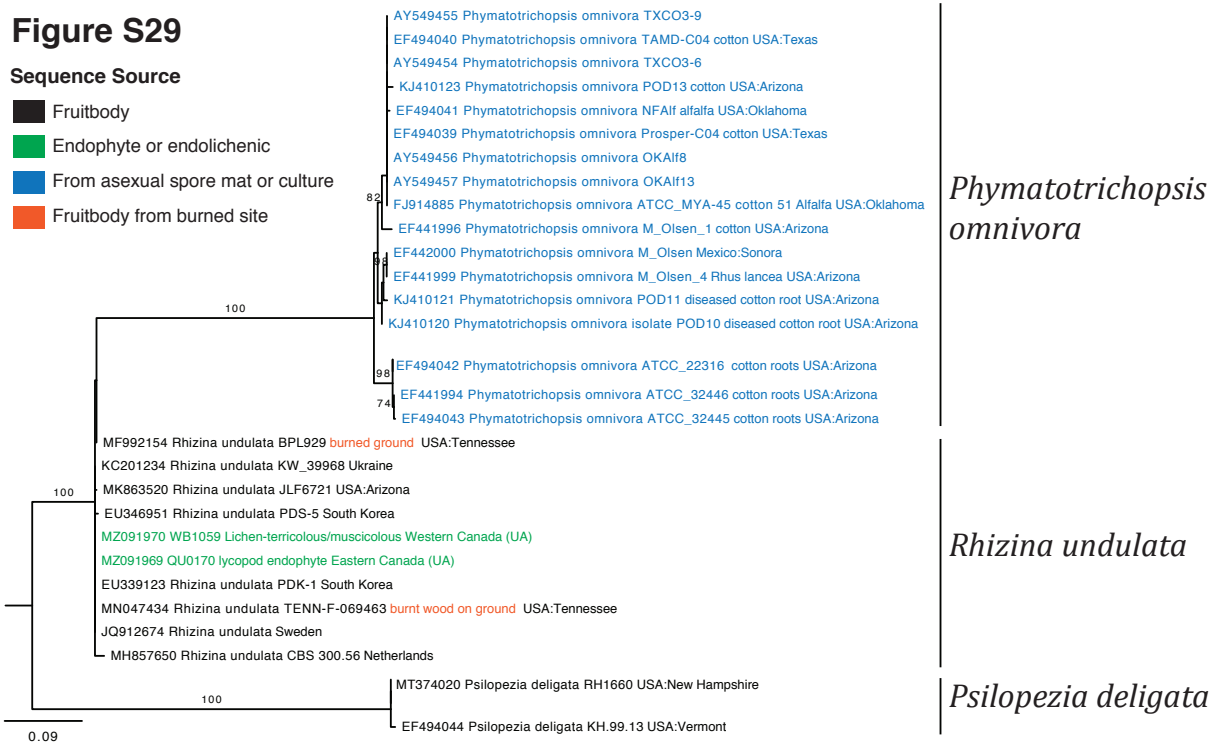


Fig. S30 Phylogeny based on ITS sequences of Sarcoscyphaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; air, gray). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with “UA”. Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with “GB” if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S30

