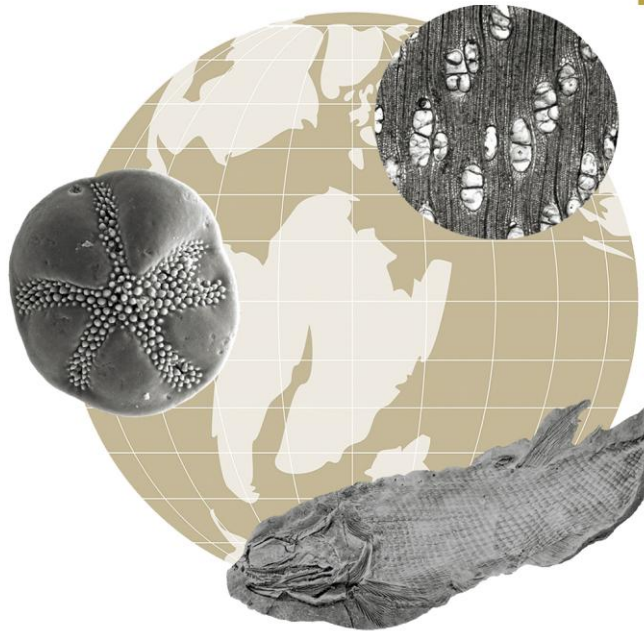




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Digital reconstruction of the mandible of *Sahitisuchus fluminensis*: a case study of imaging and modelling vertebrate fossils

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26 pages; 4 figures; 0 tables

Header: Ruiz et al.: Digital reconstruction of a sebecid

Short description: Digital reconstruction of the *Sahitisuchus fluminensis* mandible expands anatomical knowledge, improves phylogenetic character scoring, and promotes open access to rare fossils.

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27

28 **ABSTRACT**

29 Virtual palaeontology (e.g., studying fossils based on three-dimensional digital models)
30 has become an essential component of contemporary research, facilitating broader access
31 to rare specimens and fostering an array of approaches that use modelled materials as
32 primary sources of information. Among notosuchian crocodyliforms, *Sebecoidea* is a
33 clade with an often poorly preserved mandibular anatomy, limiting detailed
34 morphological and phylogenetic investigations through traditional methods. Here we
35 present a digital reconstruction of the mandible of *Sahitisuchus fluminensis*, a *Sebecoidea*
36 from the Itaboraí Basin (Eocene), Brazil. The holotypic mandible (MCT.R.1730) is
37 preserved attached to the cranium but is fractured and has some segments displaced from
38 their original position, hampering detailed assessment of relevant anatomical features.
39 Using digital segmentation and three-dimensional modelling based on computed
40 tomography data (CT), we repaired the mandibular elements and restored their original
41 morphology. We also conducted a comparative phylogenetic analysis to evaluate the
42 impact of the model on character scoring. The repaired mandible improves the
43 identification of phylogenetically relevant morphological characters, facilitating
44 comparisons with other taxa and enabling morphological and evolutionary analyses based
45 on quantitative techniques. Given the scarcity of well-preserved mandibular material of
46 *Sebecoidea*, this reconstruction provides an important anatomical framework for future
47 studies. Furthermore, the availability of the digital model enhances access to this unique
48 specimen and highlights the importance of digitising fossil collections to promote
49 research, education, and long-term preservation of palaeontological heritage.

50 **KEYWORDS:** *Notosuchia*, *Sebecidae*, CT scan, Digital reconstruction, Digitisation

51

Reconstrucción digital de la mandíbula de *Sahitisuchus fluminensis*: un caso de estudio sobre la obtención de imágenes y el modelado de fósiles de vertebrados

RESUMEN

La paleontología virtual (p. ej., el estudio de fósiles mediante modelos digitales tridimensionales) se ha convertido en un componente esencial de la investigación contemporánea, al facilitar un acceso más amplio a especímenes raros y promover diversas aproximaciones que utilizan modelos digitales como principales fuentes de información. Entre los cocodriliformes notosuquios, *Sebecoidea* constituye un clado cuya anatomía mandibular suele estar pobremente preservada, lo que limita los estudios morfológicos y filogenéticos detallados mediante métodos tradicionales. En este trabajo presentamos una reconstrucción digital de la mandíbula de *Sahitisuchus fluminensis*, un *Sebecoidea* de la Cuenca de Itaboraí (Eoceno), Brasil. La mandíbula del holotipo (MCT.R.1730) se conserva articulada al cráneo, pero presenta fracturas y varios segmentos desplazados de su posición original, lo que dificulta la evaluación detallada de caracteres anatómicos relevantes. Mediante segmentación digital y modelado tridimensional basados en datos de tomografía computarizada, reconstruimos los elementos mandibulares y restauramos su morfología original. Además, realizamos un análisis filogenético comparativo para evaluar el impacto del modelo en la codificación de caracteres. La mandíbula reconstruida mejora la identificación de caracteres morfológicos de importancia filogenética, facilita las comparaciones con otros taxones y permite realizar análisis morfológicos y evolutivos basados en técnicas cuantitativas. Dada la escasez de material mandibular bien preservado en *Sebecoidea*, esta reconstrucción proporciona un importante marco anatómico para futuros estudios. Asimismo, la disponibilidad del modelo digital amplía el acceso a este espécimen único

77 y destaca la importancia de la digitalización para promover la investigación, la educación
78 y la preservación a largo plazo del patrimonio paleontológico.

79 **PALABRAS CLAVE:** *Notosuchia*, *Sebecidae*, Tomografía computarizada,
80 Reconstrucción digital, Digitalización

81

INTRODUCTION

Modern imaging is essential for contemporary palaeontology, allowing new avenues of investigation that otherwise would be impaired or prevented (see Cunningham et al., 2014). Virtual palaeontology, including the study of fossils through three-dimensional digital models (*sensu* Sutton et al., 2014), is widely used in morphofunctional and evolutionary studies (e.g., phylogenetics, geometric morphometrics, finite element analyses, and hydrodynamic flow modelling; Rayfield, 2007; Sutton et al., 2016; Dal Sasso et al., 2017; Martin et al., 2022; Hedrick, 2023). These 3D models can be generated by different means, including photogrammetry and surface scanning, X-ray computed tomography (CT scan), and synchrotron imaging, that is applied across a range from whole-body imaging to cellular-level structures (Pérez-Ramos & Figueirido, 2020). These techniques enable the visualisation and subsequent modelling of fossil material in the digital environment, including the reconstruction of specimens that are broken, deformed, and/or incomplete (Lautenschlager, 2016; Pérez-Ramos & Figueirido, 2020; Ruiz et al., 2024).

Another important reason for digitalising fossil material is to promote communication of primary anatomical information through access to the models, which ultimately improve scrutiny and reproducibility, elevating the scientific standards of anatomy-based studies. Online platforms hosting digitised fossils grant access to researchers and the general public worldwide, reducing inequality and promoting more democratic access to palaeontological data (Uhen et al., 2013; Cunningham et al., 2014). This is particularly relevant for specimens that have been exported from their countries of origin (e.g., in colonial scientific campaigns) or that are housed in institutions with limited accessibility (e.g., smaller collections far from larger centres); such gaps in accessibility can generate sampling biases that may ultimately affect our understanding

of the evolution of entire clades (Marshall et al., 2018; Cisneros et al., 2022; Raja et al., 2022; Dean & Thompson, 2025). These advances are particularly relevant for diverse fossil clades such as *Notosuchia*, in which imaging-based approaches are increasingly contributing to anatomical and evolutionary studies.

Notosuchia (sensu Ruiz et al., 2021, Leardi et al., 2024) is a diverse clade of crocodyliforms that has been pivotal to the understanding of phylogeny and morphofunction of extinct and extant members of this clade (Bronzati et al., 2015; Stubbs et al., 2013, 2021; Montefeltro et al., 2020; Srinivas et al., 2025; Paiva et al., 2026). With a fossil record arguably encompassing nearly 150 million years, *Notosuchia* is characterised by a wide range of morphological and ecological specializations (Godoy, 2020; Pochat-Cottiloux, 2025; Ruiz et al., 2025), but studies of this clade based on imaging are only now becoming common. Examples of digital studies of notosuchians include extensive use of CT images but also scanning electron microscopy and micrograph images (e.g., Kley et al., 2010; Augusta & Zaher, 2019; Dias et al. 2019; Montefeltro et al., 2020; Darlim et al., 2021; Nieto et al., 2021; Santos et al., 2022; Sena et al., 2023, 2025; Iori et al. 2024; Aureliano et al., 2025; Fachini et al., 2025; Muscioni et al., 2025; Srinivas et al., 2025).

