

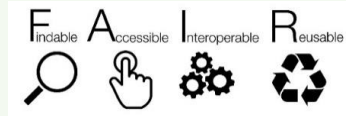
# The GlobalFungi database

GlobalFungi dataset release 5.0 (16.11.2023). Taxonomy based on UNITE version 9.0 (16.10.2022).  
Actual number of samples in the database: 84972; actual number of studies included: 846.  
Number of ITS sequence variants: 593 399 355; number of ITS1 sequences 1 233 820 630; number of ITS2 sequences 3 474 636 588.

How to use GlobalFungi Database (tutorial) | How to Submit your Study (tutorial)

World map showing fungal occurrences (yellow dots) and a pie chart showing the geographical distribution of samples across continents and oceans.

<https://globalfungi.com/>



SCIENTIFIC DATA

OPEN DATA DESCRIPTOR

GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies

Tomáš Větrovský<sup>1,4</sup>, Daniel Morais<sup>1,5</sup>, Petr Kohout<sup>1,4</sup>, Clémentine Lepinay<sup>1,4</sup>, Camella Algora<sup>1</sup>, Sandra Awokunle Hollá<sup>1</sup>, Barbara Doreen Bahmann<sup>1</sup>, Květa Bilohradská<sup>1</sup>, Vendula Brabcová<sup>1</sup>, Federica D'Alò<sup>1</sup>, Zander Rainier Human<sup>1</sup>, Mayuko Jomura<sup>1</sup>, Miroslav Kolařík<sup>1</sup>, Jana Kvasničková<sup>1</sup>, Salvador Lladó<sup>1</sup>, Rubén López-Mondéjar<sup>1</sup>, Tijana Martinović<sup>1</sup>, Tereza Mašínová<sup>1</sup>, Lenka Meszárosóvá<sup>1</sup>, Lenka Michalčíková<sup>1</sup>, Tereza Michalová<sup>1</sup>, Sunil Mundra<sup>1,5</sup>, Diana Navrátilová<sup>1</sup>, Inaki Odriozola<sup>1</sup>, Sarah Piché-Choquette<sup>1</sup>, Martina Štursová<sup>1</sup>, Karel Švec<sup>1</sup>, Vojtěch Tláškal<sup>1</sup>, Michaela Urbanová<sup>1</sup>, Lukáš Vlček<sup>1</sup>, Jana Vorišková<sup>1</sup>, Lucía Žifčáková<sup>1</sup> & Petr Baldrian<sup>1,10</sup>



# Initiative of the GlobalFungi database

► Initiative from the Laboratory of Environmental Microbiology from the Institute of Microbiology at the Czech Academy of Sciences



Petr Baldrian  
> *project leader*



Tomáš Vetrovsky  
> *perform bioinformatic, design online database*



Petr Kohout  
> *valorization of the database*



Clémentine Lepinay

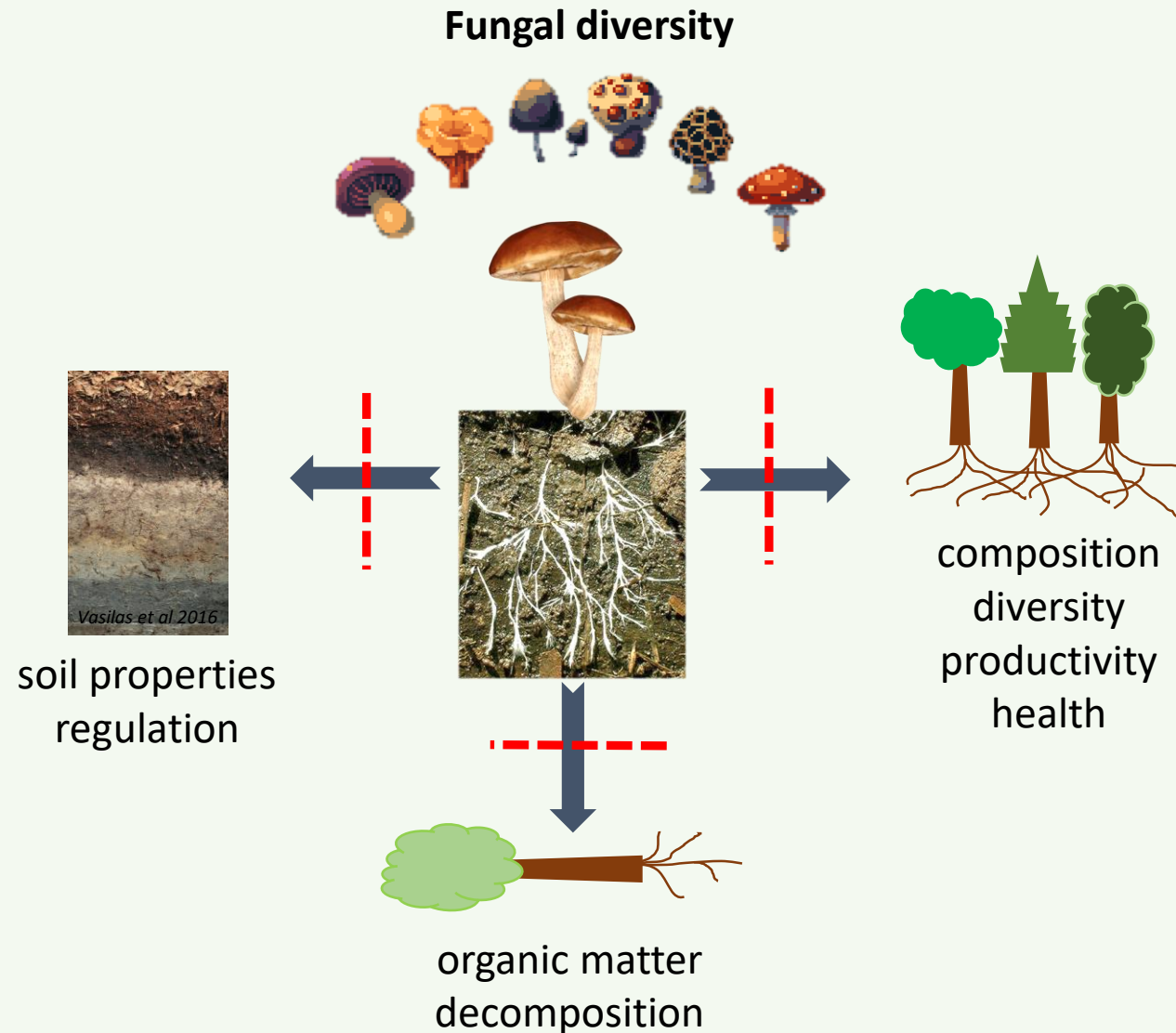
> *coordinate data acquisition*

A **COLLABORATIVE** project on a **national** and **international** scale



Project funded by grants from the Czech Science Foundation. ELIXIR CZ research infrastructure project by the Ministry of Education, Youth and Sports of the Czech Republic is hosting the database and provides access to computing and storage facilities.

## ► Major ecological and economic roles of fungi



➡ Ecosystem services

--- Environmental filters determining fungal diversity and distribution

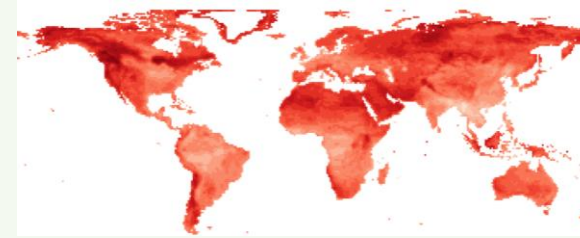
- Climate
- Soil characteristics
- Plant community composition

At global scale...  
What is where and why ?



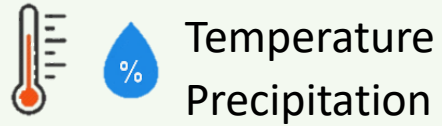
# Objectives of the GlobalFungi database

- ▶ Characterize the distribution of fungal diversity worldwide

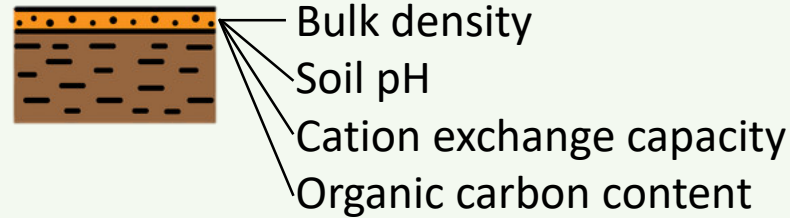


- ▶ Determine which environmental factors could best explain the distribution of fungal diversity