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Air

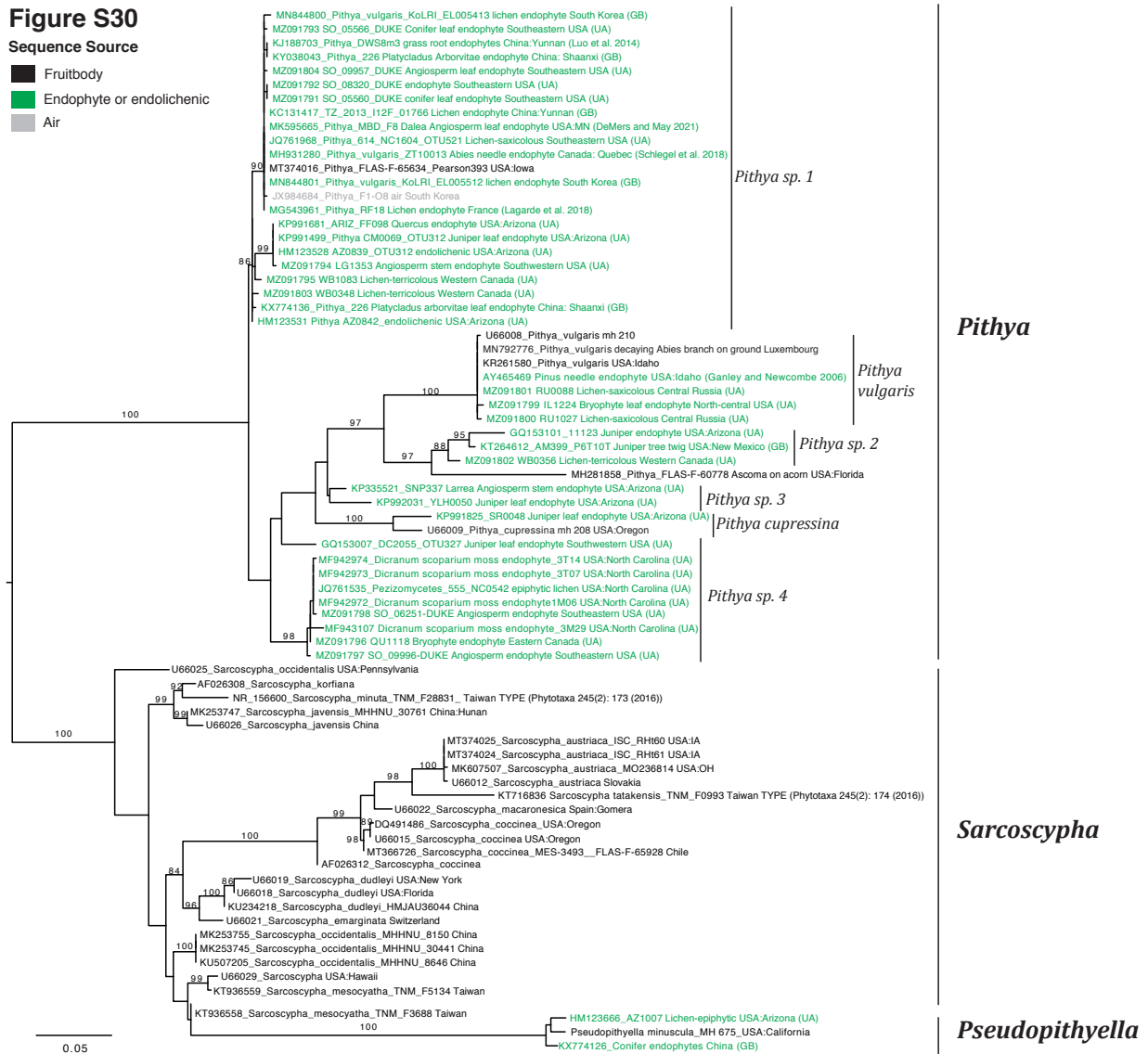


Fig. S31 Phylogeny based on ITS sequences of Sarcosomataceae (*Donadinia*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green). All endophyte and endolichenic sequences originated from the University of Arizona and are indicated with “UA”. Sequences from type specimens include the reference for the sequence.

Figure S31
Sequence Source

- Fruitbody
- Endophyte or endolichenic

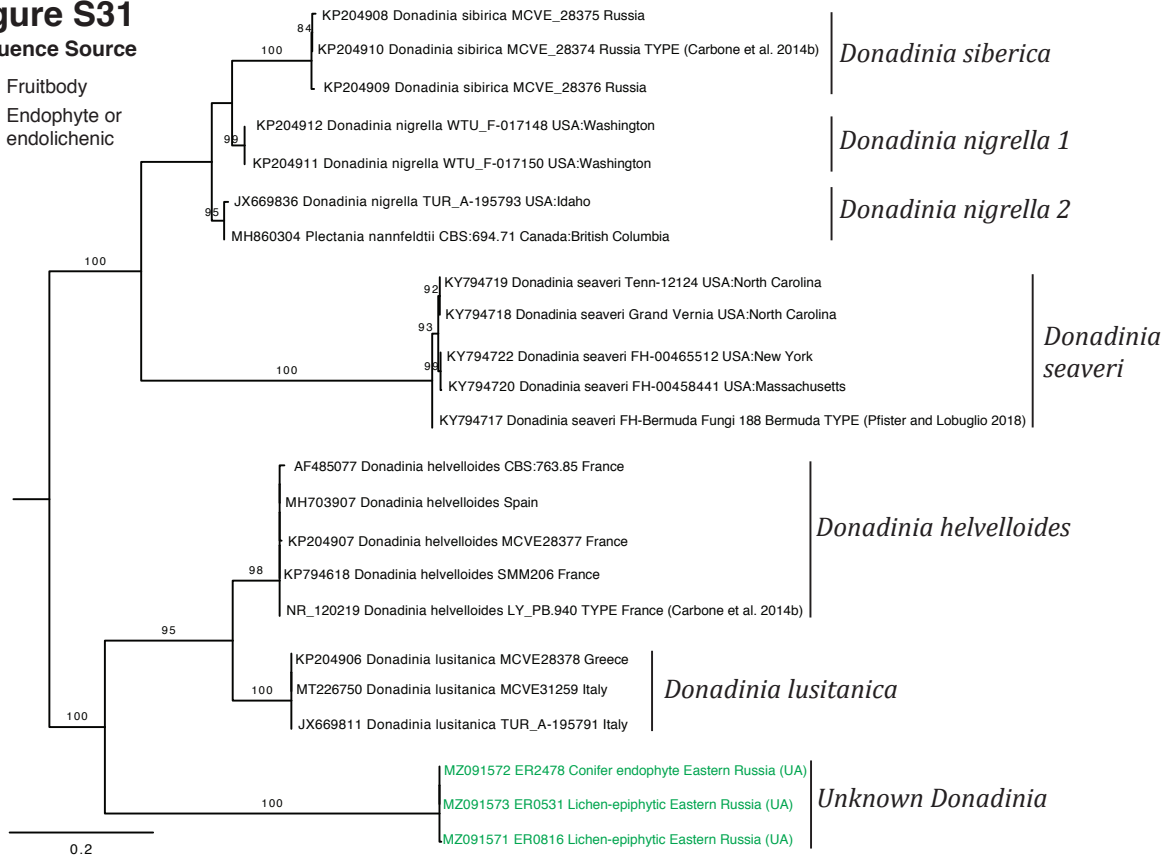


Fig. S32 Phylogeny based on ITS sequences of Sarcosomataceae (*Galiella*, *Plectania*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mat, blue; dead leaf, gray brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication or thesis where they were obtained.

