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SUPPLEMENTARY MATERIAL**

**A new diapsid with a unique tooth structure from the
Middle Triassic (Ladinian) of Germany**

GABRIELA SOBRAL,^{1*} HANS-DIETER SUES,² AND RAINER SCHOCH¹

¹Staatliches Museum für Naturkunde, Rosenstein 1, 70191 – Stuttgart, Germany, gabriela.sobral@smns-bw.de,
rainer.schoch@smns-bw.de;

²Department of Paleobiology, National Museum of Natural History, Smithsonian Institution, MRC 121, P.O.
Box 37012, Washington, D.C. 20013-7012, U.S.A., sush@si.edu

* Corresponding author

PHYLOGENETIC ANALYSIS

For the phylogenetic placement of *Stauromatodon mohli* (SMNS 91427) four different analyses were performed. The data set used was the morphological data only from Bittencourt et al. (2020). For the Bayesian analysis, the search parameters were maintained. The analysis was run in MrBayes 3.2.6 on the CIPRES Science Gateway (phylo.org). The resulting tree topology (Fig. S1) shows several groups collapsed at the saurian node, together with single taxa including *Stauromatodon*. The posterior probabilities were generally very low, in contrast with the original results.

The parsimony analyses were performed in the software TNT (Goloboff et al., 2003). In the equal weight maximum parsimony analysis, a TBR search with 1,000 replications each and 100 trees stored per replication was applied. The result yielded 60 MPTs with a length of 2,284 steps (Fig. S2). The consistency index is 0,18 and the retention index is 0,64. Support values were also very low. Most branches collapse with a decay index of 1 and all of them with 5. Most branches collapse with a cutoff lower than 50 in the Bootstrap and Jackknife analyses with 1.000 replicates. The topology of the majority rule consensus tree shows *Stauromatodon* in a politomy with saurosphargids. The monophyly of this clade is supported by five synapomorphies, of which only two are scored for *Stauromatodon* and one for all three taxa, namely crown apices lingually concave. In this analysis, the clade is found in Sauropterygia.

We also performed an equal weight parsimony Tree Analysis using New Technology on the software TnT with 1,000 random addition sequences each and 100 rounds for the RSS and CSS sectoral searches, as well as Rachtet and tree fusing searches. It resulted in 179 MPTs of 2284 steps each (Fig. S3). The tree topology of the majority rule consensus is the same as in the previous analysis, albeit with less support. The consistency and retention indexes are the same as above, and the Bremer support is also very similar. The supporting synapomorphies are also the same.

For the implied weight parsimony analysis a TBR search with 1,000 replications each and 100 trees stored per replication, together with a k value of 8 was used. The analysis resulted in 3 MPTs of 2,294 steps each (Fig. S4). The consistency index is 0,17 and the retention index is 0,64. Other support values were generally similar to the equal weight maximum parsimony analysis. The topology of the majority rule consensus tree is the most diverging of the four analyses, showing SMNS 91427 in a politomy with the paramacellodids lepidosaurs *Neokotus*, *Blackesius*, and *Paramacellodus*. Two synapomorphies support the monophyly of this clade, the labiolingual expansion at tooth base only and the crown apices lingually concave.