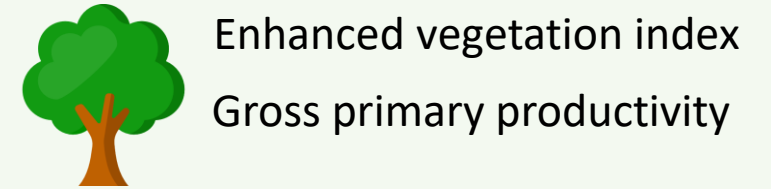
## Climate



## Soil characteristics

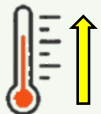


## Plant community



- ▶ Assess the impact of global change on fungal diversity

## Warming



## Drought



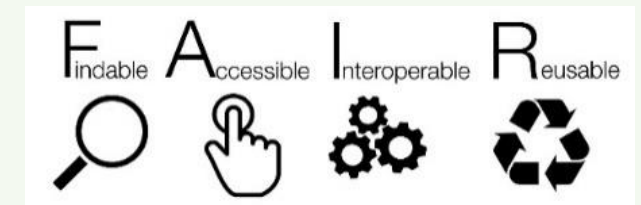
## Nitrogen deposition



## Elevated CO<sub>2</sub>



- ▶ Create an open database fitting with the FAIR principles and continuously enriched with recent data



# Methods (1/2) – Source of data

► **Join the efforts** of the scientific community to collect **fungal diversity data** worldwide by compiling **high-throughput sequencing results** from papers reporting fungal community composition in **environmental samples**

- **Environmental samples** (soil, air, water, coral, fungal sporocarp, lichen, mosses, algae, plant material)
- **Exclude manipulated** environments/studies (microcosms, greenhouse experiments...) → *specific category for manipulated samples (T°C, water, CO<sub>2</sub>, N) in field conditions*
- **Include** samples from environments following **usual agricultural practices**
- Sequencing primers should be **general for fungi** and target the **ITS region of rDNA** → *specific category for AMF fungi*
- Sequencing data must result from **high-throughput sequencing** methods
- **raw sequencing data** (FASTQ format) available into the paper or requested to the authors
- **GPS coordinates** must be provided

Published papers

- Internal collaboration
- International collaboration
- Annual paper search with keywords

Check for eligibility criteria

- GPS coordinates
- Raw sequencing data
- Set of metadata (x16 mandatory and x32 optional; *geographic, sampling, DNA extraction, soil characteristics, sequencing, description of manipulation for specific category of manipulated samples*)

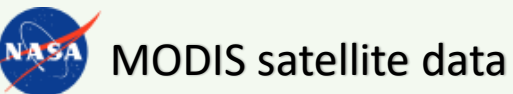
Extraction of a set of data and metadata

Checking/homogenization

- Ensure data quality
- Communication with authors

Retrieval of metadata from external databases

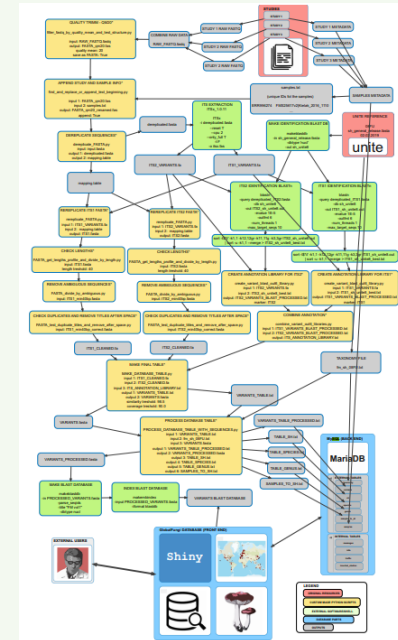
- Climate
- Soil characteristics
- Vegetation



## Data processing



SEED pipeline  
(Větrovský *et al.* 2018)



- Raw sequencing data quality filtered
- Extraction ITS1 and/or ITS2 fungal region
- ITS sequences classified according to the representative sequence of the closest UNITE species hypothesis (SH) using BLASTn (98.5% similarity threshold)
- All representative sequences unclassified were used to build database library of unique nucleotide sequences (sequence variants)

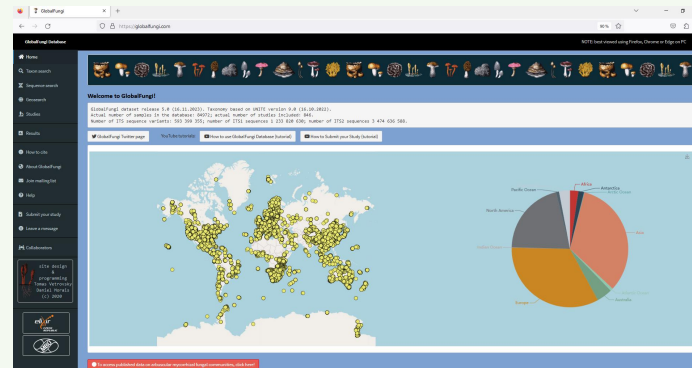
www.nature.com/scientificdata

# SCIENTIFIC DATA

OPEN DATA DESCRIPTOR

## GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies

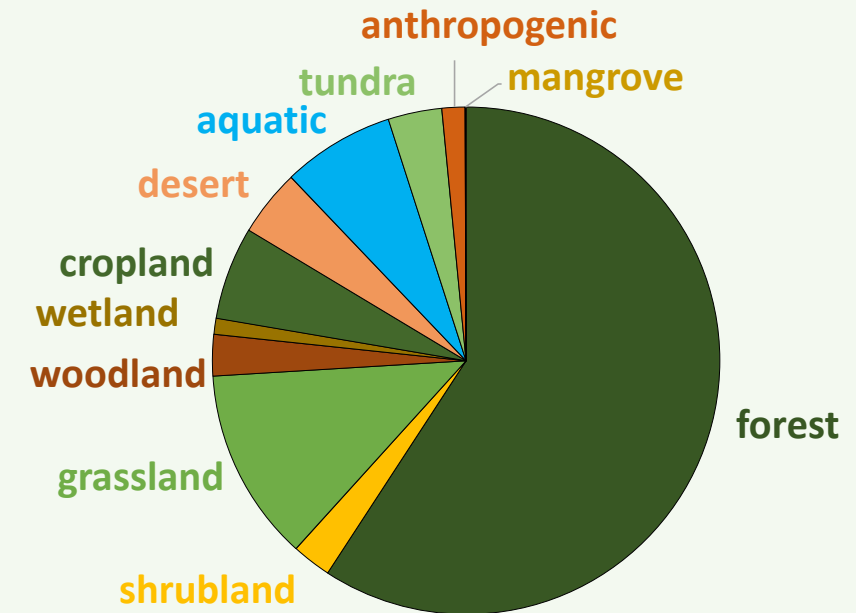
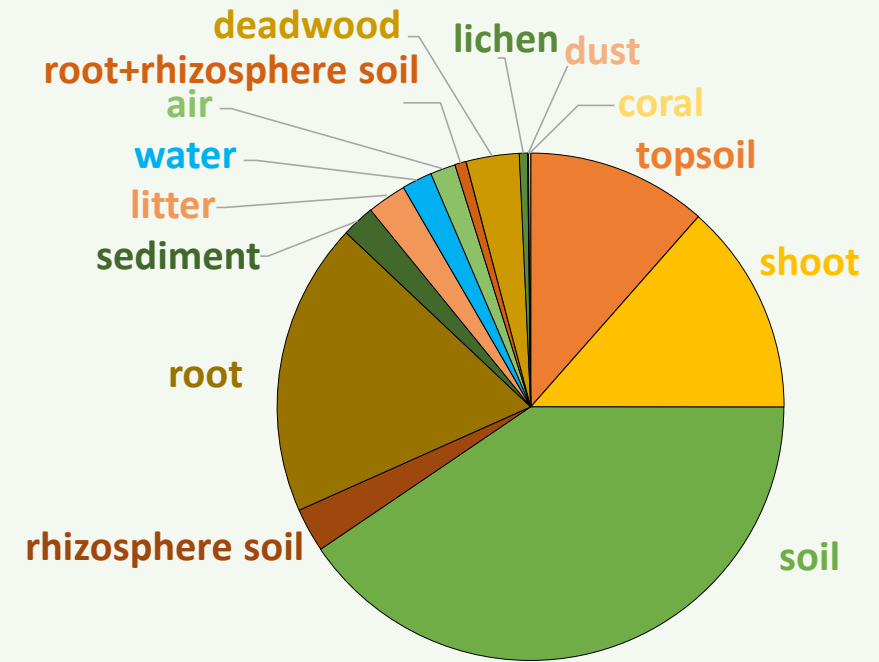
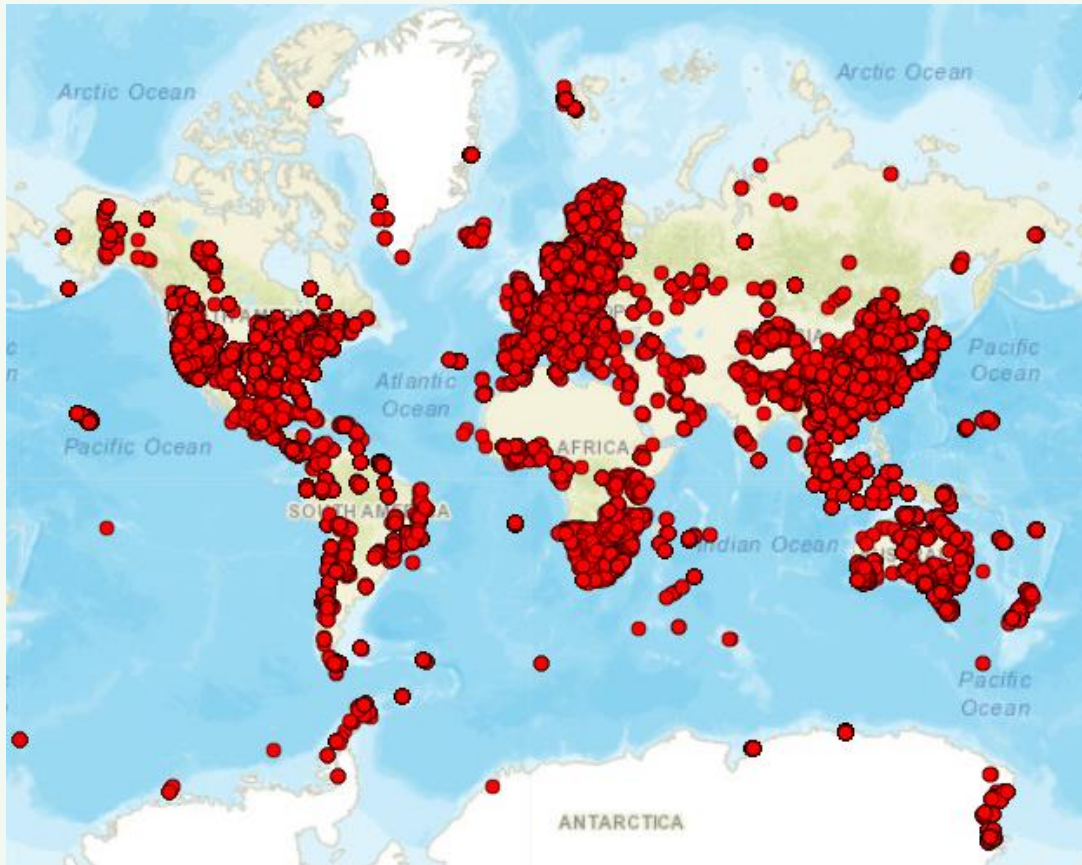
Tomáš Větrovský<sup>1,6</sup>, Daniel Morais<sup>1,6</sup>, Petr Kohout<sup>1,6</sup>, Clémentine Lepinay<sup>1,6</sup>, Camelia Algora<sup>1</sup>, Sandra Awokunle Hollá<sup>1</sup>, Barbara Doreen Bahnmann<sup>1</sup>, Květa Bilohnědá<sup>1</sup>, Vendula Brabcová<sup>1</sup>, Federica D'Alò<sup>2</sup>, Zander Rainier Human<sup>1</sup>, Mayuko Jomura<sup>3</sup>, Miroslav Kolařík<sup>1</sup>, Jana Kvasničková<sup>4</sup>, Salvador Lladó<sup>1</sup>, Rubén López-Mondéjar<sup>1</sup>, Tijana Martinović<sup>2</sup>, Tereza Mašínová<sup>1</sup>, Lenka Meszárosová<sup>1</sup>, Lenka Michalčíková<sup>1</sup>, Tereza Michalová<sup>1</sup>, Sunil Mundra<sup>4,5</sup>, Diana Navrátilová<sup>1</sup>, Iñaki Odriozola<sup>3</sup>, Sarah Piché-Choquette<sup>1</sup>, Martina Štursová<sup>1</sup>, Karel Švec<sup>1</sup>, Vojtěch Tláškal<sup>1</sup>, Michaela Urbanová<sup>1</sup>, Lukáš Vlk<sup>1</sup>, Jana Voříšková<sup>1</sup>, Lucia Žifčáková<sup>1</sup> & Petr Baldrian<sup>1,6</sup>



