GlobalFungi: Global database of fungal records from high-throughput-sequencing metabarcoding studies

Tomáš Větrovský¹, Daniel Morais¹, Petr Kohout¹, Clémentine Lepinay¹, Camelia Algora Gallardo¹, Sandra Awokunle Hollá¹, Barbara Doreen Bahnmann¹, Květa Bílohněd¹, Vendula Brabcová¹, Federica D'Alò², Zander Rainier Human¹, Mayuko Jomura³, Miroslav Kolařík¹, Jana Kvasničková¹, Salvador Lladó¹, Rubén López-Mondéjar¹, Tijana Martinović¹, Tereza Mašíňová¹, Lenka Meszárošová¹, Lenka Michalčíková¹, Tereza Michalová¹, Sunil Mundra⁴, Diana Navrátilová¹, Iľaki Odriozola¹, Sarah Piché-Choquette¹, Martina Štursová¹, Karel Švec¹, Vojtěch Tláškal¹, Michaela Urbanová¹, Lukáš Vlk¹, Jana Voříšková¹, Lucia Žifčáková¹, Petr Baldrian¹

Affiliations

1. Institute of Microbiology of the Czech Academy of Sciences, Vídeňská 1083, 14220 Praha 4, Czech Republic
2. Laboratory of Systematic Botany and Mycology, University of Tuscia, Largo dell'Università snc, Viterbo 01100, Italy
3. Department of Forest Science and Resources, College of Bioresource Sciences, Nihon University, Fujisawa, Kanagawa, Japan
4. Department of Biology, United Arab Emirates University, Al Ain, Abu Dhabi, United Arab Emirates

corresponding author: Petr Baldrian (baldrian@biomed.cas.cz)

Tomáš Větrovský, Daniel Morais, Petr Kohout and Clémentine Lepinay contributed equally to this work.

Abstract

Fungi are key players in vital ecosystem services, spanning carbon cycling, decomposition, symbiotic associations with cultural and wild plants and pathogenicity. The high importance of fungi in the ecosystem processes contrasts with the incompleteness of understanding of the patterns of fungal biogeography and the environmental factors that drive it. To close this gap of knowledge, we have here collected and validated data published on the composition of soil fungal communities in terrestrial environments including soil and plant-associated habitats and made them publicly accessible through a user interface at <http://globalfungi.com>. The GlobalFungi database contains over 650 million observations of fungal sequences across >20 000 samples with geographical locations and additional metadata contained in 207 original studies with millions of unique sequence variants of the fungal internal transcribed spacers (ITS) 1 and 2 representing fungal species and genera. As it is, the study represents the most comprehensive atlas of fungal distribution on the global scale open to further additions.

Background & Summary

Fungi play fundamental roles in the ecosystem processes across all terrestrial biomes. As plant symbionts, pathogens or major decomposers of organic matter they substantially influence plant primary production, carbon mineralization and sequestration, and act as crucial regulators of the soil carbon balance^{1,2}. The activities of fungi and their communities contribute to the production of clean water, food, and air and the suppression of disease-causing soil organisms. Soil biodiversity is thus increasingly recognized to provide services critical to food safety and human health³.

It is of high importance to determine how environmental factors affect the diversity and distribution of fungal communities. So far, only a few studies focused on fungal distribution and diversity on global scale⁴⁻⁶. Importantly, these single survey studies focused either on a limited number of biomes^{4,5}, narrower taxonomical group within the Fungal kingdom⁶, or were restricted only to fungi inhabiting soil. While the benefit of a focused study is the fact that it can rely on standardized sample analysis and metadata collection, its limitation is the inability to cover large sampling efforts in space and time. On the other hand, since the advent of the high-throughput-sequencing methods, large amounts of sequencing data exist for fungi from terrestrial environments with sufficient metadata that allow their evaluation⁷. Recently, the meta-analysis of 36 papers reporting global diversity of soil fungi collected >3000 samples and helped to indicate that climate is an important factor for the global distribution of soil fungi and identify the hotspots of fungal diversity outside the tropics⁸. This approach clearly demonstrated the utility of a meta-study approach to address fungal biogeography, ecology and diversity. In addition, the compilation of these data demonstrated the fact that symbiotic mycorrhizal fungi that aid cultural and wild plants to access nutrients, are more likely to be affected by rapid changes of climate than other guilds of fungi, including plant pathogens⁸ and helped to identify which fungi tend to follow alien plants invading new environments⁹.

Here, we have undertaken a comprehensive collection and validation of data published on the composition of soil fungal communities in terrestrial environments including soil and plant-associated habitats. This approach enabled us to construct the GlobalFungi database containing, on March 16, 2020, over 120 million of unique sequence variants¹⁰ of the fungal internal transcribed spacers (ITS) 1 and 2, covering >20 000 samples contained in 207 original studies (Figure 1). The dataset of sequence variant frequencies across samples, accompanied by metadata retrieved from published papers and in global climate databases is made publicly available at <http://globalfungi.com>. To achieve the goal to make published data findable, accessible, interoperable and reusable, the user interface at the above address allows the users to search for individual sequences, fungal species hypotheses¹¹, species or genera, to get a visual representation of their distribution in the environment and to access and download sequencing data and metadata. In addition, the user interface also allows authors to submit data from studies not yet covered and in this way to help to build the resource for the community of researchers in mycology, biogeography and ecology of fungi.

Methods

Data selection. We explored papers that used high-throughput sequencing for the analysis of fungal communities that were published until the beginning of 2019; in total, we explored 843 papers. The following selection criteria were used for the inclusion of samples (and, consequently, studies) into the dataset: (1) samples came from terrestrial biomes of soil, dead or live plant material (e.g., soil, litter, rhizosphere soil, topsoil, lichen, deadwood, root and shoot) and were not subject to experimental treatment; (2) the precise geographic location of each sample was recorded (GPS coordinates); (3) the whole fungal community was subject to amplicon sequencing (studies using group-specific primers were excluded); (4) the internal transcribed spacer regions (ITS1, ITS2, or both) were subject to amplification; (5) sequencing data (either in fasta or fastq format) were publicly available or provided by the authors of the study upon request, and the sequences were unambiguously assigned to samples; (6) the samples could be assigned to biomes according to the Environment Ontology (<http://www.ontobee.org/ontology/ENVO>)⁸. In total, there were 209 publications contained samples that matched our criteria (Online-Only Table 1).

Processing of sequencing data.

For the processing of data, see Figure 2. Raw datasets from 207 studies, covering 20 009 individual samples were quality filtered by removing all sequences with the mean quality phred scores below 20. Each sequence was labelled using the combination of a sample ID and sequence ID, and the full ITS1 or ITS2 fungal region was extracted using Perl script ITSx v1.0.11¹². ITS extraction resulted in a total of 416 291 533 full ITS1 and 231 278 756 full ITS2 sequences. The extracted ITS sequences were classified according to the representative sequence of the closest UNITE species hypothesis (SH) using BLASTN, considering the SH created using a 98.5% similarity threshold (general release 8.1 from 2.2.2019¹¹). The sequence was classified to the best best hit SH only when the following thresholds were met: e-value <10e⁻⁵⁰, sequence similarity >=98.5%. All representative sequences annotated as nonfungal were discarded. All representative sequences classified to any fungal SH and all unclassified sequences were used to build database sequence variant library. The number of sequence variants (unique nucleotide sequences) accessible through the database is 119 566 862.

Sample metadata. Sample metadata were collected from the published papers and/or public repositories where they were submitted by the authors. In some cases, metadata were obtained from the authors of individual studies upon request. The samples were assigned to continents, countries or specific locations, and all sites were categorized into biomes following the classification of Environment Ontology to a maximum achievable depth for each sample. The complete list of metadata included in the database is in Table 1.

In addition to metadata provided by the authors of each study, we also extracted bioclimatic variables from the global CHELSA¹³ and WorldClim 2¹⁴ databases for each sample based on its GPS location. Since the results based on CHELSA and WorldClim 2 were comparable, we decided to include those from CHELSA, because precipitation patterns are better captured in the CHELSA dataset, in particular for mountain sites¹³.

For each sequence variant that was classified to SH, fungal species name and genus name was retrieved from the UNITE database¹¹, when available.

Data Records

The raw sequencing reads used to create the database are available at the following locations: One part of the raw ITS sequencing reads can be found from the National Center for Biotechnology Information (NCBI) Sequence Read Archive under accession numbers SRP001058¹⁵, SRP001175¹⁶, SRP006078¹⁷, SRP012868¹⁸, SRP013695¹⁹, SRP013944²⁰, SRP015735²¹, SRP016090²², SRP026207²³, SRP028404²⁴, SRP033719²⁵, SRP035356²⁶, SRP040314²⁷, SRP040786²⁸, SRP041347²⁹, SRP043106³⁰, SRP043706³¹, SRP043982³², SRP044665³³, SRP045166³⁴, SRP045587³⁵, SRP045746³⁶, SRP045933³⁷, SRP046049³⁸, SRP048036³⁹, SRP048856⁴⁰, SRP049544⁴¹, SRP051033⁴², SRP052222⁴³, SRP052716⁴⁴, SRP055957⁴⁵, SRP057433⁴⁶, SRP057541⁴⁷, SRP058508⁴⁸, SRP058555⁴⁹, SRP058851⁵⁰, SRP059280⁵¹, SRP060838⁵², SRP061179⁵³, SRP061305⁵⁴, SRP061904⁵⁵, SRP062647⁵⁶, SRP063711⁵⁷, SRP064158⁵⁸, SRP065817⁵⁹, SRP066030⁶⁰, SRP066284⁶¹, SRP066331⁶², SRP067301⁶³, SRP067367⁶⁴, SRP068514⁶⁵, SRP068608⁶⁶, SRP068620⁶⁷, SRP068654⁶⁸, SRP069065⁶⁹, SRP069742⁷⁰, SRP070568⁷¹, SRP073070⁷², SRP073265⁷³, SRP074055⁷⁴, SRP074496⁷⁵, SRP075989⁷⁶, SRP079403⁷⁷, SRP079521⁷⁸, SRP080210⁷⁹, SRP080428⁸⁰, SRP080680⁸¹, SRP082472⁸², SRP082976⁸³, SRP083394⁸⁴, SRP083434⁸⁵, SRP083901⁸⁶, SRP087715⁸⁷, SRP090261⁸⁸, SRP090335⁸⁹, SRP090490⁹⁰, SRP090651⁹¹, SRP091741⁹², SRP091855⁹³, SRP091867⁹⁴, SRP092609⁹⁵, SRP092777⁹⁶, SRP093592⁹⁷, SRP093928⁹⁸, SRP094708⁹⁹, SRP097883¹⁰⁰, SRP101553¹⁰¹, SRP101605¹⁰², SRP102378¹⁰³, SRP102417¹⁰⁴, SRP102775¹⁰⁵, SRP106137¹⁰⁶, SRP106774¹⁰⁷, SRP107174¹⁰⁸, SRP107743¹⁰⁹, SRP109164¹¹⁰, SRP109773¹¹¹, SRP110522¹¹², SRP110810¹¹³, SRP113348¹¹⁴, SRP114697¹¹⁵, SRP114821¹¹⁶, SRP115350¹¹⁷, SRP115464¹¹⁸, SRP115599¹¹⁹, SRP117302¹²⁰, SRP118875¹²¹, SRP118960¹²²,