Figure S32

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Asexual spore mat
- Dead leaf

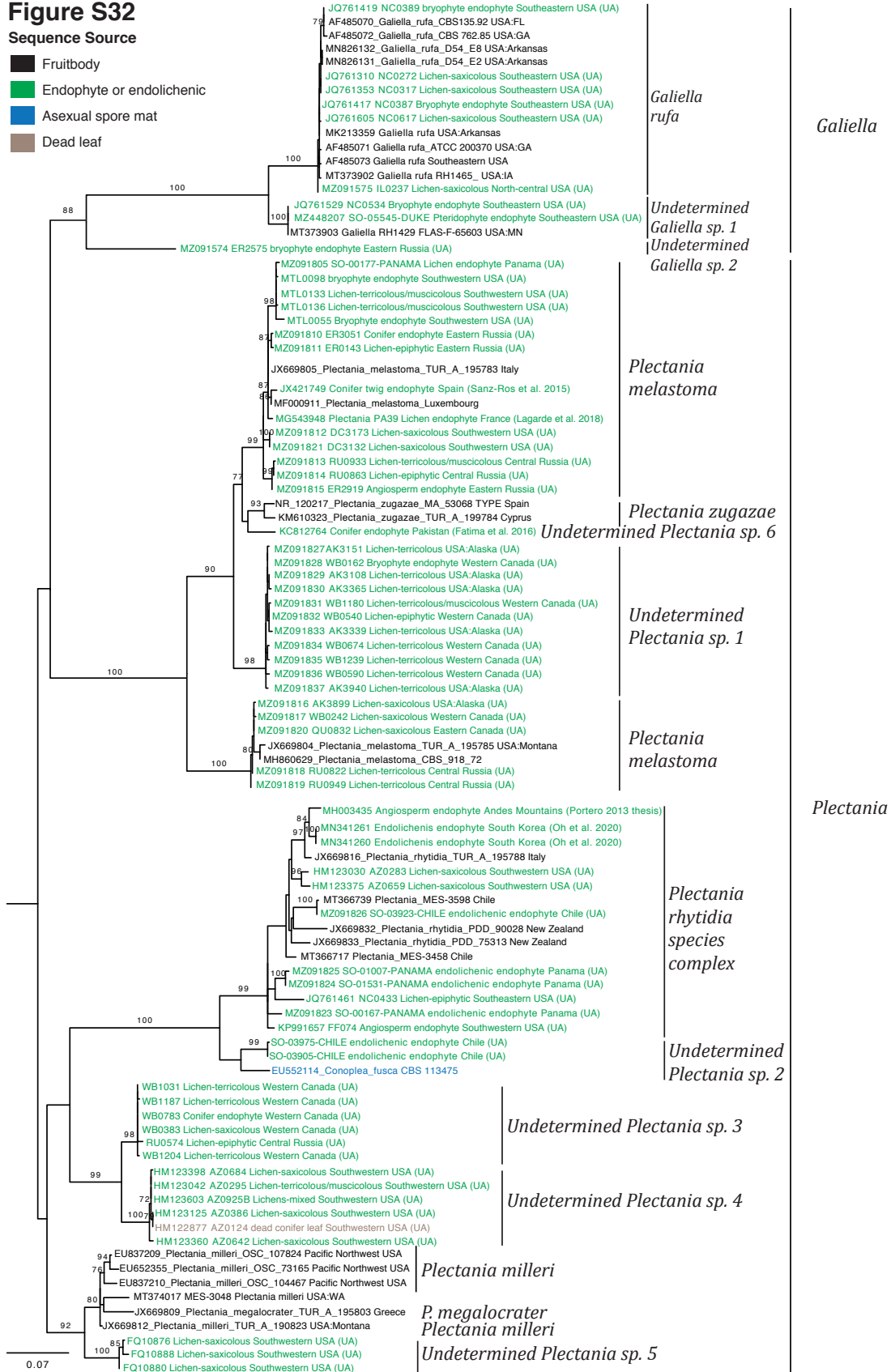


Fig. S33 Phylogeny based on ITS sequences of Sarcosomataceae (*Pseudoplectania*, *Sarcosoma*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; dead leaf, gray brown). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication where they were obtained or are labeled with "GB" if they are unpublished and were obtained directly from GenBank (NCBI). Sequences from type specimens include the reference for the sequence.

Figure S33

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Dead leaf



Fig. S34 Phylogeny based on ITS sequences of Sarcosomataceae (*Urnula*) and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; asexual spore mat, blue). Endolichenic sequence originated from the University of Arizona and is indicated with “UA”. Sequences from type specimens include the reference for the sequence.

