

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	CorelDraw X9 and Adobe Photoshop CC for image processing. Dragonfly v4.1.7 for 3-D reconstruction of the fossils. FigTree 1.4.4 for visualization of phylogenetic tree. Microsoft Excel 2019 for coding phylogenetic matrices.
Data analysis	ImageJ v. 1.8.0 for the measurement of Sunella carapace. Data is provided as Supplementary Data 1. MrBayes v.3.2.6 x64 and TNT V 1.5 for phylogenetic analysis. Code is provided as Supplementary Data 2. Tracer v1.7.2 for convergence. Data is provided as Supplementary Data 3. R packages for ancestral state reconstruction. Data is provided as Supplementary Data 4 and Data 5. Inkscape was used to create outlines from photographs. Momocs package in R used for elliptical Fourier analysis. Data is provided as Supplementary Data 6.

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 data analysed in this paper are available as part of the Article, Supplementary Data 1 to 6.

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

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

This study is a palaeontological investigation involving collection, description, comparison and Micro-CT scanning, phylogenetic analyses, geometric morphometrics analysis, and ancestral state reconstruction of fossil material from the lower Cambrian of Yunnan, China

Research sample

A total of 30 new specimens were sampled from five localities of the Chengjiang biota, i.e., the Chengjiang, Dapoutou, Jianshan, Sanjiezi, and Tanglipo (CJ, DPT, JS, SJZ, TLP).

Sampling strategy

All fossils of the same type encountered during the excavation were collected.

Data collection

All the studied specimens have been deposited in the Shaanxi Key Laboratory of Early Life and Environments (LELE), Northwest University, Xi'an.

Timing and spatial scale

Collection of the fossil specimens at the Yu'an-shan shale Member (or Yu'an-shan Formation) of the Helinpu Formation

Timing and spatial scale	(=Chiungchussu Formation), Eoredlichia-Wutingaspis assemblage zone, Cambrian Series 2, Stage 3.
Data exclusions	No data exclusions.
Reproducibility	All new fossil specimens will become available upon publication.
Randomization	No data randomization.
Blinding	No blinding as no biological experiments performed in this study.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Fossil specimens were manually from well-exposed outcrops of fossiliferous claystone.
Location	Specimens were collected from the five localities (Chengjiang, Dapoutou, Jianshan, Sanjiezi, and Tanglipo sections) of Eastern Yunnan, China.
Access & import/export	All the studied specimens have been deposited in the Shaanxi Key Laboratory of Early Life and Environments (LELE), Northwest University, Xi'an.
Disturbance	Disturbance to the quarry area was minimised through small-scale manual excavation. Reclamation of the quarry will proceed in accordance with procedures stipulated by the local government.

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
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☐	☒ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

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

Palaeontology and Archaeology

Specimen provenance	Specimens described here were collected from the five localities (Chengjiang, Dapoutou, Jianshan, Sanjiezi, and Tanglipo sections) of Eastern Yunnan, China.
Specimen deposition	All the studied specimens have been deposited in the Shaanxi Key Laboratory of Early Life and Environments (LELE), Northwest University, Xi'an.
Dating methods	No new dates are provided.
☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	State Key Laboratory of Continental evolution and Early Life, Shaanxi Key Laboratory of Early Life and Environments approved the study protocol.

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

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.