SRP119174¹²³, SRP125864¹²⁴, SRP132277¹²⁵, SRP132591¹²⁶, SRP132598¹²⁷, SRP136886¹²⁸, SRP139483¹²⁹, SRP142723¹³⁰, SRP148813¹³¹, SRP150527¹³², SRP151262¹³³, SRP153934¹³⁴, SRP160913¹³⁵, SRP161632¹³⁶ and SRP195764¹³⁷, in the European Nucleotide Archive (ENA) Sequence Read Archive under accession numbers ERP001713¹³⁸, ERP003251¹³⁹, ERP003790¹⁴⁰, ERP005177¹⁴¹, ERP005905¹⁴², ERP009341¹⁴³, ERP010027¹⁴⁴, ERP010084¹⁴⁵, ERP010743¹⁴⁶, ERP011924¹⁴⁷, ERP012017¹⁴⁸, ERP013208¹⁴⁹, ERP013987¹⁵⁰, ERP014227¹⁵¹, ERP017480¹⁵², ERP017851¹⁵³, ERP017915¹⁵⁴, ERP019580¹⁵⁵, ERP019924¹⁵⁶, ERP020657¹⁵⁷, ERP022511¹⁵⁸, ERP022742¹⁵⁹, ERP023275¹⁶⁰, ERP023718¹⁶¹, ERP023855¹⁶², ERP106131¹⁶³, ERP107634¹⁶⁴, ERP107636¹⁶⁵, ERP110188¹⁶⁶ and ERP112007¹⁶⁷, in the DNA Data Bank of Japan (DDBJ) under the accession numbers DRA000926¹⁶⁸, DRA000937¹⁶⁹, DRA001737¹⁷⁰, DRA002424¹⁷¹, DRA002469¹⁷², DRA003024¹⁷³, DRA003730¹⁷⁴, DRA004913¹⁷⁵, DRA006519¹⁷⁶, DRP002783¹⁷⁷, DRP003138¹⁷⁸ and DRP005365¹⁷⁹, in the Dryad Digital Repository under the DOIs <https://doi.org/10.5061/dryad.2fc32>¹⁸⁰, <http://dx.doi.org/10.5061/dryad.n82g9>¹⁸¹, <http://dx.doi.org/10.5061/dryad.2343k>¹⁸², <https://doi.org/10.5061/dryad.gp302>¹⁸³, <http://dx.doi.org/10.5061/dryad.cq2rb>¹⁸⁴, <https://doi.org/10.5061/dryad.8fn8j>¹⁸⁵ and <https://doi.org/10.5061/dryad.216tp>¹⁸⁶, in the MG-RAST repository under the accession numbers 4783710.3¹⁸⁷, 4702703.3¹⁸⁸, 4524551.3¹⁸⁹, 4544233.3¹⁹⁰, 4683808.3¹⁹¹, 4684008.3¹⁹², 4696490.3¹⁹³, 4715213.3¹⁹⁴, 4563787.3¹⁹⁵, 4563788.3¹⁹⁶, 4620497.3¹⁹⁷, 4620498.3¹⁹⁸, mgp13293¹⁹⁹, mgp1617²⁰⁰ and mgp9003²⁰¹, in the PlutoF repository under the URLs <https://plutof.ut.ee/#/filerepository/view/1561672>²⁰², <https://plutof.ut.ee/#/filerepository/view/1562683>²⁰³, <https://plutof.ut.ee/#/doi/10.1515/BIO/100002>²⁰⁴ and <https://plutof.ut.ee/#/doi/10.1515/BIO/587446>²⁰⁵, in the UNITE database under the URL http://unite.ut.ee/454_EcM_CMZ.zip²⁰⁶, in GenBank under the accessions KAYV00000000.1²⁰⁷, KAYU00000000.1²⁰⁸, KAYT00000000.1²⁰⁹, SAMN02934078²¹⁰ and SAMN02934079²¹¹, in the database of the Australian Antarctic Data Center under DOI <http://dx.doi.org/10.4225/15/526f42ada05b1>²¹², in the supplemental data of papers under URLs https://static-content.springer.com/esm/art%3A10.1038%2Fismej.2012.84/MediaObjects/41396_2012_BFismej201284_MOESM78_ESM.zip²¹³ and https://static-content.springer.com/esm/art%3A10.1038%2Fismej.2015.238/MediaObjects/41396_2016_BFismej2015238_MOESM67_ESM.zip²¹⁴, and on server of the Czech Academy of Sciences under URLs www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0001.zip²¹⁵, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0002.zip²¹⁶, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0003.zip²¹⁷, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0004.zip²¹⁸, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0005.zip²¹⁹, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0006.zip²²⁰, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0007.zip²²¹, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0008.zip²²², www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0009.zip²²³, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0010.zip²²⁴, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0011.zip²²⁵, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0012.zip²²⁶.

The database contains two data types: sequence variants (individual nucleotide sequences) and samples. For each sequence variant, the following information is stored: sequence variant code, identification of samples where sequence variant occurs and the number of observations, the SH of best hit (when available), fungal species name (when available), fungal genus name (when available). For each sample, metadata information is stored (Table 1). Sequencing data and metadata are accessible at Figshare (GlobalFungi_ITS_variants.zip, GlobalFungi_metadata.xlsx). All database content is accessible using a public graphical user interface at <http://globalfungi.com>.

Technical Validation

The technical validation included the screening of the data sources, sequencing data and data reliability. Regarding the data source screening, the data sources (published papers) were screened to fulfil the criteria outlined in the Methods section. The dataset was thoroughly checked for duplicities and for all records that appeared in multiple publications, only the first original publication of the dataset was considered as a datasource. Considering sequence quality, we have only utilized those primer pairs that are generally accepted to target general fungi^{7,227}. Sequences were quality filtered by removing all sequences with the mean quality phred scores below 20 and sequences that did not represent complete ITS1 or ITS2 after extraction or those that were identified as chimeric by the ITS extraction software¹² were removed. All representative sequences where the BLASTn search against the UNITE database¹¹ resulted in a nonfungal organism, were discarded.

For data reliability, the geographic location represented by the GPS coordinates was validated first. For each sample set, the geographic location of the sample described in the text of the study was confronted with the location on the map. For those samples, where disagreement was recorded (e.g., terrestrial samples positioned in the ocean, location in another region than described in the text), the authors of each study were asked for correction. If impossible, such samples were deleted. The quality of sample metadata was checked and if they were outside the acceptable range (such as content of elements or organic matter >100%), these invalid metadata were removed.

Usage Notes

The user interface at <http://globalfungi.com> enables the users to access the database in several ways (Figure 3). In taxon search, it is possible to search for genera and species of fungi and for the 98.5% SH species hypotheses of UNITE, contained in the general release 8.1 from 2.2.2019. The search results open the options to download corresponding SH or corresponding sequence variants. It is also possible to view breakdown of samples by type, biome, mean annual temperature, mean annual precipitation, pH and continents. The results also contain an interactive map of the taxon distribution with relative abundances of sequences of the taxon across samples and a list of samples with metadata. Several modes of filtering of results are available as well.

In sequence search, it is possible to search for multiple nucleotide sequences by exact match or BLAST retrieving the sequence variant best hit in the database, and alternatively, blasting a single sequence can deliver multiple ranked high score hits among the sequence variants. It is also possible to open individual studies and access their content and to select a group of samples on the map with a range of tools and retrieve data for these samples (such as the FASTA file with all occurring sequence variants).

Importantly, the database is intended to grow, both by the continuing activity of the authors and using the help of the scientific community. For that, web interface enabling the submission of studies not yet represented is available to users. The submission tool guides the submitting person through the steps where details about the publication, samples, sample metadata and sequences are sequentially collected. The submitted data will be added to the existing dataset after processing and validation by the authors.

Code Availability

The workflow included several custom made python scripts (labelled by star) which are accessible here: <https://github.com/VetrovskyTomas/GlobalFungi>.

Acknowledgements

We acknowledge funding from the Czech Science Foundation Grant No 18-26191S. ELIXIR CZ research infrastructure project LM2015047 by the Ministry of Education, Youth and Sports of the Czech Republic is acknowledged for hosting the database. All corresponding authors of published studies that provided additional information on the samples included in the database are gratefully acknowledged.

Author contributions

T.V., P.K. and P.B. jointly conceived the study. C.L. and coordinated data acquisition, T.V., D.M., M.K. and P.B. designed the database, T.V. and D.M. developed the database and created the user interface. C.A.G., S.A.H., B.D.B., K.B., V.B., F.D., R.Z.H., M.J., J.K., C.L., S.L., R.L.M., T.Mar., T.Maš., L.Me., L.Mi., T.Mi., S.M., D.N., I.O., S.P.C., M.Š., K.Š., V.T., M.U., L.V., J.V. and L.Ž. identified data sources, processed and analysed sequencing information, collated and analysed metadata. P.B. drafted the manuscript along with T.V., C.L. and P.K. All authors wrote and reviewed the manuscript. T.V., D.M., P.K. and C.L. contributed equally to this work.

Competing interests

The authors declare no competing interests.

References

1. Crowther, T.W., Todd-Brown, K.E.O., Rowe, C.W., Wieder, W.R., Carey, J.C., Machmuller, M.B., Snoek, B.L., Fang, S., Zhou, G., Allison, S.D., Blair, J.M., Bridgman, S.D., Burton, A.J., Carrillo, Y., Reich, P.B., Clark, J.S., Classen, A.T., Dijkstra, F.A., Elberling, B., Emmett, B.A., Estiarte, M., Frey, S.D., Guo, J., Harte, J., Jiang, L., Johnson, B.R., Kroel-Dulay, G., Larsen, K.S., Laudon, H., Lavalley, J.M., Luo, Y., Lupascu, M., Ma, L.N., Marhan, S., Michelsen, A., Mohan, J., Niu, S., Pendall, E., Penuelas, J., Pfeifer-Meister, L., Poll, C., Reinsch, S., Reynolds, L.L., Schmidt, I.K., Sistla, S., Sokol, N.W., Templer, P.H., Treseder, K.K., Welker, J.M. & Bradford, M.A. Quantifying global soil carbon losses in response to warming. *Nature* **540**, 104-108 (2016).
2. Peay, K.G., Kennedy, P.G. & Talbot, J.M. Dimensions of biodiversity in the Earth mycobiome. *Nature Rev. Microbiol.* **14**, 434-447 (2016).
3. Wall, D.H., Nielsen, U.N. & Six, J. Soil biodiversity and human health. *Nature* **528**, 69-76 (2015).
4. Tedersoo, L., Bahram, M., Polme, S., Koljalg, U., Yorou, N.S., Wijesundera, R., Ruiz, L.V., Vasco-Palacios, A.M., Thu, P.Q., Suija, A., Smith, M.E., Sharp, C., Saluveer, E., Saitta, A., Rosas, M., Riit, T., Ratkowsky, D., Pritsch, K., Poldmaa, K., Piepenbring, M., Phosri, C., Peterson, M., Parts, K., Partel, K., Otsing, E., Nouhra, E., Njouonkou, A.L., Nilsson, R.H., Morgado, L.N., Mayor, J., May, T.W., Majuakim, L., Lodge, D.J., Lee, S.S., Larsson, K.H., Kohout, P., Hosaka, K., Hiiesalu, I., Henkel, T.W., Harend, H., Guo, L.D., Greslebin, A., Grelet, G., Geml, J., Gates, G., Dunstan, W., Dunk, C., Drenkhan, R., Dearnaley, J., De Kesel, A., Dang, T., Chen, X., Buegger, F., Brearley, F.Q., Bonito, G., Anslan, S., Abell, S. & Abarenkov, K. Global diversity and geography of soil fungi. *Science* **346**, 1256688 (2014).
5. Bahram, M., Hildebrand, F., Forslund, S.K., Anderson, J.L., Soudzilovskaia, N.A., Bodegom, P.M., Bengtsson-Palme, J., Anslan, S., Coelho, L.P., Harend, H., Huerta-Cepas, J., Medema, M.H., Maltz, M.R., Mundra, S., Olsson, P.A., Pent, M., Polme, S., Sunagawa, S., Ryberg, M.,

