

1 Table S1. Barcodes and adapter/sequencing primers for metatranscriptome

Sample	Barcode	5' adapter/sequencing primer	3' adapter/sequencing primer
Dec .8	AAACT	AGTTTAGATCGGAAGAGCGGTTC AGCAGGAATGCCGAG	ACACTCTTTCCCTACACGA CGCTCTTCCCATCTAAACT
Dec. 9	AAAGC	AGTTTAGATCGGAAGAGCGGTTC AGCAGGAATGCCGAG	ACACTCTTTCCCTACACGA CGCTCTTCCCATCTAAACT
Dec. 10	AACAA	AGTTTAGATCGGAAGAGCGGTTC AGCAGGAATGCCGAG	ACACTCTTTCCCTACACGA CGCTCTTCCCATCTAAACT
Dec. 11	AACTG	AGTTTAGATCGGAAGAGCGGTTC AGCAGGAATGCCGAG	ACACTCTTTCCCTACACGA CGCTCTTCCCATCTAAACT

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3 Table S2. LSU barcodes and primers

Sample	Forward barcode	Reverse barcode	Full barcode	Forward primer (LR0R)	Reverse primer (LR3)
Dec .8	TAATTC	AATATC	AATATCTAATTC	ACCCGCTGA ACTTAAGC	CCGTGTTTC AAGACGGG
Dec. 9	TACACA	AATATC	AATATCTACACA	ACCCGCTGA ACTTAAGC	CCGTGTTTC AAGACGGG
Dec. 10	CCCTAA	AATATC	AATATCCCCTAA	ACCCGCTGA ACTTAAGC	CCGTGTTTC AAGACGGG
Dec. 11	CCGAGG	AATATC	AATATCCCGAGG	ACCCGCTGA ACTTAAGC	CCGTGTTTC AAGACGGG

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5 Table S3. Air sequence summary statistics

Sample	# Metatranscriptome Sequences	# rRNA sequences (metatranscriptome)	# LSU amplicon sequences
Dec. 8	331,765	51,361	5,377
Dec. 9	601,828	97,871	20,766
Dec. 10	0	0	18,778
Dec. 11	4,231,592	1,766,762	10,493

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1 Table S3. Relative abundances of fungal families

	Total				Active		
	12/8	12/9	12/10	12/11	12/8	12/9	12/11
Sordariomycetidae	0.00	0.00	0.00	0.00	1.11	4.63	5.06
Lachnocladiaceae	0.34	3.74	2.66	4.37	0.03	0.00	0.03
Capnodiales family	10.86	0.29	0.40	0.37	0.20	0.00	0.03
Hymenochaetaceae	2.77	2.43	4.37	3.40	0.03	0.03	0.31
Saccharomycetaceae	0.09	1.66	0.54	0.06	1.89	2.60	7.57
Sclerotiniaceae	0.57	0.00	0.06	0.00	9.57	8.86	3.31
Mycosphaerellaceae	0.46	0.11	0.31	0.14	10.29	8.46	3.23
Schizoporaceae	6.26	8.46	8.63	5.91	0.00	0.00	0.09
Coriolaceae	10.43	7.20	7.54	8.63	0.20	0.00	0.20
Physciaceae	0.00	0.00	0.00	0.00	19.34	21.03	7.86
Xylariaceae	0.51	0.31	0.54	0.97	20.49	22.57	9.74
Polyporaceae	40.37	42.11	45.97	40.49	0.09	0.14	0.63
Other family	27.34	33.69	28.97	35.66	36.77	31.69	61.94