Studies based on 3D imaging are essential for advancing our understanding of notosuchian diversity and morphofunction, especially considering the increasing availability of quantitative analytical methods in modern palaeontology. In this context, we digitally reconstructed the mandible of the sebecid (*Sebecidae* sensu Leardi et al., 2024) *Sahitisuchus fluminensis* from the Itaboraí Basin (Early Eocene of Brazil; Kellner et al., 2014; Bergqvist et al., 2024), generating a three-dimensional digital model intended to facilitate broader access to this unique taxon and to support future morphofunctional and comparative analyses within *Notosuchia*. To test its usability in an evolutionary

perspective, we also conducted phylogenetic analyses using an updated dataset based on the new information made available by the digital model.

Institutional abbreviations: **HUPE:** Hospital Universitário Pedro Ernesto, Universidade Estadual do Rio de Janeiro (UERJ), Rio de Janeiro, Brazil; **IGM:** Museo Geológico Nacional "José Royo y Gómez", Servicio Geológico Colombiano, Bogotá, Colombia; **IPUW:** Institute für Paläontologie der Universität Wien, Vienna, Austria; **MCT.R:** Museu de Ciências da Terra, subcoleção Répteis, Rio de Janeiro, Brazil; **MN:** Museu Nacional, Rio de Janeiro, Brazil; **PVL:** Instituto Miguel Lillo, Universidad Nacional de Tucuman, San Miguel de Tucuman, Argentina; **TMM:** Texas Memorial Museum, The University of Texas at Austin, U.S.A.; **UCMP:** University of California Museum of Paleontology, Berkeley, U.S.A.

MATERIAL AND METHODS

Specimen and segmentation: The reconstruction was based on the CT scan of the *Sahitisuchus fluminensis* holotype, MCT.R.1730, a roughly complete skull with associated vertebral elements (**Fig. 1**; Kellner et al., 2014). The mandible is, in general, well preserved but fragmented in places, with some portions displaced from their original positions (**Fig. 1**). The left hemimandible is almost fully preserved, whereas the right hemimandible lacks the posterior portion, including the articular and retroarticular process. Both lateral and medial surfaces are well preserved. The anterodorsal portion of the symphysis, from the first to the third dentary teeth, is missing in both hemimandibles; posterior to the toothrow, the dorsal surface of both hemimandibles is difficult to observe on direct examination of the specimen due to the contact with the cranium. Most of the erupted crowns are broken or missing, but the alveoli positions and crown sizes can be assessed from the CT slices.

The scan was performed using a medical CT scanner at the radiology department of HUPE. The following parameters were employed: an electric voltage of 120kV (selected to optimize bone penetration while minimizing radiation exposure); a 38 cm field of view (FOV) to encompass the entire specimen; a matrix size of 512x512 pixels for high-resolution imaging; 735 slices acquired with a 0.65mm slice thickness and a 0.325mm slice interval, with a 50% slice overlap to improve 3D reconstruction.

The segmentation was performed in three steps by using two tools, the software Amira 3D 2022.2 and the free online platform Biomedisa (Lösel et al., 2020). The first step was the segmentation of the mandible in selected, non-continuous slices in Amira 3D, which were then exported as labels (.AM) and imported in Biomedisa for the second step (following the protocol of Lösel et al., 2020). A new surface (.PLY) of the complete mandible was then automatically generated and imported to Amira 3D to be edited in step 3. This last step included the reconstruction of tooth crowns. The segmentation process, thus, ensured the full modelling of the lower jaw and its dentition (**Fig. 1**).

Digital reconstruction: The mandible was digitally reconstructed in Blender 4.5.2 (available at <https://www.blender.org>), with the almost complete left hemimandible serving as the base of the process. The reconstruction aimed to correct taphonomic deformation, restore missing anatomical structures, and generate a realistic three-dimensional model suitable for subsequent analyses. Initially, fragmented and displaced regions of the posterior portion of the mandible were separated into discrete objects and retrodeformed to approximate their inferred original positions based on the better-preserved morphology of the right hemimandible and the reference material, namely, photos of the mandible of the closely related *Bretesuchus bonapartei* (PVL 4735).

The right caniniform, the only one preserved, was used as the basis for the reconstruction of this tooth; its preserved portions guided the size, cross-sectional shape

and curvature of the modelled crown. The caniniforms of *Sebecus ayrampu* (holotype; missing only the apical tip; Bravo et al. 2021) and *Eremosuchus* (UOK 347; juvenile; Nicholl et al. 2025) were consulted for general sebecoid crown morphology but not used as direct templates, since the caniniform of *Sahitisuchus fluminensis* is proportionally more robust than those of other sebecids. Extant crocodylian caniniforms served as a general visual reference for crown proportions. The entire region was then isolated, mirrored, and fused in place of the corresponding damaged area on the left side. The mandibular symphysis was subsequently reconstructed by digitally sculpting the mandible of *Dentaneosuchus crassiprорatus* (Martin et al., 2022) as the main comparative reference. Three front teeth were also added to the model based on the morphology and spacing of the preserved alveoli of the comparative material. The lingual surface of the mandible was conservatively reconstructed. Due to its preservation in close contact with the cranium, this region is largely obscured and difficult to segment accurately from the surrounding matrix and associated elements. Consequently, reconstruction of the lingual surface was restricted to minimal modifications, necessary to produce a continuous geometry while avoiding speculative anatomical interpretations.

Following the reconstruction, fractures, discontinuities generated during fragment repositioning, and segmentation artefacts were filled and smoothed. The mandible was then oriented in orthographic view, and the left hemimandible trimmed along the sagittal plane so that, when duplicated and mirrored, the resulting angle between both hemimandibles closely matched that observed in the reference specimen of *Bretesuchus bonapartei*.

The final model (**Fig. 2**) was assessed for mesh errors (bad geometries) using the Blender add-on “3D Print Toolbox”. Non-manifold geometries were corrected automatically where possible, whereas intersecting faces were removed manually. The

completed model was exported in .PLY format and processed in Instant Meshes (Jakob et al., 2015), where it was retopologised and remeshed into an isotropic triangular mesh. The final reconstructed mandible was then exported in .STL format for downstream analyses and visualisation.

Phylogenetic analyses: To test the potential of the reconstructed model for the understanding of evolutionary relationships, phylogenetic analyses were conducted based on the dataset of Nicholl et al. (2025), which contains the largest sampling of *Sebecoidea* taxa (sensu Bravo et al., 2025), including *Sahitisuchus fluminensis*. This dataset includes 80 discrete characters related to the mandible and dentition: of those, eight were rescored for *Sahitisuchus fluminensis* by analysing the reconstructed digital model alone, without reference to the CT-images (81, 88, 166, 168, 183, 196, 413, and 450; see **Supplementary Online Information**). Overall, these characters are directly related to the mandible shape, attributes readily observable in the reconstructed model (e.g., dentary and surangular dorsal shape, teeth relative size and width, external surface of the symphysis etc.) Other characters in the matrix, including continuous characters, were retained unchanged from Nicholl et al. (2025).

Two maximum parsimony analyses under equal character weighting were conducted in TNT v.1.5 (Goloboff et al., 2008; Goloboff & Catalano, 2016), one with the original dataset and a second with the updated dataset (hereafter “**original analysis**” and “**updated analysis**”, respectively). These analyses followed the search strategy “Analysis 1” of Nicholl et al. (2025), including the same character ordering scheme and treatment of continuous characters. *Gracilisuchus stipanicorum* was set as the outgroup, and the operational taxonomic units (OTUs) *Coringasuchus anisodontis*, *Pabwehshi pakistanensis*, *Pehuenchesuchus enderi*, *Sebecus huilensis* (= *Langstonia huilensis*;

Paolillo & Linares, 2007), *Neuquensuchus universitas*, the “Lumbrera form”, and the “Fayum form” were excluded from all analyses, following Nicholl et al. (2025).