- Tedersoo, L. & Bork, P. Structure and function of the global topsoil microbiome. *Nature* **560**, 233-237 (2018).
6. Egidio, E., Delgado-Baquerizo, M., Plett, J.M., Wang, J., Eldridge, D.J., Bardgett, R.D., Maestre, F.T. & Singh, B.K. A few Ascomycota taxa dominate soil fungal communities worldwide. *Nature Commun.* **10**, 2369 (2019).
7. Nilsson, R.H., Anslan, S., Bahram, M., Wurzbacher, C., Baldrian, P. & Tedersoo, L. Mycobiome diversity: high-throughput sequencing and identification of fungi. *Nature Rev. Microbiol.* **17**, 95-109 (2019).
8. Větrovský, T., Kohout, P., Kopecký, M., Machac, A., Man, M., Bahnmann, B.D., Brabcová, V., Choi, J., Meszárošová, L., Human, Z.R., Lepinay, C., Lladó, S., Lopez-Mondejar, R., Martinovic, T., Mašínová, T., Morais, D., Navrátilová, D., Odriozola, I., Štursová, M., Švec, K., Tláškal, V., Urbanová, M., Wan, J., Žifčáková, L., Howe, A., Ladau, J., Peay, K.G., Storch, D., Wild, J. & Baldrian, P. A meta-analysis of global fungal distribution reveals climate-driven patterns. *Nature Commun.* **10**, 5142 (2019).
9. Vlk, L., Tedersoo, L., Antl, T., Větrovský, T., Abarenkov, K., Pergl, J., Albrechtová, J., Vosátka, M., Baldrian, P., Pyšek, P. & Kohout, P. Early successional ectomycorrhizal fungi are more likely to naturalize outside their native range than other ectomycorrhizal fungi. *New Phytol.* in press, doi: 10.1111/nph.16557.
10. Thompson, L.R., Sanders, J.G., McDonald, D., Amir, A., Ladau, J., Locey, K.J., Prill, R.J., Tripathi, A., Gibbons, S.M., Ackermann, G., Navas-Molina, J.A., Janssen, S., Kopylova, E., Vázquez-Baeza, Y., González, A., Morton, J.T., Mirarab, S., Zech Xu, Z., Jiang, L., Haroon, M.F., Kanbar, J., Zhu, Q., Jin Song, S., Kosciulek, T., Bokulich, N.A., Lefler, J., Brislawn, C.J., Humphrey, G., Owens, S.M., Hampton-Marcell, J., Berg-Lyons, D., McKenzie, V., Fierer, N., Fuhrman, J.A., Clauset, A., Stevens, R.L., Shade, A., Pollard, K.S., Goodwin, K.D., Jansson, J.K., Gilbert, J.A. Knight, R. & The Earth Microbiome Project, C. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* **551**, 457-463 (2017).
11. Nilsson, R.H., Larsson, K.H., Taylor, A.F.S., Bengtsson-Palme, J., Jeppesen, T.S., Schigel, D., Kennedy, P., Picard, K., Glockner, F.O., Tedersoo, L., Saar, I., Koljalg, U. & Abarenkov, K. The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. *Nucleic Acids Res.* **47**, D259-D264 (2019).
12. Bengtsson-Palme, J., Ryberg, M., Hartmann, M., Branco, S., Wang, Z., Godhe, A., De Wit, P., Sanchez-Garcia, M., Ebersberger, I., de Sousa, F., Amend, A.S., Jumpponen, A., Unterseher, M., Kristiansson, E., Abarenkov, K., Bertrand, Y.J.K., Sanli, K., Eriksson, K.M., Vik, U., Veldre, V. & Nilsson, R.H. Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences of fungi and other eukaryotes for analysis of environmental sequencing data. *Meth. Ecol. Evol.* **4**, 914-919 (2013).
13. Karger, D.N., Conrad, O., Bohner, J., Kawohl, T., Kreft, H., Soria-Auza, R.W., Zimmermann, N.E., Linder, H.P. & Kessler, M. Data Descriptor: Climatologies at high resolution for the earth's land surface areas. *Scientific Data* **4**, 170122 (2017).
14. Fick, S.E. & Hijmans, R.J. WorldClim 2: new 1-km spatial resolution climate surfaces for global land areas. *International J. Climatol.* **37**, 4302-4315 (2017).
15. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP001058> (2010).
16. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP001175> (2010).
17. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP006078> (2011).
18. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP012868> (2012).
19. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP013695> (2012).
20. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP013944> (2016).
21. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP015735> (2015).
22. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP016090> (2015).
23. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP026207> (2014).
24. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP028404> (2015).
25. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP033719> (2015).

26. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP035356> (2015).
27. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP040314> (2014).
28. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP040786> (2015).
29. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP041347> (2015).
30. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP043106> (2015).
31. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP043706> (2017).
32. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP043982> (2015).
33. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP044665> (2016).
34. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP045166> (2015).
35. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP045587> (2016).
36. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP045746> (2014).
37. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP045933> (2015).
38. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP046049> (2016).
39. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP048036> (2016).
40. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP048856> (2015).
41. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP049544> (2015).
42. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP051033> (2016).
43. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP052222> (2017).
44. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP052716> (2015).
45. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP055957> (2015).
46. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP057433> (2016).
47. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP057541> (2016).
48. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP058508> (2016).
49. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP058555> (2016).
50. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP058851> (2018).
51. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP059280> (2016).
52. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP060838> (2016).
53. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP061179> (2016).
54. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP061305> (2017).
55. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP061904> (2015).
56. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP062647> (2016).
57. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP063711> (2017).
58. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP064158> (2017).
59. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP065817> (2017).
60. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP066030> (2016).
61. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP066284> (2017).
62. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP066331> (2017).
63. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP067301> (2017).
64. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP067367> (2016).
65. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP068514> (2016).
66. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP068608> (2016).
67. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP068620> (2016).
68. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP068654> (2016).
69. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP069065> (2017).
70. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP069742> (2017).
71. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP070568> (2016).
72. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP073070> (2016).
73. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP073265> (2017).
74. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP074055> (2016).
75. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP074496> (2016).
76. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP075989> (2017).
77. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP079403> (2017).

78. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP079521> (2018).
79. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP080210> (2016).
80. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP080428> (2017).
81. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP080680> (2017).
82. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP082472> (2017).
83. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP082976> (2017).
84. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP083394> (2017).
85. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP083434> (2017).
86. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP083901> (2017).
87. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP087715> (2017).
88. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP090261> (2016).
89. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP090335> (2017).
90. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP090490> (2017).
91. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP090651> (2017).
92. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP091741> (2017).
93. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP091855> (2018).
94. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP091867> (2016).
95. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP092609> (2019).
96. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP092777> (2017).
97. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP093592> (2017).
98. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP093928> (2017).
99. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP094708> (2017).
100. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP097883> (2017).
101. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP101553> (2017).
102. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP101605> (2018).
103. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP102378> (2017).
104. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP102417> (2018).
105. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP102775> (2018).
106. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP106137> (2018).
107. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP106774> (2018).
108. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP107174> (2017).
109. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP107743> (2017).
110. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP109164> (2017).
111. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP109773> (2017).
112. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP110522> (2017).
113. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP110810> (2017).
114. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP113348> (2018).
115. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP114697> (2017).
116. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP114821> (2018).
117. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP115350> (2018).
118. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP115464> (2018).
119. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP115599> (2018).
120. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP117302> (2018).
121. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP118875> (2018).
122. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP118960> (2018).
123. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP119174> (2017).
124. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP125864> (2016).
125. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP132277> (2018).
126. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP132591> (2018).
127. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP132598> (2018).
128. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP136886> (2012).
129. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP139483> (2019).

130. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP142723> (2018).
131. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP148813> (2018).
132. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP150527> (2019).
133. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP151262> (2018).
134. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP153934> (2018).
135. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP160913> (2018).
136. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP161632> (2018).
137. NCBI Sequence Read Archive, <https://identifiers.org/ncbi/insdc.sra:SRP195764> (2019).
138. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP001713> (2014).
139. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP003251> (2013).
140. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP003790> (2015).
141. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP005177> (2015).
142. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP005905> (2015).
143. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP009341> (2015).
144. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP010027> (2017).
145. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP010084> (2016).
146. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP010743> (2016).
147. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP011924> (2016).
148. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP012017> (2016).
149. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP013208> (2016).
150. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP013987> (2017).
151. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP014227> (2016).
152. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP017480> (2018).
153. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP017851> (2017).
154. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP017915> (2017).
155. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP019580> (2017).
156. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP019924> (2017).
157. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP020657> (2017).
158. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP022511> (2019).
159. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP022742> (2017).
160. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP023275> (2018).
161. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP023718> (2018).
162. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP023855> (2018).
163. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP106131> (2018).
164. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP107634> (2019).
165. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP107636> (2019).
166. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP110188> (2019).
167. European Nucleotide Archive, <https://identifiers.org/ena.embl:ERP112007> (2019).
168. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA000926> (2014).
169. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA000937> (2014).
170. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA001737> (2016).
171. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA002424> (2016).
172. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA002469> (2016).
173. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA003024> (2016).
174. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA003730> (2016).

175. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA004913> (2017).
176. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/submission?acc=DRA006519> (2018).
177. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/study?acc=DRP002783> (2015).
178. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/study?acc=DRP003138> (2016).
179. DNA Data Bank of Japan, <https://trace.ddbj.nig.ac.jp/DRAsearch/study?acc=DRP005365> (2019).
180. Dryad Digital Repository, <https://doi.org/10.5061/dryad.2fc32> (2015).
181. Dryad Digital Repository, <http://dx.doi.org/10.5061/dryad.n82g9> (2017).
182. Dryad Digital Repository, <http://dx.doi.org/10.5061/dryad.2343k> (2015).
183. Dryad Digital Repository, <https://doi.org/10.5061/dryad.gp302> (2015).
184. Dryad Digital Repository, <http://dx.doi.org/10.5061/dryad.cq2rb> (2016).
185. Dryad Digital Repository, <https://doi.org/10.5061/dryad.8fn8j> (2017).
186. Dryad Digital Repository, <https://doi.org/10.5061/dryad.216tp> (2013).
187. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4783710.3> (2012).
188. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4702703.3> (2016).
189. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4524551.3> (2014).
190. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4544233.3> (2016).
191. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4683808.3> (2017).
192. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4684008.3> (2016).
193. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4696490.3> (2016).
194. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4715213.3> (2016).
195. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4563787.3> (2015).
196. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4563788.3> (2015).
197. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4620497.3> (2015).
198. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=4620498.3> (2015).
199. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=mgp13293> (2012).
200. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=mgp1617> (2013).
201. MG-RAST, <https://www.mg-rast.org/mgmain.html?mgpage=search&search=mgp9003> (2014).
202. PlutoF repository, <https://plutof.ut.ee/#/filerepository/view/1561672> (2017).
203. PlutoF repository, <https://plutof.ut.ee/#/filerepository/view/1562683> (2017).
204. PlutoF repository, <https://plutof.ut.ee/#/doi/10.1515/BIO/100002> (2015).
205. PlutoF repository, <https://plutof.ut.ee/#/doi/10.1515/BIO/587446> (2017).
206. UNITE database, http://unite.ut.ee/454_EcM_CMZ.zip (2010).

207. Schappe, T., Alborno, F.E., Turner, B.L., Neat, A., Condit, R. and Jones, F.A. TLS: uncultured fungus internal transcribed spacer 1, targeted locus study. Genbank <https://identifiers.org/ncbi/insdc:KAYV00000000.1> (2017).
208. Schappe, T., Alborno, F.E., Turner, B.L., Neat, A., Condit, R. and Jones, F.A. TLS: uncultured fungus internal transcribed spacer 1, targeted locus study. Genbank <https://identifiers.org/ncbi/insdc:KAYU00000000.1> (2017).
209. Schappe, T., Alborno, F.E., Turner, B.L., Neat, A., Condit, R. and Jones, F.A. TLS: uncultured fungus internal transcribed spacer 1, targeted locus study. Genbank <https://identifiers.org/ncbi/insdc:KAYT00000000.1> (2017).
210. Vaz, A.B., Fonseca, P.L., Leite, L.R., Badotti, F., Salim, A.C., Araujo, F.M., Cuadros-Orellana, S., Duarte, A.A., Rosa, C.A., Oliveira, G. and Goes-Neto, A. MIMS Environmental/Metagenome sample from biofilm metagenome. Genbank <https://identifiers.org/ncbi/insdc:SAMN02934078> (2017).
211. Vaz, A.B., Fonseca, P.L., Leite, L.R., Badotti, F., Salim, A.C., Araujo, F.M., Cuadros-Orellana, S., Duarte, A.A., Rosa, C.A., Oliveira, G. and Goes-Neto, A. MIMS Environmental/Metagenome sample from biofilm metagenome. Genbank <https://identifiers.org/ncbi/insdc:SAMN02934079> (2017).
212. Australian Antarctic Data Center, <http://dx.doi.org/10.4225/15/526f42ada05b1> (2016).
213. Hartmann, M., Howes, C.G., VanInsberghe, D., Yu, H., Bachar, D., Christen, R., Nilsson, R.H., Hallam, S.J. and Mohn, W.W. Significant and persistent impact of timber harvesting on soil microbial communities in Northern coniferous forests. Supplementary Data 2 https://static-content.springer.com/esm/art%3A10.1038%2Fismej.2012.84/MediaObjects/41396_2012_BFismej201284_MOESM78_ESM.zip (2012).
214. Rime, T., Hartmann, M. and Frey, B. Potential sources of microbial colonizers in an initial soil ecosystem after retreat of an alpine glacier. Supplementary Information https://static-content.springer.com/esm/art%3A10.1038%2Fismej.2015.238/MediaObjects/41396_2016_BFismej2015238_MOESM67_ESM.zip (2016).
215. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0001.zip.
216. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0002.zip,
217. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0003.zip,
218. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0004.zip,
219. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0005.zip,
220. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0006.zip,
221. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0007.zip,
222. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0008.zip,
223. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0009.zip,
224. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0010.zip,
225. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0011.zip,
226. Czech Academy of Sciences, www.biomed.cas.cz/mbu/lbwrf/metastudy_datasets/GF0012.zip.

227. Anslan, S., Nilsson, R.H., Wurzbacher, C., Baldrian, P., Tedersoo, L. & Bahram, M. Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. *Mycokeys* **39**, 29-40 (2018).

Figure Legends

Figure 1: **Map of locations of samples contained in the GlobalFungi database.** Each point represents one or several samples where fungal community composition was reported using high-throughput-sequencing methods targeting the ITS1 or ITS2 marker of fungi. The map was created using the 'leaflet' package that uses an open-source JavaScript library for mobile-friendly interactive maps (GNU GENERAL PUBLIC LICENSE).

Figure 2: **Processing of raw sequencing data for the GlobalFungi database.** Workflow of processing of sequencing data included in the GlobalFungi database.

Figure 3: **User interface to access the GlobalFungi database.**

Tables

Table 1: **List of metadata contained in the GlobalFungi database.** The table lists identifiers, units and sources of metadata contained in the database with the description of their content. Data source "original paper" may also represent additional metadata provided by the authors of the paper.

Metadata identifier	Unit	Description of content	Source
Sample ID		unique identifier	generated
Longitude	degrees	Geographical longitude	original paper
Latitude	degrees	Geographical latitude	original paper
Continent		One of the following: Africa/Antarctica/Asia/Australia/Europe/North America/South America	original paper
Sample type		One of the following: soil/rhizosphere soil/litter/litter+humus/deadwood/lichen/shoot/root	original paper
Biome		One of the following: forest biome/woodland biome/shrubland biome/grassland biome/desert biome/tundra biome/mangrove biome/anthropogenic terrestrial biome/marine biome/freshwater biome/polar desert biome	original paper
Sampling year		Year of sample collection	original paper
Primers		Primers used	original paper
pH		pH	original paper
ITS total		Number of full ITS sequences extracted	generated
MAT (°C)	°C	Mean annual temperature from CHELSA database	CHELSA
MAP (mm)	mm	Mean annual precipitation from CHELSA database	CHELSA

Online-only Table 1: List of papers that were used as data sources for GlobalFungi database with digital object identifiers.

Paper	Doi:
Almario, J., et al.: 2017. Root-associated fungal microbiota of nonmycorrhizal <i>Arabidopsis alpina</i> and its contribution to plant phosphorus nutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> 114(44):E9403-E9412.	10.1073/pnas.1710455114
Alvarez-Garrido, L., et al.: 2019. Distributional shifts in ectomycorrhizal fungal communities lag behind climate-driven tree upward migration in a conifer forest-high elevation shrubland ecotone. <i>Soil Biology & Biochemistry</i> 137:107545.	10.1016/j.soilbio.2019.107545
Alzarhany, A. K., et al.: 2019. Are drivers of root-associated fungal community structure context specific?. <i>ISME Journal</i> 13(5):1330-1344.	10.1038/s41396-019-0350-y
Anthony, M. A., et al.: 2017. Fungal community homogenization, shift in dominant trophic guild, and appearance of novel taxa with biotic invasion. <i>Ecosphere</i> 8(9):e01951.	10.1002/ecs2.1951
Bahram, M., et al.: 2016. Stochastic distribution of small soil eukaryotes resulting from high dispersal and drift in a local environment. <i>ISME Journal</i> 10(4):885-896.	10.1038/ismej.2015.164
Bach, E. M., et al.: 2018. Greatest soil microbial diversity found in micro-habitats. <i>Soil Biology & Biochemistry</i> 118:217-226.	10.1016/j.soilbio.2017.12.018
Baldrian, P., et al.: 2012. Active and total microbial communities in forest soil are largely different and highly stratified during decomposition. <i>ISME Journal</i> 6(2):248-258.	10.1038/ismej.2011.95
Baldrian, P., et al.: 2016. Fungi associated with decomposing deadwood in a natural beech-dominated forest. <i>Fungal Ecology</i> 23:109-122.	10.1016/j.funeco.2016.07.001
Barnes, C. J., et al.: 2016. Unexpectedly High Beta-Diversity of Root-Associated Fungal Communities in the Bolivian Andes. <i>Frontiers in Microbiology</i> 7:1377.	10.3389/fmicb.2016.01377
Bergottini, V. M., et al.: 2017. Exploring the diversity of the root-associated microbiome of <i>Ilex paraguariensis</i> St. Hil. (Yerba Mate). <i>Applied Soil Ecology</i> 109:23-31.	10.1016/j.apsoil.2016.09.013
Bickford, W. A., et al.: 2018. Root endophytes and invasiveness: no difference between native and non-native <i>Phragmites</i> in the Great Lakes Region. <i>Ecosphere</i> 9(12):e02526.	10.1002/ecs2.2526
Bissett, A., et al.: 2016. Introducing BASE: the Biomes of Australian Soil Environments soil microbial diversity database. <i>GigaScience</i> 5(1):21.	10.1186/s13742-016-0126-5
Buee, M., et al.: 2009. 454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. <i>New Phytologist</i> 184(2):449-456.	10.1111/j.1469-8137.2009.03003.x