# Current status of the GlobalFungi database

→ Actual number of samples in the database: 84972

→ Actual number of studies included: 846








# How to use the GlobalFungi database

- Home
- Taxon search
- Sequence search
- Geosearch
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- Results
- How to cite
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- Join mailing list
- Help
- Submit your study
- Leave a message
- Collaborators

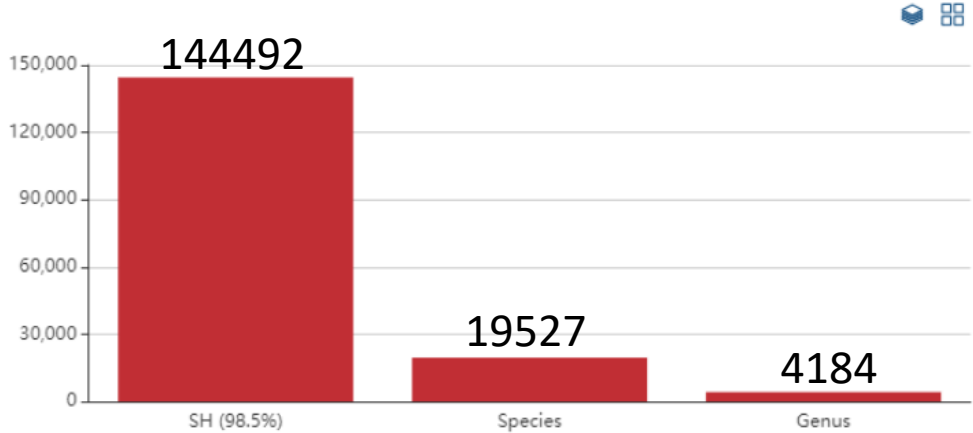
 **Search by taxonomy!**

SH Species Genus

Select species:  
Start typing here

Search

Breakdown of search options



Search Option	Count
SH (98.5%)	144492
Species	19527
Genus	4184

Save as .png

# How to use the GlobalFungi database

Save as .fasta

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Here are the results for species covering 5611 samples

Botrytis cinerea

19896 sequence variant(s) found  
Download FASTA

Species	Kingdom	Phylum	Class	Order	Family	Genus
Botrytis cinerea	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytis

Original result is covering 5611 samples

**Ignore singletons:**  
 ignore

**Add manipulated samples (81):**  
 add

**Filter biome:**

- anthropogenic
- aquatic
- cropland
- desert
- forest
- grassland
- mangrove
- shrubland
- tundra
- wetland
- woodland

**Filter type:**

- air
- deadwood
- lichen
- litter
- rhizosphere soil
- root
- root + rhizosphere soil
- sediment
- shoot
- soil
- topsoil
- water

**Sampling year:**

2005 2007 2009 2011 2013 2015 2017 2019 2021

include NA

Apply filters

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Filtered result is covering 5611 samples (NO FILTERS APPLIED)

SHs **Sample type & Biome** MAT & MAP pH Geography Map Metadata

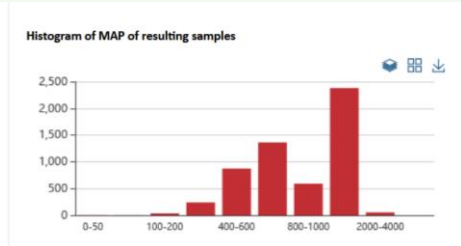
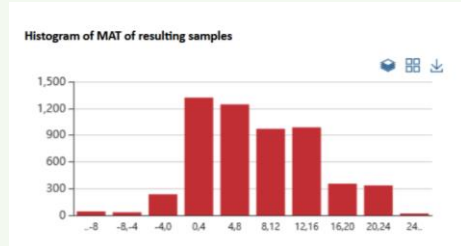
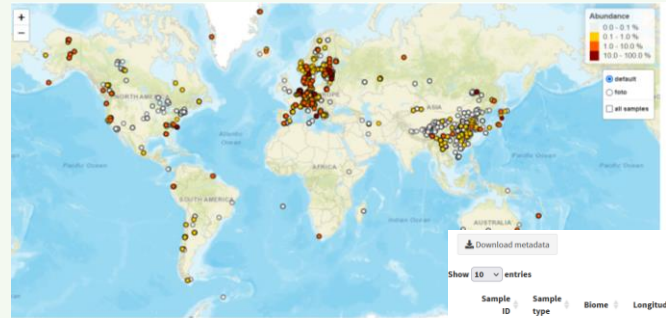
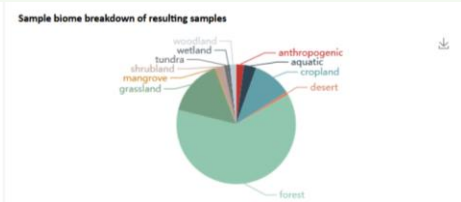
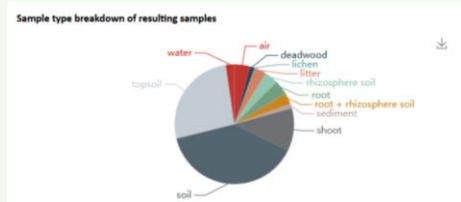
Download SH list **Save as .txt**

Show 10 entries Search:

	SH	Kingdom	Phylum	Class	Order	Family	Genus	Species
1	SH1152451.08FU	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytis	Botrytis cinerea
2	SH1152452.08FU	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytis	Botrytis cinerea
3	SH1152462.08FU	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytis	Botrytis cinerea
4	SH1152477.08FU	Fungi	Ascomycota	Leotiomycetes	Helotiales	Sclerotiniaceae	Botrytis	Botrytis cinerea