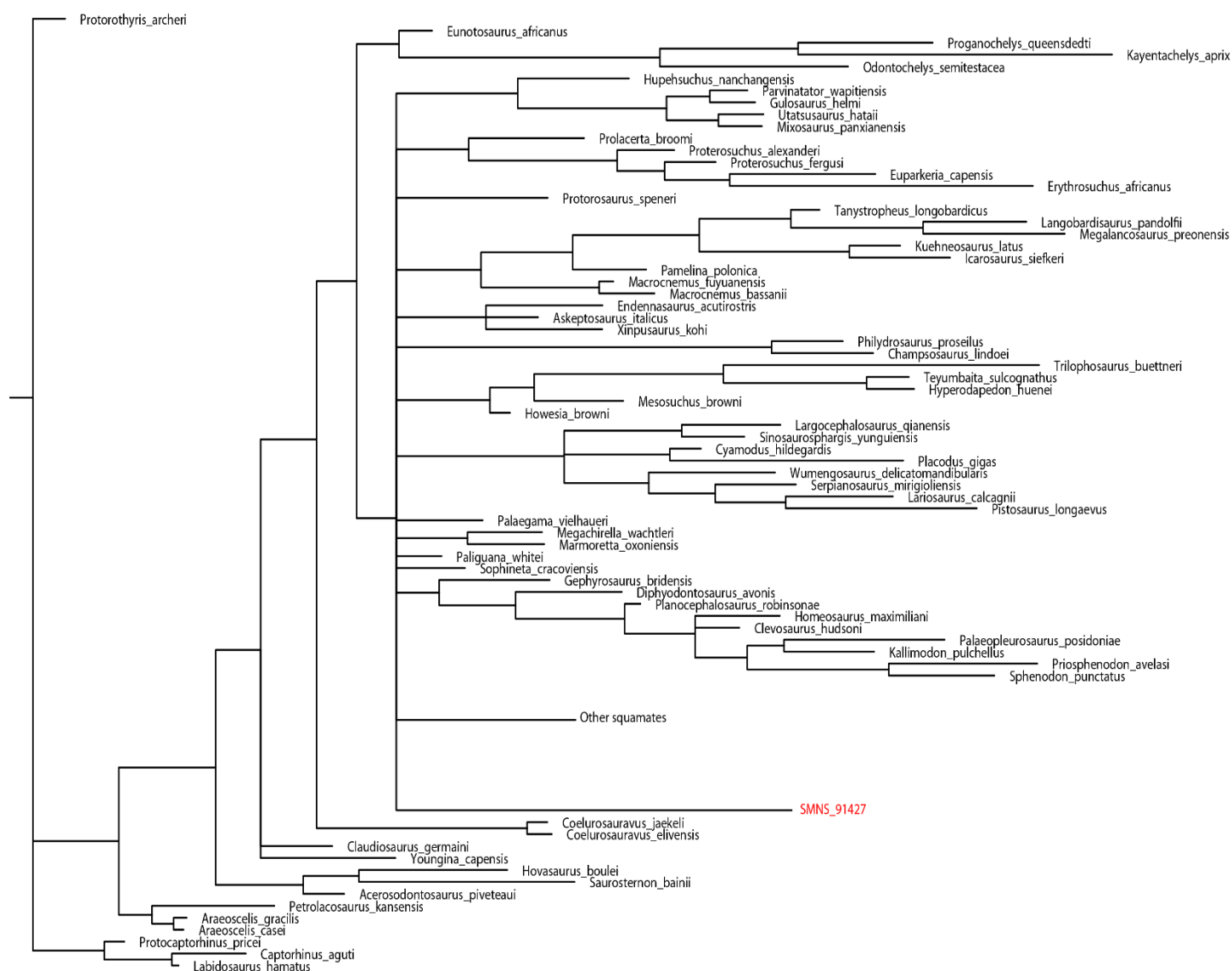


FIGURE S1. Majority rule consensus of the Bayesian inference analysis. Numbers indicate posterior probabilities. Branch lengths are not to scale.

