

Are Turtles Diapsid Reptiles?

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Abstract

It has been argued that, based on a neighbor-joining analysis of a broad set of fossil reptile morphological data that turtles are diapsid reptiles. A Bayesian phylogenetic analysis does not sustain this view.

Keywords: Turtles, diapsid, neighbor-joining, Bayesian phylogenetic

1.0 Introduction

The traditional classification of reptiles is based on a single key character, the presence and style of fenestration in the temporal region of the skull. Snakes, lizards, crocodiles, dinosaurs and others are 'diapsids': they have (at least in a rudimentary form) two holes in the temporal region. Reptiles in which the skull is completely roofed, with no temporal fenestration, are called 'anapsids'. These include many Palaeozoic forms such as captorhinomorphs, procolophonids and pareiasaurs, but also include Testudines (turtles and tortoises). Consistent with this assumption, recent analyses of the affinities of Testudines have included Palaeozoic taxa only, placing them as akin to captorhinomorphs or procolophonids or

nested within pareiasaurs. [4], in contrast, maintains turtles are diapsid reptiles, based on a neighbor-joining (NJ) assessment ([2]) of fossil reptile morphological data.

2.0 Method

The taxon descriptors in [5] were reformatted under Microsoft *Notebook* to be compatible with the variable coding requirements of [1]. The resulting descriptors were then analyzed under a Bayesian phylogenetic ([2]) software package (*MRBAYES*, [1]; see Figure 1). The software was run on a Dell Inspiron 545 with an Intel Core2 Quad CPU Q8200 clocked at 2.33 GHz, with 8.00 GB RAM, under *Windows Vista Home Premium/SP2*.


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Owenetta      2000?010??1??0011112000211111001110{01}00?000?0002001?0??01?
Araeoscelidia 2001?000??0??001001100000100010000100000000010010000000001
Claudiosaurus 200??100??0??0010011100001?1010000101000?0011011000010111?
Younginiiformes 2001?000??00?0010001100011??0?00?1101000000110010001?0{01}1{01}1
Kuehneosauridae 20?1?01??0??001??0?0?001?0??10?1101000100?11?1110?10??
Testudines
20101111101{01}{01}0211{01}2113{02}011111101{01}1??11{01}{02}011{01}0?1001111010
Rhynchocephalia 2{01}01?0111{01}010001110210001101011011111000{01}01?1001{01}001101121
Squamata
200{01}0{01}111101{01}0011{01}12010{012}11{01}{01}1110{01}11110001{02}{01}1100110011{01}1
{01}21
Choristodera 210110011?01??0111010101010?01?01110100011011011100110111?
Rhynchosauria 211010010?01?00210{01}21000111110101112100010011001000110111?
Prolacertiformes
21011{01}10??01?001000{12}1000{01}1?10100111010001{02}0?1{01}11{01}001101101
Trilophosaurus 211?10111101?0011012110211100??01112100?1{12}011011000?10111?
Archisauriformes
2{01}1111?111011{01}01110{12}100{012}{01}1{01}10100?11010001{012}0?1{01}11{01}101101111
Placodus 2001?1101101?1201202010111100101110100000?111111?1?1110
Eosauropterygia
2{01}01??11101?1201{01}?2110{01}{01}10?0110?110{01}0?01{01}1?11111010101{01}{01}0

Seymouriadae 00000000000000000000000000000000000000000000000000000000000000?00
Diadectomorpha 00000000000000000000000000000000000000000000000000000000000000?00
Caseidae 10000000000000000000000000000000000000000000000000000000000000?00
Ophiacodontidae {01}00000000000000000000000000000000000000000000000000000000000000?00
Edaphosauridae 10000000000000??0000000000000001?00??0?0??0?0?0?00
Sphenacodontidae 10000000000000000000000000000000000000000000000000000000000000?00
Gorganopsia 1000000001200010100011012101011122101000010020000?0?
Cynodontia 1200?0100220011110101111211011121101010011021100?01
Captorhinidae 00010000020000000000000000000000000000000000000000000000000000?00
Paleothyris 00010001010000000000000000000000000000000000000000000000000000?00
Millerettidae 00?00?01?1?00?0?0100000000??00?100001000?10?00100?00
Acleistorhinus ??????????????????????????????????????????????????????????????0??
Lanthanosuchidae 0????0?????????????????????????????????????????????????????????0?
Macroleter 10?1000001000000010001000001?001000010000100010001000?0?
Bradysaurus 11?10000?2200100011011000001000110001000021020011001
Scutosaurus 11?10000?2200100011011001001000110001000021020011211
Anthodon 21?10010?2200100010011001001000110001000021020012111
Procolophon 10?100{01}00210010001001100000100011100100002011001{01}000
Owenetta ???10000?10101?0100?0000??0?01?0????0?????1??0?00
Araeoscelidia 000100010{12}0000000000000000000000000000000000000000000000000000000000000?00
Claudiosaurus 00100101121001010000101?01110001000000000010100100?00
Younginiiformes ?010000011{02}0{01}1010100101?0101100100000100110101100?00
Kuehneosauridae 0010000101012?111?00101?0101??10?????0?10101?00?01
Testudines 22?01{01}1111{02}1011{01}110001011011111110{01}11100211200{01}201?
Rhynchocephalia 00100001{01}12000111000101{01}01010111110{01}111120101100?00
Squamata 0010001111{02}10{01}111000101{01}0101{01}1111011111{01}20101100?01
Choristodera ?010000011{02}121110?00101001111??10?101110?10?01100?00
Rhynchosauria 0010{01}0001101011000011011010111120101110110101110?00
Prolacertiformes 001000001201{12}111{01}001101?0101100120{01}{01}11{01}0{01}10101100?00
Trilophosaurus 1010000012010000000110110101100120101110110101100?00
Archisauriformes
{01}010{01}{01}01{01}1110111000110103{12}{01}11011201{01}1110010101101000
Placodus 00101111110121??1?00101001111?01000110000?01000020?0
Eosauropterygia
20101{01}1111{01}{01}{12}11?1?00101{01}0{01}11{01}10100011000020100000??0
;
end;

```

