nature portfolio

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Last updated by author(s): *YYYY-MM-DD*

# 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<br>*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<br>*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 | Data were compiled from open-access databases including Index Fungorum (http://www.indexfungorum.org), MycoBank (http://www.mycobank.org), the Global Biodiversity Information Facility (GBIF; https://www.gbif.org), and the Mycological Specimen Portal (MyCoPortal; https://www.mycoportal.org), as well as from taxonomic literature and specimen records. |
| Data analysis | All data preprocessing, statistical analyses, and visualizations were conducted in the R programming environment (version 4.5.2). The specific R packages used are listed as follows: Data imputation and multivariate analyses: The missMDA package was used for PCA-based missing value imputation, and the FactoMineR package was used for principal component analysis (PCA). Mixed-effects models: The lme4 package (version 1.1-35.1) was used for fitting linear mixed-effects models, with marginal and conditional $R^2$ calculated using the MuMIn package (version 1.47.5). Categorical trait modeling: The base glm function was used for binomial logistic regression, with Firth's penalized likelihood correction applied via the logistf package (version 1.26.0). Model evaluation: The pROC package (version 1.18.5) was used to calculate the Area Under the Curve (AUC). Multiple testing correction: The base p.adjust function was used for Benjamini–Hochberg False Discovery Rate (FDR) correction. Data visualization: The ggplot2 package (version 3.4.4) was used for graphical visualizations. Other analyses, including Generalized Additive Models (GAMs), ensemble species distribution modeling (combining random forests, GAMs, and maximum entropy models), spatial autocorrelation analyses, and raster-based spatial extraction for environmental variables, were performed using standard R functions and custom scripts as detailed in the Methods section. |

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 data and articles supporting the results of this study can be accessed for publication

## 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 | We conducted a global macroecological study by synthesizing 26 functional traits (12 continuous and 14 categorical) across 7,454 wood-inhabiting fungal species. We integrated this trait database with approximately 4.58 million georeferenced occurrence records to investigate multidimensional trait trade-offs (the fungal economics spectrum) and environmental driving mechanisms. We further employed ensemble species distribution models to project future shifts in fungal functional traits under two climate scenarios (SSP1-2.6 and SSP5-8.5). |
| Research sample | The research sample comprises 7,454 valid wood-inhabiting macrofungi species within the class Agaricomycetes, representing 22 orders, 121 families, and 759 genera globally. The species checklist was constructed based on authoritative taxonomic systems (Index Fungorum and MycoBank). Occurrence records were sourced from global databases (GBIF, MyCoPortal) and extensive field surveys/ specimen collections accumulated over the past three decades. The sample aims to represent the global functional diversity of wood-inhabiting fungi. |
| Sampling strategy | No statistical method was used to predetermine the sample size. Our sampling strategy aimed for comprehensive global coverage rather than a specific statistical power calculation. The sample size (7,454 species) was chosen because it represents a near-complete representative sampling at the order and family levels of known wood-inhabiting fungi, particularly including all major lineages involved in lignocellulose degradation. For geographic data, a sample-based rarefaction analysis was conducted across three latitudinal zones to ensure sample sizes met the robustness prerequisites for subsequent statistical analyses. |
| Data collection | Data were collected by the authors and team members. Trait data were extracted from taxonomic literature, mycological monographs, and scientific expedition reports. Distribution data were retrieved from GBIF and MyCoPortal using species scientific names and synonyms as keywords, alongside physical specimen records verified by morphological and molecular data. Environmental variables were derived from ERA5-Land climate reanalysis products and global DEM datasets. |
| Timing and spatial scale | Spatial scale: Global (covering latitudinal zones from 0° to 80°, with a particular focus on China for field surveys). Temporal scale: The compiled data and literature were published before June 2025. For future projections, baseline climate conditions were defined as 1970–2000, and future conditions as 2071–2100. |

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| Data exclusions | For geographic occurrence records, exact duplicates were removed using gbifID. Records were filtered based on spatial extent, temporal validity, and coordinate completeness. Observations lacking precise coordinates were assigned the geometric centroid of their respective administrative or biogeographical unit. In trait analyses, trait matrices were filtered to remove variables with excessive missingness or near-zero variance prior to PCA imputation. |
| Reproducibility | To ensure reproducibility, all data sources (literature references, database IDs) are documented in the Appendix and Supplementary Tables. The R codes needed to reproduce the statistical results and figures are publicly available. The taxonomic statuses were cross-validated and dynamically updated using Index Fungorum and MycoBank. |
| Randomization | N/A |
| Blinding | N/A |

Did the study involve field work? ☒ Yes ☐ No

## Field work, collection and transport

| | |
|---|---|
| Field conditions | Field surveys and specimen collections were conducted globally over the past three decades (with a particular focus on China) across diverse forest ecosystems. Because the records span a 30-year period and broad geographic gradients, specific micro-environmental parameters (e.g., exact temperature and rainfall at the time of each collection) were not uniformly recorded for all historical specimens. However, the spatial distribution records were subsequently linked to macro- and micro-environmental variables (e.g., annual precipitation, mean temperature, elevation, and LAI) derived from ERA5-Land climate reanalysis products and global DEM datasets for statistical analyses. |
| Location | The field surveys and specimen collections were conducted globally, with a primary focus on China. The distribution records span latitudinal zones from 0° to 80° (tropical-subtropical to boreal-polar). Detailed geographic coordinates (latitude and longitude) and elevation information for each verified specimen record are provided in the compiled occurrence dataset, which forms the basis of this study. |
| Access & import/export | Field surveys and specimen collections were conducted in accordance with local, national, and international regulations. Because this study is a macroecological synthesis, the vast majority of distribution records were compiled from public databases (e.g., GBIF, MyCoPortal) and published literature, rather than requiring physical transport of specimens to the analysis site. All specimens are deposited in the Fungal Herbarium of the Institute of Microbiology, Beijing Forestry University (BJFC, Beijing, China). |
| Disturbance | The field work involved non-destructive sampling (collecting fruiting bodies) of macrofungi. No significant disturbance to the habitats, forest ecosystems, or protected species occurred. Sampling was restricted to a minimal number of individuals required for taxonomic identification (morphological observation and molecular analysis), thereby minimizing any ecological impact on the local fungal populations and the surrounding environment. |

# 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 |

## Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

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|---|---|
| Laboratory animals | N/A |
| Wild animals | N/A |

| | |
|---|---|
| Reporting on sex | N/A |
| Field-collected samples | Field-collected samples consisted of fungal fruiting bodies (specimens). Specimens were collected using non-destructive methods and deposited in recognized fungaria/herbaria for morphological and molecular identification. No live animals were involved, and thus no housing, maintenance, or end-of-experiment protocols for animals were required. |
| Ethics oversight | N/A |

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

## Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

| | |
|---|---|
| Clinical trial registration | N/A |
| Study protocol | N/A |
| Data collection | N/A |
| Outcomes | N/A |

## Plants

| | |
|---|---|
| Seed stocks | N/A |
| Novel plant genotypes | N/A |
| Authentication | N/A |