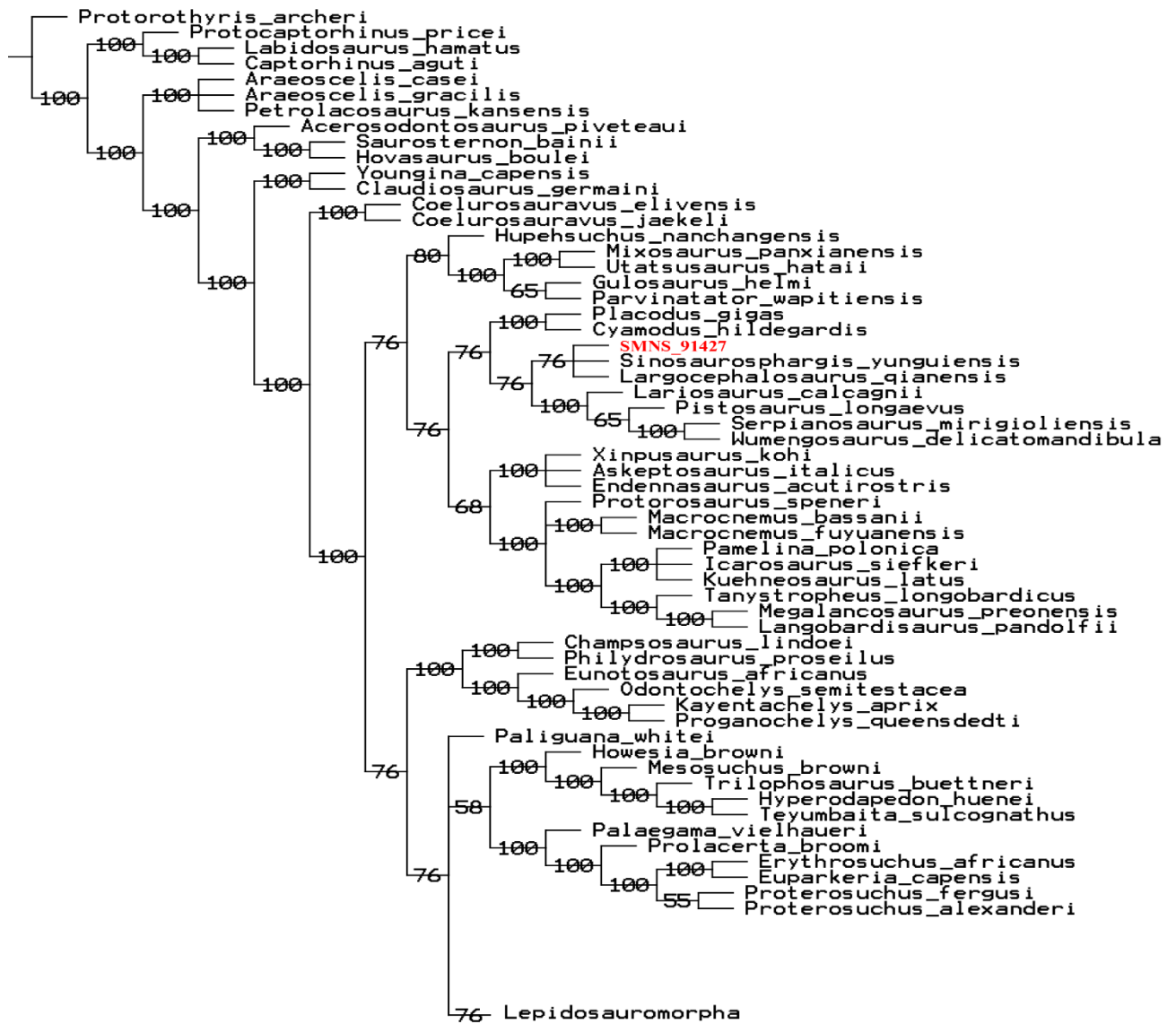


FIGURE S2. Majority rule consensus of the Equal Weight parsimony analysis with TBR search. Branch numbers indicate frequency of appearance. Branch lengths are not to scale.



FIGURE S3. Majority rule consensus of the Equal Weight parsimony analysis with TNT search.

Branch numbers indicate frequency of appearance. Branch lengths are not to scale.



FIGURE S4. Pruned majority rule consensus topology of the best fit trees of the Implied Weight parsimony analysis focusing on squamates. Branch numbers indicate frequency of appearance. Branch lengths are not to scale.