Figure S34

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Asexual spore mat

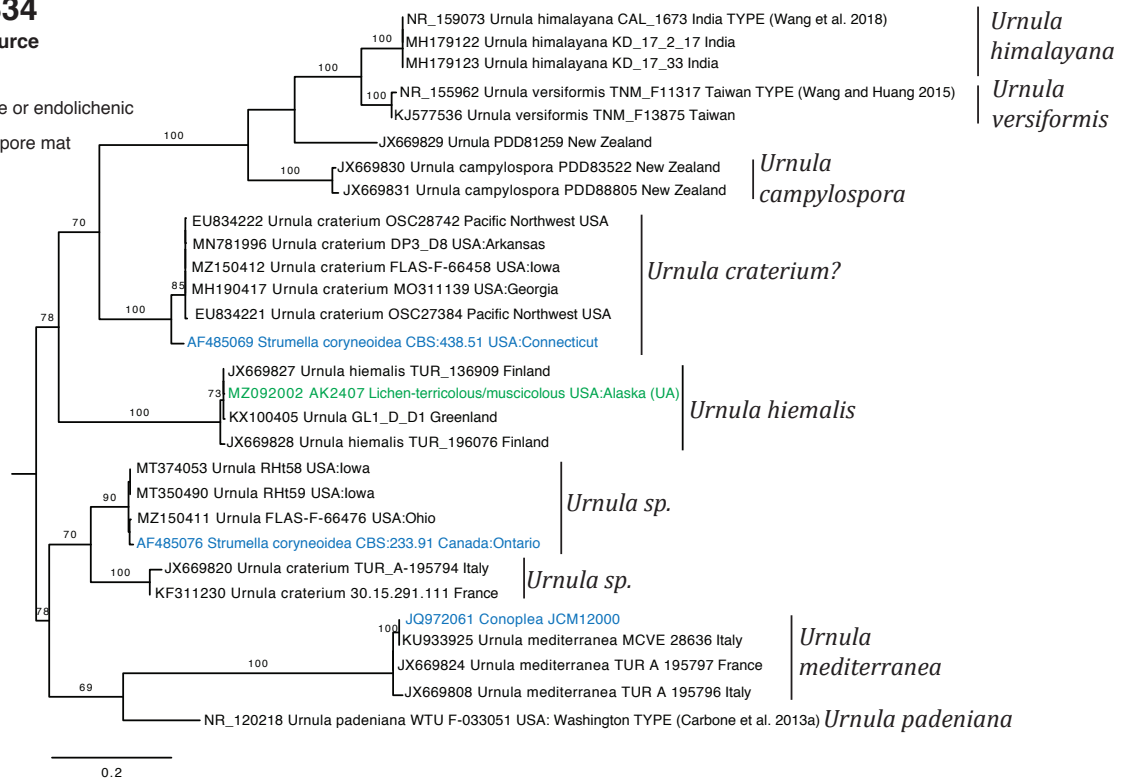


Fig. S35 Phylogeny based on ITS sequences of Tarzettaceae and related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from Type specimens are indicated with "TYPE". Sequences from ectomycorrhizas are designated with the abbreviation "ECM" preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish-brown; orchid root, purple; dead leaf, gray brown; asexual spore mat, blue; soil, gray) and substrates for fruitbodies are color coded if they were collected on a burnt substrate (orange). Endophyte and endolichenic sequences originating from the University of Arizona are indicated with "UA". Endophyte and endolichenic sequences that are not from the UA database include a reference to the publication or thesis where they were obtained or are labeled with "GB" if they are unpublished and were obtained directly from GenBank (NCBI). *Geopyxis* is currently a paraphyletic genus. The clade that includes a sequence from *Geopyxis carbonaria* (the type species for *Geopyxis*) is the clade referred to as "sensu stricto". The clade without the type species is referred to as "sensu lato". Sequences from type specimens include the reference for the sequence.

Figure S35

Sequence Source

-  Fruitbody
-  Endophyte or endolichenic
-  Ectomycorrhiza
-  Orchid root
-  Dead leaf
-  Asexual spore mat
-  Soil
-  Fruitbody from burned site