The phylogenetic search was performed using “New Technology Search”, enabling all four algorithms: sectorial searches (10 drifting cycles), drift (10 cycles), ratchet (10 iterations), and tree fusing (10 rounds). The minimum tree length was recovered 100 times. All other parameters were not changed from default. The trees obtained from this procedure were subsequently used as starting trees for an extra round of analysis with “Traditional Search” conducted using Tree Bisection–Reconnection (TBR) with “trees from RAM”. To identify potentially unstable taxa that could generate polytomies or prevent a better resolution of the topology, we applied the IterPCR protocol (Pol & Escapa, 2009) to the MPTs of the updated analysis. As *Eremosuchus elkoholicus* was identified as unstable, a third analysis based on the “updated dataset” but excluding this taxon was conducted to evaluate whether its removal resolves the polytomy recovered in the strict consensus (see **Results** and **Supplementary Online Information**).

RESULTS

Phylogenetic analysis: The original analysis produced 12 most parsimonious trees (MPTs) with a total tree length of 184690.5, matching the same results of Nicholl et al. (2025). The updated analysis produced 34 MPTs with a total tree length of 184790.5 (**Supplementary Online Information, Figs. S1-2**). As summarised by the strict consensus, the topology recovered in the updated analysis differs slightly from that of the original analysis, with *Lorosuchus nodosus* as sister to *Sebecidae* in both trees (**Fig. 3**). The main difference is within *Sebecidae*, including the position of *Sahitisuchus fluminensis*. In the topology obtained from the original analysis, it forms a polytomy with *Sebecus querejazus* (= *Zulmasuchus querejazus*; Paolillo & Linares, 2007) and a clade

comprising all other sebecids, whereas a broader polytomy was found in the updated topology, including four additional taxa (*Ayllusuchus fernandezi*, *Eremosuchus elkoholicus*, *Bretesuchus bonapartei*, and *Sebecus icaeorhinus*). IterPCR identified *Eremosuchus elkoholicus* as the only unstable taxon, as it attaches to different positions within *Sebecoidea* in different MPTs. Its exclusion resolved the polytomy, yielding a reduced consensus with a topology identical to that of the original analysis (**Supplementary Online Information, Fig. S3**), except for the absence of *Eremosuchus*.

The updated analysis recovered two new autapomorphies for *Sahitisuchus fluminensis* in addition to the 19 autapomorphies of the original analysis (see **Supplementary Online Information**). These include the absence of a mandibular fenestra (char. 82, state 1) and a posteroventral orientation of the basioccipital and ventral occipital condyle (char. 119, state 1). The latter highlights how modifications to mandibular character scoring can indirectly influence the optimization of characters from other anatomical regions through changes in recovered topology. The updated analysis also recovered three new synapomorphies for *Sebecidae*, in addition to the four from the original analysis. These include the participation of the ectopterygoid in the choanal groove (char. 233, unknown for *Sahitisuchus fluminensis*), the contact between the jugal and ectopterygoid (char. 406, unknown for *Sahitisuchus fluminensis*), and the relative distance between the lower teeth 4 and 5 (char. 450, state 0 for *Sahitisuchus fluminensis*).

DISCUSSION

Sebecoidea is a clade that encompasses several Cretaceous and Cenozoic taxa from South America, Europe, Africa, and the Caribbean (Bravo et al., 2025; Nicholl et al., 2025; Viñola Lopez et al., 2025). They are particularly important because they were one of the few major terrestrial vertebrates to survive the end-Cretaceous extinction event, yet they

later died out before the present day. Unfortunately, the degree of preservation of the mandibular apparatuses in these taxa varies considerably, and complete mandibles are rare (**Fig. 4**), which hinders our understanding of their anatomical, functional, and dietary diversity. Fossils of *Barinasuchus arveloi*, *Eremosuchus elkoholicus*, *Sebecus ayrampu*, *Sebecus huilensis* (UCMP 37877, IGM 250816, TMM 41658-8), *Pehuenchesuchus enderi*, *Doratodon ibericus*, *Iberosuchus macrodon*, and *Bergisuchus dietrichbergi* preserve only the anterior portion of the mandible; in few cases, preservation extends posteriorly to the mandibular fenestra.

Doratodon carcharidens is otherwise known from fragmentary mandibular remains, including fragments of the anterior portion of the mandible (see Muscioni et al., 2025), but the specimen IPUW 2349/57 preserves an almost complete right hemimandible, lacking the angular process and most teeth (**Fig. 4**). Although the right hemimandible of *Lorosuchus nodosus* is preserved along its entire length, including the symphyseal region (see Pol & Powell, 2011), most of the ventral portion on the anterior half is very fractured, obscuring its original morphology and making its overall shape difficult to assess in lateral view (**Fig. 4**). The mandible of *Sebecus icaeorhinus* is mostly known from fragmented and isolated elements from different parts of the jaw, which limits direct anatomical interpretations and requires reconstruction based on comparative inference (see Gasparini, 1972 and Molnar, 2010). In contrast, although the mandible of *Dentaneosuchus crassiprорatus* is also known from several fragments, its overall morphology can be better inferred by integrating these preserved elements as digital models (see Martin et al., 2022).

Among *Sebecoidea*, the mandible is fully preserved in *Bretesuchus bonapartei* and *Sahitisuchus fluminensis*. The former preserves a non-deformed, isolated mandible with a complete left hemimandible, whereas the mandible of *Sahitisuchus fluminensis* is

attached to the cranium and exhibits several fractures, with some segments noticeably displaced from its original position (**Fig. 4**). Nevertheless, these taxa represent valuable proxies for systematic and morphological studies within a clade that generally has few well-preserved mandibular elements, and the digital reconstruction of the mandible of *Sahitisuchus fluminensis* significantly expands this anatomical information.

At a basic level, the reconstruction enables accessing regions and relative proportions that are not observable in the fossil due to its articulation with the cranium, facilitating the description and identification of morphological features. It may also contribute to phylogenetic studies, as demonstrated by the updated analysis conducted here. By rescored eight characters, the updated analysis recovered a different topology (**Fig. 3**), highlighting the potential use of digital models in character scoring. Comparison between the original and updated analyses further indicates that the impact of these modifications extends beyond the rescored characters themselves. Although only one of the rescored characters was recovered as a synapomorphy of Sebecidae (char. 450, see **Supplementary Online Information**), and none were recovered as autapomorphies of *Sahitisuchus fluminensis*, the updated analysis recovered additional autapomorphies and synapomorphies because changes in the recovered topology altered character optimization, including for characters from anatomical regions not directly affected by rescored. This suggests that incorporating digitally reconstructed anatomical information can influence phylogenetic interpretations not only by refining individual character states, but also indirectly by altering the recovered topology, which subsequently affects the optimization of morphological traits across the tree.

Continuous characters can also be refined through measurements obtained from 3D digital models, overcoming simplifications associated with translating three-dimensional structures into two-dimensional representations. This approach may

contribute to reducing perspective and scaling issues, a significant challenge in morphometric analyses (Arnqvist & Martensson, 1998). Although 3D models may occasionally produce inaccurate measurements, such issues can be minimised through good methodological practices and do not outweigh the benefits these models provide (Engelkes et al., 2019).

As a caveat, access to finer anatomical details such as sutures, enamel structures, small foramina, etc., depends both on the quality of the original imaging data (e.g., there are often fewer details in models generated from surface scanners than from μ CT) and on the process of reconstruction (e.g., smoothing fragmented surfaces). For example, a specific character from the continuous dataset (char. 4) could not be scored because it is related to the splenial extension on the mandibular symphysis, a jaw portion not preserved in MCT.R.1730 and, therefore, not reconstructed in full detail in the final model. Nonetheless, the case presented here highlights the broader phylogenetic perspective that digital models can provide, and we highly recommend their consideration in future analyses, when available. By enabling alternative approaches to quantifying morphological information (e.g., through atomising characters), digital models can not only improve character assessment but also contribute to reducing biases such as subjective inclusion and discretisation of phenotypic variation (Garcia et al., 2017; Celik et al., 2025).