Showing 1 to 4 of 4 entries

Previous 1 Next



Download metadata


Show 10 entries Search:


Sample ID	Sample type	Biome	Longitude	Latitude	MAT (°C)	MAP (mm)	pH	Sampling year	Primers	ITS observed	ITS total	Manipulated
1	topsoil	forest	100.167	27.167	0.8	1063	NA	2015	gITS7ngp/ITS4ngpUni	27	51089	false
2	soil	forest	12.021	36.7584	16.6	533	6.23	2013	ITS3/ITS4	2	437042	false
13	soil	forest	-71.3318	42.4094	10.1	1279	5.4	2013	ITS7/ITS4	2	178186	false
4	soil	forest	-123.267	54.3333	3.6	670	4.9	2015	ITS86F/ITS4	1	205499	false
5	topsoil	forest	100.17	27.12	1.2	1179	NA	2014	gITS7ngp/ITS4ngpUni	3	731474	false
6	topsoil	forest	100.17	27.12	1.2	1179	NA	2017	gITS7ngp/ITS4ngpUni	5	938441	false
7	topsoil	forest	100.17	27.12	1.2	1179	NA	2014	gITS7ngp/ITS4ngpUni	21	1037162	false
8	soil	woodland	126.728	33.478	14.3	1934	NA	2015	ITS3/ITS4	3	52865	false
9	topsoil	forest	101.02	24.53	12.9	1557	NA	2014	gITS7ngp/ITS4ngpUni	1	902545	false
10	topsoil	forest	100.17	27.12	1.2	1179	NA	2014	gITS7ngp/ITS4ngpUni	28	935353	false


Showing 1 to 10 of 5,611 entries


Previous 1 2 3 4 5 ... 562 Next


# How to use the GlobalFungi database


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
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 Collaborators



Search by sequence!

## Paste your sequence

```
CCGAAGTACAGGCCCTCTCGTAGGGCTAAACTTCCACCCTTTGTTTATCATACCATGTTGCTTTGGCGAGACGTCCTCGGACCACCGGCCCTCGGGCGGGTGCGCGCTCGCCAGAGAAAAA  
TCAAACCCAAACCATTTAGTAGTAGTCTGAAAACAAGTTTCAATTATTA
```


## Choose FASTA file

Browse... No file selected


Reset/Clear Input

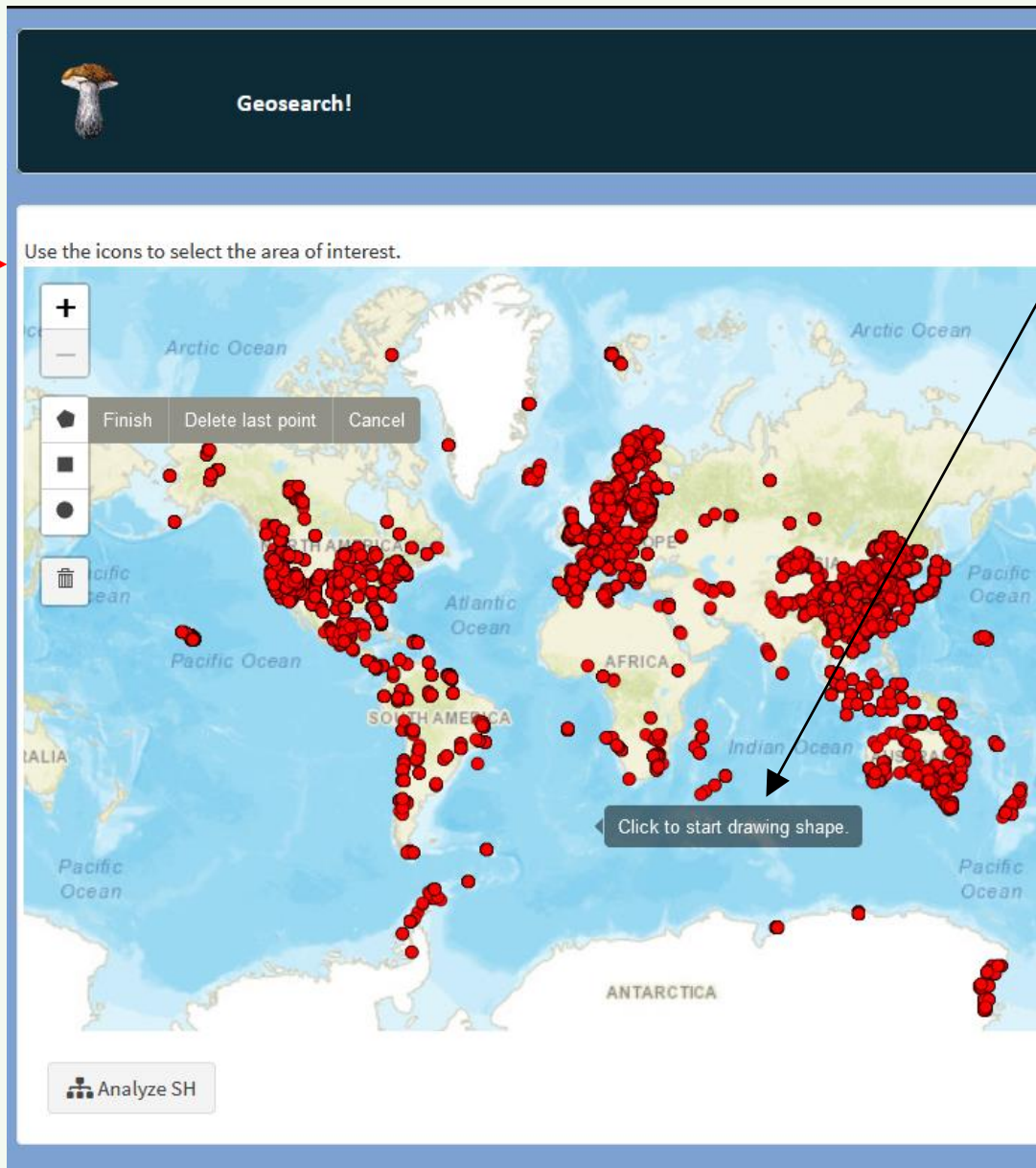
## Search type:

- Exact hit (input 1-100 sequences; only complete ITS1 or ITS2)
- BLAST - best hit (input 1-100 sequences; ITS1 or ITS2)
- BLAST - group results (input 1 sequence; ITS1 or ITS2)

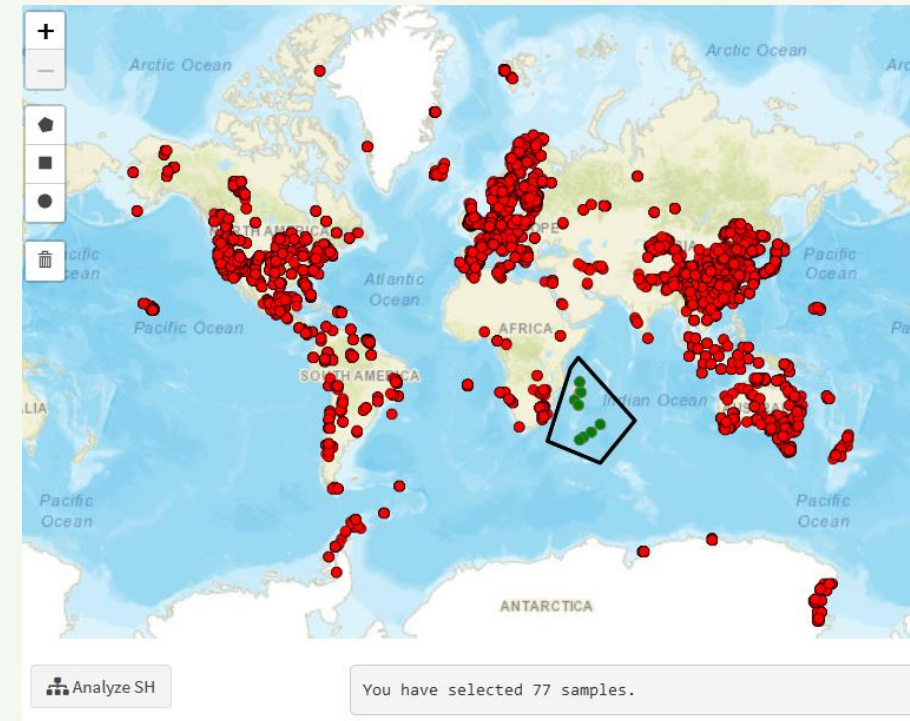
 Search

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1) Delimit an area



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## Geosearch!

Use the icons to select the area of interest.

+

−

Finish Delete last point Cancel

▣

●

🗑️

Click to start drawing shape.

