

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	Bone microstructure data was collected using VGSTUDIO MAX v. 3.5 (RRID:SCR_017997) and ImageJ 1.52i (RRID:SCR_003070) with the BoneJ 1.4.3 plug-in. Landmark data for geometric morphometrics was collected using the software Amira 5.5.0 (Thermo Fisher Scientific, USA) and 3D Slicer v5.8.1. Phylogenetic data was compiled in Mesquite (v. 3.7);
Data analysis	Analysis were performed in the phylogenetic software T.N.T v. 1.1 and MrBayes developer's version (future MrBayes 3.2.8). Diagnostic values assessed with Tracer v. 1.7.1. Statistical analyses and graphic plots were conducted/produced in R v. 4.4.1 using customized scripts and packages reported in the Methods section. All the necessary code for phylogenetic analyses and R scripts are provided as supplementary data.

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](#)

CT scan data including reconstructed slices and surface volume files for all segmented elements of the holotype are available online as Supplementary Data S1 in MorphoSource at <https://doi.org/10.17602/M2/L868201> (Project ID: 000780586).

Phylogenetic data (morphological and molecular) generated and analysed, along with trees and log files, are available online as Supplementary Data S2. GenBank accession numbers for molecular data are provided in Supplementary Data S2. Input data and output files from geometric morphometric analyses and bone microstructure analyses are available as Supplementary Data S3 and S4, respectively. MorphoSource accession numbers for publicly available specimens used for geometric morphometrics are provided in Supplementary Data S3. All Supplementary Data files S2-S4 are openly available online at Simões Lab Dataverse at <https://doi.org/10.7910/DVN/C6WXM0>.

Life Science Identifiers for the new genera and species have been registered at Zoobank as: 'Tametara' (urn:lsid:zoobank.org:act:AC526A67-E75D-4972-8955-56BEF0DC9699) and 'Tametara mirim' (urn:lsid:zoobank.org:act:459A4E86-0203-4E7A-8328-42C08E9A5C1C).

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	Description of new snake fossil species, including anatomical data collection using micro-CT scanning, and comparative anatomy and phylogenetic analyses. Central nervous system endocasts were produced based on CT scans Phylogenetic analyses include 166 species of lepidosaurian reptiles based on morphological and molecular data, using multiple optimality criteria, including maximum parsimony, non-clock bayesian inference, and relaxed clock bayesian inference using total evidence dating. Geometric morphometric analyses on brain endocasts of 60 species of squamates were conducted, and subsequently used to produce a phylogenetically informed principal component analysis and linear discriminant analysis. Bone microstructure based on linear measurements of CT-scan cross-sections of 106 species of squamates were conducted, and subsequently used to produce a phylogenetically informed principal component analysis.
Research sample	Phylogenetic analyses include 166 species of lepidosaurian reptiles; Geometric morphometric analyses on brain endocasts used 60 species of squamates; Bone microstructure used 166 species of squamates.
Sampling strategy	Sampling strategy was used to maximize diversity, including at least one representative across all major groups of squamates.

Data collection	Data collection for all analyses were based on digital models produced from micro-CT scans available on MorphoSource or scanned by the authors. Sources for all digital models are available as Supplementary Data S2-S4.
Timing and spatial scale	Data collection was not performed in time series. Spatial scale is at global level of representation.
Data exclusions	No data was excluded a priori from analyses
Reproducibility	Sensitive measurements were conducted by specialists in squamate anatomy and measurements on fossils were conducted by at least two different authors.
Randomization	Randomization is not relevant because sampling strategy is to maximize diversity
Blinding	<i>Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.</i>

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
☒	☐ 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 was discovered by W.R.N. and G.M.X.P. in 2020, in William's Quarry 2 at Sítio Paleontológico 'José Martin Suárez' (Presidente Prudente municipality, State of São Paulo, Brazil); Adamantina Formation, Bauru Group, Bauru Basin.
Specimen deposition	Holotype (and single specimen) MPM 420 deposited at Museu de Paleontologia de Marília, Marília, State of São Paulo, Brazil.
Dating methods	Dates are relative based on biostratigraphic correlation (late Santonian to early Campanian age, ca. 85–75 million years ago). Calibration ages for all fossil species used in total evidence dating are available as Supplementary Information S2 and were obtained from the literature resources provided in the original publication of the dataset (ref. 6)
☒ 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 for guidance was required for fossil collection according to Brazilian legislation

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