nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Open source code R 4.3.2 is used for data collection (R core team). The R packages are: landscapemetrics (v2.1.2) – for calculating landscape metrics; vegan (v2.6-6.1) – for calculating community diversity indices and dissimilarity. Environmental and spatial data were obtained and processed using: Copernicus Global Land Service (100 m resolution land cover maps); WorldClim 2 (v2.1, 1 km resolution elevation data); CHELSA (v2.1, 1 km resolution climate data).Global Soil Information Database (SoilGrids) – for soil property data.
Data analysis	Open source code R 4.3.2 is used for statistical analyses (R core team). The code that used for data analysis are openly available on figshare at https://doi.org/10.6084/m9.figshare.26377660.v5. The packages used for data analysis include: gamlss (v5.4-22) – for fitting multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS); metafor (v4.8-0) – for random-effects meta-analysis; plspm (v0.5.1) – for Partial Least Squares Path Modeling (PLSPM); gdm (v1.6.0-7) – for Generalized Dissimilarity Modeling (GDM).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The raw sequencing data generated in this study have been deposited in the NCBI Sequence Read Archive (SRA) under accession code PRJNA1045969. The source data underlying all figures are available on Figshare at https://doi.org/10.6084/m9.figshare.26377660.v5. All other data supporting the findings of this study are provided in the Supplementary Information.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	n/a
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	n/a
Recruitment	n/a
Ethics oversight	n/a

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This is a global field survey with 511 soil samples collected worldwide to study the effect of landscape complexity on global soil pathogenic fungal diversity across spatial scales, compared with local environmental variables.
Research sample	We classified fungal phylotypes (from all the analyzed 511 soil samples) into pathogenic fungi, including aboveground leaf/fruit/seed-associated (LFSA) fungi and below-ground root-associated (RA) fungi.
Sampling strategy	Soil samples were collected from the International Soil Biogeography Consortium (iSBio, https://home.uni-leipzig.de/idiv/isbio). Sampling strategy can be found in Heintz-Buschart et al. (2020).
Data collection	Soil samples were collected from 511 plots, across 290 sites located in 32 countries and six continents, in natural environmental conditions. Soil samples were collected following a standard sampling protocol to identify the soil pathogenic fungal diversity and soil properties (see Methods for details). Landscape complexity was calculated from a land cover map with 100 m resolution from Copernicus Global Land Service. The geographic variables included elevation, longitude, and latitude. The longitude and latitude were measured on site, and elevation was taken from WorldClim 2 with 1 km resolution. The climatic variables included mean annual temperature (MAT) and mean annual precipitation (MAP) that were extracted from a processed global layer CHELSA with 1 km resolution.
Timing and spatial scale	All the samples were collected during summer in 2018 (the northern hemisphere), or 2019 (the southern hemisphere). Landscape complexity was calculated across six spatial scales: 250, 500, 1,000, 2,000, 5,000, and 10,000 m radius around the sampling coordinate.
Data exclusions	Based on 290 sites that composed of two homogeneous plots, we should collect 580 samples in total, but 3 of which were lost during transportation and 66 samples were lost due to sequencing failure, resulting in a final 511 soil samples.

Reproducibility	Each site was composed of two homogeneous plots to ensure representativeness.
Randomization	In each plot, four randomly distributed soil samples were collected and pooled into one composite sample.
Blinding	Blinding is not revelant since we performed no artificial control in the experimental design.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Of the 290 sites, 145 were categorized as forest ecosystems (dominated by trees or shrubs), 109 were grassland ecosystems (including grasslands, meadows, or pastures), and 36 were other ecosystems (including tundra, desert, plantation, salt marsh, or croplands). Temperature and precipitation vary across site, with Mean annual temperature (MAT) ranged from -13.9°C to 26.4°C, with an average of 7.8°C. Mean annual precipitation (MAP) varied from 24.0 mm yr^{-1} to 3127.5 mm yr^{-1}, averaging 931.3 mm yr^{-1}. Detailed information can be found in Figshare (https://doi.org/10.6084/m9.figshare.26377660.v5.)
Location	Field sampling sites were distributed globally, ranging from 51.916°S to 73.135°N latitude and 149.247°W to 148.289°E longitude. Sampling elevations ranged from 0.5 m to 2951.8 m a.s.l., with a mean elevation of 626.4 m a.s.l..The locations of all the 511 soil plots can be found in Figshare (https://doi.org/10.6084/m9.figshare.26377660.v5.)
Access & import/export	All research activities complied with relevant ethical regulations and were conducted under permits MAE-DNB-CM-2016-0043 and 006-2021-EXP-CM-FAU-DBI/MAAE issued by the Galapagos National Park Directorate and the Ecuadorian Ministry of Environment, Water and Ecological Transition.
Disturbance	This study did not cause any environmental disturbance.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study	
☒	☐	Antibodies
☒	☐	Eukaryotic cell lines
☒	☐	Palaeontology and archaeology
☒	☐	Animals and other organisms
☒	☐	Clinical data
☒	☐	Dual use research of concern
☒	☐	Plants

Methods

n/a	Involved in the study	
☒	☐	ChIP-seq
☒	☐	Flow cytometry
☒	☐	MRI-based neuroimaging

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a