

Reporting Summary

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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 to collect data, except for the linear dimensions of the skull of <i>Mellisuga minima</i> : Lars Schmitz took measurements of a scaled digital model in Meshlab 2016.12.
Data analysis	All data were analysed in R 3.5.0 using routine phylogenetic comparative methods. Custom scripts are available in the Supplementary Information. Figures were made using Adobe CS 2018. Phylogenetic analysis was run using TNT 1.0. CT data was processed using ImageJ 1.4 and VG StudioMax 1.2, 2.1 and 2.4.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data are available in the Supplementary Information.

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	We describe the anatomy of a new fossil enclosed in Burmese amber, facilitated through synchrotron microtomography. We also performed large-scale phylogenetic comparative analysis of the scaling of eye socket size with respect to skull length, and visualization of eye shape through scleral ring and eye socket anatomy. Both approaches facilitate the comparison of the fossil with modern birds and lizards.
Research sample	The fossil we are describing in this paper is curated in the Hupoge Amber Museum, identified through the unique collection number HPG-15-3. To facilitate comparative analyses, data on eye socket and skull length were collected for a total of 206 extant species of birds. These samples were chosen to reflect all major clades of living birds, providing an overview of the overall pattern found across birds. Data on eye shape (orbit length, external and internal scleral ring diameter) and diel activity patterns of lizards and birds are from a previous study (Schmitz and Motani, 2011, Science).
Sampling strategy	Samples were chosen to reflect all major clades of living birds. Whenever possible, multiple individuals per species were measured; all analyses were performed with the average values of species. Regression analyses of smaller sample sizes (n=50, randomly chosen from the 206 species) revealed very similar results, hence the sample size used for the final analysis is deemed adequate.
Data collection	Li Gang and and Yi Qiru conducted the CT scans and reconstruction - HPG-15-3 was imaged nondestructively using propagation phase contrast Synchrotron Radiation X-ray microtomography (PPC-SRX-μCT) on beamline 13W of the Shanghai Synchrotron Radiation Facility (SSRF). The SR beam was monochromatized at 22 keV using the double Si (111) crystal monochromator. The distance between sample and detector (propagation distance) was 60 mm to obtain the phase contrast. The physical pixel size of CCD sensor was 6.5μm×6.5μm and we used a 2× microscope objective; the isotropic voxel size was 3.25 μm. The pixel number of our detector was 2048 × 2048 and its dynamic range was 16 bit. The field of the view of our detector was 6.6 mm × 6.6 mm. 6 μCT scans under the same conditions were performed to image the whole specimen due to the fact its size in the vertical direction is much larger than the FOV of our detector. The off-axis scanning 360° mode was adopted to 3 scans because the sample's size in horizontal direction was larger than detector's FOV. In this mode 6000 projections were collected for a single CT scan. The exposure time of single projection was 0.3 s. In the off-axis scanning data preprocessing, the image stitching was the first step that always required to consider the image alignment, the contrast unification, and the tilt of the rotation axis. We obtained 3000 stitched images with enlarged horizontal FOV, about 6.6 mm × 13 mm, for 3000 project angle. The phase retrieval and slice reconstruction of all the six projection data sets were performed using PITRE-3 software [S12]. After all the reconstruction, the six segments CT slice sets were stitched again in the vertical direction. The CT slices for the entire sample consisted of 36 GB data. To reduce the amount of memory used, the sampling interval was set as one pixel in all 3 directions so that the data were reduced to one-eighth of its original size. The amber and all impurities surrounding the skull were removed using the image segmentation function. The rotation correction was performed using ImageJ software. The 3-D data processing, segmentation, and analysis was performed using VG StudioMax 1.2 and 2.1. The 3d morphology of the endocast was obtained through manual segmentation using ImageJ 1.4 and rendered using VG studio Max 2.4. Jingmai O'Connor performed the phylogenetic analysis using TNT. HPG-15-3 was scored into an modified version of the matrix published by Atterholt et al. 2018 which in turn is a modified version of the 2013 matrix published by O'Connor and Zhou. In order to elucidate the phylogenetic position of HPG-15-3 we added five new cranial characters - O'Connor scored these characters from published data. The modified matrix consists of 36 birds scored across 257 morphological characters with Dromaeosauridae as the outgroup, which was analyzed using TNT (Goloboff et al 2008). First, a heuristic search was conducted using tree-bisection reconnection (TBR) retaining the single shortest tree from every 1,000 replications. This produced 46 trees with a length of 728 steps; an additional round of TBR produced 2,044 trees of the same length, producing a large polytomy in the Nelson Strict Consensus tree. Early avian evolution is extremely homoplastic thus we utilized implied weighting. We explored k values from one to 20 and 25 and found that the position of Oculudentavis stabilized at k values higher than one and that enantiornithine interrelationships stabilized at k values higher than 11 (enantiornithine relationships are also stable from k equals 2 to 11 and differ from higher k values only in the relative placement of a few deeply nested taxa). In the presented analysis we conducted a heuristic search using TBR, retaining the single shortest tree from every 1,000 replications with a k value of 16. This produced three most parsimonious trees with a score of 21.3. These trees differed only in the relative placement of the most derived enantiornithines, which form a small polytomy in the strict consensus tree (Consistency Index = 0.47; Retention Index = 0.645). Lars Schmitz collected data of the skull length and eye socket length of birds with digital calipers, in the collections of the Los Angeles County Museum of Natural History (LACM), California State University Long Beach (CSULB, now integrated with the LACM collections), and the Smithsonian National Museum of Natural History (USNM). Collection numbers of all specimens are provided in the data table. A cranium of <i>Mellisuga minima</i> (UF 19832) was CT scanned by Edward Stanley at the Nanoscale Research Facility at the University of Florida, Gainesville, and uploaded to Morphosource (identifier: S21840). CT acquisition data are provided at Morphosource (https://www.morphosource.org/Detail/MediaDetail/Show/media_id/39924).

Timing and spatial scale	N/A
Data exclusions	No data were excluded.
Reproducibility	During the design phase of the study, linear dimensions were taken repeatedly for the same individual skeleton to ensure consistency. All repeated measurements were successful.
Randomization	Grouping of birds and lizards by diel activity pattern was taken from a previously published study.
Blinding	Blinding was not possible and also not relevant for this study. All bird specimens in museum collections are properly labeled hence it is impossible to not know what bird taxon is measured. Given that the main goal was to characterize the overall scaling of eye socket size, irrespective of taxon or ecological group, blinding was not deemed necessary.
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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Palaeontology

Specimen provenance	Angbamo locality, Hukawng Valley, Kachin Province, Myanmar; the source and preservation of HPG-15-3 are in full compliance with the laws of Myanmar and China, including Myanmar's import and export regulations of jewelry and China's laws and regulations on museum. All extant bird specimens that were included in this study are curated in the collections of the LACM (including the CSULB specimens), USNM, and the University of Florida.
Specimen deposition	HPG-15-3 is housed and displayed in the Hupoge Amber Museum (HPG), Tengchong City Amber Association, China.
Dating methods	No new dates are provided.
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	