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Reporting Summary

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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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P 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 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 analysis

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 Supporting data and three appendices (Appendix 1, Appendix 2 and Appendix 3) that support the findings of this study are available in Figshare at https://doi.org/10.6084/m9.figshare.29270048

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Here, we conduct a comprehensive global meta-analysis to investigate the patterns of the species richness-ecological uniqueness relationship (RUR) across taxa groups and to evaluate the relative importance of four ecological hypotheses (i.e. species pool attributes, dispersal limitation, environmental filtering and spatial grain size).
Research sample	We incorporated three distinct approaches to allow for a broad and representative collection of studies or datasets (See Supplementary Note 1-2 for details). (1) Peer-reviewed literature studies: First, we searched for peer-reviewed journal articles using the ISI Web of Science using predefined keyword combinations to obtain an extensive collection of primary studies that focused on ecological uniqueness globally. The search was conducted using the ISI Web of Science Core Collection database, accessed via the institutional subscription of the University of Chinese Academy of Sciences. This process was conducted in adherence to the Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) 2020 statement. Additionally, as a supplementary strategy, we also performed a citation tracking search and investigated all studies that cited Legendre & De Cáceres, 2013, on December 1, 2024. This is because this seminal paper provided both the conceptual foundation and terminology of ecological uniqueness (i.e. the metric of local contributions to beta diversity), and which has become a cornerstone in this research domain. Collectively, 1763 records were obtained from these combined search methods (i.e. records of keyword-based searching: 876; records of seminal literature citation tracking: 887) and 1542 records were retained after removing duplicated records (2) Public data repositories: Second, we compiled several additional raw datasets across different taxonomic groups from data repository, because ecological uniqueness and species richness were both computable from raw species composition datasets. We separately used the following keywords to search for biological community composition datasets in Dryad digital repository (http://datadryad.org/): (taxonomic composition) OR (species composition) OR (species assemblage) OR (community composition) OR (community assemblage) OR (species abundance) OR (presence absence). (3) Compiled datasets: Third, we compiled a series of additional raw datasets from our own data. These datasets were mainly acquired through: (1) direct correspondence with principal investigators maintaining unpublished datasets, or (2) using the existing data sources including: GrassPlot, sPlot and CESTES by ourselves. The detailed procedures are now described in Supplementary Note 1 and Supplementary Note 2.
Sampling strategy	Not applicable
Data collection	Authors Y.C. and X.W. extracted relevant data from the publications, directly from text and tables. We list the source of the data in Supplementary Data file and Supplementary information. The attribution of effect sizes to different categories (moderators and random effects) is explained in the manuscript and Supplementary information.
Timing and spatial scale	The last search of literatures and datasets were done on December 1, 2024. The year of studies or datasets included in the synthesis ranged from 2011 to 2024
Data exclusions	We established several criteria to exclude several studies (Supplementary Fig. 1), these are: (1) We excluded experimental studies because their species combinations are typically artificially manipulated or intentionally set in each community or study unit (Reason 1, 5 studies; Supplementary Fig. 1). (2) We excluded studies that failed to provide taxonomic information at the species level. For instance, several studies limited their taxonomic resolution to the family, subfamily, OTU or other levels, which did not reflect species level richness characteristics (Reason 2, 44 studies; Supplementary Fig. 1). (3) We excluded studies that did not report the distributions of both species richness and ecological uniqueness values, or studies that only report related statistics (e.g. regression