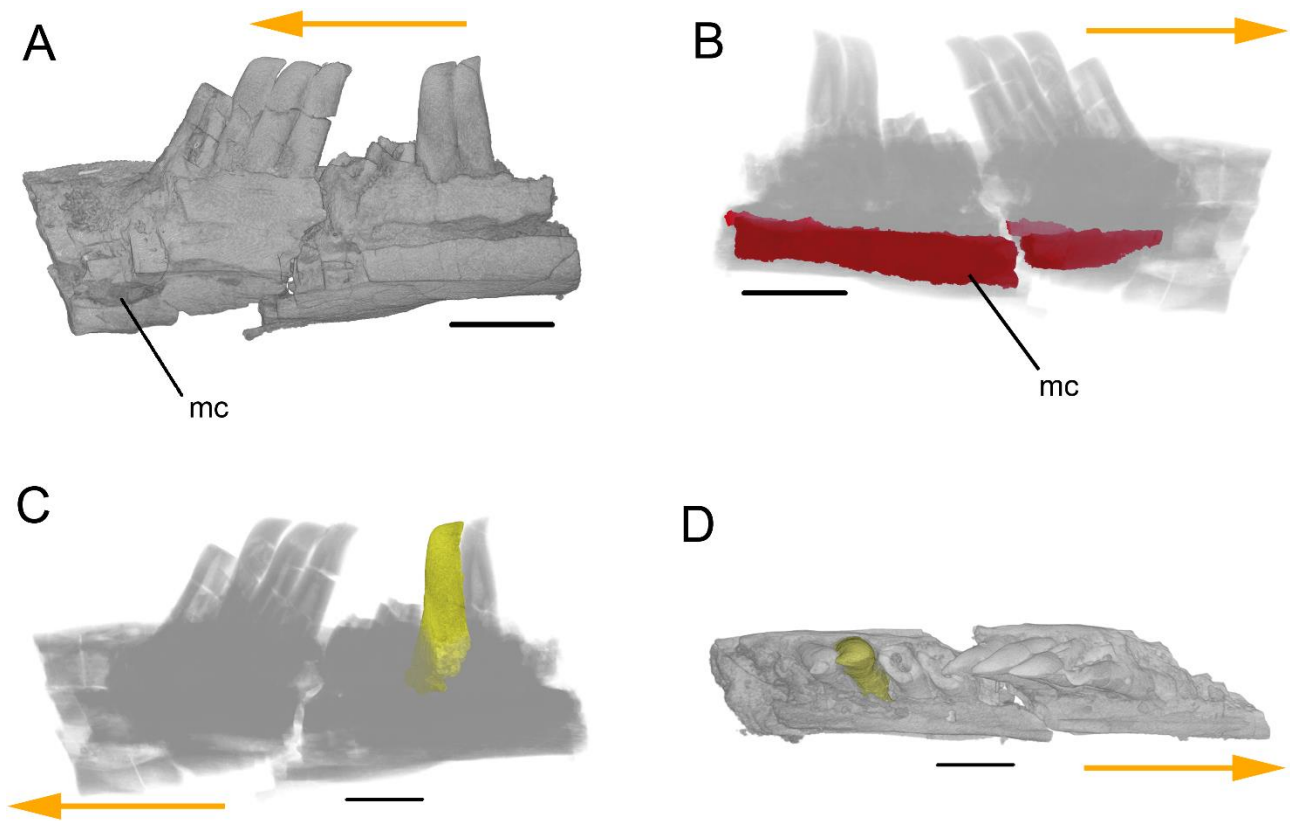


FIGURE S5. Segmented 3D models of *Stauromatodon mohli* (SMNS 91427). A) left labial view of the material, B) left lingual view with material rendered transparent and Meckelian canal marked in red, and position of the penultimate tooth (yellow) in the mandible in C) left labial view with material transparent and D) dorsal view (anterior to the right). Arrows indicate anterior direction. Abbreviation: **mc**, Meckelian canal. Scale bars: 4 mm in A–B and 3 mm in C–D.