Analyze SH

## 2) Analyse the results

Save as .txt

Analyze SH You have analyzed 77 samples. (covering 2503 SH)

SH selection Selected samples

Download SH list

Show 10 entries Search:

SH	Kingdom	Phylum	Class	Order	Family	Genus	Species	
1	SH1141087.08FU	Fungi	Basidiomycota	Agaricomycetes	Thelephorales	Thelephoraceae	unidentified	Thelephoraceae sp.
2	SH1142333.08FU	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Didymellaceae	Didymella	Didymella bryoniae
3	SH1142362.08FU	Fungi	Basidiomycota	Tremellomycetes	Tremellales	Trimorphomycetaceae	Trimorphomyces	Trimorphomyces sp.
4	SH1142520.08FU	Fungi	Ascomycota	Dothideomycetes	Venturiales	Venturiaceae	Venturia	Venturia sp.
5	SH1142555.08FU	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporales_fam_Incertae_sedis	Berkleasium	Berkleasium sp.
6	SH1142617.08FU	Fungi	Ascomycota	Dothideomycetes	Pleosporales	unidentified	unidentified	Pleosporales sp.
7	SH1142847.08FU	Fungi	Ascomycota	Dothideomycetes	Pleosporales	Pleosporaceae	Alternaria	Alternaria carthami
8	SH1142966.08FU	Fungi	Basidiomycota	Agaricomycetes	Cantharellales	unidentified	unidentified	Cantharellales sp.
9	SH1142993.08FU	Fungi	unidentified	unidentified	unidentified	unidentified	unidentified	Fungi sp.
10	SH1143036.08FU	Fungi	unidentified	unidentified	unidentified	unidentified	unidentified	Fungi sp.

Showing 1 to 10 of 2,503 entries Previous 1 2 3 4 5 ... 251 Next

Save as .txt

Analyze SH You have analyzed 77 samples. (covering 2503 SH)

SH selection Selected samples

Download metadata

Show 10 entries Search:


ID	primers	longitude	latitude	type	ITS tot.	Biome	MAT	MAP	pH	year
1	2867 5.8S_Fun/ITS4_Fun	57.2782	-32.7057	sediment	83763	aquatic	NA_	NA_	NA_	2015
2	3083 ITS9/ITS4	47.8583	-14.7333	soil	167445	forest	26.7	1531	4.25	2016
3	3098 ITS9/ITS4	48.4638	-18.9751	soil	128932	forest	18	1960	4.35	2016
4	3340 5.8S_Fun/ITS4_Fun	57.2782	-32.7057	sediment	216342	aquatic	NA_	NA_	NA_	2015
5	3363 ITS9/ITS4	48.4647	-18.979	soil	123770	forest	18.1	1916	3.967	2016
6	4475 ITS9/ITS4	48.4647	-18.979	soil	133503	forest	18.1	1916	3.967	2016
7	5693 ITS3/ITS4	47.917	-18.9162	soil	6031	forest	17.7	1965	2.58	2010
8	5867 ITS9/ITS4	48.4638	-18.9751	soil	230740	forest	18	1960	4.35	2016
9	6385 ITS3/ITS4	46.8687	-25.0621	soil	7103	forest	23.9	1557	4.55	2010
10	6867 ITS9/ITS4	48.4661	-18.979	soil	109853	forest	18.1	1916	4.787	2016

Showing 1 to 10 of 77 entries Previous 1 2 3 4 5 ... 8 Next

# How to use the GlobalFungi database

Information about all the samples from the study

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 **Studies**

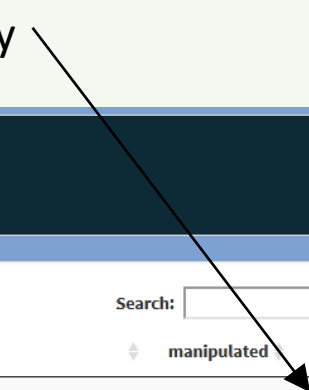
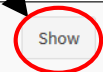
Show  entries

Search:

	Date	Title	Authors	Journal	Year	DOI	manipulated	Actions
1	21.07.2022	Revealing cues for fungal interplay in the plant-air interface in vineyards.	Abdelfattah, A., Sanzani, S.M., Wisniewski, M., Berg, G., Cacciola, S.O. and Schena, L.	Frontiers in plant science	2019	10.3389/fpls.2019.00922	false	Show
2	21.07.2022	Reindeer grazing history determines the responses of subarctic soil fungal communities to warming and fertilization.	Ahonen, S.H., Yläanne, H., Väisänen, M., Ruotsalainen, A.L., Männistö, M.K., Markkola, A. and Stark, S.	New Phytologist	2021	10.1111/nph.17623	true	Show
3	21.07.2022	Ectomycorrhizal community composition and function in a spruce forest transitioning between nitrogen and phosphorus limitation.	Almeida, J. P., Rosenstock, N. P., Forsmark, B., Bergh, J., & Wallander, H.	Fungal Ecology	2019	10.1016/j.funeco.2018.05.008	true	Show
4	21.07.2022	Plant invasion impacts on fungal community structure and function depend on soil warming and nitrogen enrichment.	Anthony, M.A., Stinson, K.A., Moore, J.A. and Frey, S.D.	Oecologia	2020	10.1007/s00442-020-04797-4	true	Show
5	21.07.2022	Fungal Diversity and Composition of the Continental Solar Saltern in Añana Salt Valley (Spain).	Azpiazu-Muniozguren, M., Perez, A., Rementeria, A., Martinez-Malaxetxebarria, I., Alonso, R., Laorden, L., Gamboa, J., Bikandi, J., Garaizar, J. and Martinez-Ballesteros, I.	Journal of Fungi	2021	10.3390/jof7121074	false	Show
6	21.07.2022	Next-generation sequencing of root fungal communities in continuous cropping soybean.	Bai, L., Sun, H., Zhang, X. and Cai, B.	Chilean journal of agricultural research	2018	10.4067/S0718-58392018000400528	false	Show
7	21.07.2022	Analyzing Ash Leaf-Colonizing Fungal Communities for Their Biological Control of Hymenoscyphus fraxineus.	Becker, R., Ulrich, K., Behrendt, U., Kube, M. and Ulrich, A.	Frontiers in Microbiology	2020	10.3389/fmicb.2020.590944	false	Show
8	21.07.2022	Evidence for Co-evolutionary History of Early Diverging Lycopodiaceae Plants With Fungi.	Benucci, G. M. N., Burnard, D., Shepherd, L. D., Bonito, G. and Munkacsy, A. B.	Frontiers in Microbiology	2020	10.3389/fmicb.2019.02944	false	Show
9	21.07.2022	Partner turnover and changes in ectomycorrhizal fungal communities during the early life stages of European beech ( <i>Fagus sylvatica</i> L.).	Boeraeve, M., Everts, T., Vandekerckhove, K., De Keersmaeker, L., Van de Kerckhove, P. and Jacquemyn, H.	Mycorrhiza	2021	10.1007/s00572-020-00998-0	false	Show
10	21.07.2022	Forest edge effects on the mycorrhizal communities of the dual-mycorrhizal tree species <i>Alnus glutinosa</i> (L.) Gaertn.	Boeraeve, M., Honnay, O. and Jacquemyn, H.	Science of the Total Environment	2019	10.1016/j.scitotenv.2019.02.290	false	Show

Showing 1 to 10 of 515 entries

Previous  2 3 4 5 ... 52 Next



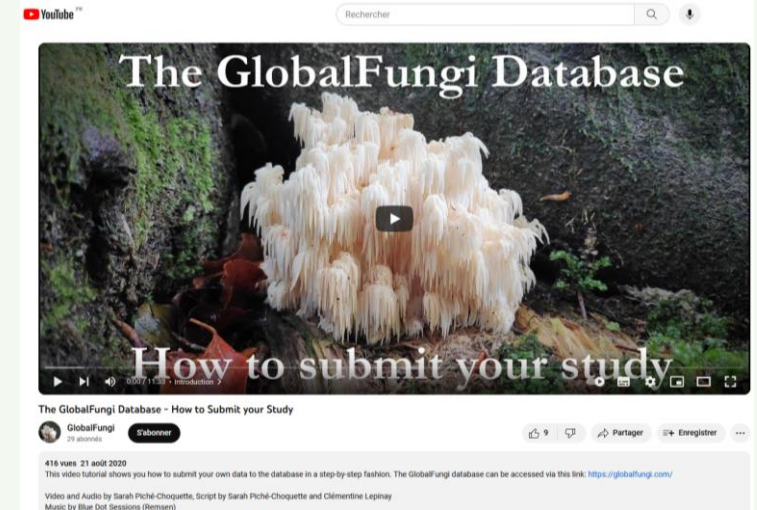
# How to use the GlobalFungi database

Větrovský T., Morais D., Kohout P., Lepinay C., *et al.* GlobalFungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies. *Scientific Data* 7, 228 (2020). <https://doi.org/10.1038/s41597-020-0567-7>

Brief presentation,  
record of each release,  
links to tutorial videos ...



