

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	No software was used.
Data analysis	Tomographic data were segmented in Mimics v.20 (http://biomedical.materialise.com/mimics ; Materialise, Leuven, Belgium). Surface meshes were then exported into and imaged in Blender v2.79 (http://blender.org ; Stitching Blender Foundation, Amsterdam, the Netherlands). Phylogenetic analyses were performed in TNT v1.5 and MrBayes v.3.2.6. Trait analyses were performed in R using the package phytools (Revell, L. J. phytools: an R package for phylogenetic comparative biology (and other things). <i>Methods in Ecology and Evolution</i> 3, 217-223 (2012).)

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](#)

The specimen described in this study is deposited in the collections of the Harvard Museum of Comparative Zoology. The CT raw projection series, reconstructed .TIFF stack, and .OBJ file of all segmented 3D objects are available on Morphosource.org (https://www.morphosource.org/concern/biological_specimens/000417029). The Mimics file can be downloaded upon request from the Department of Vertebrate Paleontology at the Museum of

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 a fossil specimen, with a phylogenetic analysis, fossil birth-death analysis and body size.
Research sample	MCZ VPF 5114, a nearly complete fish preserved in part and counterpart, missing snout, anterior portion of lower jaw, and caudal fin, from the mid-Famennian Chadakoin Formation, Warren, Pennsylvania, USA. Phylogenetic analysis dataset modified from Latimer & Giles (2018) and Figueroa et al. (2021) with the addition of ten taxa, giving a total of 121 taxa and 292 characters. Body size dataset compiled from specimen analysis and the published literature.
Sampling strategy	n/a
Data collection	n/a
Timing and spatial scale	n/a
Data exclusions	n/a
Reproducibility	n/a
Randomization	n/a
Blinding	n/a
Did the study involve field work?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> 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	Involves in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input type="checkbox"/>	<input checked="" type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involves in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Palaeontology and Archaeology

Specimen provenance	MCZ VPF 5114 is from the "Chemung" of Warren, Pennsylvania, USA. This corresponds to the Chadakoin Formation, which lies within the <i>Palmatolepis marginifera</i> Conodont Zone (Kirchgasser), Goniatite Zone II-G, and Fa2c subdivision of Spore Zone GF, indicating a mid-Famennian age, providing a constraint of 367.9-367.2 Ma. The specimen was collected in the early 1900s.
Specimen deposition	The specimen described in this study is deposited in the collections of the Harvard Museum of Comparative Zoology.

Dating methods

n/a

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight

Ethical approval was not needed as the studied specimen is from US deposits and deposited in a US museum.

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