Clemmensen, K. E., et al.: 2015. Carbon sequestration is related to mycorrhizal fungal community shifts during long-term succession in boreal forests. <i>New Phytologist</i> 205(4):1525–1536.	10.1111/nph.13208
Cline, L. C., et al.: 2018. Ecological and functional effects of fungal endophytes on wood decomposition. <i>Functional Ecology</i> 32(1):181-191.	10.1111/1365-2435.12949
Coleine, C., et al.: 2018. Antarctic cryptoendolithic fungal communities are highly adapted and dominated by Lecanoromycetes and Dothideomycetes. <i>Frontiers in Microbiology</i> 9:1392.	10.3389/fmicb.2018.01392
Cordier, T., et al.: 2012. Spatial variability of phyllosphere fungal assemblages: genetic distance predominates over geographic distance in a European beech stand (<i>Fagus sylvatica</i>). <i>Fungal Ecology</i> 5:509-520.	10.1016/j.funeco.2011.12.004
Cox, F., et al.: 2016. Not poles apart: Antarctic soil fungal communities show similarities to those of the distant Arctic. <i>Ecology Letters</i> 19(5):528-536.	10.1111/ele.12587
Cross, H., et al.: 2017. Fungal diversity and seasonal succession in ash leaves infected by the invasive ascomycete <i>Hymenoscyphus fraxineus</i> . <i>New Phytologist</i> 213(3):1405–1417.	10.1111/nph.14204
Davey, M. L., et al.: 2012. Seasonal trends in the biomass and structure of bryophyte-associated fungal communities explored by 454 pyrosequencing. <i>New Phytologist</i> 195(4):844-856.	10.1111/j.1469-8137.2012.04215.x
Davey, M. L., et al.: 2013. Amplicon-pyrosequencing-based detection of compositional shifts in bryophyte-associated fungal communities along an elevation gradient. <i>Molecular Ecology</i> 22(2):368-383.	10.1111/mec.12122
Davey, M. L., et al.: 2014. Forestry impacts on the hidden fungal biodiversity associated with bryophytes. <i>FEMS Microbiology Ecology</i> 90(1):313-325.	10.1111/1574-6941.12386
De Beeck, M. O., et al.: 2014. Comparison and Validation of Some ITS Primer Pairs Useful for Fungal Metabarcoding Studies. <i>PLoS One</i> 9(6):e97629.	10.1371/journal.pone.0097629
Dean, S. L., et al.: 2017. A study of Glycine max (soybean) fungal communities under different agricultural practices. <i>Plant Gene</i> 11:8-16.	10.1016/j.plgene.2016.11.003
DeBeeck, M. O., et al.: 2015. Impact of metal pollution on fungal diversity and community structures. <i>Environmental Microbiology</i> 17(6):2035-2047.	10.1111/1462-2920.12547
Delgado-Baquerizo, M., et al.: 2017. Soil microbial communities drive the resistance of ecosystem multifunctionality to global change in drylands across the globe. <i>Ecology Letters</i> 20(10):1295-1305.	10.1111/ele.12826
Elliott, D. R., et al.: 2015. Bacterial and Fungal Communities in a Degraded Ombrotrophic Peatland Undergoing Natural and Managed Re-Vegetation. <i>PLoS One</i> 10(5):e0124726.	10.1371/journal.pone.0124726

Fan, K., et al.: 2018. Wheat rhizosphere harbors a less complex and more stable microbial co-occurrence pattern than bulk soil.. <i>Soil Biology & Biochemistry</i> 125:251-260.	10.1016/j.soilbio.2018.07.022
Fernandez, C. W., et al.: 2017. Ectomycorrhizal fungal response to warming is linked to poor host performance at the boreal-temperate ecotone. <i>Global Change Biology</i> 23(4):1598-1609.	10.1111/gcb.13510
Fernandez-Martinez, M. A., et al.: 2017. Microbial succession dynamics along glacier forefield chronosequences in Tierra del Fuego (Chile). <i>Polar Biology</i> 40(10):1939-1957.	10.1007/s00300-017-2110-7
Fernandez-Mendoza, F., et al.: 2017. ITS1 metabarcoding highlights low specificity of lichen mycobiomes at a local scale. <i>Molecular Ecology</i> 26(18):4811-4830.	10.1111/mec.14244
Frey, B., et al.: 2016. Microbial diversity in European alpine permafrost and active layers. <i>FEMS Microbiology Ecology</i> 92(3):fiw018.	10.1093/femsec/fiw018
Fukasawa, Y. and Matsuoka, S.: 2015. Communities of wood-inhabiting fungi in dead pine logs along a geographical gradient in Japan. <i>Fungal Ecology</i> 18:75-82.	10.1016/j.funeco.2015.09.008
Galazka, A. and Grzadziel, J.: 2018. Fungal Genetics and Functional Diversity of Microbial Communities in the Soil under Long-Term Monoculture of Maize Using Different Cultivation Techniques.. <i>Frontiers in Microbiology</i> 9:76.	10.3389/fmicb.2018.00076
Gannes, V., et al.: 2016. Microbial Community Structure and Function of Soil Following Ecosystem Conversion from Native Forests to Teak Plantation Forests. <i>Frontiers in Microbiology</i> 7:1976.	10.3389/fmicb.2016.01976
Gao, C., et al.: 2015. Community assembly of ectomycorrhizal fungi along a subtropical secondary forest succession. <i>New Phytologist</i> 205(2):771-785.	10.1111/nph.13068
Ge, Z. W., et al.: 2017. Soil pH and mineral nutrients strongly influence truffles and other ectomycorrhizal fungi associated with commercial pecans (<i>Carya illinoensis</i>). <i>Plant and Soil</i> 418(1-2):493-505.	10.1007/s11104-017-3312-z
Gehring, C. A., et al.: 2016. Cheatgrass invasion alters the abundance and composition of dark septate fungal communities in sagebrush steppe. <i>Botany</i> 94(6):481-491.	10.1139/cjb-2015-0237
Geml, J., et al.: 2014. The Contribution of DNA Metabarcoding to Fungal Conservation: Diversity Assessment, Habitat Partitioning and Mapping Red-Listed Fungi in Protected Coastal <i>Salix repens</i> Communities in the Netherlands. <i>PLoS One</i> 9(6):e99852.	10.1371/journal.pone.0099852
Geml, J., et al.: 2015. Long-term warming alters richness and composition of taxonomic and functional	10.1093/femsec/fiv095

groups of arctic fungi. *FEMS Microbiology Ecology* 91(8):fiv095.

George, P. B., et al.: 2019. Divergent national-scale trends of microbial and animal biodiversity revealed across diverse temperate soil ecosystems.. *Nature Communications* 10:1107. 10.1038/s41467-019-09031-1

Glassman, S. I., et al.: 2016. Ectomycorrhizal fungal spore bank recovery after a severe forest fire: some like it hot. *ISME Journal* 10(5):1228-1239. 10.1038/ismej.2015.182

Glassman, S. I., et al.: 2017. Environmental filtering by pH and soil nutrients drives community assembly in fungi at fine spatial scales. *Molecular Ecology* 26(24):6960-6973. 10.1111/mec.14414

Glynou, K., et al.: 2018. Facultative root-colonizing fungi dominate endophytic assemblages in roots of nonmycorrhizal *Microthlaspi* species. *New Phytologist* 217(3):1190-1202. 10.1111/nph.14873

Goldmann, K., et al.: 2015. Forest Management Type Influences Diversity and Community Composition of Soil Fungi across Temperate Forest Ecosystems. *Frontiers in Microbiology* 6:1300. 10.3389/fmicb.2015.01300

Goldmann, K., et al.: 2016. Divergent habitat filtering of root and soil fungal communities in temperate beech forests. *Scientific Reports* 11:31439. 10.1038/srep31439

Gomes, S. I. F., et al.: 2017. Arbuscular mycorrhizal interactions of mycoheterotrophic *Thismia* are more specialized than in autotrophic plants. *New Phytologist* 213(3):1418-1427. 10.1111/nph.14249

Gomes, S. I. F., et al.: 2017. Fungal-host diversity among mycoheterotrophic plants increases proportionally to their fungal-host overlap. *Ecology and Evolution* 7(10):3623-3630. 10.1002/ece3.2974

Gourmelon, V., et al.: 2016. Environmental and Geographical Factors Structure Soil Microbial Diversity in New Caledonian Ultramafic Substrates: A Metagenomic Approach. *PLoS One* 11(12):e0167405. 10.1371/journal.pone.0167405

Grau, O., et al.: 2017. Abrupt changes in the composition and function of fungal communities along an environmental gradient in the high Arctic. *Molecular Ecology* 26(18):4798-4810. 10.1111/mec.14227

Guo, J. et al.: 2019. Soil fungal assemblage complexity is dependent on soil fertility and dominated by deterministic processes. *New Phytologist* 226(1):232-243. 10.1111/nph.16345

Harrison, J. G., et al.: 2016. Vertical stratification of the foliar fungal community in the world's tallest trees. *American Journal of Botany* 103(12):2087-2095. 10.3732/ajb.1600277

Hartmann, M., et al.: 2012. Significant and persistent impact of timber harvesting on soil microbial communities in Northern coniferous forests. *ISME Journal* 6(12):2199-2218. 10.1038/ismej.2012.84

He, D., et al.: 2017. Diversity and co-occurrence network of soil fungi are more responsive than those of bacteria to shifts in precipitation seasonality in a subtropical forest. <i>Soil Biology & Biochemistry</i> 115:499-510.	10.1016/j.soilbio.2017.09.023
He, F., et al.: 2016. Changes in composition and diversity of fungal communities along <i>Quercus mongolica</i> forests developments in Northeast China. <i>Applied Soil Ecology</i> 100:162-171.	10.1016/j.apsoil.2015.12.014
Hiiesalu, I., et al.: 2017. Plant species richness and productivity determine the diversity of soil fungal guilds in temperate coniferous forest and bog habitats. <i>Molecular Ecology</i> 26(18):4846-4858.	10.1111/mec.14246
Hoppe, B., et al.: 2015. Linking molecular deadwood-inhabiting fungal diversity and community dynamics to ecosystem functions and processes in Central European forests. <i>Fungal Diversity</i> 77(1):367-379.	10.1007/s13225-015-0341-x
Chaput, D. L., et al.: 2015. Profiling Microbial Communities in Manganese Remediation Systems Treating Coal Mine Drainage. <i>Applied and Environmental Microbiology</i> 81(6):2189-2198.	10.1128/AEM.03643-14
Ihrmark, K., et al.: 2012. New primers to amplify the fungal ITS2 region - evaluation by 454-sequencing of artificial and natural communities. <i>FEMS Microbiology Ecology</i> 82(3):666-677.	10.1111/j.1574-6941.2012.01437.x
Izuno, A., et al.: 2016. Structure of phyllosphere fungal communities in a tropical dipterocarp plantation: A massively parallel next-generation sequencing analysis. <i>Mycoscience</i> 57(3):171-180.	10.1016/j.myc.2015.12.005
Izuno, A., et al.: 2016. Vertical Structure of Phyllosphere Fungal Communities in a Tropical Forest in Thailand Uncovered by High-Throughput Sequencing. <i>PLoS One</i> 11(11):e0166669.	10.1371/journal.pone.0166669
Jarvis, S. G., et al.: 2015. Strong altitudinal partitioning in the distributions of ectomycorrhizal fungi along a short (300 m) elevation gradient. <i>New Phytologist</i> 206(3):1145-1155.	10.1111/nph.13315
Ji, M., et al.: 2016. Microbial diversity at Mitchell Peninsula, Eastern Antarctica: a potential biodiversity "hotspot". <i>Polar Biology</i> 39(2):237-249.	10.1007/s00300-015-1776-y
Jiao, S., et al.: 2018. Soil microbiomes with distinct assemblies through vertical soil profiles drive the cycling of multiple nutrients in reforested ecosystems. <i>Microbiome</i> 6(1):146.	10.1186/s40168-018-0526-0
Johansen, R. B., et al.: 2016. A native and an invasive dune grass share similar, patchily distributed, root-associated fungal communities. <i>Fungal Ecology</i> 23:141-155.	10.1016/j.funeco.2016.08.003
Jumpponen, A. and Jones, K. L.: 2010. Seasonally dynamic fungal communities in the <i>Quercus macrocarpa</i> phyllosphere differ between urban and	10.1111/j.1469-8137.2010.03197.x