From a broader comparative perspective, the model also enables morphological, palaeoecological, and evolutionary analyses based on virtual palaeontology approaches, including geometric morphometrics (GMM), multibody dynamics (MBD), and finite element analysis (FEA), providing an important anatomical framework for future quantitative and functional studies of *Notosuchia*. None of these studies would be possible, however, without making the digital model available to the scientific

community. The holotype of *Sahitisuchus fluminensis* is housed at the Museu de Ciências da Terra, Rio de Janeiro, Brazil (Kellner et al., 2014). With the exception of the right maxilla of *Sebecus* sp. (Price & Paula Couto, 1946) and an isolated tooth attributed to *Sebecus huilensis* from the Miocene of the Solimões Formation (Pinheiro et al., 2025), *Sahitisuchus fluminensis* is the only Brazilian sebecid described so far; thus, limited access to the fossil may reduce its inclusion in comparative studies. This situation may help explain why, despite several phylogenetic analyses of *Sebecoidea* led by researchers from outside Brazil in recent years (e.g., Bravo et al., 2021, 2025; Martin et al., 2022; Nicholl et al., 2025, and earlier iterations of these datasets), this taxon was only occasionally included (e.g., Nicholl et al., 2025; but see Bravo et al., 2025). Additionally, direct examination of fossil specimens may be hindered due to their fragile condition as well as bureaucratic and logistical barriers to access (Hublin, 2013; Skinner et al., 2013). The digitisation of fossils and their dissemination in online platforms can help overcome these limitations, improving data accessibility and broadening the scope of research on notosuchian evolution.

Different open-access online platforms (e.g., Digimorph, Morphosource, Morphomuseum, Sketchfab) can significantly improve the usability of morphological data from museum collections worldwide (Lebrun & Orliac, 2017). As a key example, a valuable source for the reconstruction in our study was the three-dimensional digital model of *Dentaneosuchus crassiproratus* mandibular elements, made available by Martin et al. (2022), which proved crucial for the identification of relevant characters, including overall morphology, teeth, and bone surfaces. Apart from the scientific use, these models can also be downloaded to be 3D-printed and used as teaching and educational tools (Pérez-Ramos & Figueirido, 2020), expanding the use of biological materials for an academic outreach perspective.

Finally, digital copies of fossil specimens can be an important safeguard in cases when the original specimen is lost or damaged. Even considering the costs of digitising, they are arguably insignificant compared to the cost of recovering lost data (Davies et al., 2017). In the case of *Sahitisuchus fluminensis*, a cast of it was, until recently, housed at the National Museum of Brazil (Kellner et al., 2014). This institution was destroyed by a catastrophic fire in 2018, which severely affected its natural history collections, including the palaeontological ones (Serejo et al., 2026). The current condition of some fossils remains unknown, including that of certain notosuchian taxa such as *Coringasuchus anisodontis* (MN 7128-V, holotype and only known material; Kellner et al., 2009) and *Pepesuchus deiseae* (MN 7005-V, holotype; Campos et al., 2011). Efforts to digitise the collections are under way (Carvalho & Juliace, 2025; Serejo et al., 2026), providing another example of the importance of maintaining digital records of specimens for long-term preservation and scientific access.

CONCLUSION

With this contribution, we aim to expand the scientific and educational potential of one of the most complete parts (mandible) of the *Sahitisuchus fluminensis* holotype, which corresponds to one of the best preserved *Sebecoidea* lower jaws, enabling new research focused on the morphology and evolution, as well as improving access to the specimen and its safeguarding. By focusing on the mandible, we reconstructed an important biological structure, representing a first step toward broader digitisation efforts of notosuchians. This effort promotes broader scientific and educational use of this resource by a worldwide community, while also contributing to the ongoing digital documentation of this unique clade of vertebrates.

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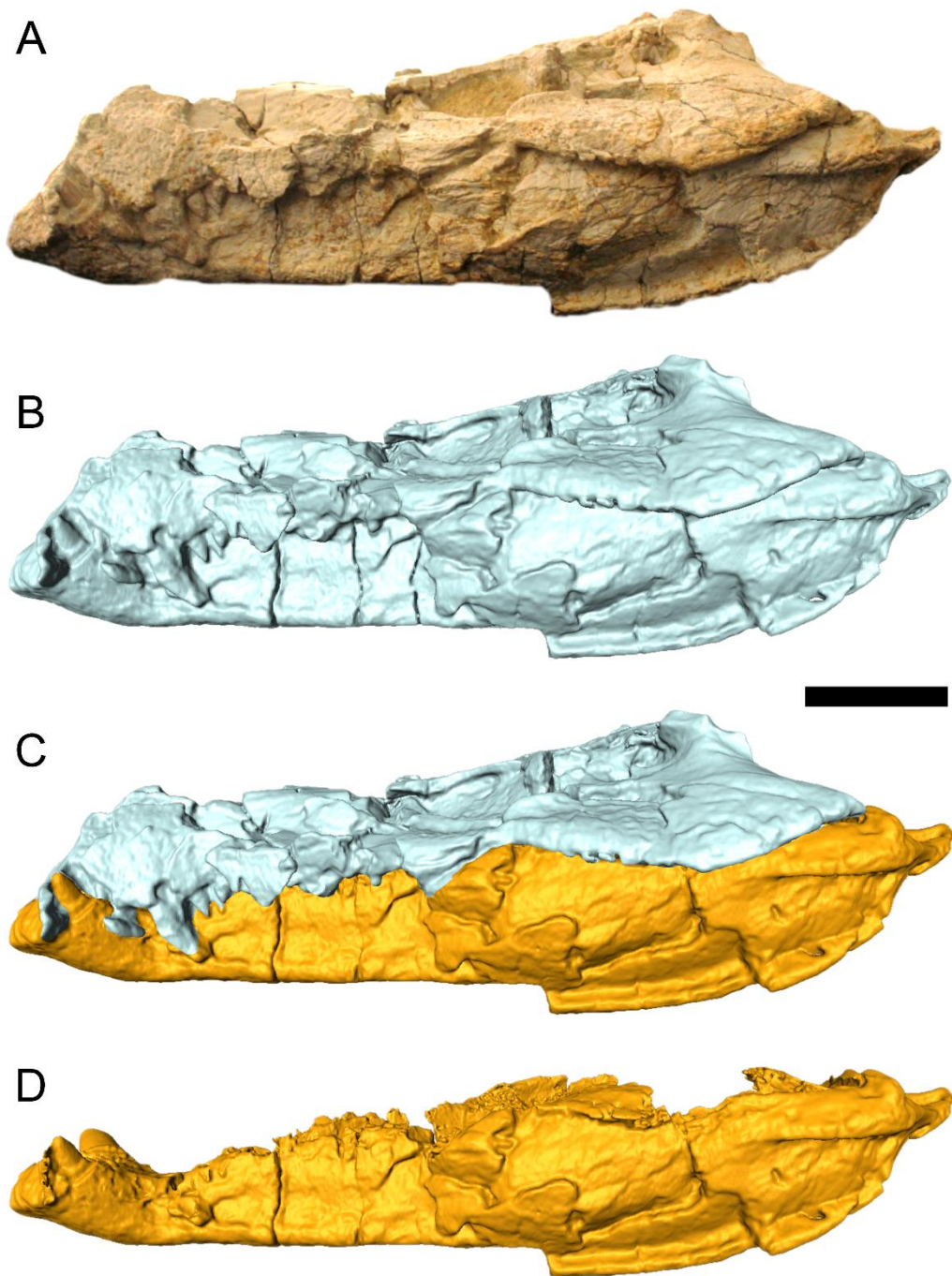
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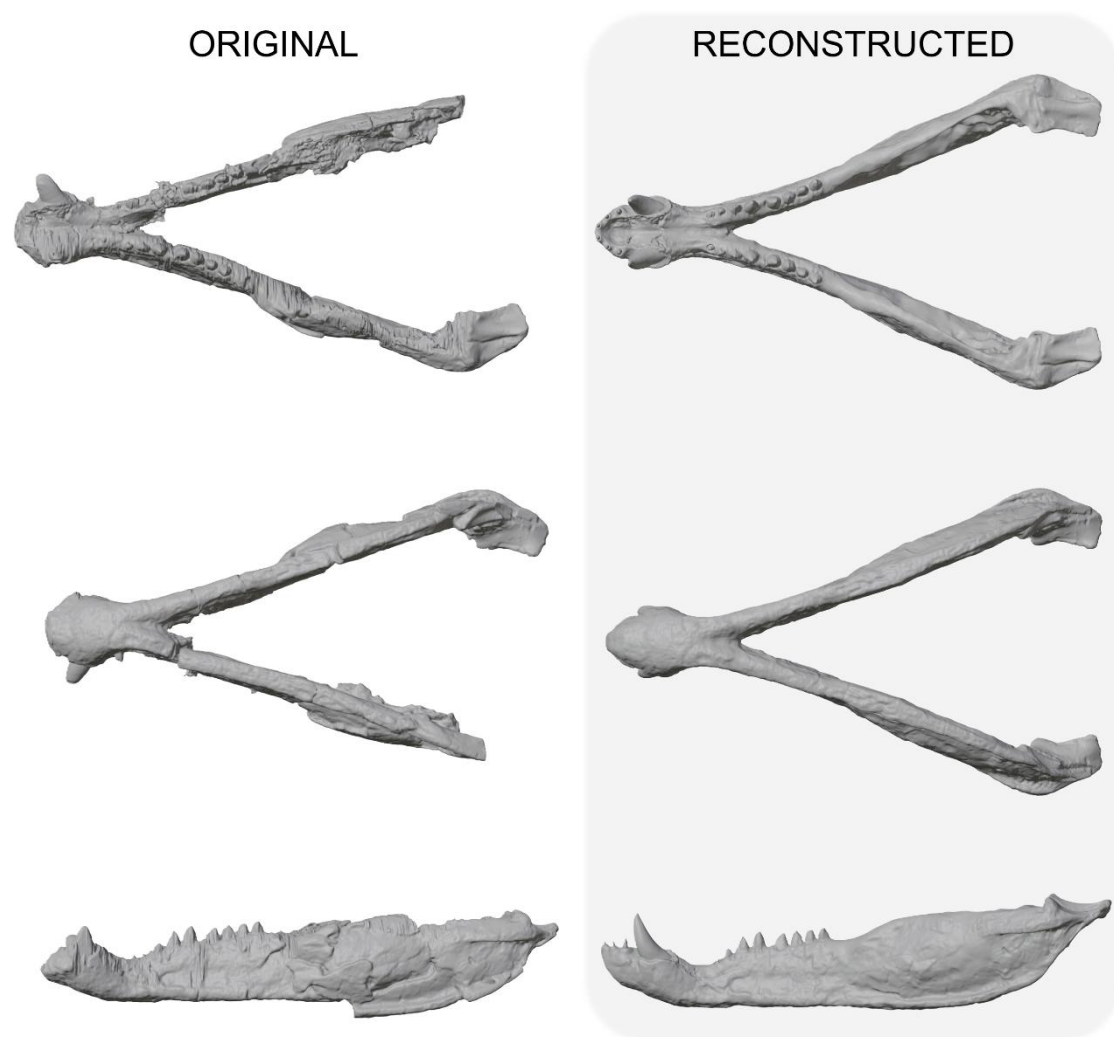
SUPPLEMENTARY ONLINE INFORMATION

