

THE SKULL AND ENDOCRANIUM OF A LOWER JURASSIC ICHTHYOSAUR BASED ON DIGITAL RECONSTRUCTIONS

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SUPPLEMENTARY INFORMATION

Phylogenetic methods

Matrix. The matrix was completed by addition of BRLSI M1399 and modification of *Hauffiopteryx typicus* to that of Fischer *et al.* (2013). The codings for *Hauffiopteryx typicus* and BRLSI M1399 are shown below – characters of BRLSI M1399 that are different to *H. typicus* are shown in boldface. Modified characters for *Hauffiopteryx typicus* are shown in bold for that taxon. We noted a discrepancy that the character codings in the included supplementary material (Fischer *et al.* 2013, pp 15–17) do not match the matrix supplied by Dr Fischer and present on Morphobank (<http://dx.doi.org/10.7934/P955>). Specifically, character 39 of *Ophthalmosaurus icenicus* is coded with state 2 – deltopectoral crest as large as dorsal process and surrounded by concave areas – in the supplement, but with character 1 – deltopectoral crest as large as dorsal process – in the Morphobank matrix. We used the latter in our analysis, as this matches our observations of the material (BCM, pers. obs.), and the previous coding of *O. icenicus* (Fischer *et al.* 2012), and the results – excluding BRLSI M1399 – match those of Fischer *et al.* (2013).

Phylogenetic character list can be found in the supplementary information of Fischer *et al.* (2013); no characters have been changed, added, nor subtracted.

Character states.

Hauffiopteryx typicus

1??0??00? ?**01?1**111?? ????100???1 1?1100?**010** 000**00**10000
10001100**10** 000100

BRLSI M1399

1001001010 0010101100 **10100?00??** ????0000?0 0000010000
0000110**1?0** 000**000**

Character states for the other taxa have not been changed and can be found in the supplementary information of Fischer *et al.* (2013). Differences in coding are indicated in bold.

Analysis. Phylogenetic analysis was done in TNT version 1.1 for Mac OS X (August 2014; Goloboff *et al.* 2008). The small size of this analysis (27 taxa, 66 characters) facilitates exact searching using implicit enumeration, which is guaranteed to find the most parsimonious trees (Fig. S1). This took 7.2 hours on a 2.2 GHz Intel Core i7 processor. *Mikadocephalus gracilirostris* was used as the outgroup. Clade support values were calculated in TNT. Bremer

supports were calculated with suboptimal searches using tree bisection and reconnection swapping from the most parsimonious tree. Symmetrical resampling was used to calculate clade frequencies by heuristic methods with 10 000 replicates and probability of replacement 33% (Goloboff *et al.* 2003). Unambiguous common clade synapomorphies were derived for the most parsimonious trees. The code used is presented below; the script 'STATS.RUN' is included in the TNT download.

```
/*create log 'Marek2015.out', increase RAM, show taxon names, clade numbers, and time*/
log Marek2015.out; mxram 200; taxname =; naked -; watch =;

/*load matrix and increase trees held in memory*/
proc Marek2015.tnt; hold 200000;
/*set outgroup*/
outgroup 0;
/*run implicit enumeration (exact search)*/
ienum;

/*save tree to 'Marek2015.tmp.tre' in parenthesis format*/
tsave * Marek2015.tmp.tre; save; tsave /;

/*tree statistics: CI and RI*/
run STATS.RUN;

/*optimize, find and list common apomorphies*/
apo [; apo [-;

/*compute consensus and save*/
nelsen*; tsave * Marek2015.nelsen.tre; save 9; tsave/; tchoose
{ strict };

/*Bremer support*/
/*find suboptimal trees by TBR and compare*/
sub 20; bsupport !!+0;

/*symmetrical resampling*/
resample = [mul=hol;] sym rep 10000 prob 33 freq from 0;

/*close log and quit*/
log/; quit;
```

Apomorphies. Unambiguous apomorphies are listed for all trees, ambiguous are listed for some. See also Figure S1 below.

Mikadocephalus gracilirostris:

All trees:

No autapomorphies:

Hudsonelpidia brevirostris:

All trees:

Char. 58: 0 → 1

Macgowania janiceps:

All trees:

No autapomorphies:

Leptonectes tenuirostris:

All trees:

Char. 3: 0 → 1

Char. 45: 1 → 0

Char. 55: 0 → 1

Excalibosaurus costini:

All trees:

Char. 35: 0 → 1

Eurhinosaurus longirostris:

All trees:

Char. 46: 0 → 1

Temnodontosaurus:

All trees:

Char. 6: 1 → 0

Char. 14: 0 → 1

Suevoleviathan disinteger:

All trees:

Char. 47: 0 → 1

Char. 53: 0 → 1

Char. 58: 0 → 1

Ichthyosaurus communis:

All trees:

Char. 47: 0 → 1

Char. 48: 0 → 1

Char. 52: 0 → 1

Char. 53: 0 → 1

Hauffiopteryx typicus:

All trees:

Char. 8: 1 → 0

Char. 50: 0 → 1

Char. 58: 0 → 1

Stenopterygius quadriscissus:

All trees:

Char. 12: 1 → 0

Char. 53: 0 → 1

Some trees:

Char. 34: 0 → 1

Chacaicosaurus cayi:

All trees:

No autapomorphies.