[https://www.youtube.com/watch?v=0\\_opE1hOXwY](https://www.youtube.com/watch?v=0_opE1hOXwY)



<https://www.youtube.com/watch?v=HmGyr26Hhso>

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- Results
- How to cite
- About GlobalFungi
- Join mailing list
- Help
- Submit your study
- Leave a message
- Collaborators

Mailing list (new releases)

Presentation of each section

[info@globalfungi.com](mailto:info@globalfungi.com)

List of all the collaborators

 <https://twitter.com/globalfungi>



# Call for collaborations !

- ▶ Follow the written instructions + video tutorial + request help if necessary (Clémentine or [info@globalfungi.com](mailto:info@globalfungi.com))
- ▶ Easy process: one Excel file to fill (including the accession numbers allowing to download the Fastq/Fasta files of the raw sequencing data from public repositories)

	A	B	C
2	Please use dot . as floating point!		
3	Empty fields fill with "NA_"		
4			
5	VARIABLE	OPTIONS	HINTS
6	Latitude	TEXT - Mandatory!	Geographical latitude where the sample has been collected, in decimal degrees and using the WGS 84 geodetic system (i.e., following the format: "12.345" if North or "-12.345" if South. If necessary, you can convert 'degrees, minutes, seconds' in 'decimal degrees' with <a href="https://www.gps-coordinates.net/">https://www.gps-coordinates.net/</a> ).
7	Longitude	TEXT - Mandatory!	Geographical longitude where the sample has been collected, in decimal degrees and using the WGS 84 geodetic system (i.e., following the format: "56.789" if East or "-56.789" if West. If necessary, you can convert 'degrees, minutes, seconds' in 'decimal degrees' with <a href="https://www.gps-coordinates.net/">https://www.gps-coordinates.net/</a> ).
8	Elevation study (m)	TEXT - optional	Elevation in meter above sea level, , or meter below sea level for aquatic samples, with a minus sign (example: "-3300").
9	Continent/Ocean	<i>One of the following: Africa/Antarctica/Asia/ Australia/Europe/North America/South America/Atlantic Ocean/Arctic Ocean/Indian Ocean/Pacific Ocean/Southern Ocean</i>	<i>Specify the continent/ocean where the sample has been collected (select from the proposed list).</i>
10	Country	TEXT - optional	Country where the sample has been collected. For aquatic samples, please specify the country to which the water area is reattached or leave empty if you are not sure.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	TEXT - Mandatory!	TEXT - Mandatory!	TEXT - optional	One of the fo	TEXT - option	TEXT - option	One of the fo	One of the follo	TEXT - optional	TEXT - option	TEXT - option	TEXT - Mand	TEXT - option
2	Latitude	Longitude	Elevation study (m)	Continent/ Ocean	Country	Location	Sample type	Environment classification	Environment classification (ENVO)	MAT (°C)	MAP (mm) study	Sample ID in study	Area covered by sampling (m2)
3													
4													
5													
6													

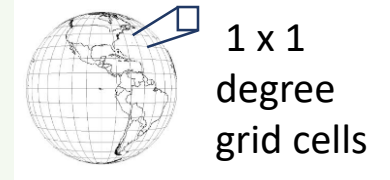
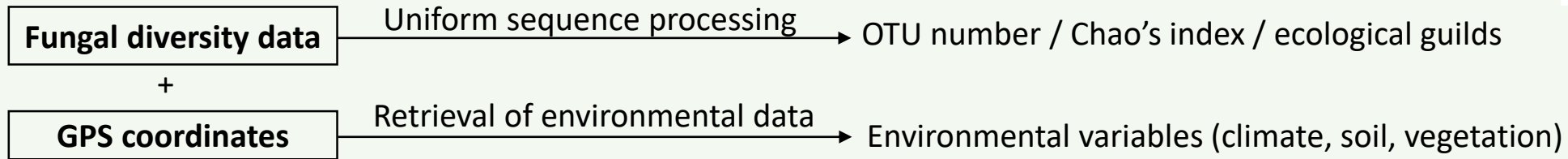
## Why to submit your study?

- + your data will be accessible in an **easily accessible form**
- + your work **gets visibility** and the international community gets the access to **additional resources**
- + **data sharing** is important
- + your name and affiliation can be added into the **list of collaborators**
- + you can have your name added to the **GlobalFungi Authorship Group** to be mentioned in future publications

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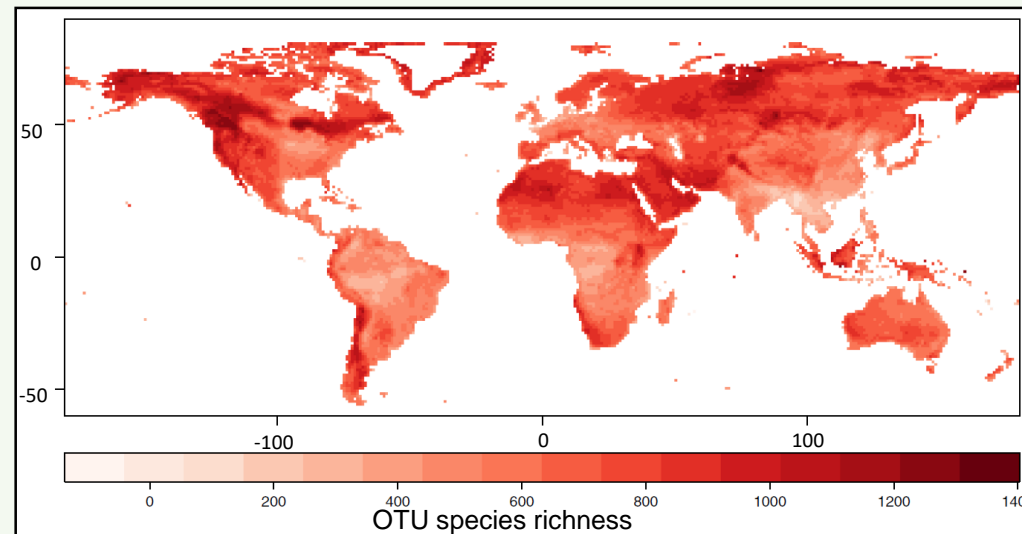
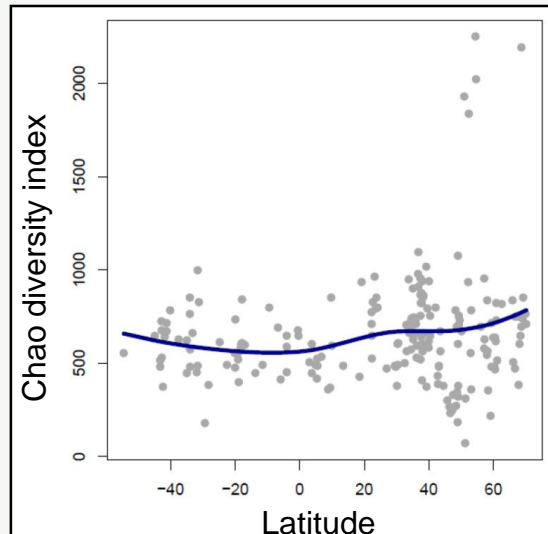
# What about our initial research questions?

Detailed analysis of 3084 soil samples from 36 studies (Větrovský, T., *et al.* 2019 Nature Communications)



## ► Characterize the distribution of fungal diversity worldwide:

- Non-parametric smoothing (Generalized linear models (GLMs) with a second-degree polynomial function)
- Climate-based generalized linear models (18 million GLMs with combinations of bioclimatic variables (max. 10 variables/model; R package *leaps*, Lumley 2017). Best model based on adjusted  $R^2$ , AIC, and BIC)

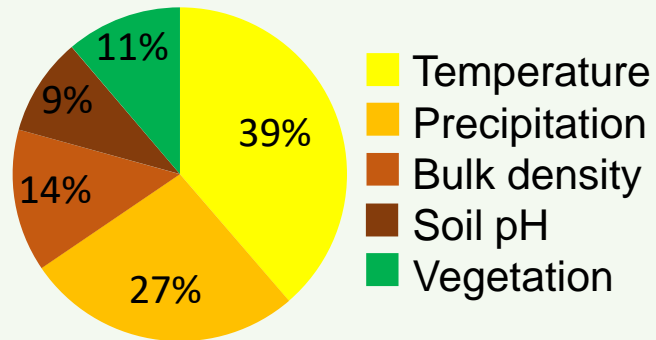


- High latitudes harbour the most diverse fungal communities
- Significant variation in diversity in temperate regions (peaks in the boreal forests of Eurasia and North America)
- Low diversity in the Southern Hemisphere