The reconstructed mandible of MCT.R.1730 will be made available at Morphosource. Supplementary file 1 includes details of the phylogenetic analyses.

612 **FIGURE CAPTIONS**

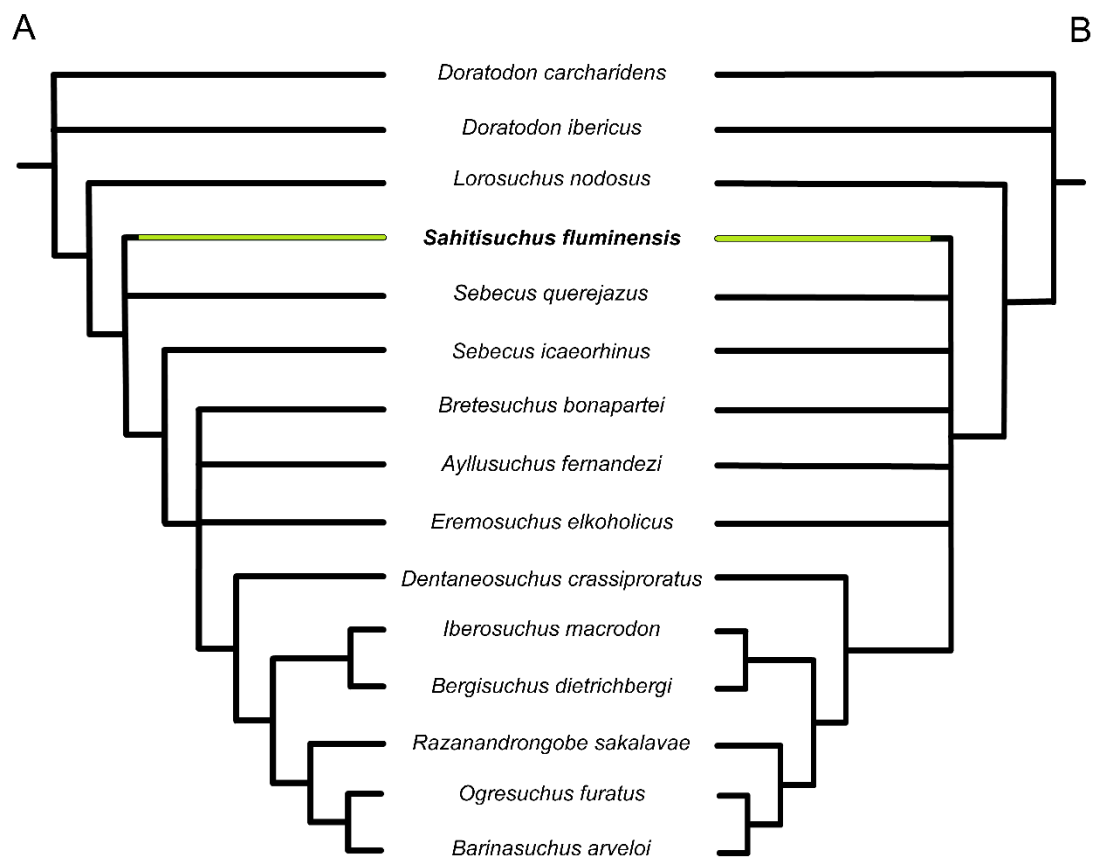


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614 **Figure 1.** Segmentation of the *Sahitisuchus fluminensis* mandible (left lateral views). **A**,
615 Holotype MCT.R.1730, an almost complete skull; **B**, CT scan of the skull; **C**,
616 Segmentation of the mandible after Biomedisa; **D**, Rough digital model of the isolated
617 mandible. Scale bar equals 5 cm.