MZ091581 DC2572 Conifer endophyte Southwestern USA (UA)
MZ091582 AK1929 Bryophyte endophyte USA:Alaska (UA)
MZ091583 AK2004 Angiosperm endophyte USA:Alaska (UA)
MZ091584 F010874 Lichen-saxicolous Southwestern USA (UA)
MZ091585 AK2796 Lichen-saxicolous USA:Alaska (UA)
MF347755 Pinus endophyte_F11_20 USA:Colorado (Albertson 2017 thesis)
MF347782 Pinus endophyte A11_3 USA:Colorado (Albertson 2017 thesis)
JQ759147 AK0744 Lichen-saxicolous USA:Alaska (UA)
HM122764_Conifer dead leaf endophyte_AZ0006 USA:Arizona (UA)
KX909110_Conifer dead leaf endophyte_AK1735 USA:Alaska (UA)
Z96889 Geopyxis carbonaria ascomata after fire Norway
JQ759396 AK1030 endolichenic USA:Alaska (UA)
JQ759645 AK1308 Lichen-terricolous/muscicolous USA:Alaska (UA)
HM122869 AZ0118 Bryophyte Endophyte USA:Arizona (UA)
KX909055 AK1690 dead leaf endophyte USA:Alaska (UA)
Z96985 Geopyxis carbonaria ascomata after fire Norway
KX909094 AK1700 Conifer dead leaf endophyte USA:Alaska (UA)
GQ153135 AEA 11171 Conifer endophyte USA:Southwestern USA (UA)
KP335212 SNP006 Angiosperm stem endophyte USA:Arizona (UA)
KP335360 SNP159 Angiosperm leaf endophyte USA:Arizona (UA)
GQ153171 AEA 11229 Conifer endophyte USA:Arizona (UA)
GQ153191 AEA 11256 Conifer endophyte USA:Arizona (UA)
MZ091586 AK2085 Lichen-terricolous USA:Alaska (UA)
MZ091587 AK3617 Angiosperm endophyte USA:Alaska (UA)
MF347808 Pinus needle endophyte USA:Colorado (Albertson 2017 thesis)
MK886737 Geopyxis carbonaria PBM4072 fire associated USA:Tennessee
MZ091589 AK3893 Lichen-saxicolous USA:Alaska (UA)
MZ091590 AK3816 Lichen-terricolous USA:Alaska (UA)
KX909148 AK1619 Salix endophyte USA:Alaska (UA)
JQ758661 AK0175 Cassiope tetragona endophyte USA:Alaska (UA)
JQ759686 AK1370 endolichenic USA:Alaska (UA)
MZ091591 AK2176 Lichen-terricolous/muscicolous USA:Alaska (UA)
MZ091592 AK2109 Lichen-terricolous USA:Alaska (UA)
KP335313 SNP108 Angiosperm stem endophyte Southwestern USA (UA)
MZ091593 AK2199 Lichen-terricolous/muscicolous USA:Alaska (UA)
MZ091620 AK2077 Angiosperm endophyte USA:Alaska (UA)
KP335323 SNP118 Angiosperm stem endophyte Southwestern USA (UA)
MZ091594 AK3277 Lichen-saxicolous USA:Alaska (UA)
JQ759259 AK0869 Lichen-terricolous USA:Alaska (UA)
KU932496 Geopyxis carbonaria TK1243 Finland
HM122879 AZ0126 Conifer dead needle endophyte Southwestern USA (UA)
KX909151 AK1638 Angiosperm dead leaf endophyte USA:Alaska (UA)
MZ091595 WB1792 Lichen-saxicolous Western Canada (UA)
HM122783 AZ0026A Bryophyte endophyte Southwestern USA (UA)
KX909126_Conifer dead leaf endophyte_AK1766 USA:Alaska (UA)
HM122804 AZ0047 Lichen-epiphytic Southwestern USA (UA)
MZ091596 AK2030 Angiosperm endophyte USA:Alaska (UA)
KP335458 SNP271 Angiosperm stem endophyte Southwestern USA (UA)
HM122950 AZ0201 Lichen-epiphytic Southwestern USA (UA)
MZ091597 AK3054 Lichen-saxicolous USA:Alaska (UA)
MZ091598 AK3235 Lichen-saxicolous USA:Alaska (UA)
KP335428 SNP238 Angiosperm stem endophyte Southwestern USA (UA)
HM123008 AZ0260 Bryophyte endophyte Southwestern USA (UA)
MZ091599 WB0429 Lichen-saxicolous Western Canada (UA)
KX909087_Conifer dead leaf endophyte_AK1605 USA:Alaska (UA)
HM122850 AZ0097 Conifer dead leaf endophyte Southwestern USA (UA)
MZ091600 QU1323 Lichen-terricolous Eastern Canada (UA)
MZ091601 WB0924 Lichen-epiphytic Western Canada (UA)
JQ759042 AK0614 Lichen-terricolous USA:Alaska (UA)
MZ091602 WB0038 Lycopod endophyte Western Canada (UA)
GQ153149 AEA 11193 Conifer needle endophyte Southwestern USA (UA)
KU932495 Geopyxis carbonaria PRM149720 Czech Republic TYPE of G. foetida (Wang et al. 2016)
HM122797 AZ0040 Bryophyte endophyte Southwestern USA (UA)
HM122763 AZ0005 Conifer dead leaf endophyte Southwestern USA (UA)
HM123498 AZ0801 Conifer needle endophyte Southwestern USA (UA)
MZ091603 AK3146 Lichen-terricolous USA:Alaska (UA)
KX909069 AK1608 Conifer dead leaf endophyte USA:Alaska (UA)
MK886736 Geopyxis carbonaria fire associated USA:Tennessee
JQ759622 AK1536 Lichen-saxicolous USA:Alaska (UA)
HM123020 AZ0271B Bryophyte endophyte Southwestern USA (UA)
MZ091604 AK1957 Bryophyte endophyte USA:Alaska (UA)
KX909122 AK1761 Conifer dead leaf endophyte USA:Alaska (UA)
JQ759358 AK0991 Lichen-terricolous USA:Alaska (UA)
MZ091605 AK2043 Angiosperm endophyte USA:Alaska (UA)
MZ091606 AK3964 Lichen-terricolous USA:Alaska (UA)
MZ091607 AK3356 Lichen-terricolous USA:Alaska (UA)
MZ091608 DC3378 Lichen-saxicolous Southwestern USA (UA)
MK886731 Geopyxis carbonaria TFB14655 fire associated USA:Tennessee
KP335312 SNP107 Angiosperm stem endophyte Southwestern USA (UA)
JQ758887 AK0435 Lichen-saxicolous USA:Alaska (UA)
MZ091609 WB1576 Lichen-saxicolous Western Canada (UA)
MZ091610 AK2175 Lichen-terricolous/muscicolous USA:Alaska (UA)
MZ091611 AK2053 Angiosperm endophyte USA:Alaska (UA)
MZ091612 WB1361 Lichen-terricolous Western Canada (UA)
KX909113 AK1740 Conifer dead leaf endophyte USA:Alaska (UA)
MZ091613 RU1020 Lichen-epiphytic Central Russia (UA)
JQ759041 AK0613 Lichen-terricolous USA:Alaska (UA)
JQ759459 AK1103 Bryophyte endophyte USA:Alaska (UA)
WB1409 Lichen-epiphytic Western Canada (UA)
KF673826 Angiosperm endophyte DM0075 Southwestern USA (UA)
MZ091614 WB1610 Lichen-saxicolous Western Canada (UA)
JQ759162 AK0760 Lichen-saxicolous USA:Alaska (UA)
KP335339 SNP359 Parkinsonia Endophyte Southwestern USA (UA)
KX909066 AK1802 Conifer dead leaf endophyte USA:Alaska (UA)
HM123331 AZ0614 Lichen-epiphytic Southwestern USA (UA)
MZ091616 AK2179 Lichen-terricolous/muscicolous USA:Alaska (UA)
JQ759054 AK0628 Lichen-terricolous USA:Alaska (UA)
MZ091617 AK3376 Lichen-terricolous USA:Alaska (UA)
JQ759320 AK0941 Lichen-saxicolous USA:Alaska (UA)
JQ758737 AK0284 Angiosperm endophyte USA:Alaska (UA)
KX909090 AK1656 Conifer dead leaf endophyte USA:Alaska (UA)
MZ091618 WB1793 Lichen-saxicolous Western Canada (UA)
MZ091619 QU1179 Lichen-terricolous/muscicolous Eastern Canada (UA)
JQ759254 AK0864 Lichen-terricolous USA:Alaska (UA)

*Geopyxis
carbonaria*

*Geopyxis
sensu stricto*

Figure S35
(Cont.)