Ophthalmosaurus icenicus:

All trees:

Char. 0: 1 → 0

Char. 25: 0 → 1

Ophthalmosaurus natans:

All trees:

Char. 27: 1 → 0

Some trees:

Char. 1: 1 → 0

Char. 34: 0 → 1

Mollesaurus periallus:

Some trees:

Char. 15: 1 → 0

Char. 21: 1 → 0

Acamptonectes densus:

Some trees:

Char. 21: 0 → 1

Brachypterygius extremus:

Some trees:

Char. 6: 1 → 0

Char. 9: 1 → 0

Char. 42: 0 → 1

Char. 52: 1 → 0

Arthropterygius chrisorum:

Some trees:

Char. 19: 1 → 2

Caypullisaurus bonapartei:

All trees:

Char. 14: 1 → 0

Some trees:

Char. 34: 0 → 1

Char. 57: 0 → 1

Aegirosaurus leptospondylus:

Some trees:

Char. 2: 1 → 0

Platypterygius australis:

All trees:

Char. 12: 1 → 0
 Char. 15: 01 → 2
 Some trees:
 Char. 8: 1 → 0
 Char. 62: 0 → 1

Platypterygius hercynicus:

All trees:
 Char. 3: 1 → 0
 Some trees:
 Char. 6: 01 → 1
 Char. 16: 0 → 1
 Char. 61: 0 → 1

Maiaspondylus lindoei:

All trees:
 Char. 3: 1 → 0
 Some trees:
 Char. 1: 0 → 1
 Char. 50: 1 → 0
 Char. 61: 0 → 1

Athabascasaurus bitumineus:

Some trees:
 Char. 0: 0 → 1
 Char. 1: 01 → 0
 Char. 8: 1 → 0
 Char. 9: 01 → 1
 Char. 13: 1 → 0

Sveltonectes insolitus:

All trees:
 Char. 62: 0 → 1
 Some trees:
 Char. 0: 0 → 1
 Char. 42: 01 → 0

Malawania anachronus:

All trees:
 No autapomorphies:

BRLSI M1399:

All trees:
 Char. 15: 1 → 0
 Char. 20: 0 → 1
 Char. 22: 0 → 1
 Char. 57: 0 → 1
 Char. 63: 1 → 0

Node 28:

All trees:
No synapomorphies

Node 29:
All trees:
Char. 0: 0 → 1
Char. 16: 0 → 1
Char. 30: 1 → 0

Node 30:
All trees:
Char. 54: 1 → 0

Node 31:
All trees:
Char. 45: 0 → 1

Node 32:
All trees:
Char. 4: 0 → 1

Node 33:
All trees:
Char. 63: 0 → 1

Node 34:
All trees:
Char. 39: 0 → 1
Char. 43: 0 → 1
Char. 50: 0 → 1

Node 35:
All trees:
Char. 8: 0 → 1
Char. 16: 0 → 1
Char. 32: 0 → 1
Char. 55: 0 → 1

Node 36:
All trees:
Char. 23: 0 → 1

Node 37:
All trees:
Char. 0: 0 → 1
Char. 3: 0 → 1
Char. 12: 0 → 1
Char. 14: 0 → 1

Node 38:

All trees:

Char. 35: 0 → 1

Char. 43: 0 → 1

Char. 46: 0 → 1

Char. 56: 0 → 1

Char. 60: 0 → 1

Some trees:

Char. 34: 0 → 1

Node 39:

All trees:

Char. 21: 0 → 1

Char. 51: 0 → 1

Node 40:

All trees:

Char. 20: 0 → 1

Some trees:

Char. 18: 0 → 1

Char. 50: 0 → 1

Char. 59: 0 → 1

Node 41:

All trees:

Char. 19: 0 → 12

Char. 37: 0 → 1

Char. 47: 0 → 1

Some trees:

Char. 40: 0 → 1

Time calibration. Time calibration was done in R v. 3.1.2 using the packages ape v. 3.2 and strap v. 1.4 (Paradis *et al.* 2004; Bell and Lloyd 2015). Trees were imported in Newick, self-converted from TNT parenthesis format. Taxon ranges used occurrence data from the literature, to ammonite or conodont biozone level where possible, that was converted into a date using the Geologic Time Scale 2012 (Table S1; Gradstein *et al.* 2012). The time-calibrated tree was created with DatePhylo command of strap, with node ages calculated using the equal-age method of Brusatte *et al.* (2008). A root length of 1.41 Ma was used as this is the smallest age difference between *M. gracilirostris* (242.57 Ma) and its temporally nearest outgroup (*Cymbospondylus piscosus*; 243.99 Ma), as suggested by Bell and Lloyd (2015). This tree was plotted against a geological timescale with geoscalePhylo. Code is presented below.

```
# install and load all of these libraries [install.packages(...)]
library(ape)
library(strap)

# 1.Import tree
tree<-read.tree("Marek2015.ie.newick.tre")

# 2. Time calibrate
```

```

times<-read.table("Marek2015.ie.occurrences.txt",row.names=1,
col.names=c("Taxon", "FAD", "LAD"))
# import taxon ranges table
timeTree<-DatePhylo(tree, times, rlen = 1.41, method =
"equal", add.terminal = FALSE)
# time-calibrate tree

# 3. Plot tree against timescale
geoscalePhylo(ladderize(timeTree), times, upwards=FALSE,
units=c("Age"), boxes="Age", tick.scale="myr", cex.age=0.4,
cex.ts=0.4, cex.tip=0.4, width=1, ts.col=TRUE, ranges=TRUE,
vers="ICS2012")
# ladderizes tree, age timescale and vertical boxes, myr scale, timescale colours, taxon ranges,
ICS version 2012

```

Taxon	First occurrence (Ma)	Last occurrence (Ma)
<i>Mikadocephalus gracilirostris</i>	242.57	240.3
<i>Hudsonelpidia brevirostris</i>	226.5	221.25
<i>Macgowania janiceps</i>	220	216.9
<i>Temnodontosaurus</i>	200.1	174.15
<i>Leptonectes tenuirostris</i>	201.3	190.8
BRLSI M1399	182.7	180.36
<i>Excalibosaurus costini</i>	199.3	197.8
<i>Eurhinosaurus longirostris</i>	182.7	180.36
<i>Suevoleviathan disinteger</i>	181.7	180.36
<i>Hauffiopteryx typicus</i>	182.7	180.36
<i>Ichthyosaurus communis</i>	201.3	196.31
<i>Malawania anachronus</i>	131	125
<i>Stenopterygius quadriscissus</i>	182.7	180.36
<i>Chacaicosaurus cayi</i>	170.3	169.45
<i>Arthropterygius chrisorum</i>	163.47	152.06
<i>Mollesaurus periallus</i>	170.3	169.45
<i>Ophthalmosaurus icenicus</i>	165.59	161.39
<i>Ophthalmosaurus natans</i>	163.5	157.3
<i>Acamptonectes densus</i>	132.9	129.4
<i>Brachypterygius extremus</i>	157.3	148
<i>Maiaspondylus lindoei</i>	111.27	110.22
<i>Aegirosaurus leptospondylus</i>	152.06	149.87
<i>Sveltonectes insolitus</i>	129.41	126.3
<i>Platypterygius hercynicus</i>	118.02	103.13
<i>Caypullisaurus bonapartei</i>	152.1	143.57
<i>Platypterygius australis</i>	113	100.5
<i>Athabascasaurus bitumineus</i>	113	111.5

TABLE S1. Occurrence dates for taxa included in the phylogenetic analysis.

REFERENCES

- BELL, M. A. and LLOYD, G. T. 2014. strap: an R package for plotting phylogenies against stratigraphy and assessing their stratigraphic congruence. *Palaeontology*, **58**, 379–389.
- BRUSATTE, S. L., BENTON, M. J., RUTA, M. and LLOYD, G. T. 2008. Superiority, competition, and opportunism in the evolutionary radiation of dinosaurs. *Science*, **321**, 1485–1488.
- FISCHER, V., APPLEBY, R. M., NAISH, D., LISTON, J., RIDING, J. B., BRINDLEY, S. and GODEFROIT, P. 2013. A basal thunnosaurian from Iraq reveals disparate phylogenetic origins for Cretaceous ichthyosaurs. *Biology Letters*, **9**, 20130021.
- MAISCH, M. W., NAISH, D., KOSMA, R., LISTON, J., JOGER, U., KRÜGER, F. J., PARDO PÉREZ, J., TAINSH, J. and APPLEBY, R. M. 2012. New ophthalmosaurid ichthyosaurs from the European Lower Cretaceous demonstrate extensive ichthyosaur survival across the Jurassic–Cretaceous boundary. *PLoS ONE*, **7**, e29234.
- GOLOBOFF, P. A., FARRIS, J. S. and NIXON, K. C. 2008. TNT, a free program for phylogenetic analysis. *Cladistics*, **24**, 774–786.
- KÄLLERSJÖ, M., OXELMAN, B., RAMÍREZ, M. J. and SZUMIK, C. A. 2003. Improvements to resampling measures of group support. *Cladistics*, **19**, 324–332.
- GRADSTEIN, F. M., OGG, J. C., SCHMITZ, M. D. and OGG, G. M. (eds.) 2012. The Geologic Time Scale 2012. Elsevier, Oxford, 1143 pp.
- PARADIS, E., CLADE, J. and STRIMMER, K. 2004. APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289–290.