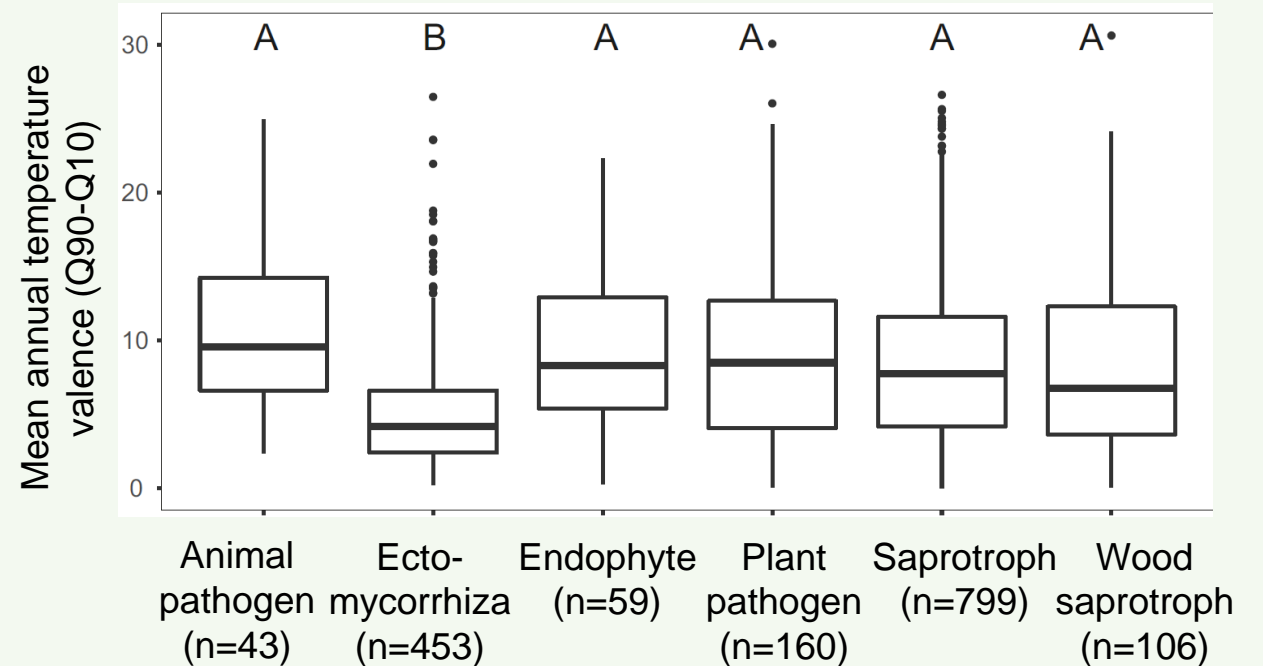
# What about our initial research questions?

## ► Determine which environmental factors could best explain the distribution of fungal diversity:

→ Random forest (Comparison between trees containing randomly sampled 2/3 of the observations and 1/3 of the predictors and the remaining observations (Breiman 2001; Liaw & Wiener 2002 for R package *randomForest*))



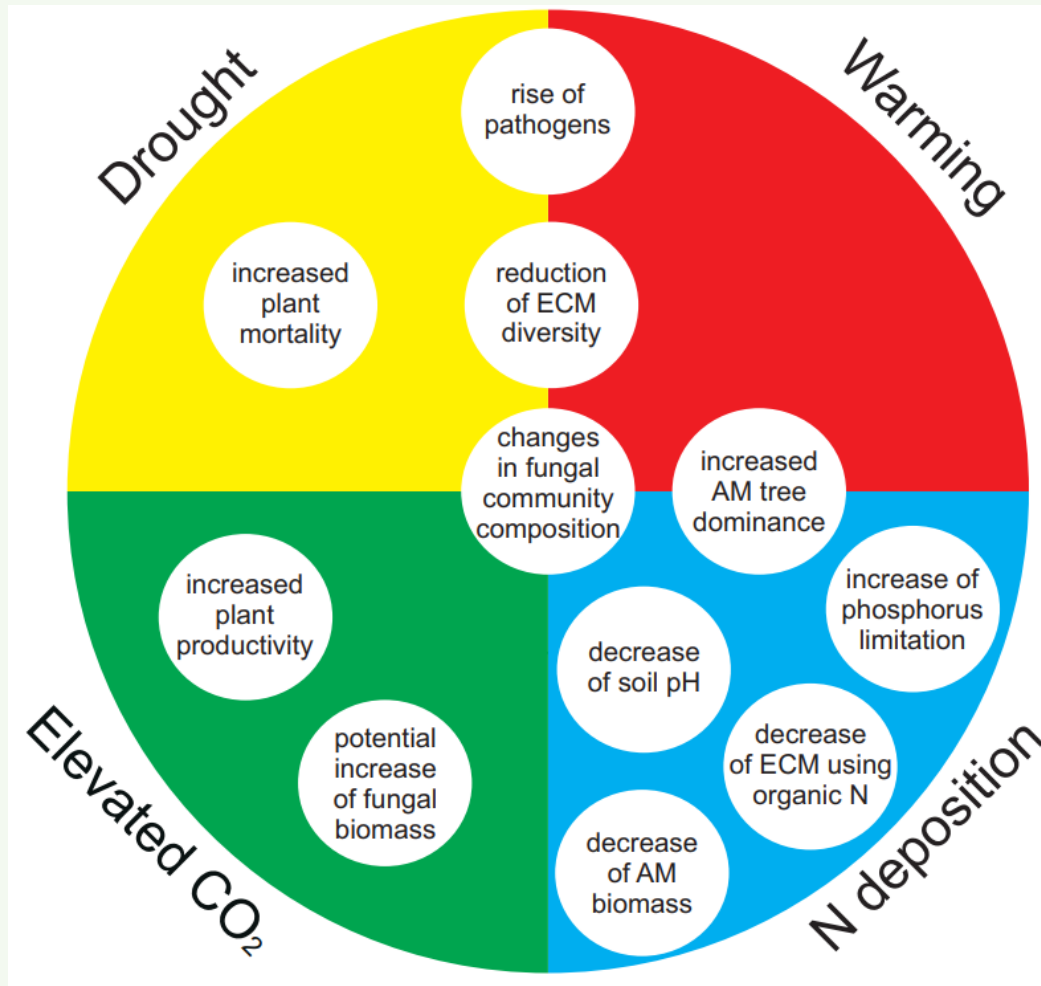
- Climate variables contribute to the explanation of biogeographic distribution for 97% of the 469 top taxa (Species Hypothesis in >5% of samples)
- Ectomycorrhizal fungi have a narrower climate niche than other guilds



# What about our initial research questions?



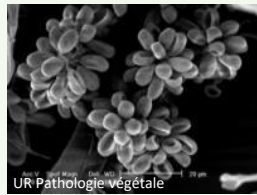
## ► Assess the impact of global change on the distribution of fungal diversity