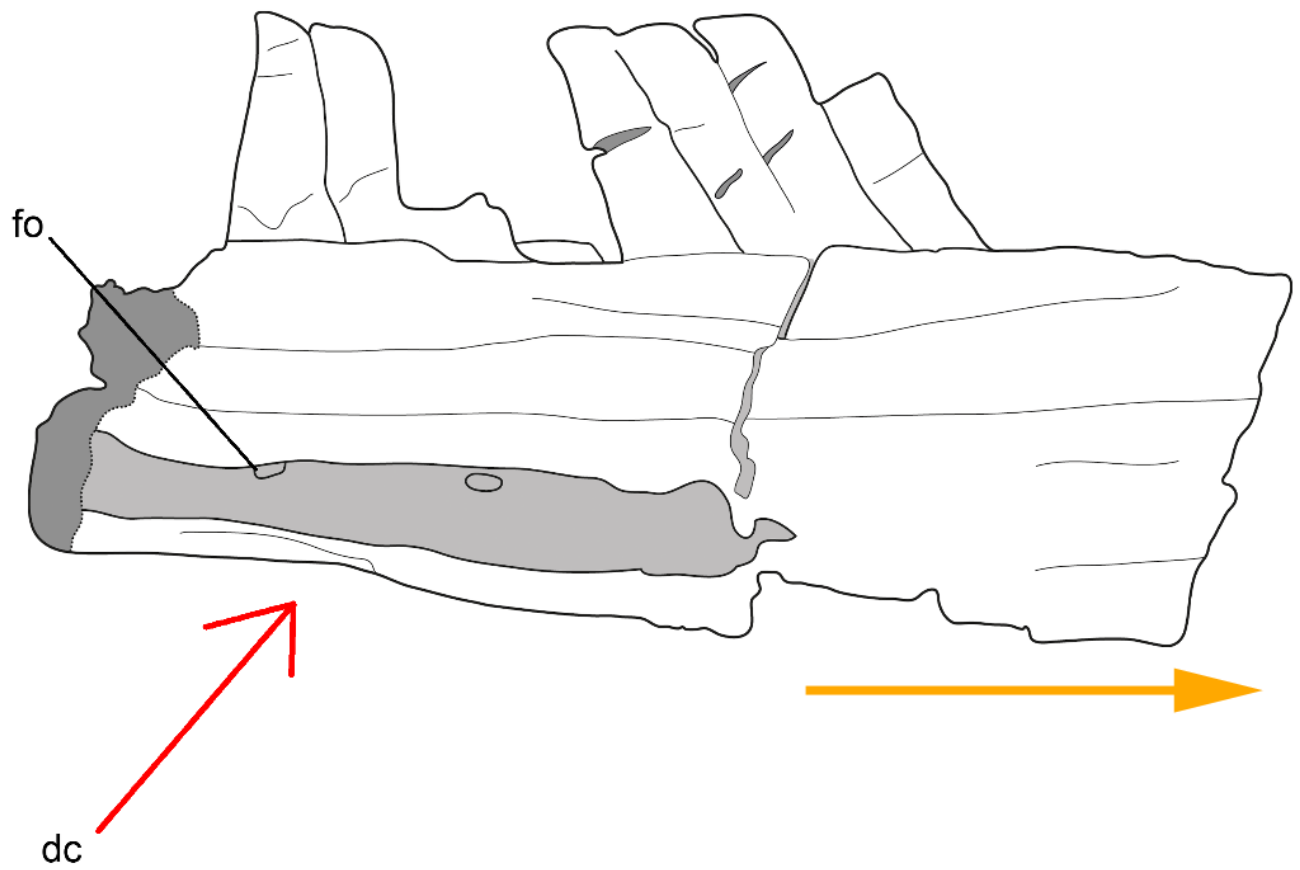


FIGURE S6. Line drawing of the main text figure 2B emphasizing the constriction in the ventral border of the dentary (red arrow). Orange arrow indicates anterior direction. Abbreviations: **dc**, dental constriction; **fo**, foramen.