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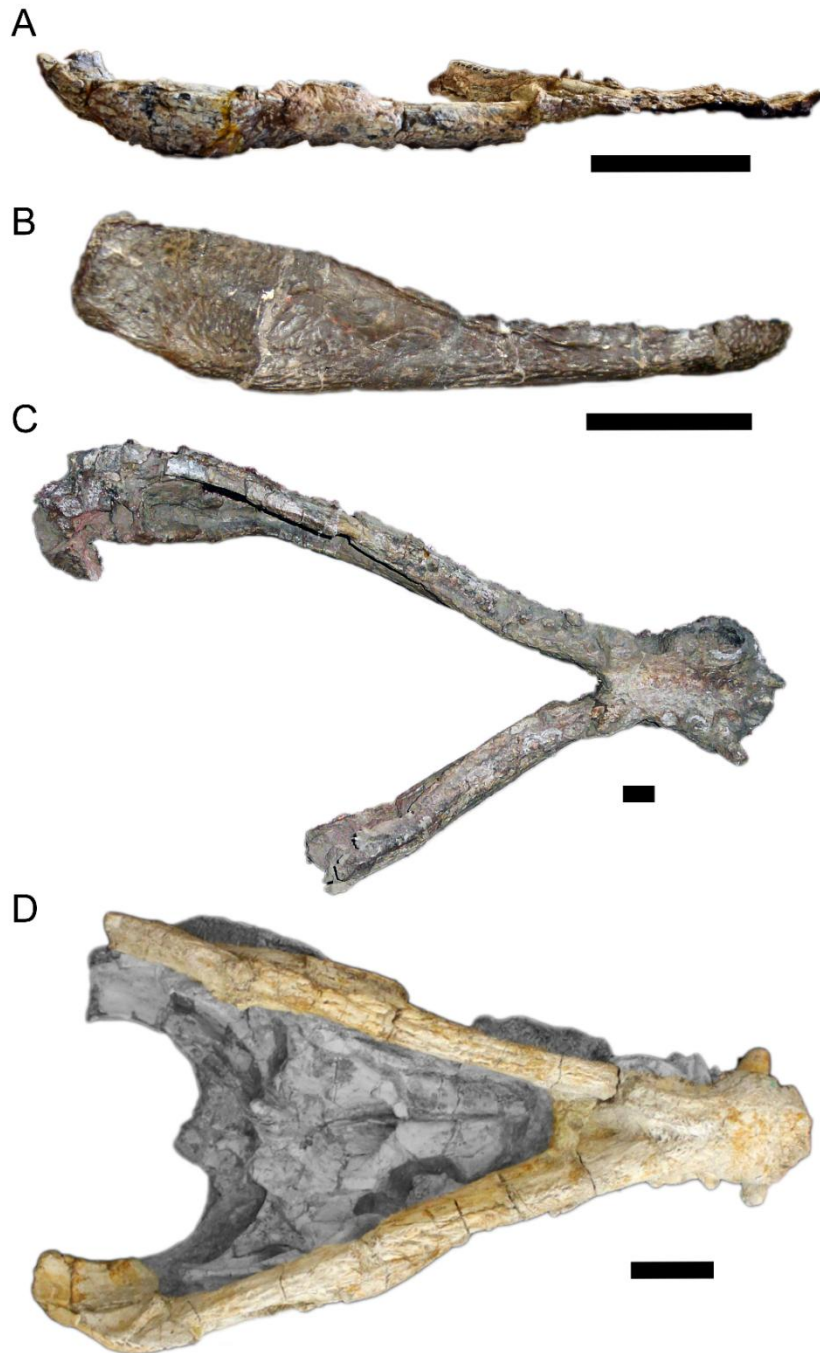
619 **Figure 2.** Original and reconstructed mandible models of *Sahitisuchus fluminensis* in
 620 dorsal (upper), ventral (midline), and left lateral (bottom) views.



621

622 **Figure 3.** Strict consensus topology recovered for *Sebecoidea* in **A**, original analysis;

623 and **B**, updated analysis.



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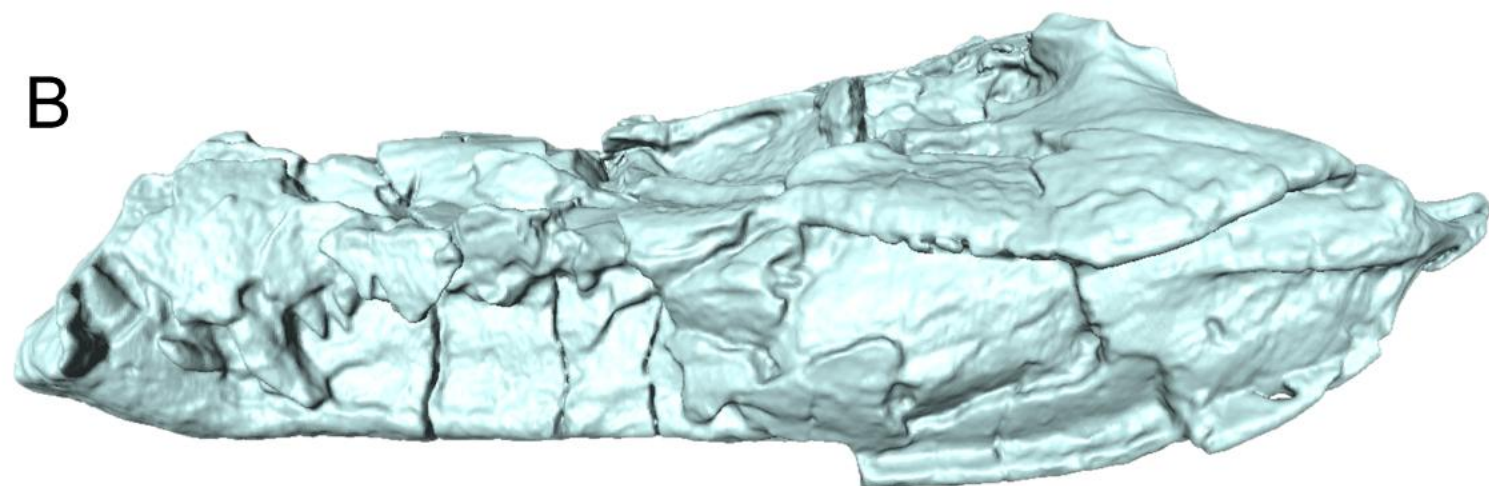
625 **Figure 4.** Examples of the better-preserved mandibular elements among *Sebecoidea*. **A**,
 626 Right lateral view of the *Lorosuchus nodosus* mandible (PVL 6219), with a heavily
 627 fractured anteroventral region; **B**, Right lateral view of the right *Doratodon carcharidens*
 628 hemimandible (IPUW 2349/57), missing the angular process and most teeth; **C**, Dorsal
 629 view of the *Bretesuchus bonapartei* mandible (PVL 4735), missing the posterior portion
 630 of the right hemimandible; **D**, Ventral view of the of *Sahitisuchus fluminensis* mandible

- 631 (MCT.R.1730, highlighted), missing the posterior portion of the right hemimandible.
- 632 Scale bars equal 4 cm.