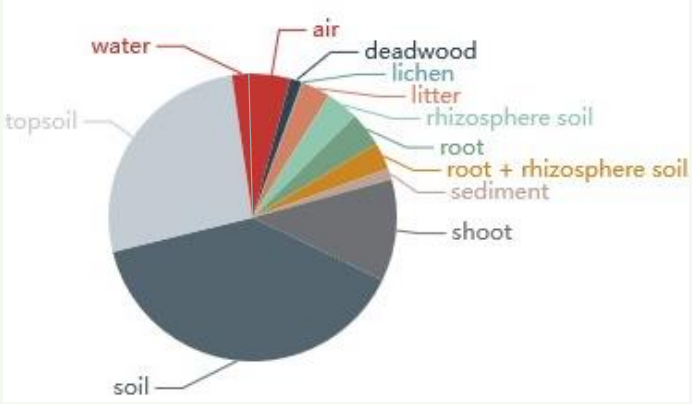
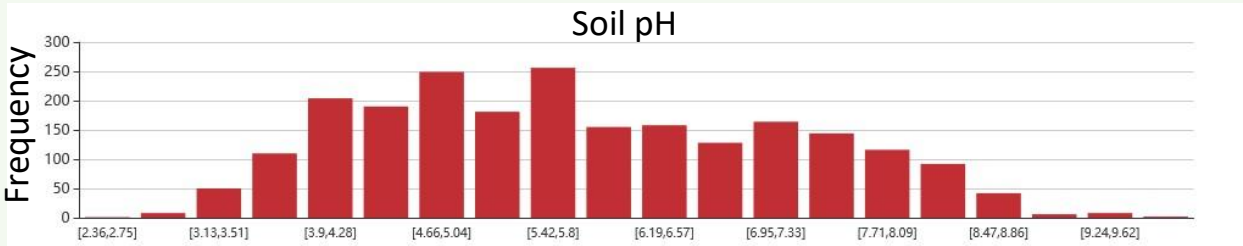
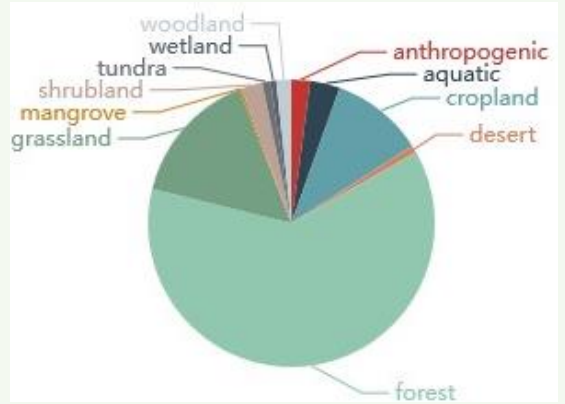
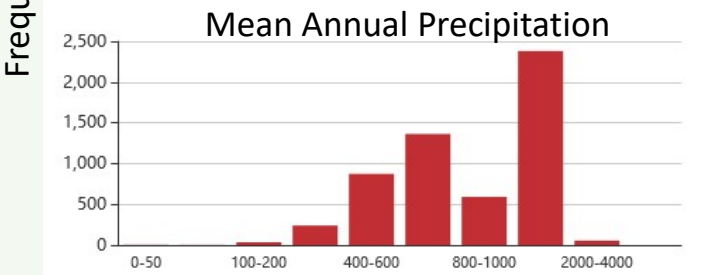
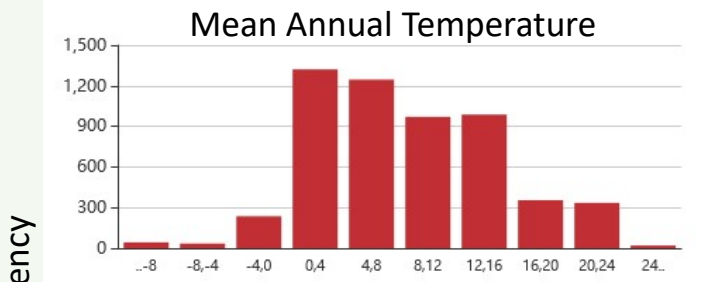
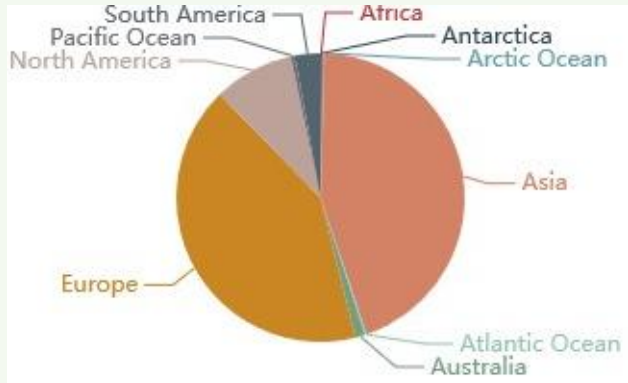
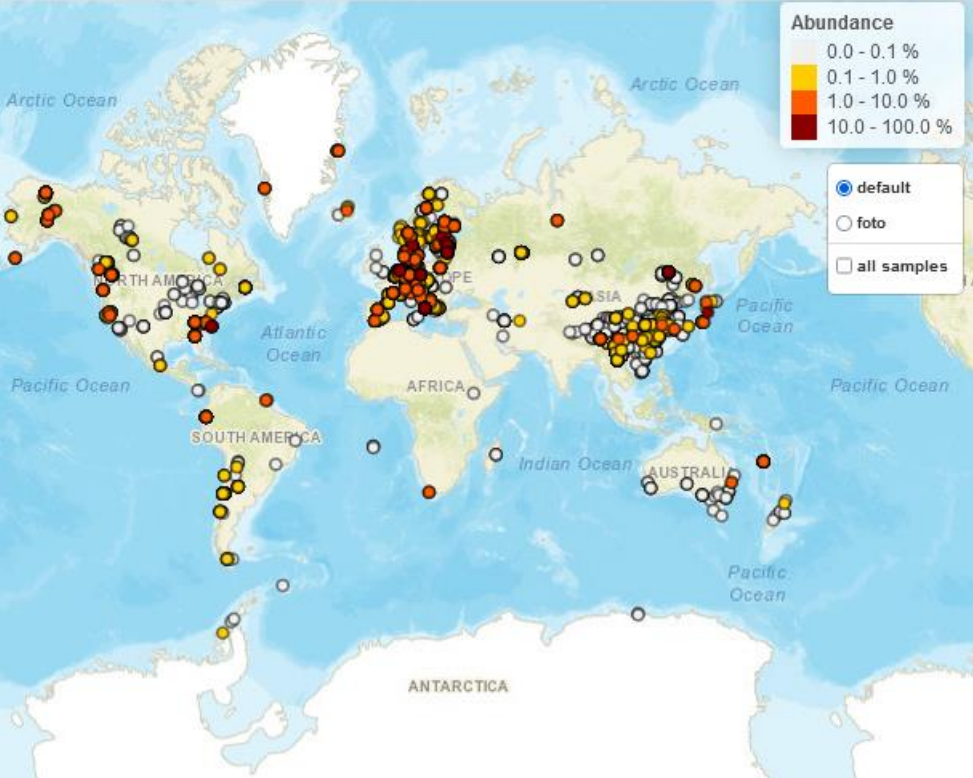
- Strong effect of N deposition on fungal communities
- Increase in abundance and dispersal of plant pathogenic fungi
- plant-mutualistic fungal guilds (ectomycorrhizal fungi and arbuscular mycorrhizal fungi) strongly and negatively affected by N deposition and warming
- Effect of size and duration of change + local conditions

# How to use the database in plant pathology?

► Example of the airborne pathogenic fungi *Botrytis cinerea*



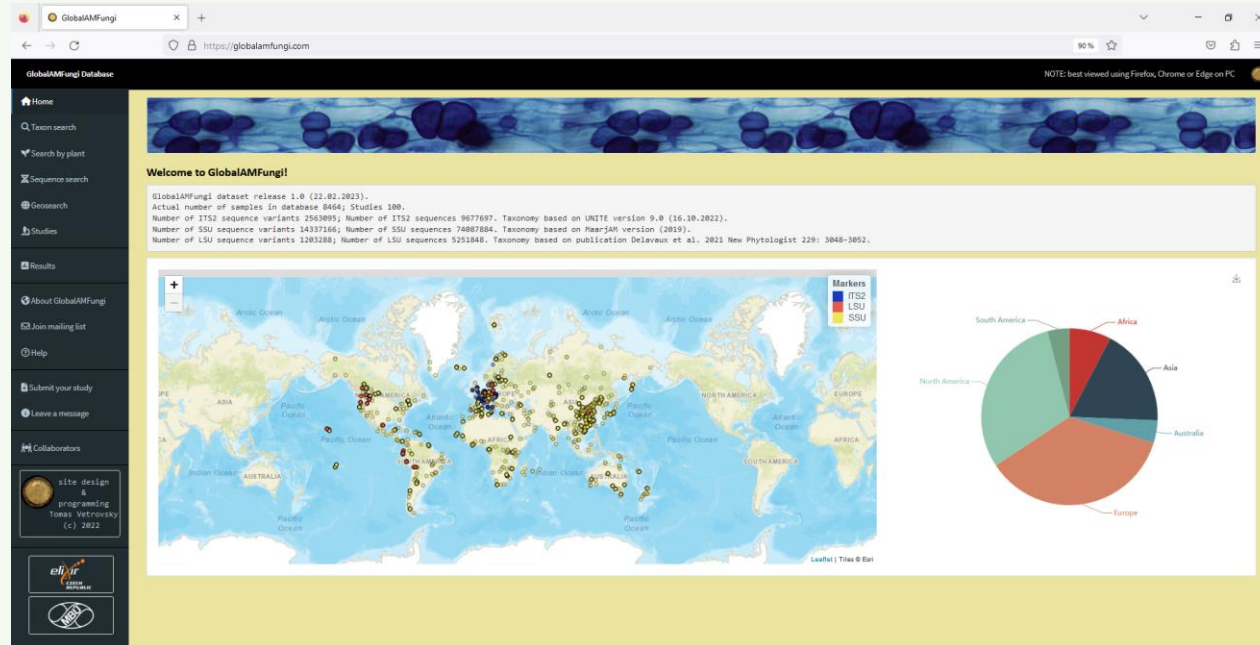
*Botrytis cinerea*



## ► Open to many other scientific questions ...



## ► Similar project developed for arbuscular mycorrhizal fungi (AMF): <https://globalamfungi.com/>



### Methods

## GlobalAMFungi: a global database of arbuscular mycorrhizal fungal occurrences from high-throughput sequencing metabarcoding studies

Tomáš Větrovský<sup>1</sup>, Zuzana Kolaříková<sup>2</sup>, Clémentine Lepinay<sup>1</sup>, Sandra Awokunle Hollá<sup>1</sup>, John Davison<sup>3</sup>, Anna Fleyberková<sup>1</sup>, Anastasiia Gromyko<sup>1</sup>, Barbora Jelínková<sup>1</sup>, Miroslav Kolařík<sup>1</sup>, Manuela Krüger<sup>2</sup>, Renata Lejsková<sup>1</sup>, Lenka Michalčíková<sup>1</sup>, Tereza Michalová<sup>1</sup>, Mari Moora<sup>3</sup>, Andrea Moravcová<sup>1,4</sup>, Štěpánka Moulíková<sup>1</sup>, Iñaki Odriozola<sup>1</sup>, Maarja Öpik<sup>3</sup>, Monika Pappová<sup>1</sup>, Sarah Piché-Choquette<sup>1</sup>, Jakub Skřivánek<sup>1,4</sup>, Lukáš Vlk<sup>1</sup>, Martin Zobel<sup>3</sup>, Petr Baldrian<sup>1</sup> and Petr Kohout<sup>1,4</sup>

Accepted: 4 September 2023



**Thank you for your attention**

