

Reporting Summary

Nature Research 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 Research 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
<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 No software was used in the data collection process.

Data analysis Computer software use for the analyses are: BEAST2.5.1, TreePL, Geneious, ClustalW, RAxMLv.8, R, and python.

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

GenBank accession numbers for sequence data, sequence alignments, phylogenetic trees and fossil information that support the findings of this study are available within the supplementary information files of the paper and at Zenodo with the identifier doi.org/10.5281/zenodo.382087855. The fossil calibration list is available at Zenodo with the identifier doi.org/10.5281/zenodo.382807156. The geographic data are available from the Global Biodiversity Information Facility with the identifier doi.org/10.15468/dl.iftsjs.

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	To perform divergence time estimation and spatial analyses for all families of extant angiosperms. For this we sampled 1,209 species in all 435 families, used 238 fossils for time-tree calibration, and integrated the results with over 16 million occurrence records for extant angiosperms.
Research sample	We describe our molecular and fossil sample in the Supplementary Methods. Detailed information for the species and fossils are available in the accompanying supplementary files.
Sampling strategy	We conducted the molecular and fossil sampling based on previous studies and attempted to cover angiosperm diversity at the family level. The molecular sampling covered all orders and families of extant angiosperms, which is sufficient to address the questions of the study.
Data collection	Molecular data collection was based on available sequence data in GenBank. Fossil data collection was based on literature review. Geographical data was collected from the Global Biodiversity Information Facility (GBIF).
Timing and spatial scale	The study addresses geological timing relevant to the evolution of angiosperms as a whole and we compiled global scale geographic distribution data to address the questions of the study.
Data exclusions	No data were excluded.
Reproducibility	The phylogenetic results, divergence time estimates, and geographic analyses can be reproduced from the data provided in the accompanying supplementary files.
Randomization	Molecular sampling was designed to cover all angiosperm families.
Blinding	Blinding is not relevant to our study.
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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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