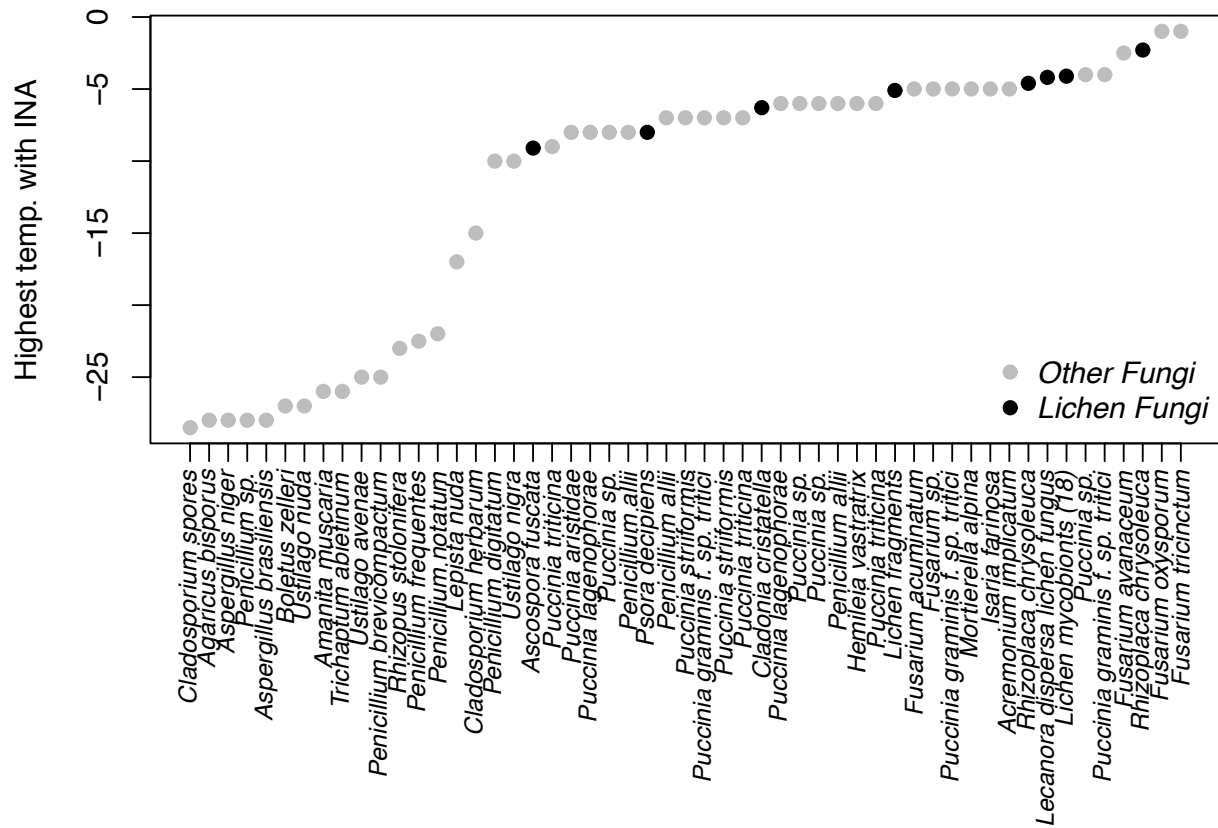
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1 Table S4. IN taxa in Figure S1 that were detected in Amazon air samples. Counts are based on
 2 rarefied data.

Genus name	# Total	# Active	Temp (°C)	Reference(s)
<i>Agaricus</i>	0	1	-28	Haga et al., 2014
<i>Amanita</i>	0	3	-26	Haga et al., 2014
<i>Aspergillus</i>	0	2	-28	Haga et al., 2014
<i>Boletus</i>	0	1	-27	Haga et al., 2014
<i>Cladosporium</i>	2	0	-15 to -28	Jayaweera and Flanagan, 1982; Iannone et al., 2011
<i>Fusarium</i>	1	0	-5 to -1	Pouleur et al., 1992; Tsumuki et al. 1992; Richard et al. 1996
<i>Lepsita</i>	0	1	-17	Haga et al., 2014
<i>Mortierella</i>	0	15	-5	Fröhlich-Nowoisky et al., 2015
<i>Acremonium</i>	8	0	-5	Huffman et al., 2013
<i>Puccinia</i>	0	1	-9 to -4	Morris et al., 2013
<i>Rhizopus</i>	6	13	-23	Jayaweera and Flanagan, 1982
<i>Cladonia</i>	0	2	-6.3	Kieft and Ahmadjian, 1989

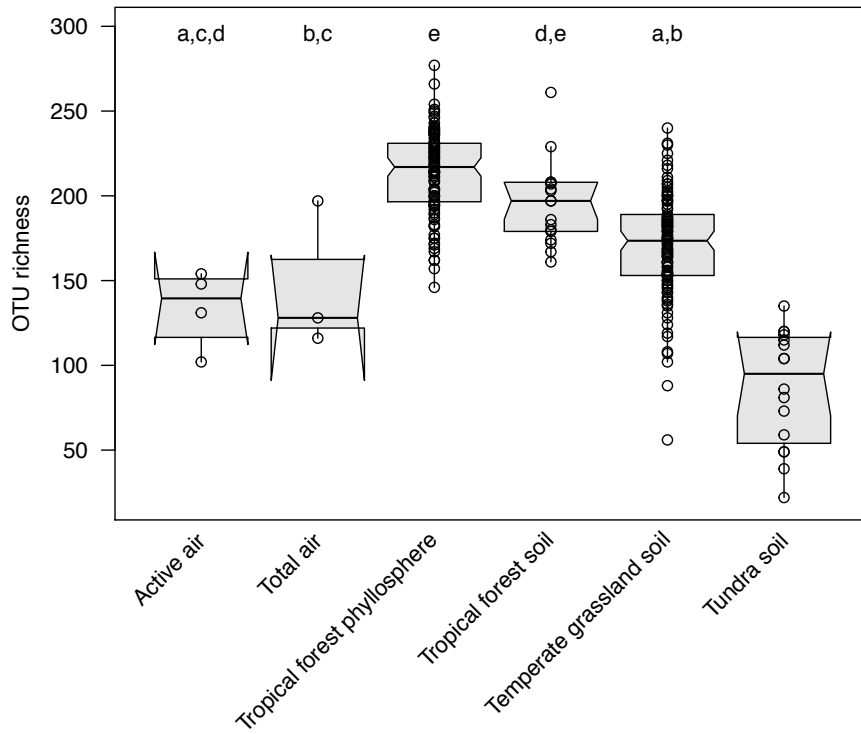
1 Table S5. Multi-environment sequence summary statistics