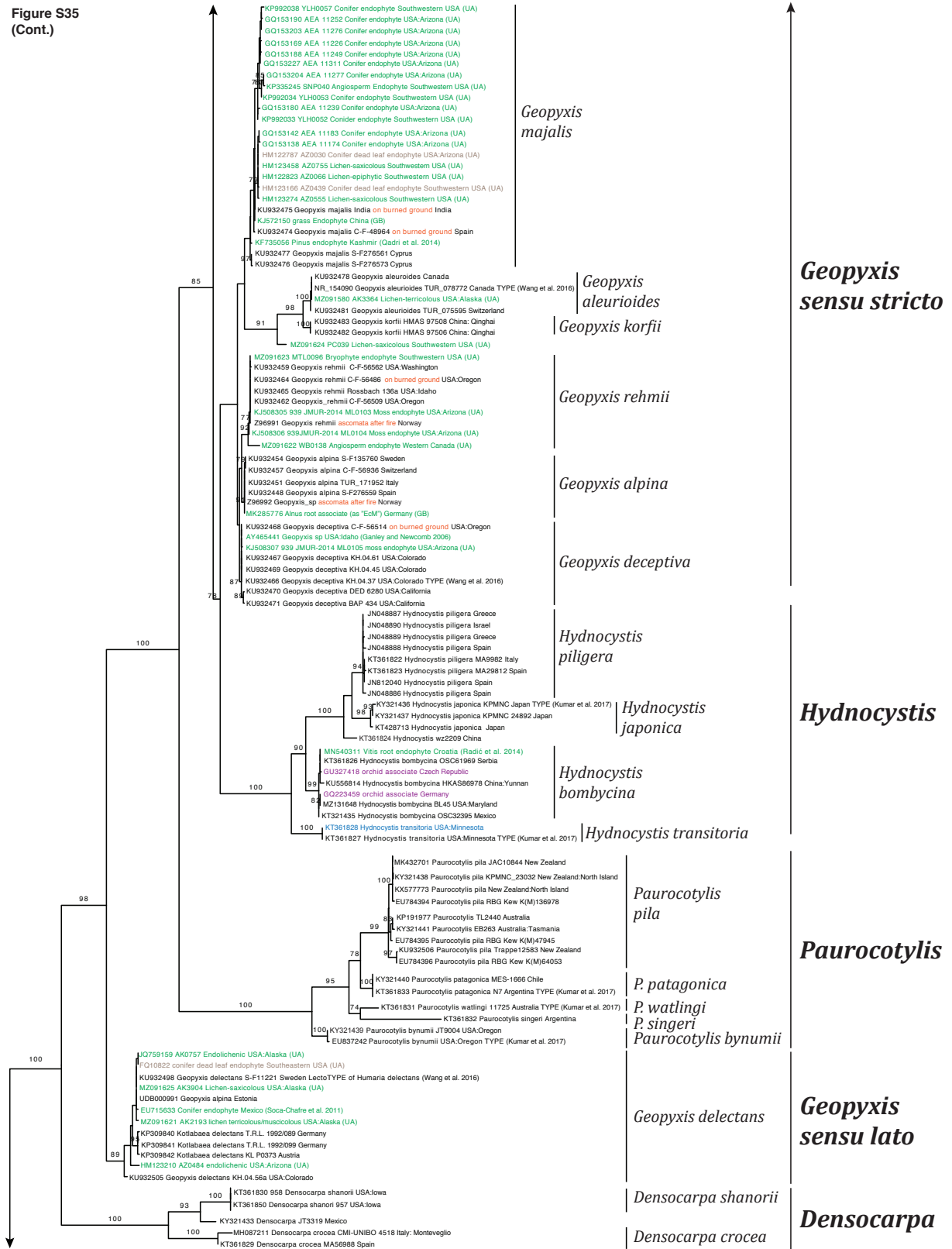


Figure S35
(Cont.)