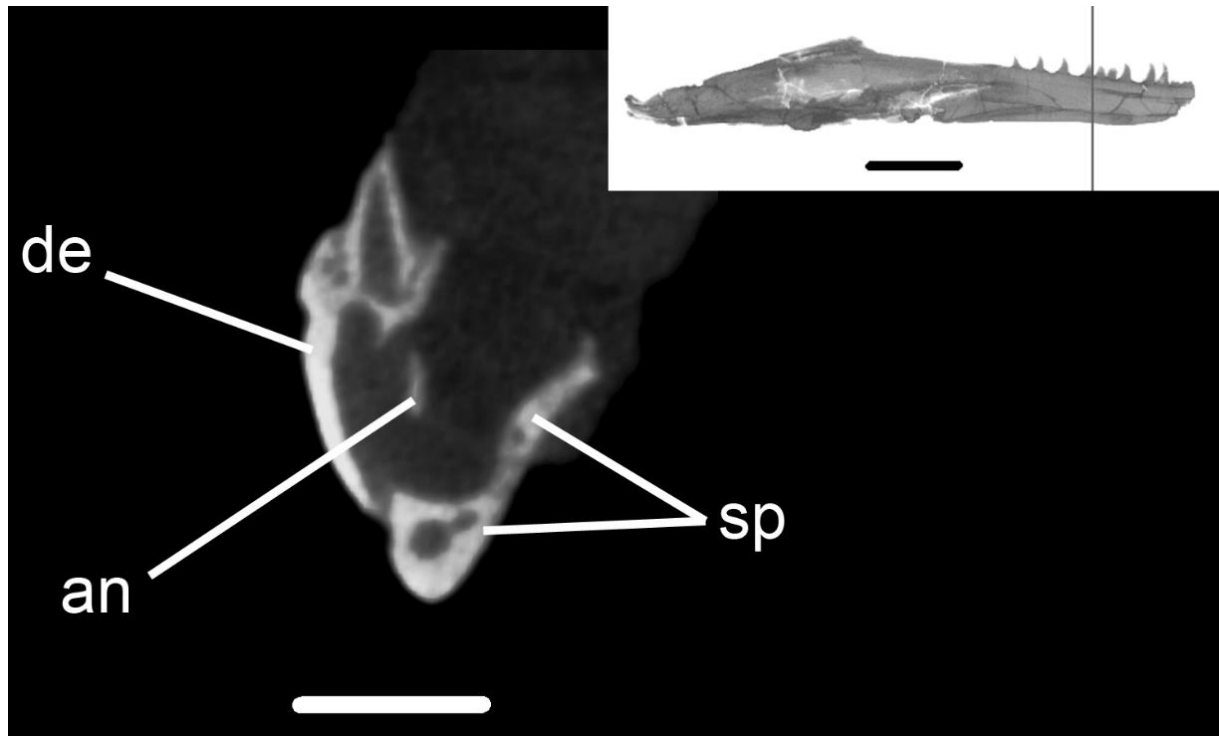


FIGURE S7. Cross-section of the mid-anterior portion of the right lower jaw (inset) of the holotype of *Prolacerta broomi* (UCMZ 2003.41R) in anterior view. Abbreviations: **an**, angular; **de**, dentary; **sp**, splenial. Scale bars equal 2 mm and 7.5 mm (detail).

