

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

The new titanosaurian sauropod dinosaur taxon described in this study is represented by a single partial skeleton, MUVF 200. A sauropod ulna (MUVF 201) was recovered ~20 m from MUVF 200 and is described in the online supplement.

2. Data exclusions

Describe any data exclusions.

No relevant data were excluded from the analysis.

3. Replication

Describe whether the experimental findings were reliably reproduced.

No experiments (in the strict sense of the word) were performed; hence, this field does not apply to our study.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

There were no experimental groups; hence, this field does not apply.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

There was no group allocation; hence, this field does not apply.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- ☒ ☐ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ A statement indicating how many times each experiment was replicated
- ☒ ☐ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☒ ☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☒ ☐ The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
- ☒ ☐ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

The phylogenetic and palaeobiogeographic methods used in our study are extensively described in the Methods section of our main text and in our online supplement. Parsimony analyses were conducted using PAUP v4.0a157. Tip-dating Bayesian phylogenetic analyses were conducted using BEAST v2.4.4. The R package BEASTmasterR was used to construct all XML files. The BEASTlabs, BDSKY, SA, phylodynamics, and CA packages were installed into BEAUTi v2.4.4 so that the tip-dating analyses would operate properly. Convergence, effective sample size (greater than 200) of pertinent parameters, and model likelihood scores were calculated in Tracer v1.6. The R package BioGeoBEARS was used to conduct palaeobiogeographic analyses on the variable rates tip-dated Bayesian topologies.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

No unique materials were used.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used.

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

No laboratory animals were used.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

The study did not involve human research participants.