- nonurban environments. *New Phytologist* 186(2):496-513.
- Jumpponen, A., et al.: 2010. Massively parallel 454-sequencing of fungal communities in *Quercus* spp ectomycorrhizas indicates seasonal dynamics in urban and rural sites. *Molecular Ecology* 19(1):41-53. 10.1111/j.1365-294X.2009.04483.x
- Kadowaki, K., et al.: 2014. Detection of the horizontal spatial structure of soil fungal communities in a natural forest. *Population Ecology* 56(2):301-310. 10.1007/s10144-013-0424-z
- Kamutando, C. N., et al.: 2017. Soil nutritional status and biogeography influence rhizosphere microbial communities associated with the invasive tree *Acacia dealbata*. *Scientific Reports* 7:6472. 10.1038/s41598-017-07018-w
- Kazartsev, I., et al.: 2018. Decaying *Picea abies* log bark hosts diverse fungal communities. *Fungal Ecology* 33:1-12. 10.1016/j.funeco.2017.12.005
- Kerfahi, D., et al.: 2016. Rainforest Conversion to Rubber Plantation May Not Result in Lower Soil Diversity of Bacteria, Fungi, and Nematodes. *Microbial Ecology* 72(2):359-371. 10.1007/s00248-016-0790-0
- Kielak, A. M., et al.: 2016. Bacterial Community Succession in Pine-Wood Decomposition. *Frontiers in Microbiology* 7:231. 10.3389/fmicb.2016.00231
- Kolarikova, Z., et al.: 2017. Root-associated fungal communities along a primary succession on a mine spoil: Distinct ecological guilds assemble differently. *Soil Biology & Biochemistry* 113:143-152. 10.1016/j.soilbio.2017.06.004
- Kyaschenko, J., et al.: 2017. Shift in fungal communities and associated enzyme activities along an age gradient of managed *Pinus sylvestris* stands. *ISME Journal* 11(4):863-874. 10.1038/ismej.2016.184
- Lanzen, A., et al.: 2016. Multi-targeted metagenetic analysis of the influence of climate and environmental parameters on soil microbial communities along an elevational gradient. *Scientific Reports* 6:28257. 10.1038/srep28257
- Leff, J. W., et al.: 2015. Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. *Proceedings of the National Academy of Sciences of the United States of America* 112(35):10967-10972. 10.1073/pnas.1508382112
- Li, Y., et al.: 2016. Changes of soil microbial community under different degraded gradients of alpine meadow. *Agriculture, Ecosystems and Environment* 222:213-222. 10.1016/j.agee.2016.02.020
- Liu, C., et al.: 2016. The influence of soil properties on the size and structure of bacterial and fungal communities along a paddy soil chronosequence. *European Journal of Soil Biology* 76:9-18. 10.1016/j.ejsobi.2016.06.002
- Liu, J., et al.: 2015. Soil carbon content drives the biogeographical distribution of fungal communities in the black soil zone of northeast China. *Soil Biology & Biochemistry* 83:29-39. 10.1016/j.soilbio.2015.01.009

Marin, C., et al.: 2017. Functional land-use change effects on soil fungal communities in Chilean temperate rainforests. <i>Journal of Soil Science and Plant Nutrition</i> 17(4):985-1002.	10.4067/S0718-95162017000400011
Martirosyan, V., et al.: 2016. Desert Perennial Shrubs Shape the Microbial-Community Miscellany in Laimosphere and Phyllosphere Space. <i>Microbial Ecology</i> 72(3):659-668.	10.1007/s00248-016-0822-9
Matsuoka, S., et al.: 2016. Disentangling the relative importance of host tree community, abiotic environment and spatial factors on ectomycorrhizal fungal assemblages along an elevation gradient. <i>FEMS Microbiology Ecology</i> 92(5):fiw044.	10.1093/femsec/fiw044
Matsuoka, S., et al.: 2016. Temporal distance decay of similarity of ectomycorrhizal fungal community composition in a subtropical evergreen forest in Japan. <i>FEMS Microbiology Ecology</i> 92(5):fiw061.	10.1093/femsec/fiw061
Matsuoka, S., et al.: 2018. Taxonomic, functional, and phylogenetic diversity of fungi along primary successional and elevational gradients near Mount Robson, British Columbia. <i>Polar Science</i> 21:165-171.	10.1016/j.polar.2018.09.004
McHugh, T. A. and Schwartz, E.: 2015. Changes in plant community composition and reduced precipitation have limited effects on the structure of soil bacterial and fungal communities present in a semiarid grassland. <i>Plant and Soil</i> 388(1-2):175-186.	10.1007/s11104-014-2269-4
McHugh, T. A., et al.: 2014. Minor Changes in Soil Bacterial and Fungal Community Composition Occur in Response to Monsoon Precipitation in a Semiarid Grassland. <i>Microbial Ecology</i> 68(2):370-378.	10.1007/s00248-014-0416-3
Mello, A., et al.: 2011. ITS-1 versus ITS-2 pyrosequencing: a comparison of fungal populations in truffle grounds. <i>Mycologia</i> 103(6):1184-1193.	10.3852/11-027
Mendoza, J. R., et al.: 2017. Understanding the mycobiota of maize from the highlands of Guatemala, and implications for maize quality and safety. <i>Crop Protection</i> 101:5-11.	10.1016/j.cropro.2017.07.009
Mirmajlessi, S. M., et al.: 2018. Survey of Soil Fungal Communities in Strawberry Fields by Illumina Amplicon Sequencing.. <i>Eurasian Soil Science</i> 51(6):682-691.	10.1134/S106422931806011X
Miura, T., et al.: 2017. Is microbial terroir related to geographic distance between vineyards?. <i>Environmental Microbiology Reports</i> 9(6):742-749.	10.1111/1758-2229.12589
Montagna, M., et al.: 2018. Differential biodiversity responses between kingdoms (plants, fungi, bacteria and metazoa) along an Alpine succession gradient. <i>Molecular Ecology</i> 27(18):3671-3685.	10.1111/mec.14817
Moussa, T. A. A., et al.: 2017. Comparative metagenomics approaches to characterize the soil fungal communities of western coastal region, Saudi Arabia. <i>PLoS One</i> 12(9):e0185096.	10.1371/journal.pone.0185096

Muller, L. A. H. and Hilger, H. H.: 2015. Insights into the effects of serpentine soil conditions on the community composition of fungal symbionts in the roots of <i>Onosma echinoides</i> . <i>Soil Biology & Biochemistry</i> 81:1-8.	10.1016/j.soilbio.2014.10.027
Mundra, S., et al.: 2015. Arctic fungal communities associated with roots of <i>Bistorta vivipara</i> do not respond to the same fine-scale edaphic gradients as the aboveground vegetation. <i>New Phytologist</i> 205(4):1587-1597.	10.1111/nph.13216
Nacke, H., et al.: 2016. Fine Spatial Scale Variation of Soil Microbial Communities under European Beech and Norway Spruce. <i>Frontiers in Microbiology</i> 7:2067.	10.3389/fmicb.2016.02067
Newsham, K. K., et al.: 2016. Relationship between soil fungal diversity and temperature in the maritime Antarctic. <i>Nature Climate Change</i> 6(2):182.	10.1038/NCLIMATE2806
Nguyen, D., et al.: 2016. Do foliar fungal communities of Norway spruce shift along a tree species diversity gradient in mature European forests?. <i>Fungal Ecology</i> 23:97-108.	10.1016/j.funeco.2016.07.003
Nguyen, D., et al.: 2017. Foliar fungi of <i>Betula pendula</i> : impact of tree species mixtures and assessment methods. <i>Scientific Reports</i> 7:41801.	10.1038/srep41801
Oh, S.-Y., et al.: 2016. Distinctive Feature of Microbial Communities and Bacterial Functional Profiles in <i>Tricholoma matsutake</i> Dominant Soil. <i>PLoS One</i> 11(12):e0168573.	10.1371/journal.pone.0168573
Oja, J., et al.: 2015. Temporal patterns of orchid mycorrhizal fungi in meadows and forests as revealed by 454 pyrosequencing. <i>New Phytologist</i> 205(4):1608-1618.	10.1111/nph.13223
Oja, J., et al.: 2017. Local-scale spatial structure and community composition of orchid mycorrhizal fungi in semi-natural grasslands. <i>Mycorrhiza</i> 27(4):355-367.	10.1007/s00572-016-0755-7
Oono, R., et al.: 2017. Distance decay relationships in foliar fungal endophytes are driven by rare taxa. <i>Environmental Microbiology</i> 19(7):2794-2805.	10.1111/1462-2920.1379
Oono, R.: 2017. A confidence interval analysis of sampling effort, sequencing depth, and taxonomic resolution of fungal community ecology in the era of high-throughput sequencing. <i>PLoS One</i> 12(12):e0189796.	10.1371/journal.pone.0189796
Ovaskainen, O., et al.: 2010. Identifying wood-inhabiting fungi with 454 sequencing - what is the probability that BLAST gives the correct species?. <i>Fungal Ecology</i> 3:274-283.	10.1016/j.funeco.2010.01.001
Park, M. S., et al.: 2018. Diversity of fungi associated with roots of <i>Calanthe</i> orchid species in Korea. <i>Journal of Microbiology</i> 56(1):49-55.	10.1007/s12275-018-7319-9
Peay, K. G., et al.: 2013. Strong coupling of plant and fungal community structure across western Amazonian rainforests. <i>ISME Journal</i> 7(9):1852-1861.	10.1038/ismej.2013.66

Peay, K. G., et al.: 2017. Convergence and contrast in the community structure of Bacteria, Fungi and Archaea along a tropical elevation-climate gradient. <i>FEMS Microbiology Ecology</i> 93(5):fix045.	10.1093/femsec/fix045
Persoh, D.: 2013. Factors shaping community structure of endophytic fungi-evidence from the Pinus-Viscum-system. <i>Fungal Diversity</i> 60(1):55-69.	10.1007/s13225-013-0225-x
Polackova, T., et al.: 2016. Drivers of yeast community composition in the litter and soil of a temperate forest. <i>FEMS Microbiology Ecology</i> 93(2):fiw223.	10.1093/femsec/fiw223
Poosakkannu, A., et al.: 2017. Microbial community composition but not diversity changes along succession in arctic sand dunes. <i>Environmental Microbiology</i> 19(2):698-709.	10.1111/1462-2920.13599
Porter, T. M., et al.: 2016. Ribosomal DNA and Plastid Markers Used to Sample Fungal and Plant Communities from Wetland Soils Reveals Complementary Biotas. <i>PLoS One</i> 11(1):e0142759.	10.1371/journal.pone.0142759
Purahong, W., et al.: 2017. Characterization of Unexplored Deadwood Mycobiome in Highly Diverse Subtropical Forests Using Culture-independent Molecular Technique. <i>Frontiers in Microbiology</i> 8:574.	10.3389/fmicb.2017.00574
Purahong, W., et al.: 2018. Determinants of Deadwood-Inhabiting Fungal Communities in Temperate Forests: Molecular Evidence From a Large Scale Deadwood Decomposition Experiment. <i>Frontiers in Microbiology</i> 9:2120.	10.3389/fmicb.2018.02120
Purahong, W., et al.: 2018. Increasing N deposition impacts neither diversity nor functions of deadwood-inhabiting fungal communities, but adaptation and functional redundancy ensure ecosystem function. <i>Environmental Microbiology</i> 20(5):1693-1710.	10.1111/1462-2920.14081
Purahong, W., et al.: 2019. Characterization of the <i>Castanopsis carlesii</i> deadwood mycobiome by Pacbio sequencing of the full-length fungal nuclear ribosomal internal transcribed spacer (ITS).. <i>Frontiers in Microbiology</i> 10:983.	10.3389/fmicb.2019.00983
Rajala, T., et al.: 2015. Habitat models of wood-inhabiting fungi along a decay gradient of Norway spruce logs. <i>Fungal Ecology</i> 18:48-55.	10.1016/j.funeco.2015.08.007
Ramirez, K. S., et al.: 2019. Range-expansion effects on the belowground plant microbiome. <i>Nature Ecology and Evolution</i> 3(4):604.	10.1038/s41559-019-0828-z
Ramona, M., et al.: 2018. Rhizosheath microbial community assembly of sympatric desert speargrasses is independent of the plant host. <i>Microbiome</i> 6(1):215.	10.1186/s40168-018-0597-y
Rasmussen, P.U., et al.: 2018. Multiscale patterns and drivers of arbuscular mycorrhizal fungal communities in the roots and root-associated soil of a wild perennial herb. <i>New Phytologist</i> 220(4):1248-1261	10.1111/nph.15088

