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SUPPLEMENTARY ONLINE MATERIAL FOR

An enigmatic new archosauriform from the Carnian-Norian (Late Triassic)

Ischigualasto Formation of northwestern Argentina

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Supplementary Online Material

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Data matrix available at http://app.pan.pl/SOM/app66-Yanez_etal_SOM/DataMatrix.tnt http://app.pan.pl/SOM/app66-Yanez_etal_SOM/DataMatrix.nex

1. Phylogenetic analysis

Following the taxon sampling and character modifications outlined by Nesbitt et al. (2017), the final matrix consisted of 85 taxa and 419 characters. The following characters were treated as ordered in the matrix of Nesbitt et al. (2017): 32, 52, 121, 137, 139, 156, 168, 188, 223, 247, 258, 269, 271, 291, 297, 328, 356, 399, and 413. The data matrix in TNT format is included as a separate supplementary file.

2. Character coding for *Trialestes romeri* and *Mandasuchus tanyauchen* as OTUs in our phylogenetic analysis.

We included PVSJ 397 in the latest iteration of the Nesbitt (2011) data matrix as implemented in Nesbitt et al. (2017). To further assess the phylogenetic affinities of *Incertovenator longicollum* gen. et sp. nov. (PVSJ 397), we incorporated the holotype (PVL 2561) and referred specimen (PVL 3889) of *Trialestes romeri* as a single operational taxonomic unit (OTU) in the data matrix of Nesbitt et al. (2017). We followed the character scorings made by Lecuona et al. (2016) for their terminal taxon '*Trialestes romeri* combined' in their modified version of the Nesbitt (2011) data matrix. We also incorporated the holotype (NHMUK PV R6792) and referred specimens (NHMUK PV R36950, NHMUK PV R6793, NHMUK PV R6794 and NHMUK PV R36889) of *Mandasuchus tanyauchen* as a single OTU following the character scorings made by Butler et al. (2018) for their terminal taxon '*Mandasuchus* total' in their modified version of the Nesbitt (2011) data matrix.

In order to comply with the additions and modifications of character definitions made by Nesbitt et al. (2017) we revised the following scorings for *Trialestes romeri* (terminal taxon '*Trialestes romeri* combined' in the data matrix of Lecuona et al., 2016) and *Mandasuchus tanyauchen* (terminal taxon '*Mandasuchus* total' in the data matrix of Butler et al., 2018).

- i. Character 191: character state unchanged (0) for *Trialestes romeri*; character state unchanged (1) for *Mandasuchus tanyauchen*.
- ii. Character 273: character state changed from (2) to (1) for *Trialestes romeri;* coded as (0) for *Mandasuchus tanyauchen*.
- iii. Character 414: scored as inapplicable for *Trialestes romeri*; scored as (0) for *Mandasuchus tanyauchen*.
- iv. Character 415: scored as missing (?) for *Trialestes romeri*; scored as missing (?) for *Mandasuchus tanyauchen*.
- v. Character 416: scored as missing (?) for *Trialestes romeri*; scored as (0) for *Mandasuchus tanyauchen*.
- vi. Character 417: scored as (0) for *Trialestes romeri*; scored as (0) for *Mandasuchus tanyauchen*.
- vii. Character 418: scored as (0) for *Trialestes romeri*; scored as (0) for *Mandasuchus tanyauchen*.
- viii. Character 419: scored as (0) for *Trialestes romeri*; scored as (1) for *Mandasuchus tanyauchen*.

3. Parsimony analysis.

The matrix was analyzed under equally weighted parsimony using TNT 1.5 (Goloboff et al., 2008; Goloboff & Catalano, 2016). A heuristic search with 1000 replicates of Wagner trees (with random addition sequence) followed by TBR branch swapping (holding 10 trees per replicate) was performed. The best trees obtained from the replicates were subjected to a final round of TBR branch swapping. Zero-length branches in any of the recovered most-parsimonious trees (MPTs) were collapsed.