Study	# Samples	# Sequences	Biome	Gene region	Total # OTUs
Barnard et al., 2013	60	151,125	Temperate grassland soil	D1-D2	6,872
Kerekes et al., 2013	36	26,390	Tropical forest soil	D1-D2	3,524
Kembel and Mueller, 2014	100	771,562	Tropical forest phyllosphere	D1-D2	21,379
Penton et al., 2013	16	82,618	Tundra soil	D1-D3	1,386
Penton et al., 2013	12	93,994	Temperate grassland soil	D1-D3	2,288
Penton et al., 2014	48	451,769	Temperate grassland soil	D1-D2	8,221
This study (amplicons)	4	55,414	Tropical forest air (DNA)	D1-D2	535
This study (metatranscriptome)	3	1,915,994	Tropical forest air (RNA)	na	441

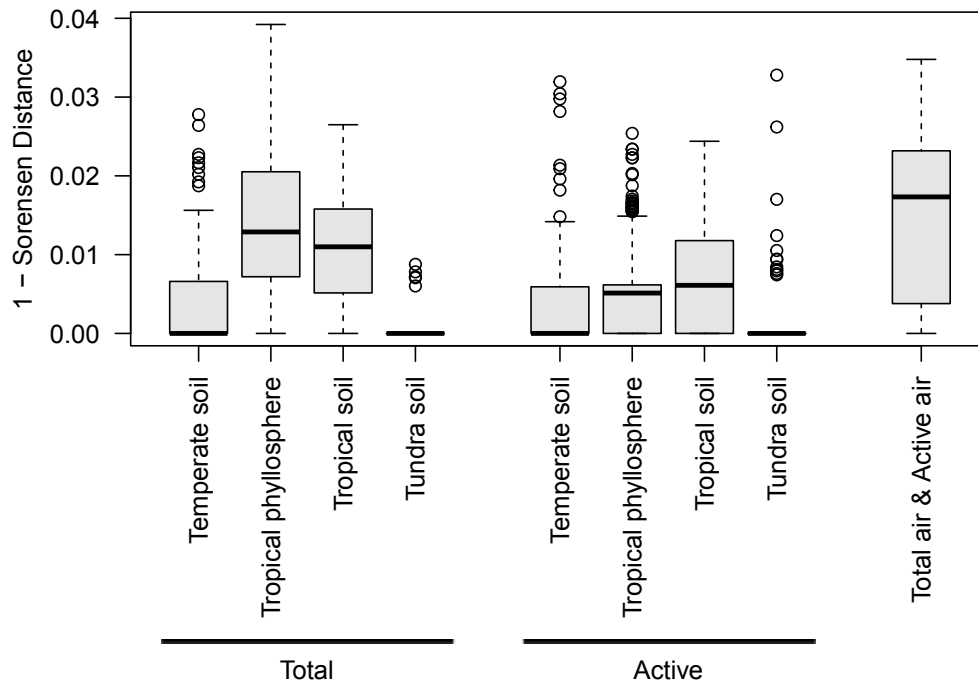


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 2 Figure S1. Highest temperatures with ice nucleation activity (INA) in lichens and other fungi.
 3 Species that occur more than once were measured in multiple studies. Data compiled from
 4 Després et al., 2012, Fröhlich-Nowoisky et al., 2015, Haga et al., 2014, Morris et al., 2013.

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 2 Figure S2. OTU richness significantly varied among environment types (ANOVA, $F(5,237) =$
 3 66.89 , $p < 0.001$). Letters above each box indicate non-significant pairs after Tukey's honestly
 4 significant difference (HSD) test (adjusted p-value > 0.05).



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 2 Figure S3. Similarity between air communities and potential source environments significantly
 3 differed among environments (ANOVA, $F(8,1655) = 106.4, p < 0.001$). Post-hoc Tukey's HSD
 4 test showed that total and active air communities were most similar to tropical phyllosphere and
 5 tropical soil communities. The following results were significant at $p < 0.001$. Total air
 6 communities were most similar to tropical phyllosphere communities than to temperate soil,
 7 tundra soil, and tropical soil. Active air communities were more similar to tropical soil than
 8 tundra soil and temperate soil and were more similar to tropical phyllosphere communities than to
 9 temperate soil. There was no significant difference in similarity between tropical soil and
 10 phyllosphere communities.