```

begin mrbayes;
  log start filename=turtle_vardata_log.log replace;
  set autoclose=yes;
  mcmc nruns=2 ngen=800000 printfreq=100
      samplefreq=100 nchains=4 savebrlens=yes
      filename=turtle_vardata;
  mcmc;
  plot filename=turtle_vardata.run1.p;

```

```

plot filename=turtle_vardata.run2.p;
sumt filename=turtle_vardata burnin=10000 contype=halfcompat;
log stop;
end;

```

Figure 1. Template of the *MRBAYES* script [1] used in this study. The script creates 8000000 (*ngen*) Markov Chain ([6]) generations, (Monte Carlo, [7]) sampling every 100 (*samplefreq*) generations. The first 10000 (*burnin*) trees are discarded. Partial tree consensus (*contype*) is allowed. For definitions of other parameters used in this script, see [1]. A description of the character coding shown in the data matrix can be found in [5]

3.0 Results

Figure 2 is the tree generated by the script shown in Figure 1 running under [1]. The time to produce this tree was ~3 hours. Based on the system monitor, two of the four cores on the system performed 99% of the computational work. Total CPU utilization ranged from about 25% to 50%. The computation required approximately 1 GB memory.

```

/-Seymouriadae (1)
|
|- Diadectomorpha (2)
|
|   /- Caseidae (3)
|   |
|   /--+ / Ophiacodontidae (4)
|   | | |
|   | | \---+ / Edaphosauridae (5)
|   | | | |
|   | | | \---+ / Sphenacodontidae (6)
|   | | | |
|   | | | \--+
|   | | | \-----+ / Gorganopsia (7)
|   | | | \-----+
|   | | | \-----+ Cynodontia (8)
|   | |
|   | /-- Captorhinidae (9)
|   | |
|   | /- Paleothyris (10)
|   | /-+|
|   | | | /- Araeoscelidia (20)
|   | | | |
|   | | | | /----- Claudiosaurus (21)
|   | | | | \---+
|   | | | | | /- Younginiiformes (22)
|   | | | | | |
|   | | | | | \-----+
|   | | | | | | /----- Kuehneosauridae (23)
|   | | | | | | |
|   | | | | | | /-- Rhynchocephalia (25)
|   | | | | | | |-----+
|   | | | | | | \---+
|   | | | | | | /-----+ \-- Squamata (26)
|   | | | | | | |
|   | | | | | | /----- Placodus (32)
|   | | | | | | \-----+
|   | | | | | | \- Eosauropterygia (33)
|   | | | | \---+
|   | | | | | /----- Choristodera (27)
|   | | | | | |
|   | | | | | | /----- Rhynchosauria (28)
|   | | | | | | |-----+
|   | | | | | | \---+
|   | | | | | | /-+ \----- Trilophosaurus (30)
|   | | | | | | | /-+
|   | | | | | | | | \---- Archisauriform~ (31)

```


will converge to the population distribution of trees; NJ cannot be guaranteed to satisfy this criterion.

5.0 Acknowledgements

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6.0 References

- [1] Ronquist F and Huelsenbeck JP. MRBAYES 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19 (2003), 1572-1574. Software is available at Ronquist F and Huelsenbeck JP. MRBAYES v3.1.2 for 64-bit Windows. http://sourceforge.net/projects/mrbayes/files/mrbayes/3.2.1/mrbayes-3.2.1_installer_WINx64.msi/download. 2012.
- [2] Felsenstein J. *Inferring Phylogenies*. Sinauer Associates. 2004.
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- [5] O. Rieppel and M. deBraga. Supplementary information for [4]. This data was once available on the *Nature* web site, URL <http://www.nature.com>, but no longer appears to be. A copy to the morphological data, together with a description of the morphological characters

(and associated references) can be obtained from me on request.

- [6] Gilks WR, Richardson S, and Spiegelhalter DJ. *Markov Chain Monte Carlo in Practice*. Chapman and Hall. 1996.
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- [8] Chung KL. *A Course in Probability Theory*. Third Edition. Academic Press. 2001.