

Supplementary material 5: Details concerning the Methodology of the geometric morphometric analysis.

In this analysis we used seven anatomical landmarks and 77 sliding landmarks in order to quantify the shape of the dentary (see Fig. 1). The landmarks and sliding landmarks were placed using the software TPSDig2 v. 2.18 [1] by a single user (C. B.) on all the specimens. Accuracy and reliability of this methodology was tested using ten pictures of 3 specimens (*A. gingivinus*: USNM 236357; USNM 236358 and USNM 236362) analyzed as mentioned below in order to check if the variability between pictures of the same specimen was lower than variability between specimens.

In order to analyze the sliding landmarks we used the software TPSrelw [2] to allow the sliding landmarks to slide from their position on the outline of the shape of the consensus specimens while minimizing the Procrustes distance [3]. The data were then analyzed in R v.3.1.2 (<https://cran.r-project.org>) using the Rmorph package [4]. After performing a Generalized Procrustes Analysis (GPA) [5,6], we performed a PCA analysis to reduce the dimensionality of the data set and retained the first seven PC axes representing a total of 91% of the recorded variability for further analyses. The allometric component of the shape data was tested using linear regression analysis of the PC axes against centroid size using the package stats v. 3.1.2 in R. Allometric differences between modern and fossil groups were tested using Procrustes ANOVA with permutation procedures with the function “procD.allometry” of the Geomorph R library [7]. These differences were visualized using the same function by plotting predicted values of dentary shape from species-specific regressions versus centroid size [8]. Allometry free shape data were obtained from the residuals of the species-specific regressions also provided by the function “procD.allometry” of the geomorph R library [7]. The Linear Discriminant Analyses (LDA) were performed using the R package Mass v.7.3 [9]. This analysis is commonly used to optimize discrimination between groups, minimizing intra-group variability and maximizing variability between groups [6,10]. Neighbor-joining trees were constructed using the Mahalanobis distances obtained from the LDA using the R libraries Rmorph [4] (function “d2mahal”) and Ape [11]. The use of Mahalanobis distances instead of Euclidian distances provides a greater weight to variables that explain the difference between groups and minimizes the weight of data representing noise in this regard. The impact of phylogeny on the shape of the dentaries of modern anoles was tested using a Kmult test [12] for multivariate data on the PC axis using the R package geomorph [7]. Phylogenetic data used in this analysis follow the work of Pyron et al. [13].

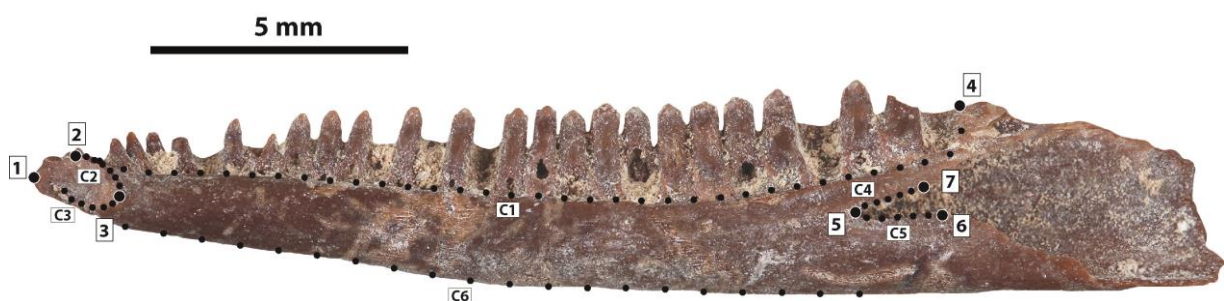


Figure 1: Landmarks (black point circled in white) and sliding landmarks (black points) used in the analysis. Each landmark is indicated by a number and the number of each series of curve of sliding landmarks is preceded by a “C”. Additional details concerning the position of each landmark can be found in appendix 2.

Description of landmarks and sliding semi-landmarks used:

Anatomical landmarks:

Landmark 1: Most anterior point of the mandibular symphysis.