coefficients, slope t-tests or model estimates) without providing richness or uniqueness distributions. Although it is methodologically feasible to convert such statistics into correlation coefficients, this exclusion was necessary because previous empirical evidence demonstrates that the RUR may exhibit either linear or nonlinear (e.g. curve-linear) relationships. Without detailed distributions of species richness and ecological uniqueness, we could not reliably characterize the association form of RUR. To empirically test the form of the relationship for each study, it was essential for us to have access to the data distributions. Moreover, relying solely on converted summary statistics would have presupposed a linear association and prevented us from verifying this key assumption. Such incomplete reporting would fundamentally limit our capacity to distinguish between alternative ecological models while introducing substantial uncertainty in the synthesis (Reason 3, 186 studies; Supplementary Fig. 1). (4) We excluded studies that exhibited methodological variation in data acquisition approaches. Specifically, studies combining multiple data sources with inconsistent sampling protocols (e.g., those integrating community data from both literature-compiled records and original field surveys within the same analysis) were excluded to ensure methodological consistency. Furthermore, we also excluded studies lacking standardized sampling protocols, particularly those with inconsistent sampling areas across sampling units. This is because studies have revealed that both species composition and species richness are both sensitive to the area of sampling unit. This exclusion criteria was implemented to minimize confounding effects and enhance comparability across studies (Reason 4, 8 studies; Supplementary Fig. 1). (5) We excluded studies that calculated ecological uniqueness metrics based on other analytical units incompatible with our spatial site-based framework. Specifically, studies employing non-spatial compositional units (e.g., temporal observations at different time points, individual organisms from distinct populations, or nodes at food webs) to obtain ecological uniqueness were excluded because these study units fail to capture site-based distributions of ecological uniqueness. This exclusion criterion ensures conceptual consistency in defining ecological uniqueness as a spatial-community property emerging from β -diversity patterns (Reason 5, 39 studies; Supplementary Fig. 1). (6) We excluded studies that solely reported species richness of specific taxonomic groups (e.g., threatened species, invasive/exotic species, or other preselected categories). This exclusion criterion was implemented because our primary focus lies in understanding RUR at the community or sampling site level (Reason 6, 7 studies; Supplementary Fig. 1). (7) We excluded methodological studies that primarily focused on synthetic/simulated data to quantify species richness or ecological uniqueness, because our analytical framework specifically investigates patterns of ecological uniqueness and species richness derived from empirical observations (Reason 7, 4 studies; Supplementary Fig. 1). (8) We also excluded studies sharing identical datasets (i.e., multiple publications analyzing the same datasets) (Reason 8, 1 study; Supplementary Fig. 1).

(1) We excluded datasets related to experimental studies because the species combinations are artificially manipulated in each sampling unit (Reason 1, 21 datasets; Supplementary Fig. 1). (2) We excluded datasets that failed to provide taxonomic information at the species level. For instance, several datasets reported richness of taxonomic levels of other types (e.g., genus, family, OTU or ASV), which did not meet the requirement of species-level richness in the analysis. Additionally, we disqualified datasets containing species with missing information (e.g., species that could not be identified or lacked pertinent data within the dataset), as these omissions made it difficult for us to calculate species richness (Reason 2, 5 datasets; Supplementary Fig. 1). (3) We excluded datasets that exhibited methodological heterogeneity in data acquisition approaches. For example, some datasets obtained part of their community data from literature sources while other parts were based on field surveys. In addition, we also found that sampling sites differed in their sampling area in certain datasets. Such studies were not included in our synthesis. Meanwhile, datasets lacking details of sampling protocols were also excluded (Reason 3, 30 datasets; Supplementary Fig. 1). (4) We excluded datasets based on other sampling unit incompatible with our spatial-community framework (e.g., temporal observations, individual organisms from distinct populations, or food web nodes) (Reason 4, 4 datasets; Supplementary Fig. 1). (5) We also excluded studies sharing identical datasets (i.e., the same dataset used in primary studies or multiple data publications containing the same datasets) (Reason 5, 11 datasets; Supplementary Fig. 1). Following the established exclusion criteria, we retrieved 243 raw datasets from the Dryad repository, encompassing 20 distinct taxonomic groups (e.g., terrestrial plants, fish, birds, terrestrial insects, invertebrates; Supplementary Table 1).

Reproducibility

All analyses are reproducible with provided datasets

Randomization

During the systematic review processes, we checked that no randomization was used when collecting the data

Blinding

We did not used blinding during acquisition or analyses of data

Did the study involve field work?

☐ Yes☒ No

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	NA
Novel plant genotypes	NA
Authentication	NA