

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
<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 for data collection. |
| Data analysis | TNT version 1.6; MrBayes 3.2.7; Tracer 1.7.1; and the R packages Claddis version 0.6.3, akima 0.6-3.4, and phytools 2.1-1. The custom code used for the disparity analysis is deposited in Figshare: https://figshare.com/s/4fc207d07da2b8ff13cd |

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 generated or analysed during the study are included as part of this article, and its supplementary information files. The datasets for phylogenetic, disparity and morphometric analyses are deposited in the Figshare repository (<https://figshare.com/s/4fc207d07da2b8ff13cd>).

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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

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

Sample size	No statistical methods were used to determine sample size. Terminals of the phylogenetic data matrices were scored based on all available, unambiguously referred specimens. Sample size was limited to available published information on phylogenetic analyses or published data on measurements of tadpoles and adult anurans.
Data exclusions	No exclusions were performed because taxonomic and character samples of the phylogenetic analyses were intended to be as broad as possible.
Replication	Our investigation considers all the available specimen of the studied species and the phylogenetic analyses include 86 taxa and 152 characters. Terminals of the phylogenetic data matrices were scored based on the type specimens and all available, unambiguously referred specimens. The parsimony phylogenetic analysis was conducted until 100 optimal results were recovered under the tree search replications. In the morphological disparity analyses, the 95% confidence intervals were generated using the two tails of values recovered from 9,999 bootstrap technical replicates. All the replications were successful.
Randomization	Not applicable. The available fossil material was included and the random and incomplete nature of the vertebrate fossil record acts as a natural randomization process.
Blinding	The taxon-character matrices for the phylogenetic analyses were built on the basis of independent observation of each taxon. Blinding was not necessary, neither possible, because we have used all available specimens for the scoring of characters in each sampled species.

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 The specimen described (MPM-PV 23540) was collected from a quarry from the Middle Jurassic La Matilde Formation (Bathonian-Callovian; ca. 168–161 Mya) in southern Patagonia, Argentina. The fieldwork and curation was performed by authors of the manuscript following the national legislation.

Specimen deposition MPM-PV 23540 is cataloged and available for study to researchers upon request at Museo Provincial Padre M.J. Molina, Santa Cruz Province, Argentina.

Dating methods No new dating methods were performed. Dates used for the Bayesian inference analysis are provided in the supplementary information.

☒ 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 or guidance was required because the study is based on previously collected fossil specimens.

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

Plants

Seed stocks N/A

Novel plant genotypes N/A

Authentication N/A