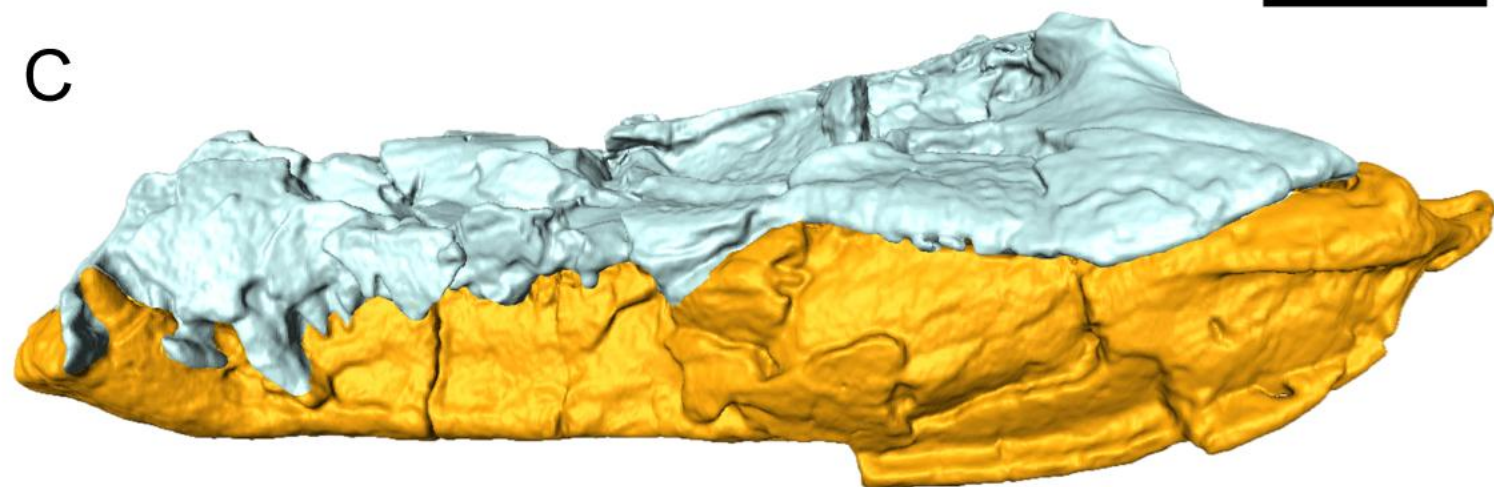
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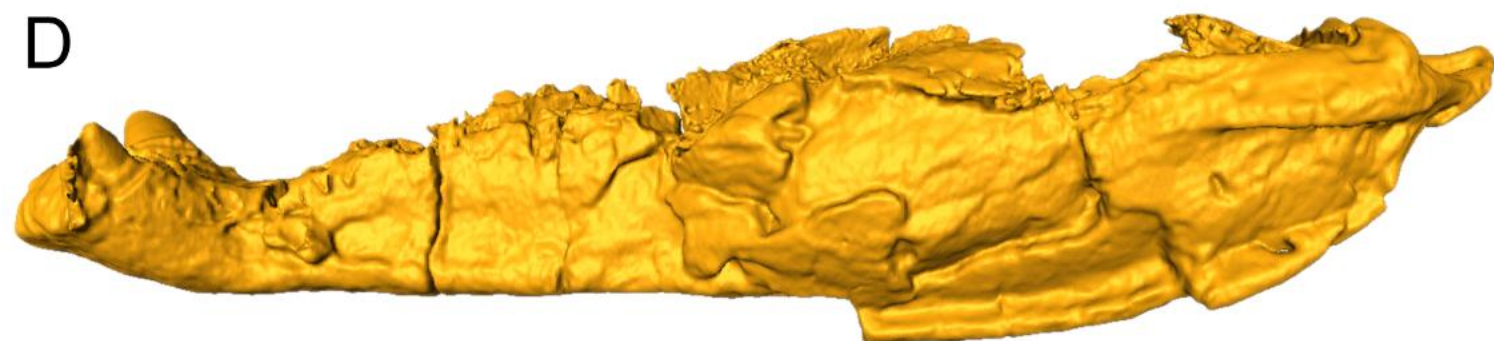
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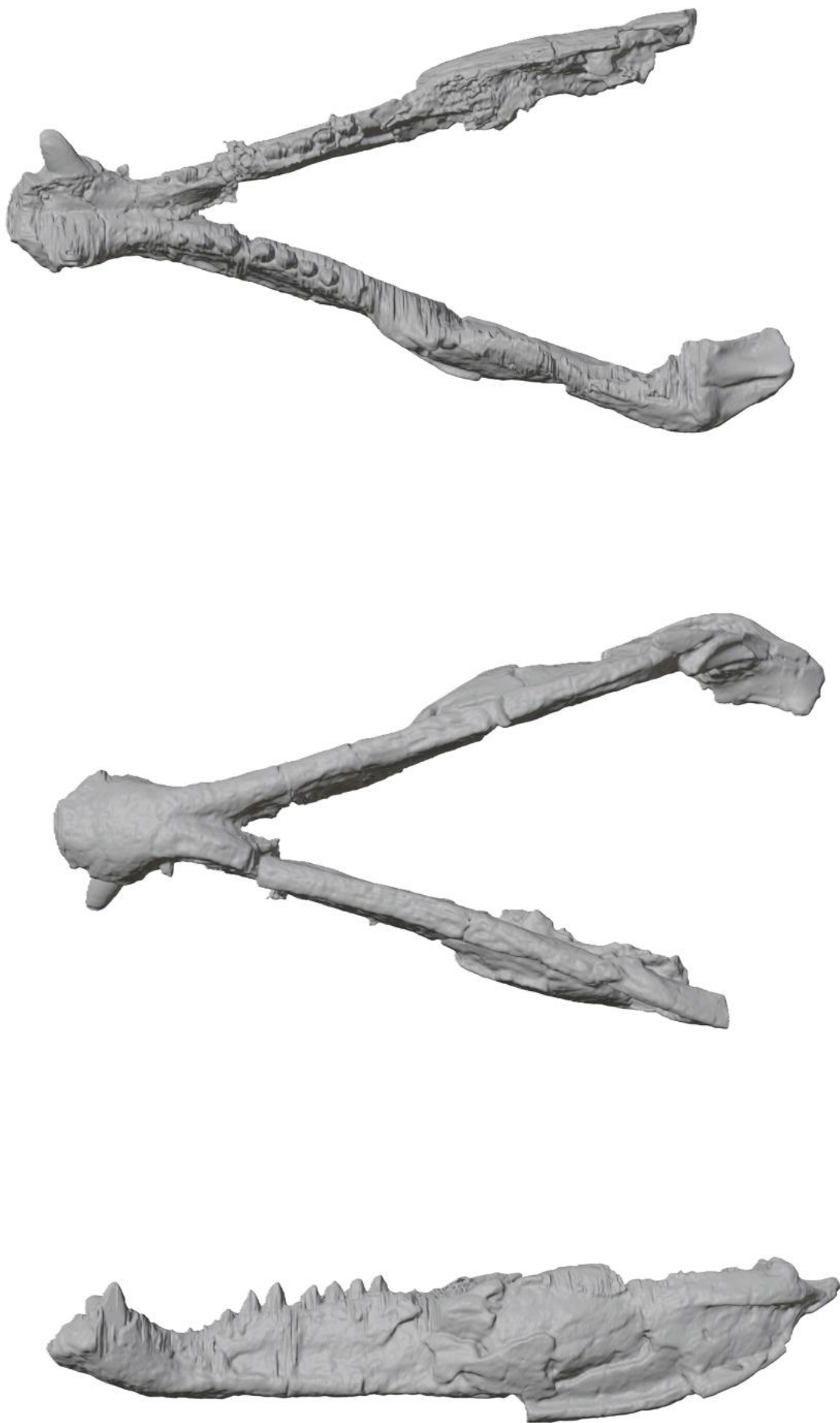
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D