Reese, A. T., et al.: 2016. Urban stress is associated with variation in microbial species composition-but not richness-in Manhattan. <i>ISME Journal</i> 10(3):751-760.	10.3389/fmicb.2017.00574
Ren, C., et al.: 2018. Differential responses of soil microbial biomass, diversity, and compositions to altitudinal gradients depend on plant and soil characteristics. <i>Science of the Total Environment</i> 610:750-758.	10.1016/j.scitotenv.2017.08.110
Rime, T., et al.: 2015. Vertical distribution of the soil microbiota along a successional gradient in a glacier forefield. <i>Molecular Ecology</i> 24(5):1091-1108.	10.1111/mec.13051
Rime, T., et al.: 2016. Potential sources of microbial colonizers in an initial soil ecosystem after retreat of an alpine glacier. <i>ISME Journal</i> 10(7):1625-1641.	10.1038/ismej.2015.238
Rincon, A., et al.: 2015. Compartmentalized and contrasted response of ectomycorrhizal and soil fungal communities of Scots pine forests along elevation gradients in France and Spain. <i>Environmental Microbiology</i> 17(8):3009-3024.	10.1111/1462-2920.12894
Rogers, T. J., et al.: 2018. Exploring variation in phyllosphere microbial communities across four hemlock species.. <i>Ecosphere</i> 9(12):e02524.	10.1002/ecs2.2524
Roy-Bolduc, A., et al.: 2016. High richness of ectomycorrhizal fungi and low host specificity in a coastal sand dune ecosystem revealed by network analysis. <i>Ecology and Evolution</i> 6(1):349-362.	10.1002/ece3.1881
Roy-Bolduc, A., et al.: 2016. Strong linkage between plant and soil fungal communities along a successional coastal dune system. <i>FEMS Microbiology Ecology</i> 92(10):fiw156.	10.1093/femsec/fiw156
Saitta, A., et al.: 2018. Tree species identity and diversity drive fungal richness and community composition along an elevational gradient in a Mediterranean ecosystem. <i>Mycorrhiza</i> 28(1):39-47.	10.1007/s00572-017-0806-8
Santalahti, M., et al.: 2016. Vertical and seasonal dynamics of fungal communities in boreal Scots pine forest soil. <i>FEMS Microbiology Ecology</i> 92(11):fiw170.	10.1093/femsec/fiw170
Santalahti, M., et al.: 2018. Reindeer grazing alter soil fungal community structure and litter decomposition related enzyme activities in boreal coniferous forests in Finnish Lapland. <i>Applied Soil Ecology</i> 132:74-82.	10.1016/j.apsoil.2018.08.013
Sapkota, R. and Nicolaisen, M.: 2018. Cropping history shapes fungal, oomycete and nematode communities in arable soils and affects cavity spot in carrot. <i>Agriculture, Ecosystems and Environment</i> 257:120-131.	10.1016/j.agee.2018.01.032
Saravesi, K., et al.: 2015. Moth Outbreaks Alter Root-Associated Fungal Communities in Subarctic Mountain Birch Forests. <i>Microbial Ecology</i> 69(4):788-797.	10.1007/s00248-015-0577-8
Semenova, T. A., et al.: 2016. Compositional and functional shifts in arctic fungal communities in	10.1016/j.soilbio.2016.06.001

response to experimentally increased snow depth. *Soil Biology & Biochemistry* 100:201-209.

Semenova-Nelsen, T. A., et al.: 2019. Frequent fire reorganizes fungal communities and slows decomposition across a heterogeneous pine savanna landscape. *New Phytologist* 224(2):916-927. 10.1111/nph.16096

Sharma-Poudyal, D., et al.: 2017. Long-term no-till: A major driver of fungal communities in dryland wheat cropping systems. *PLoS One* 12(9):e0184611. 10.1371/journal.pone.0184611

Shen, Z., et al.: 2017. Banana Fusarium Wilt Disease Incidence Is Influenced by Shifts of Soil Microbial Communities Under Different Monoculture Spans. *Microbial Ecology* 75(3):739-750. 10.1007/s00248-017-1052-5

Shigyo, N., et al.: 2019. Seasonal Dynamics of Soil Fungal and Bacterial Communities in Cool-Temperate Montane Forests. *Frontiers in Microbiology* 10:1944. 10.3389/fmicb.2019.01944

Schappe, T., et al.: 2017. The role of soil chemistry and plant neighbourhoods in structuring fungal communities in three Panamanian rainforests. *Journal of Ecology* 105(3):569-579. 10.1111/1365-2745.12752

Schlatter, D. C., et al.: 2018. Fungal community composition and diversity vary with soil depth and landscape position in a no-till wheat-based cropping system. *FEMS Microbiology Ecology* 94(7):fiy098. 10.1093/femsec/fiy098

Schlegel, M., et al.: 2018. The Endophytic Mycobiome of European Ash and Sycamore Maple Leaves – Geographic Patterns, Host Specificity and Influence of Ash Dieback. *Frontiers in Microbiology* 9:2345. 10.3389/fmicb.2018.02345

Schmidt, P-A., et al.: 2013. Illumina metabarcoding of a soil fungal community. *Soil Biology & Biochemistry* 65:128-132. 10.1016/j.soilbio.2013.05.014

Schneider-Maunoury, L., et al.: 2018. Is *Tuber melanosporum* colonizing the roots of herbaceous, non-ectomycorrhizal plants?. *Fungal Ecology* 31:59-68. 10.1016/j.funeco.2017.10.004

Schon, M. E., et al.: 2018. Belowground fungal community diversity and composition associated with Norway spruce along an altitudinal gradient. *PLoS One* 13(12):e0208493. 10.1371/journal.pone.0208493

Schroeder, J. W., et al.: 2018. Community composition and diversity of Neotropical root-associated fungi in common and rare trees. *Biotropica* 50(4):694-703. 10.1111/btp.12553

Si, P., et al.: 2018. Rhizosphere Microenvironments of Eight Common Deciduous Fruit Trees Were Shaped by Microbes in Northern China. *Frontiers in Microbiology* 9:3147. 10.3389/fmicb.2018.03147

Siles, J. A. and Margesin, R.: 2016. Abundance and Diversity of Bacterial, Archaeal, and Fungal Communities Along an Altitudinal Gradient in Alpine Forest Soils: What Are the Driving Factors?. *Microbial Ecology* 72(1):207-220. 10.1007/s00248-016-0748-2

Siles, J. A. and Margesin, R.: 2017. Seasonal soil microbial responses are limited to changes in functionality at two Alpine forest sites differing in altitude and vegetation. <i>Scientific Reports</i> 7:2204.	10.1038/s41598-017-02363-2
Smith, M. E., et al.: 2017. Investigating niche partitioning of ectomycorrhizal fungi in specialized rooting zones of the monodominant leguminous tree <i>Dicymbe corymbosa</i> . <i>New Phytologist</i> 215(1):443-453.	10.1111/nph.14570
Song, H., et al.: 2019. Tropical forest conversion to rubber plantation in southwest China results in lower fungal beta diversity and reduced network complexity. <i>FEMS Microbiology Ecology</i> 95(7):fiz092.	10.1093/femsec/fiz092
Sterkenburg, E., et al.: 2015. Changes in fungal communities along a boreal forest soil fertility gradient. <i>New Phytologist</i> 207(4):1145-1158.	10.1111/nph.13426
Stursova, M., et al.: 2016. Small-scale spatial heterogeneity of ecosystem properties, microbial community composition and microbial activities in a temperate mountain forest soil. <i>FEMS Microbiology Ecology</i> 92(12):fiw185.	10.1093/femsec/fiw185
Sun, H., et al.: 2015. Fungal Community Shifts in Structure and Function across a Boreal Forest Fire Chronosequence. <i>Applied and Environmental Microbiology</i> 81(22):7869-7880.	10.1128/AEM.02063-15
Sun, R., et al.: 2018. Tillage Changes Vertical Distribution of Soil Bacterial and Fungal Communities. <i>Frontiers in Microbiology</i> 9:699.	10.3389/fmicb.2018.00699
Talbot, J. M., et al.: 2014. Endemism and functional convergence across the North American soil mycobiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> 111(17):6341-6346.	10.1073/pnas.1402584111
Tedersoo, L., et al.: 2010. 454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. <i>New Phytologist</i> 188(1):291-301.	10.1111/j.1469-8137.2010.03373.x
Tedersoo, L., et al.: 2014. Global diversity and geography of soil fungi. <i>Science</i> 346(6213):1256688.	10.1126/science.1256688
Tedersoo, L., et al.: 2015. Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>Mycoskeys</i> 10:1-43.	10.3897/mycokeys.10.4852
Tedersoo, L., et al.: 2016. Tree diversity and species identity effects on soil fungi, protists and animals are context dependent. <i>ISME Journal</i> 10(2):346-362.	10.1038/ismej.2015.116
Thiem, D., et al.: 2017. Ectomycorrhizal and endophytic fungi associated with <i>Alnus glutinosa</i> growing in a saline area of central Poland. <i>Symbiosis</i> 75(1):17-28.	10.1007/s13199-017-0512-5
Tian, H., et al.: 2017. Changes in soil microbial communities after 10 years of winter wheat	10.1371/journal.pone.0184223

cultivation versus fallow in an organic-poor soil in the Loess Plateau of China. *PLoS One* 12(9):e0184223.