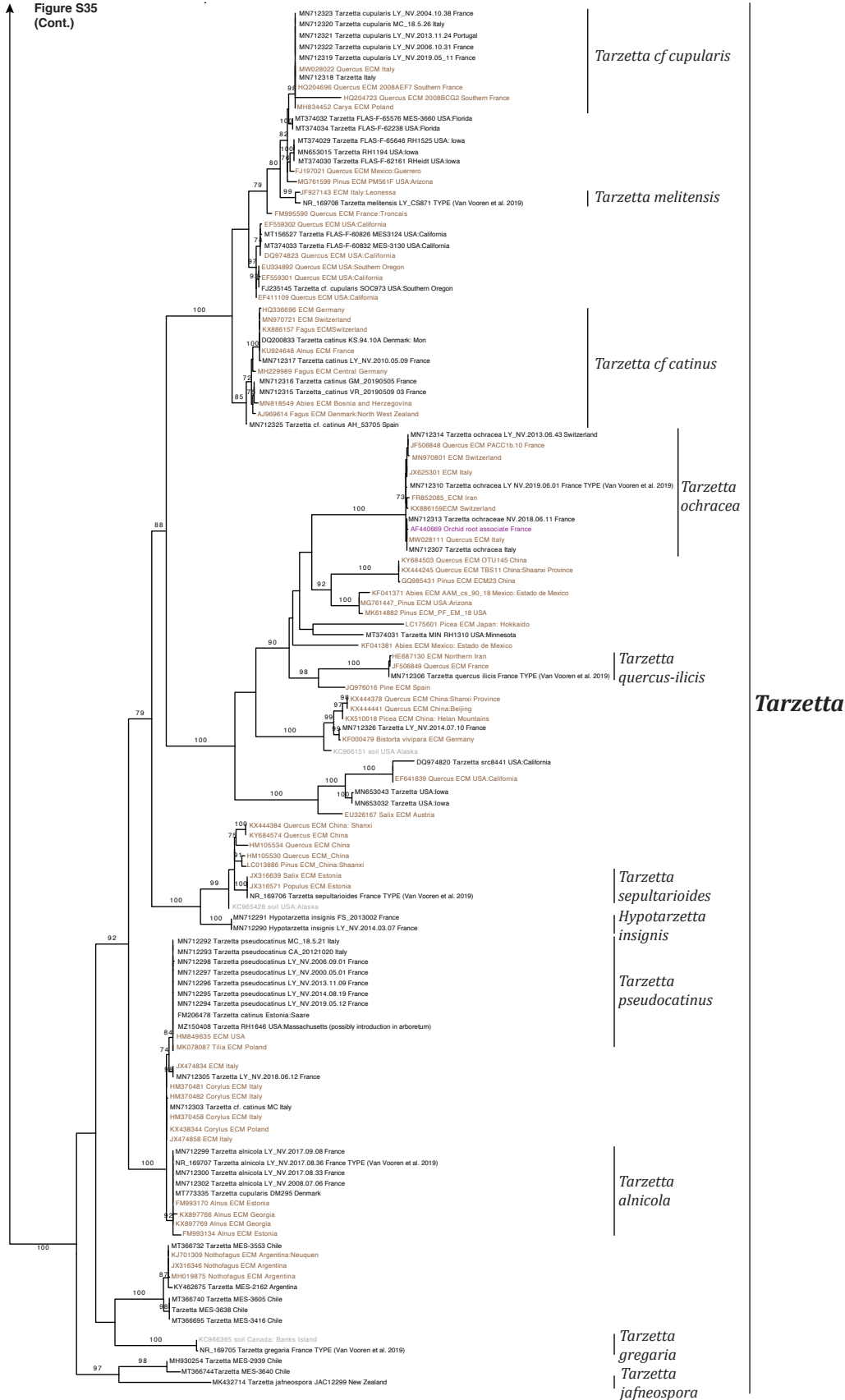
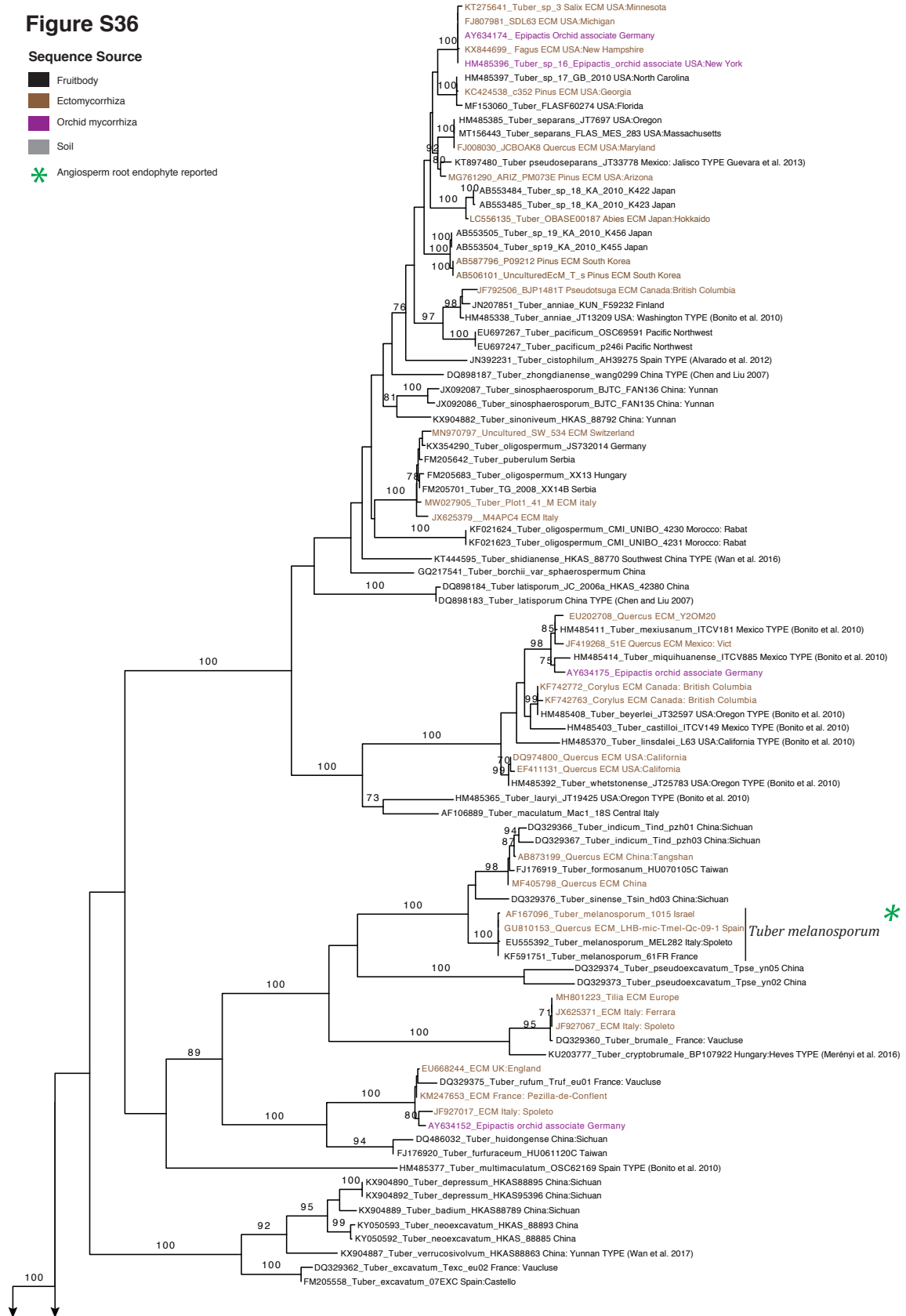


Fig. S36 Phylogeny based on ITS sequences of Tuberaceae analyzed with Maximum Likelihood. Taxa for which endophyte sequences were reported by Schneider-Maunoury *et al.* (2020) are shown with a green asterisk. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with "TYPE". Sequences from ectomycorrhizas are designated with the abbreviation "ECM" preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; ectomycorrhizae, reddish-brown; orchid root, purple; soil, gray). ITS sequences of endophytes were not available, but species for which endophytes have been reported by Schneider-Maunoury *et al.* (2020) are indicated by a green asterisk. Sequences from type specimens include the reference for the sequence.