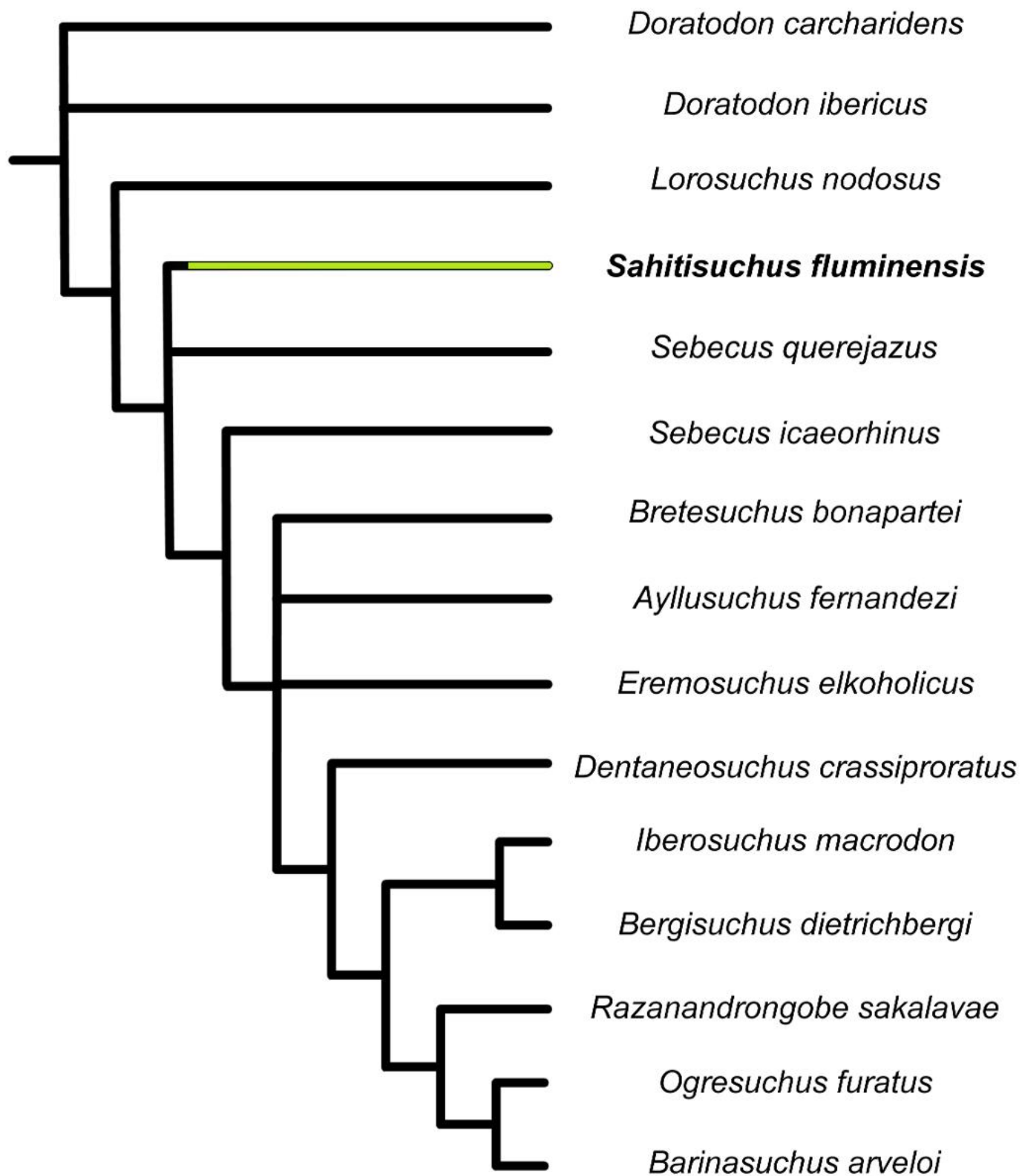
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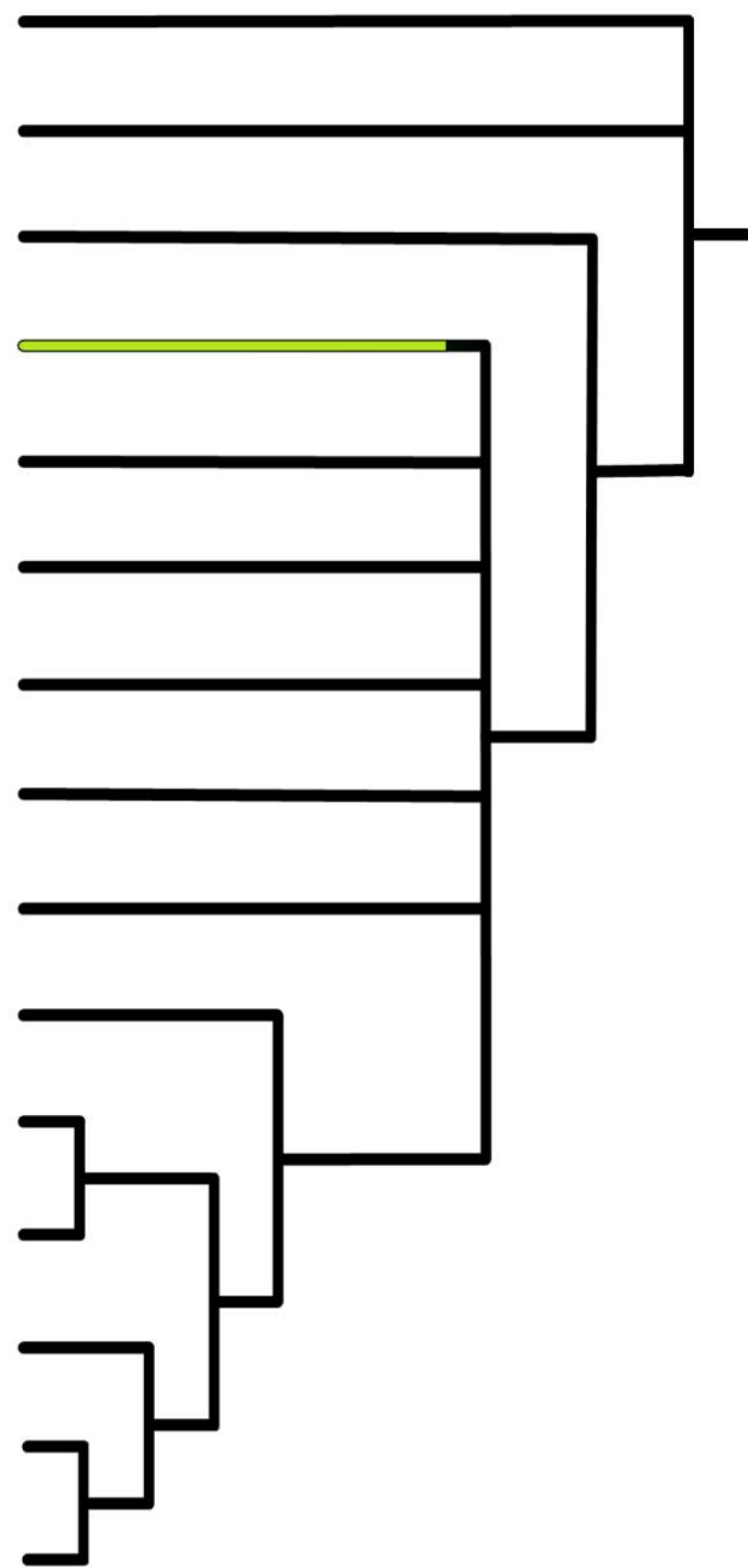
RECONSTRUCTED



A



B



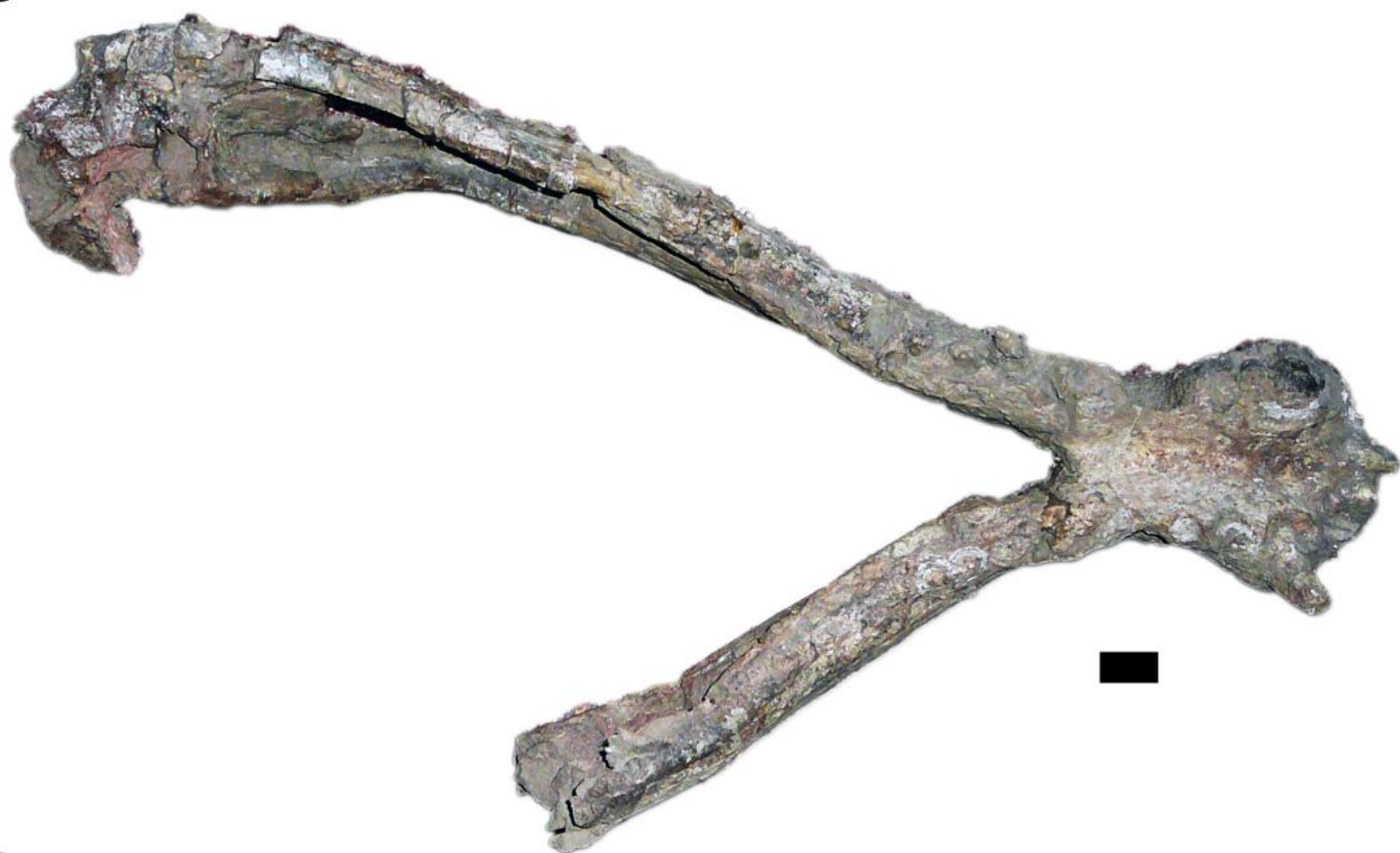
A



B



C



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