Tian, J. Q., et al.: 2017. Ecological Succession Pattern of Fungal Community in Soil along a Retreating Glacier. *Frontiers in Microbiology* 8:1028. 10.3389/fmicb.2017.01028

Tian, J. Q., et al.: 2017. Patterns and drivers of fungal diversity along an altitudinal gradient on Mount Gongga, China. *Journal of Soils and Sediments* 17(12):2856-2865. 10.1007/s11368-017-1701-9

Toju, H., et al.: 2016. Ericaceous plant-fungus network in a harsh alpine-subalpine environment. *Molecular Ecology* 25(13):3242-3257. 10.1111/mec.13680

Toju, H., et al.: 2016. Network modules and hubs in plant-root fungal biomes. *Journal of the Royal Society, Interface* 13(116):20151097. 10.1098/rsif.2015.1097

Toole, D. R., et al.: 2017. Differences in soil fungal assemblages associated with native and non-native tree species of varying weediness. *Biological Invasions* 20(4):891-904. 10.1007/s10530-017-1580-4

Truong, C., et al.: 2019. Ectomycorrhizal fungi and soil enzymes exhibit contrasting patterns along elevation gradients in southern Patagonia. *New Phytologist* 222(4):1936-1950. 10.1111/nph.15714

Tu, B., et al.: 2017. Microbial diversity in Chinese temperate steppe: unveiling the most influential environmental drivers. *FEMS Microbiology Ecology* 93(4):fix031. 10.1093/femsec/fix031

Urbanova, M., et al.: 2015. Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. *Soil Biology & Biochemistry* 84:53-64. 10.1016/j.soilbio.2015.02.011

Urbina, H., et al.: 2016. DNA-metabarcoding uncovers the diversity of soil-inhabiting fungi in the tropical island of Puerto Rico. *Mycoscience* 57(3):217-227. 10.1016/j.myc.2016.02.001

Uroz, S., et al.: 2016. Specific impacts of beech and Norway spruce on the structure and diversity of the rhizosphere and soil microbial communities. *Scientific Reports* 6:27756. 10.1038/srep2775

Valverde, A., et al.: 2016. Specific Microbial Communities Associate with the Rhizosphere of *Welwitschia mirabilis*, a Living Fossil. *PLoS One* 11(4):e0153353. 10.1371/journal.pone.0153353

van der Wal, A., et al.: 2015. Neglected role of fungal community composition in explaining variation in wood decay rates. *Ecology* 96(1):124-133. 10.1890/14-0242.1

van der Wal, A., et al.: 2016. Patterns of natural fungal community assembly during initial decay of coniferous and broadleaf tree logs. *Ecosphere* 7(7):e01393. 10.1002/ecs2.1393

van der Wal, A., et al.: 2017. Fungal diversity and potential tree pathogens in decaying logs and stumps. *Forest Ecology and Management* 406:266-273. 10.1016/j.foreco.2017.08.018

van der Wal, A., et al.: 2017. Soil-wood interactions: Influence of decaying coniferous and broadleaf logs on composition of soil fungal communities. <i>Fungal Ecology</i> 30:132-134.	10.1016/j.funeco.2017.08.006
Vannette, R. L., et al.: 2016. Forest area and connectivity influence root-associated fungal communities in a fragmented landscape. <i>Ecology</i> 97(9):2374-2383.	10.1002/ecy.1472
Varenius, K., et al.: 2017. Retention of seed trees fails to lifeboat ectomycorrhizal fungal diversity in harvested Scots pine forests. <i>FEMS Microbiology Ecology</i> 93(9):fix105.	10.1093/femsec/fix105
Vasutova, M., et al.: 2017. Distinct environmental variables drive the community composition of mycorrhizal and saprotrophic fungi at the alpine treeline ecotone. <i>Fungal Ecology</i> 27:116-124.	10.1016/j.funeco.2016.08.010
Vaz, A. B. M., et al.: 2017. Using Next-Generation Sequencing (NGS) to uncover diversity of wood-decaying fungi in neotropical Atlantic forests. <i>Phytotaxa</i> 295(1):1-21.	10.11646/phytotaxa.295.1.1
Veach, A. M., et al.: 2015. Woody plant encroachment, and its removal, impact bacterial and fungal communities across stream and terrestrial habitats in a tallgrass prairie ecosystem. <i>FEMS Microbiology Ecology</i> 91(10):fiv109.	10.1093/femsec/fiv109
Voriskova, J., et al.: 2014. Seasonal dynamics of fungal communities in a temperate oak forest soil. <i>New Phytologist</i> 201(1):269-278.	10.1111/nph.12481
Walker, D. M., et al.: 2014. A metagenomics-based approach to the top-down effect on the detritivore food web: a salamanders influence on fungal communities within a deciduous forest. <i>Ecology and Evolution</i> 4(21): 4106-4116.	10.1002/ece3.1259
Wang, M. A., et al.: 2017. Influence of Peanut Cultivars and Environmental Conditions on the Diversity and Community Composition of Pod Rot Soil Fungi in China. <i>Mycobiology</i> 45(4):392-400.	10.5941/MYCO.2017.45.4.392
Wang, W., et al.: 2016. Endophytic bacterial and fungal microbiota in sprouts, roots and stems of rice (<i>Oryza sativa</i> L.). <i>Microbiological Research</i> 188:1-8.	10.1016/j.micres.2016.04.009
Waring, B. G., et al.: 2016. Scale-dependent variation in nitrogen cycling and soil fungal communities along gradients of forest composition and age in regenerating tropical dry forests. <i>New Phytologist</i> 209(2):845-854.	10.1111/nph.13654
Wicaksono, C. Y., et al.: 2017. Contracting montane cloud forests: a case study of the Andean alder (<i>Alnus acuminata</i>) and associated fungi in the Yungas. <i>Biotropica</i> 49(2):141-152.	10.1111/btp.12394
Wilhelm, R. C., et al.: 2017. A metagenomic survey of forest soil microbial communities more than a decade after timber harvesting. <i>Scientific Data</i> 4:170092.	10.1038/sdata.2017.92

Xu, L. H., et al.: 2012. Linking fungal communities in roots, rhizosphere, and soil to the health status of <i>Pisum sativum</i> . <i>FEMS Microbiology Ecology</i> 82(3):736-745.	10.1111/j.1574-6941.2012.01445.x
Yamamoto, S., et al.: 2014. Spatial Segregation and Aggregation of Ectomycorrhizal and Root-Endophytic Fungi in the Seedlings of Two <i>Quercus</i> Species. <i>PLoS One</i> 9(5):e96363.	10.1371/journal.pone.0096363
Yang, T., et al.: 2016. Carbon constrains fungal endophyte assemblages along the timberline. <i>Environmental Microbiology</i> 18(8):2455-2469.	10.1111/1462-2920.13153
Yang, T., et al.: 2016. Fungal assemblages in different habitats in an Erman's Birch forest.. <i>Frontiers in Microbiology</i> 7:1368.	10.3389/fmicb.2016.01368
Yang, T., et al.: 2017. Fungal community assemblages in a high elevation desert environment: Absence of dispersal limitation and edaphic effects in surface soil. <i>Soil Biology & Biochemistry</i> 115:393-402.	10.1016/j.soilbio.2017.09.013
Yang, T., et al.: 2017. Soil fungal diversity in natural grasslands of the Tibetan Plateau: associations with plant diversity and productivity. <i>New Phytologist</i> 215(2):756-765.	10.1111/nph.14606
Yao, F., et al.: 2013. Substantial compositional turnover of fungal communities in an alpine ridge-to-snowbed gradient. <i>Molecular Ecology</i> 22(19):5040-5052.	10.1111/mec.12437
Yao, F., et al.: 2017. Microbial Taxa Distribution Is Associated with Ecological Trophic Cascades along an Elevation Gradient. <i>Frontiers in Microbiology</i> 8:2071.	10.3389/fmicb.2017.02071
Younginger, B. S. and Ballhorn, D. J.: 2017. Fungal endophyte communities in the temperate fern <i>Polystichum munitum</i> show early colonization and extensive temporal turnover. <i>American Journal of Botany</i> 104(8):1188-1194.	10.3732/ajb.1700149
Zhang, J., et al.: 2018. Distinct large-scale biogeographic patterns of fungal communities in bulk soil and soybean rhizosphere in China. <i>Science of the Total Environment</i> 644:791-800.	10.1016/j.scitotenv.2018.07.016
Zhang, S. W., et al.: 2017. Relations among epiphytic microbial communities from soil, leaves and grapes of the grapevine. <i>Frontiers in Life Science</i> 10(1):73-83.	10.1080/21553769.2017.1365776
Zhang, T., et al.: 2015. Diversity and distribution of lichen-associated fungi in the Ny-Alesund Region (Svalbard, High Arctic) as revealed by 454 pyrosequencing. <i>Scientific Reports</i> 5:14850.	10.1038/srep14850
Zhang, T., et al.: 2016. Soil pH is a Key Determinant of Soil Fungal Community Composition in the Ny-Ålesund Region, Svalbard (High Arctic). <i>Frontiers in Microbiology</i> 7:227.	10.3389/fmicb.2016.00227
Zhang, W. W., et al.: 2017. Impacts of conversion from secondary forests to larch plantations on the	10.1016/j.apsoil.2016.11.019

structure and function of microbial communities.
Applied Soil Ecology 111:73-83.

Zhang, Z. Q., et al.: 2017. Fungal communities in 10.1371/journal.pone.0187575
ancient peatlands developed from different periods in
the Sanjiang Plain, China. PLoS One 12(12):e0187575.

Zhou ,X. G., et al.: 2017. Conversion from long-term 10.1038/srep41502
cultivated wheat field to Jerusalem artichoke
plantation changed soil fungal communities. Scientific
Reports 7:41502.

Zhou, J., et al.: 2016. Temperature mediates 10.1038/ncomms12083
continental-scale diversity of microbes in forest soils.
Nature Communications 7:12083.

Zhou, X., et al.: 2017. Rhizospheric fungi and their link 10.1002/jobm.201700312
with the nitrogen-fixing Frankia harbored in host plant
Hippophae rhamnoides L. Journal of Basic
Microbiology 57(12):1055-1064.

Zifcakova, L., et al.: 2016. Microbial activity in forest 10.1111/1462-2920.13026
soil reflects the changes in ecosystem properties
between summer and winter. Environmental
Microbiology 18(1):288-301.

Zimmerman, N. B. and Vitousek, P. M.: 2012. Fungal 10.1073/pnas.1209872109
endophyte communities reflect environmental
structuring across a Hawaiian landscape. Proceedings
of the National Academy of Sciences of the United
States of America 109(32):13022-13027.

[Home](#)[Taxon search](#)[Sequence search](#)[Studies](#)[Geosearch](#)[How to cite](#)[About GlobalFungi](#)[Help](#)[Results](#)[Leave a message](#)[Submit your study](#)[Collaborators](#)

Welcome to GlobalFungi!

Database version v0.9.6; Release version 1.0; Taxonomy based on UNITE version 8.1(2.2.2019); Last update 27.3.2020; First release.

Actual number of samples in database 20009; Studies 207.

Number of ITS sequence variants 119566862; Number of ITS1 sequences 416291533; Number of ITS2 sequences 231278756.

site design
&
programming
Tomas Vetrovsky
Daniel Morais
2020