Figure S36

Sequence Source

- Fruitbody
- Ectomycorrhiza
- Orchid mycorrhiza
- Soil
- Angiosperm root endophyte reported



Tuber

Tuber melanosporum *

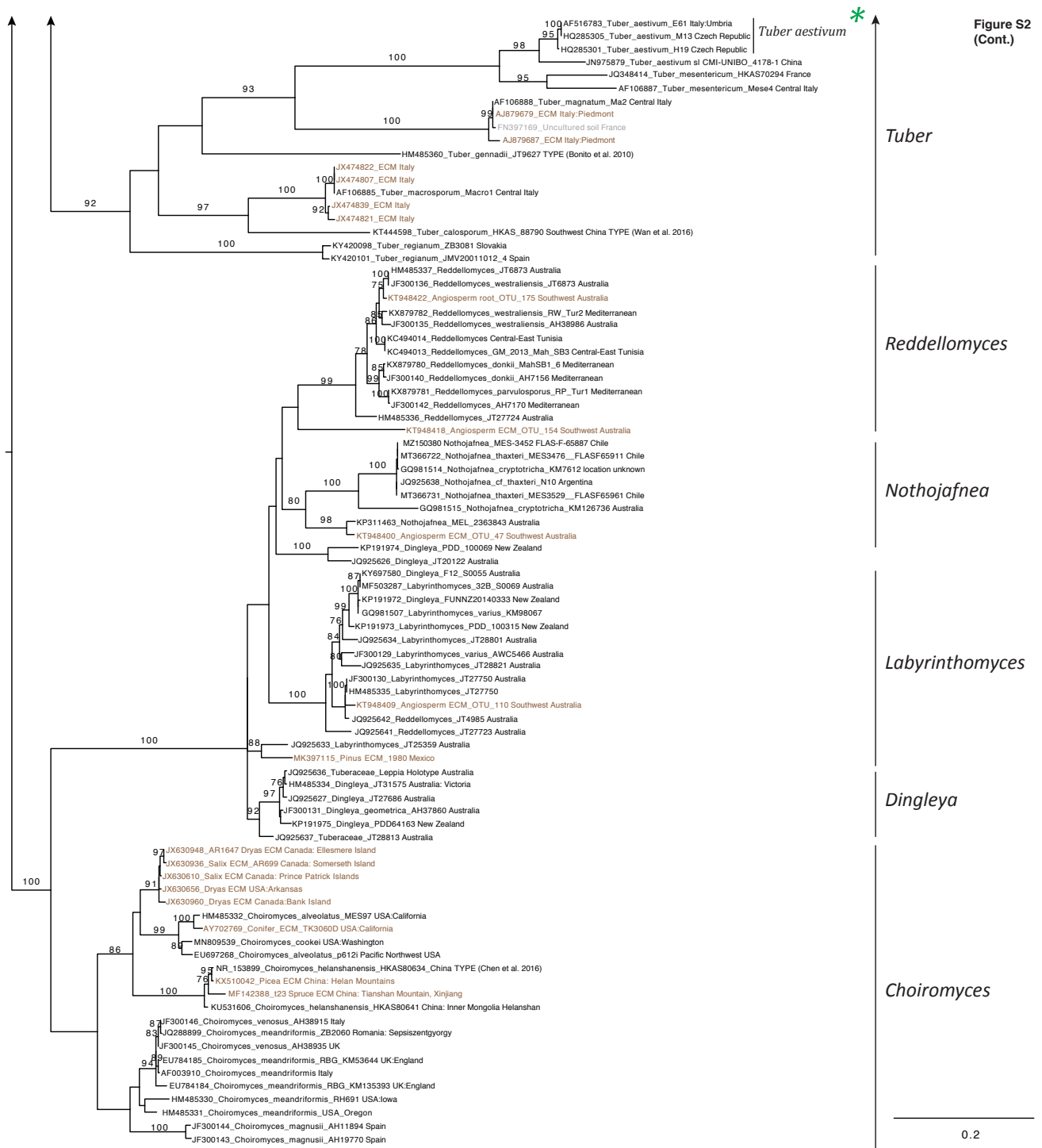


Fig. S37 Phylogeny based on ITS sequences of Geomoriaceae and an undetermined lineage of related endophytic and endolichenic fungi analyzed with Maximum Likelihood. The phylogram is a 50% majority rule tree with midpoint rooting and support based on 1000 bootstrap replicates. Bootstrap support $\geq 70\%$ is shown above each node. GenBank accession number is given on the terminal preceding other available information (organism name, herbarium voucher accession number, collection, and country). Sequences from type specimens are indicated with “TYPE”. Sequences from ectomycorrhizas are designated with the abbreviation “ECM” preceded by host name if available. Terminals are color coded by their sequence source (fruitbody, black; endophytic or endolichenic, green; ectomycorrhiza, reddish-brown). All endophyte and endolichenic sequences originated from the University of Arizona and are indicated with “UA”. Sequences from type specimens include the reference for the sequence.

Figure S37

Sequence Source

- Fruitbody
- Endophyte or endolichenic
- Ectomycorrhiza

0.07

