

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 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 <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	No additional software was used in the collection of data.
Data analysis	TNT 1.6 and MrBayes v3.2.4 for phylogenetic analyses. The settings needed to replicate these analyses are provided in the paper and its supplementary material.

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 the used data for this study are embedded in the manuscript and supplementary files.

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	Anatomical observations of newly collected fossil stems of <i>Guangdedendron micrum</i> were combined with a morphological phylogenetic analysis of Late Palaeozoic lycopsids to investigate the evolution of anatomical characters and phylogenetic relationships.
Research sample	The study examined anatomically preserved fossil stems of <i>Guangdedendron micrum</i> from the Upper Devonian Wutong Formation, together with morphological character data for Devonian–Carboniferous lycopsid taxa compiled from direct observations and published literature.
Sampling strategy	All available anatomically preserved specimens suitable for anatomical study were included. Taxa for the phylogenetic analysis were selected to represent the major Devonian and Carboniferous lycopsid lineages with sufficiently documented morphological characters. No statistical method was used to predetermine sample size.
Data collection	Anatomical observations and character scoring were performed by the authors based on direct examination of fossil specimens and published descriptions. Measurements were made from fossil specimens and published figures using standard palaeobotanical methods.
Timing and spatial scale	Fossil specimens were collected during multiple field expeditions between 2022 and 2025 from the Xinhang fossil forest, Guangde, Anhui Province, China. Phylogenetic character compilation was carried out between 2020 and 2025 using specimens and published data from Devonian and Carboniferous localities worldwide.
Data exclusions	No specimens or taxa were excluded after data collection, except where anatomical or morphological characters were unavailable and therefore coded as unknown in the phylogenetic matrix.
Reproducibility	All anatomical observations were repeatedly examined by the authors. The phylogenetic data matrix, character list, and analysis scripts are provided in the Supplementary Information to enable reproduction of the analyses.
Randomization	not applicable
Blinding	not applicable

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Field work was only used to collect fossil specimens and thus not affected by field conditions.
Location	Specimens was collected from the Leigutai Member (upper part of the Upper Devonian Wutong Formation), at the Yongchuan clay mine in Xinhang Town, Guande City, Anhui Province, China.
Access & import/export	Not applicable
Disturbance	No disturbance is caused by the study.

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

Palaeontology and Archaeology

Specimen provenance	The fossil specimens were collected by authors and their collaborators and no permit is needed for the field work.
Specimen deposition	All the specimens are deposited in the Department of Geology, Peking University.
Dating methods	No new date is provided.
☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	No ethical approval was required for this study.

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

Plants

Seed stocks	Not applicable
Novel plant genotypes	Not applicable
Authentication	Not applicable