

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	Software was not used in primary data collection. Data were collected through direct observation or taken from literature.
Data analysis	Phylogenetic data were scored in the freeware Mesquite (ver. 3.70). Phylogenetic analysis of morphological data was performed in the freeware TNT ver 1.6 (Goloboff & Morales. 2023. Cladistics DOI 10.1111/cla.12524), which is made freely available through the Willi Hennig Society (www.cladistics.org). Macroevolutionary analyses of body size and biogeography were undertaken using relevant published packages including ape (ver. 5.8-1), geoscale (ver. 2.0.1), paleotree (ver. 3.4.7), phytools (ver. 2.5-2), BioGeoBEARS (ver. 1.1.1), and STRAP (ver. 1.6-1) designed for the R computing environment. Analyses were performed in R (ver. 4.5.1.) through the RStudio (ver. 2024.12.1+563)) interface. Additional biogeographic analyses were carried out in the freeware RASP ver. 4.2 (Yu., Y, Blair, C. & He, X. Mol. Biol. Evol. 37, 604–606 (2020). All relevant code and scripts have been uploaded to Figshare and available at https://doi.org/10.6084/m9.figshare.30569894 . No proprietary software was developed for this study.

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](#)

Data including extended diagnosis, specimen measurements, and list of characters are available as supplementary information associated with this paper. The phylogenetic data matrix, which is a derivative of the TWiG family of data matrices, as well as, body mass data, and taxon ages are available as files in Figshare at <https://doi.org/10.6084/m9.figshare.30569894>

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)

Ecological, evolutionary & environmental sciences study design

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

Study description	The study presented anatomical description (including histology) and measurements of a new dinosaur specimen, including a revised diagnosis. New information on related species was also presented in the supplementary information and in the data files. The phylogenetic position of the new specimen was analyzed under the parsimony criterion, and its significance for evolution of arm length and body size as well as biogeography of alvarezsauroid theropods were analyzed quantitatively.
Research sample	The principal sample is a near-complete specimen of the alvarezsauroid dinosaur <i>Alnashetri cerropolisiensis</i> . Additionally, phylogenetic information taken from previous studies and supplemented with some new observations and characters formed the basis for phylogenetic analysis. The novel results of those analyses were used to inform the macroevolutionary and biogeographic studies.
Sampling strategy	Taxon sampling for the phylogenetic and subsequent analyses was comprehensive and focused on capturing as much of the ranges of body size and distributional information for alvarezsauroids as possible, while still being able to assess the phylogenetic relationships of those taxa. A few, extremely fragmentary taxa were excluded as they were phylogenetically unstable to such a degree that they could not reasonably be included in the analyses.
Data collection	Data collection was primarily through firsthand observation, measurement, and documentation (note-taking, photography) of specimens, supplemented with literature studies.
Timing and spatial scale	N/A
Data exclusions	A few very poorly preserved and incomplete species were omitted from the phylogenetic analysis, because we did not have the opportunity to study them firsthand, and they introduce so much missing data to analyses that not only their relationships are unrecoverable, but they also destabilize relationships among a swathe of other taxa.

Reproducibility	All analyses were repeated to ensure they are correct.
Randomization	We used randomizations in the tree calibration step of our macroevolutionary and biogeographic analyses to assess the effects of uncertainty on outcomes. Randomization procedures (i.e. bootstrapping) were employed to evaluate robustness of phylogenetic results.
Blinding	N/A
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Paleontological fieldwork in eolian and fluvial deposits of the mid-Cretaceous Candeleros Formation, Neuquén Group, Patagonia Argentina. Fossils are recovered from dune, interdune, and more mesic facies representing the edge of a dune dominated ancient desert.
Location	La Buitrera Paleontological Area, Río Negro Province, Argentina. GPS coordinates for site are on file, and a map of the area with fossil localities is provided in Extended Data Fig. 1.
Access & import/export	All fieldwork was performed with proper provincial permits. All fossils are the patrimony of Argentina, and remained within its borders during this research, and beyond. The focal specimens are housed in a museum in Río Negro province as required by federal and provincial laws.
Disturbance	N/A

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	All fieldwork was performed with proper provincial permits issued by Agencia Cultura de Río Negro to study coauthor Sebastian Apesteguía, and with the consent of local landowners. All fossils are the patrimony of Argentina, and remained in that country during this research. They are housed in a museum in Río Negro province as required by law.
Specimen deposition	The new fossil described here is the patrimony of Argentina, and remained in that country during this research. It, along with the holotype, are housed in the Museo Provincial Carlos Ameghino in Cipolletti, Río Negro province as required by law. All other specimens that feature in this work are housed in accredited institutions around the globe.
Dating methods	Dates are taken from literature. No new chronostratigraphic ages are presented herein.
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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.