Landmark 2: Most dorsal point of the mandibular symphysis.

Landmark 3: Most posterior point of the mandibular symphysis.

Landmark 4: Posterior extremity of the last dental position on the dorsal edge of the dental crest.

Landmark 5: Most anterior point of Meckel's foramen.

Landmark 6: Posteroventral extremity of Meckel's foramen.

Landmark 7: Posterodorsal extremity of Meckel's foramen.

Sliding landmarks:

Curve 1: 35 sliding landmarks from landmark 2 to 4 on the edge of the dental furrow.

Curve 2: 6 sliding landmarks from landmark 2 to 3 on the dorsal edge of the mandibular symphysis.

Curve 3: 6 sliding landmarks from landmark 3 to the ventral projection of landmark 2 on the ventral edge of the mandibular symphysis.

Curve 4: 5 sliding landmarks from landmark 5 to 7 on the dorsal edge of Meckel's foramen.

Curve 5: 5 sliding landmarks from landmark 5 to 6 on the ventral edge of Meckel's foramen.

Curve 6: 20 sliding landmarks on the ventral flange of the dentary, from the ventral projection of landmark 5 to landmark 3.

References

1. Rohlf FJ. 2016 *tpsDig2, digitize landmarks and outlines*. United States of America: Department of Ecology and Evolution, State University of New York.
2. Rohlf FJ. 2010 *TPS Relative warps*. United States of America: Department of Ecology and Evolution, State University of New York.
3. Gunz P, Mitteroecker P. 2013 Semilandmarks: a method for quantifying curves and surfaces. *Hystrix Ital. J. Mammal.* **24**, 103–109.
4. Baylac M. 2012 *Rmorph: A 'R' Geometric Multivariate Morphometrics Library*. France: Muséum national d'Histoire naturelle.
5. Rohlf FJ, Slice D. 1990 Extensions of the Procrustes method for the optimal superimposition of landmarks. *Syst. Zool.* **39**, 40–59. (doi:10.2307/2992207)

6. Baylac M, Frieß M. 2005 Fourier Descriptors, Procrustes Superimposition, and Data Dimensionality: An Example of Cranial Shape Analysis in Modern Human Populations. In *Modern Morphometrics in Physical Anthropology* (ed DE Slice), pp. 145–165. Springer US. (doi:10.1007/0-387-27614-9_6)
7. Adams D, Collyer M, Sherratt E. 2016 *geomorph: Geometric Morphometric Analyses of 2D/3D Landmark Data*. See <https://cran.r-project.org/web/packages/geomorph/index.html>.
8. Adams DC, Nistri A. 2010 Ontogenetic convergence and evolution of foot morphology in European cave salamanders (Family: Plethodontidae). *BMC Evol. Biol.* **10**, 216. (doi:10.1186/1471-2148-10-216)
9. Ripley B, Venables B, Bates DM, Hornick K, Gebhardt A, Firth D. 2016 *MASS: Support Functions and Datasets for Venables and Ripley's MASS*. See <https://cran.r-project.org/web/packages/MASS/index.html>.
10. Evin A, Cucchi T, Cardini A, Strand Vidarsdottir U, Larson G, Dobney K. 2013 The long and winding road: identifying pig domestication through molar size and shape. *J. Archaeol. Sci.* **40**, 735–743. (doi:10.1016/j.jas.2012.08.005)
11. Paradis E et al. 2015 *ape: Analyses of Phylogenetics and Evolution*. See <https://cran.r-project.org/web/packages/ape/index.html>.
12. Adams DC. 2014 A generalized K statistic for estimating phylogenetic signal from shape and other high-dimensional multivariate data. *Syst. Biol.* **63**, 685–697. (doi:10.1093/sysbio/syu030)
13. Pyron RA, Burbrink FT, Wiens JJ. 2013 A phylogeny and revised classification of Squamata, including 4161 species of lizards and snakes. *BMC Evol. Biol.* **13**, 1–53.