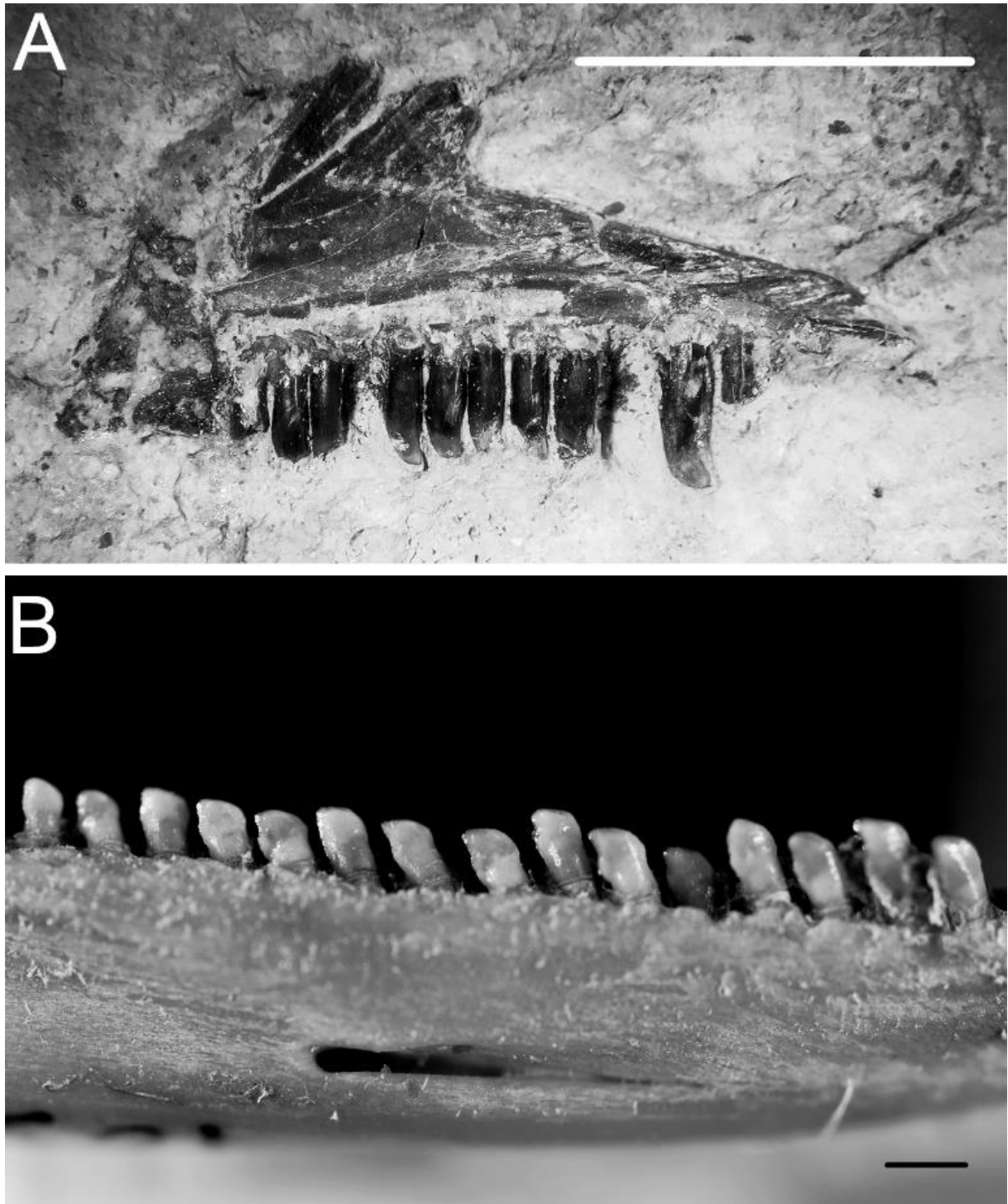


FIGURE S8. Photograph of A) right maxilla of the squamate *Paramacellodus oweni* (NHMUK R8118) in lingual view and B) right dentary of the extant salamander *Amphiuma tridactylum* (SMNS 10524) in labial view. Scale bars equal 5 mm and 1 mm, respectively.

LITERATURE CITED

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