4. Scripts used for nodal support and exploratory phylogenetic analyses.

The following scripts were coded by DP for their application in the software TNT 1.5 (Goloboff et al., 2008; Goloboff & Catalano, 2016) and were used in the different instances of the phylogenetic analyses. Both scripts can be downloaded from http://staff.mef.org.ar/en/researchers/diego-pol. We provide a short explanation of their function:

'bremsup.run': This script performs a complete Bremer support analysis (Bremer, 1994) and requires having the set of MPTs in memory before running. It creates a negative constrain and a tree search for each of the nodes of the strict consensus and provides at the end a tree with the Bremer support values on each of these nodes. For large datasets this script can be time consuming and the script 'bremer.run' distributed with TNT may be a faster option. 'swaptaxon.run': This script requires having the set of MPTs in memory before running and providing as argument the taxon number to be swapped. This taxon is moved to all possible positions on each of the trees and the tree length difference obtained for each position is printed by each node in the text output file swaptaxon.out.

'compare.run': This script compares two trees, listing which characters fit better one tree (implies less steps) than in the other. These characters are reported in the output file and characters that fit equally both trees (imply the same number of steps) are not reported.

5. Further comments on the results of the phylogenetic analysis.

In those most-parsimonious topologies where *Incertovenator longicollum* gen. et sp. nov. and *Spondylosoma absconditum* are recovered as sister taxa (and in turn being either the sister clade of the rest of aphanosaurians, the sister clade of Ornithodira, or the sister clade of Avemetatarsalia), there is no single character state optimizing as a synapomorphy (unambiguous or ambiguous) for this clade. Additionally, in each possible resolution in which *Incertovenator longicollum* is recovered as an aphanosaurian, *Spondylosoma absconditum* is recovered as a member of this clade as well.

Incertovenator longicollum further differs from *Yarasuchus deccanensis* on the presence of short and stout cervical ribs (Char. 196:1). Likewise, *Incertovenator longicollum* differs from *Mandasuchus tanyauchen* on the presence of a rugose expansion at the distal end of the cervical neural spines (Char. 191:3), dorsal vertebrae neural spines with rounded distal expansions (Char. 197:2), and an elongated preacetabular process of the ilium (Char. 269:1).

The iliac morphology of *Incertovenator longicollum* is different from all nonarchosaurian archosauromoprhs analyzed here, and resembles the condition of most early crocodylomorphs, late poposauroids, pterosaurs and dinosaurs where the preacetabular process is long and extends anterior to the acetabulum (Char. 269:1). Nevertheless, the ilium of *Incertovenator longicollum* differs from those of Dinosauriformes, Poposauroidea and Crocodylomorpha on the absence of a crest dorsal to the supraacetabular crest (Char. 265:1&2), with the notable exception of *Dibothrosuchus elaphros* and *Trialestes romeri* which also lack this crest. *Incertovenator longicollum* further differs from poposauroids on the presence of a nearly straight ventral margin of the ischial peduncle, contrasting with *Qianosuchus mixtus* and *Arizonasaurus babbitti* which possess a distinct notch (Char. 414:1).

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Figure 1. Overlapping elements of the holotype specimen of *Incertovenator longicollum* gen. et sp. nov. (PVSJ 397) and the referred specimen of *Trialestes romeri* (PVL 3889). All elements are to same scale to facilitate the comparison between specimens. Dorsal vertebrae of PVL 3889 in right lateral view (A_1); dorsal vertebrae of *Incertovenator longicollum* in right lateral view (B_1); fourth and fifth cervical vertebrae and ribs of PVL 3889 in right lateral view (A_2); axis, third, and fourth cervical vertebrae and rib of *Incertovenator longicollum* in right lateral view (B_2); sacral vertebrae of PVL 3889 in right lateral view (A_3); sacral vertebrae (S1, S2) and anterior caudal vertebrae (Ca1, Ca2) of *Incertovenator longicollum* in right lateral view (B_3); right ilium of PVL 3889 (reversed for comparison) in lateral view (A_4); left ilium of *Incertovenator longicollum* in lateral view (B_4). Scale bar represents 10 mm.





Figure 2. Strict consensus tree of the 1188 MPTs showing Bremer support values above the branches, and absolute and GC frequencies of the bootstrap resampling analysis, respectively, below the branches.