

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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give <i>P</i> values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Our tree-inventory data (March 2024 - ATDN20240303) are part of the Amazon Tree Diversity Network 8,9,44 , which contained 2,023 tree-inventory plots (Supplementary Fig. 1) with information on species composition and abundance. A total of 12 continuous environmental attributes were extracted from gridded data. A soil acidity (pH) surface for entire Amazonia was created with a loess model (with a span of 0.2, a degree of 2, using Gaussian fitting) based on measurements of soil pH from soil profiles available from several sources 68 40,41,69-72 (Supplementary Fig. 25). As a measure of nutrient availability, we used the logarithm of soil base cation concentration (SB; Ca+Mg+K), as provided by Zuquim et al. 41. Climatic data was obtained from CHELSA 73. We used three variables for temperature (mean annual temperature, temperature range, and temperature seasonality) and two for precipitation (total annual precipitation, precipitation seasonality). We also estimated the maximum climatological water deficit (MCWD), which can be considered a measure of seasonal drought. This was calculated as the cumulative rainfall deficit of consecutive months with ≤ 100 mm of precipitation from 1981-2020 as measured by CHIRPS 74-76. The water-table depth was extracted from a gridded layer produced by Fan et al. 77. Three topographic variables (elevation, multi-scale topographic index, topographic diversity index) were obtained from the digital surface models of the ALOS World 3D 78,79. In addition, we included the classification of sites into Flooded vs. Non-flooded, and Podzol vs. Non-Podzol as categorical environmental predictors.
Data analysis	All custom R code used in the analysis and visualization of the data is publicly available through FigShare (https://doi.org/10.6084/m9.figshare.26792731). This code can be used to produce all figures in main text.

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](#)

All plot metadata is included in supplementary table 2. The code to reproduce analysis and figures, the PCoA scores by plot, the grided community matrix and the mean niche position (weighted averages) and niche breadth for the species, are publicly available through FigShare 95. Additional plot-based data is available upon reasonable request by contacting the corresponding author.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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](https://www.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	The study investigates how tree species composition varies across Amazonia, with eyes on both ecological and biogeographical patterns. In addition to plot-level analyses, we also map gradients in tree species composition across Amazonia at the resolution of 0.1-degree grid cells. We then interpret the association of these broad-scale compositional differences with the climatic and edaphic variation over the region.
Research sample	The abundance of 5,188 accepted tree species within 2,023 tree-inventory plots and associated values of environmental covariates in those plots.
Sampling strategy	On each plot all trees > 10cm dbh were measure and identified to species, if possible.
Data collection	All the authors have collected data on tree inventories.
Timing and spatial scale	The first plot was sampled in 1934, the last plot was from 2023
Data exclusions	No plots were omitted
Reproducibility	All data to produce all graphs and all maps is deposited at FigShare
Randomization	Plots were grouped in forest types and regions
Blinding	NA

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Amazon forest conditions, heat, always moisture, sometimes rain.
Location	2023 plots all over the Amazon
Access & import/export	No specific sampling was needed as plot data was supplied by the co-authors
Disturbance	In most studies only small samples of trees were collected

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

Methods

n/a	Involved in the study	n/a	Involved in the study
☒	☐ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☒	☐ Palaeontology and archaeology	☒	☐ MRI-based neuroimaging
☒	☐ Animals and other organisms		
☒	☐ Clinical data		
☒	☐ Dual use research of concern		
☒	☐ Plants		

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.