

## 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 No software was used for data collection.

Data analysis Coding scripts used for this manuscript are available here (<https://doi.org/10.57760/sciencedb.27130>).

Softwares used for phylogenetic reconstruction and visualization:  
Hybpiper pipeline v.1.3.1, MAFFT v7.508, BioEdit v7.2.5, Dendroscope v3.8.10, RAxML 8.2.12, treePL 1.0, iTOL v7, TreeAnnotator v.2.7.5.

R (v4.4.1) packages for data processing and analysis:  
data.table v1.15.4, tidyverse v2.0.0, vegan v2.6-6.1, canaper v1.0.1, ape v5.8-1, ggpubr v0.6.0., phytools v2.3-0, readxl v1.4.3, future v1.67.0, rgbif v3.8.0, CoordinateCleaner v3.0.1, rnatuarearth v1.0.1, sf v1.0-16, countrycode v1.6.0, U.Taxonstand v1.3.2, rWCV v1.3.0, rangeBuilder v2.2, phangorn v2.11.1, cowplot v1.1.3, gridExtra v2.3, future.apply v1.20.0, Matrix v1.7-0

Julia packages for data processing and analysis:  
Biohistoria, DelimitedFiles, PyPlot

Spatial analysis software:  
ArcGIS 10.8.

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](#)

Sequences newly generated for this study are available in GenBank and all accession numbers are provided in Supplementary Data 6. The phylogeny and species distribution data generated in this study are available at the ScienceDB repository (<https://doi.org/10.57760/sciencedb.27130>).

## 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

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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	We provided a comprehensive spatiotemporal assessment of China's endemic vascular plants by integrating taxonomic and phylogenetic endemism. Using 49,488 sequences from 18,259 taxa, we reconstructed the most comprehensive time-calibrated phylogeny for China's vascular plants to date (99% of genera, 53% species coverage). By integrating > 1.4 million distribution records with this phylogeny, we identified centers of neo- and paleo-endemism at genus and species levels and evaluated their protection under national and global frameworks. Notably, We pinpointed Central China as a critical conservation gap, advocating its designation as a Global Biodiversity Hotspot.
Research sample	1. Our phylogeny included 18,259 taxa, representing 17,853 species and 3,288 genera, of which 16,585 species (53%) and 3,029 genera (99%) are native to China. 2. The list of China's endemic vascular plants included 124 endemic genera and 15,942 endemic species. 3. The Geographic distribution dataset contained 1,421,390 records across 941 grid cells, which encompassed 26,604 species (13,725 endemic) and 2,873 genera (116 endemic) native to China.
Sampling strategy	Phylogeny sampling: we used all publicly available molecular sequences up to September 2022. Geographic sampling: we used all available geographic distribution data after necessary data cleaning. No statistical methods were used to predetermine sample size.
Data collection	1. Our phylogeny newly included 10,023 sequences representing 3,267 species and 996 genera, of which 2,996 sequences (representing 620 species and 353 genera) were newly sequenced in this study and 7,027 (representing 2,727 species and 858 genera) were newly downloaded from GenBank. 2. Geographic distribution records of vascular plants in China were assembled from two primary sources: the gridded distribution data for angiosperms from (Zhao et al., 2024) and county-level records for gymnosperms, lycophytes, and ferns from the Chinese Virtual Herbarium ( <a href="https://www.cvh.ac.cn/">https://www.cvh.ac.cn/</a> ). 3. The coordinate point data for Chinese vascular plants used in the sensitivity analysis was downloaded from Global Biodiversity Information Facility (DOI: <a href="https://doi.org/10.15468/dl.vmupyc">https://doi.org/10.15468/dl.vmupyc</a> ).

Timing and spatial scale	We obtained all available molecular sequence data up to September 2022, and our distribution data compilation included all the data available in the corresponding database as of December 2021. GBIF coordinate data include all georeferenced records available up to 16 November 2025. The geographical scope of this study is China.
Data exclusions	1. Molecular sequence: for species with multiple sequences of the same locus, we retained the longest one. 2. List of endemic genera: we applied a strict definition of taxonomic endemism that excluded genera with updated distribution records beyond China in recent years. 3. Distribution records: Grid cells < 50% land area (i.e., < 5,000 km <sup>2</sup> ) were excluded.
Reproducibility	All code and data are publicly available at the ScienceDB repository ( <a href="https://doi.org/10.57760/sciencedb.27130">https://doi.org/10.57760/sciencedb.27130</a> ).
Randomization	Randomization was not applicable to this study as we required all available relevant records in order to capture plant diversity patterns.
Blinding	Blinding was not applicable to this study.
Did the study involve field work?	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

## Field work, collection and transport

Field conditions	The purpose of our field collection was to obtain samples for reconstructing the Tree of Life for Chinese vascular plants, field conditions are not relevant and were not recorded.
Location	We conducted sampling across China, with a focus on data-scarce regions such as Xinjiang, Yunnan, and Hainan.
Access & import/export	For all sampling locations in China, before the fieldwork, relevant national or regional authorities were contacted to obtain authorization for accession.
Disturbance	Only target samples were collected from fields and no other vegetal, animal, or soil materials were transported outside the fields. The disturbance to natural habitats was minimized.

## 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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input type="checkbox"/>	<input checked="" type="checkbox"/> Plants

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Plants

Seed stocks	The voucher information of newly sampled species was provided in Supplementary Data 6. Voucher specimens for newly sampled species were deposited at the Herbarium of Institute of Botany, Chinese Academy of Sciences (PE).
Novel plant genotypes	N/A
Authentication	N/A