SUPPLEMENTARY FIGURE

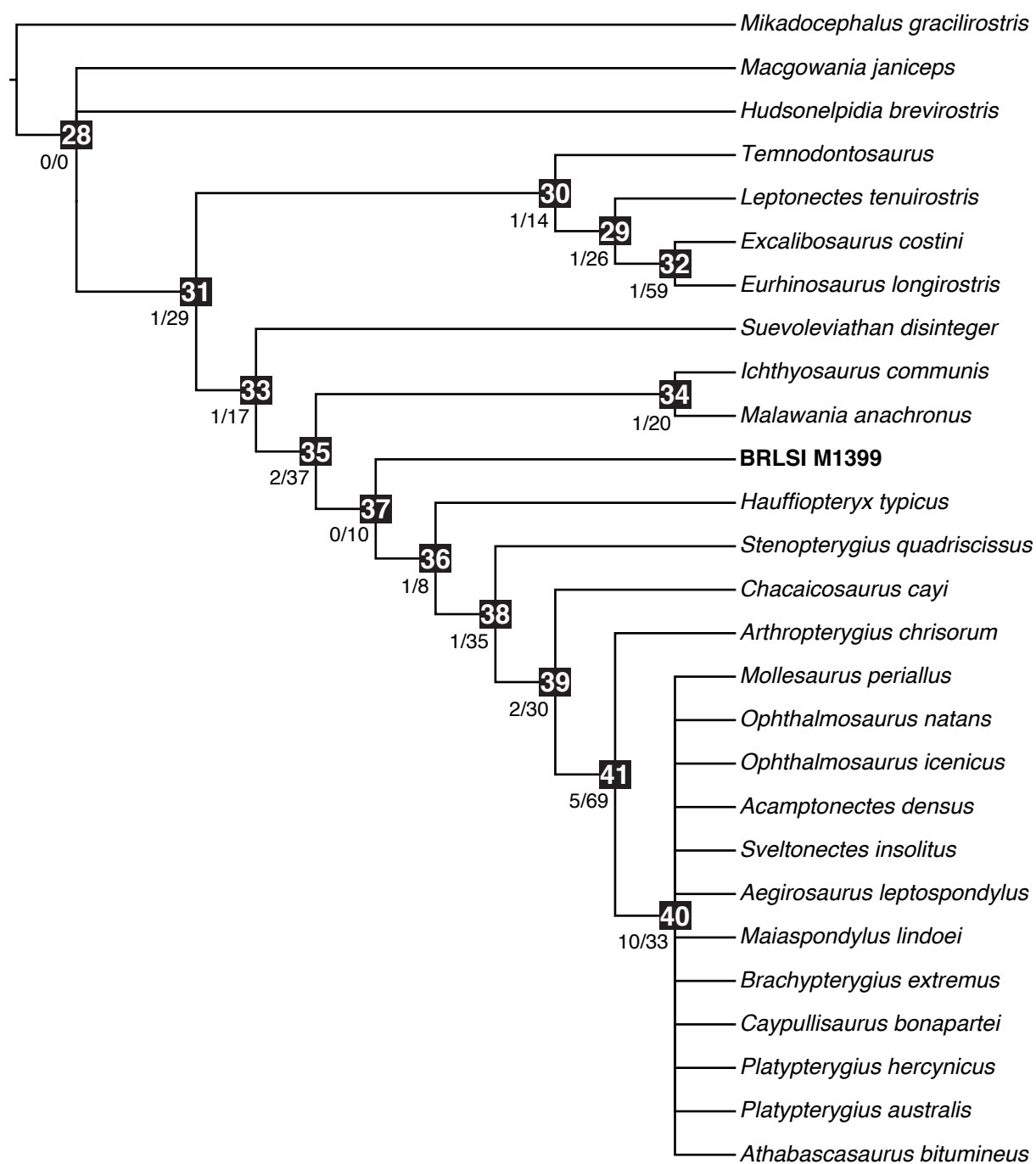


FIG. S1. Strict consensus of nine most parsimonious trees (146 steps) recovered using exact search on the matrix of Fischer *et al.* (2013) with BRLSI M1399 added as an additional taxon, and *Hauffiopteryx typicus* recoded to exclude this material. Node numbers are in squares and correspond to the apomorphies listed above. Node supports are shown to the left of nodes as Bremer supports/symmetrical resampling support (%; 10000 replicates).