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Using creation science to demonstrate evolution 2: morphological continuity within Dinosauria

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Introduction

An alarmingly large portion of the population in North America and Europe rejects evolutionary theory (Mazur, 2005; Miller et al., 2006), and political opposition to the teaching of evolution in public schools is strong (Berkman et al., 2008; Branch & Scott, 2009). This opposition is fuelled by practitioners of the discipline called creation science, the endeavour to find physical evidence supporting a literal interpretation of the biblical book of Genesis. Creation scientists publish technical accounts of their research in journals such as Journal of Creation and Creation Research Society Quarterly. The technical journals of creation science have limited readership, but research published therein is translated into ordinary language for the average reader in a vast, ever-growing collection of popular creationist literature that makes it appear that a literal interpretation of Genesis is supported by scientific studies. Some such books have even become best sellers (e.g. Strobel, 2004). This phenomenon is a problem, because it increases the already huge number of voters who believe that the creationist world view has scientific validity and empirical support.

Because of this onslaught, it is imperative to demonstrate that evolutionary theory is supported by empirical evidence. Towards this end, it is important to use methodology that is endorsed by creation science, so that creation scientists cannot reject the results of such studies without rejecting their own research. Towards that end, here I present a study using methodology endorsed and used in baraminology, the branch of creation science in which organisms are classified into separately created ‘kinds’ (baramins).

Mainstream biologists and baraminologists alike consider morphological continuity between species to be evidence of genetic relatedness. Creationists long ago abandoned the concept of fixity of species, and for many decades, they have accepted that speciation occurs within baramins (Siegler, 1978). Baraminologists measure morphological continuity among species, accepting different species as part of the same baramin if they form a continuous morphological series. They classify different groups of species into different baramins if the groups are

Keywords:
baraminology; Ceratopsia; Coelurosauria; creationism; creation science; Dinosauria; Microraptor; Ornithischia; Sauropoda; Theropoda.

Abstract

Creationist literature claims that sufficient gaps in morphological continuity exist to classify dinosaurs into several distinct baramins (‘created kinds’). Here, I apply the baraminological method called taxon correlation to test for morphological continuity within and between dinosaurian taxa. The results show enough morphological continuity within Dinosauria to consider most dinosaurs genetically related, even by this creationist standard. A continuous morphological spectrum unites the basal members of Saurischia, Theropoda, Sauropodomorpha, Ornithischia, Thyreophora, Marginocephalia, and Ornithopoda with Nodosauridae and Pachycephalosauria and with the basal ornithodirans Silesaurus and Marasuchus. Morphological gaps in the known fossil record separate only seven groups from the rest of Dinosauria. Those groups are Therizinosauroidea + Oviraptorosauria + Paraves, Tazoudasaurus + Euaurupoda, Ankylosauridae, Stegosauria, Neoceratopsia, basal Hadrosauriformes and Hadrosauridae. Each of these seven groups exhibits within-group morphological continuity, indicating common descent for all the group’s members, even according to this creationist standard.

separated from each other by a gap in morphological continuity (Robinson & Cavanaugh, 1998; Wood, 2006, 2011).

Mainstream biologists consider morphological continuity through fossil lineages to be one of the main lines of evidence for macroevolution. Morphological continuity between basal members of different lineages is one of the main lines of evidence that those lineages evolved from a common ancestor; for example, in recent years, a plethora of transitional fossils linking major dinosaurian taxa have been discovered, increasing the known morphological continuity within Dinosauria and supporting the long-standing claim by mainstream biologists that all dinosaurs are descended from a common dinosaurian ancestor (e.g. Kirkland et al., 2005; Xu et al., 2006; Choiniere et al., 2010; Yates et al., 2010). However, creationist literature claims that sufficient morphological discontinuity exists between dinosaurian taxa to effectively demonstrate special creation (e.g. Gish, 1995; Bergman, 2009). Here, I use the baraminological technique called taxon correlation to test that claim.

Taxon correlation begins with a matrix of character states for a set of taxa, e.g. the matrices of anatomical data that are routinely used by systematists in phylogenetic studies. The technique uses a Pearson correlation coefficient to measure the morphological similarity between taxa in the matrix. A detailed description is supplied by baraminologist Todd Wood (2011):

Creationists Robinson & Cavanaugh (1998) introduced the taxon correlation method, wherein a Pearson correlation coefficient is used to estimate the relative similarity of two taxa. Beginning with a set of characters with discrete states, a square distance matrix \( D \) with elements \( d_{ij} \) representing the per cent difference between the character states of taxa \( i \) and \( j \) is calculated. The relative similarity of taxa \( i \) and \( j \) is then estimated from \( D \) by calculating the Pearson correlation coefficient for rows \( i \) and \( j \) of \( D \). In theory, two taxa that are similar should have similar distances to the same third taxon and should therefore exhibit positive correlation. Negative correlation should occur between taxa that are very different (i.e. taxa that are close to \( i \) will be far from \( j \) and vice versa). Statistical significance of the correlation can be estimated using a \( t \) distribution with \( n - 2 \) degrees of freedom, where \( n \) is the number of taxa. \( P \)-values < 0.05 are considered significant. When two groups of taxa exhibit significant, negative distance correlation, a morphological discontinuity is inferred.

Simply put, after a taxon correlation analysis, positive correlation occurs between taxa that are very similar, and negative correlation occurs between taxa that are very dissimilar. If two groups of taxa exhibit significant, negative correlation, a baraminologist infers that a morphological gap exists between the two groups, and the two are considered to represent separate baramins (Robinson & Cavanaugh, 1998; Wood, 2011).

To visualize morphological distances between taxa, some baraminologists use classic multidimensional scaling (CMDS). This is a technique in which the matrix of character states is converted into a matrix of morphological distances between taxa, and from that matrix of morphological distances, a set of three-dimensional coordinates is calculated. These coordinates are used to construct a three-dimensional scatter plot in which each dot represents a taxon, and the distances between dots represent morphological distances between taxa (Wood, 2005). In a previous publication, I used CMDS to visualize morphological distances between taxa within the dinosaurian clade Coelurosauria. The resulting scatter plot appeared to show a continuous morphological spectrum linking basal, Mesozoic birds (Archaeopteryx, Sapornis and Confuciusornis) and several coelurosaurian groups (Senter, 2010). I concluded that the study demonstrated the evolutionary relatedness of these groups with each other and with basal birds in such a way as could not be countered by creation science. However, baraminologist Todd Wood subsequently pointed out that I had mistaken a mere visualization technique (CMDS) for a technique that a baraminologist would accept as a test of genetic relatedness. Taxon correlation is a method that a baraminologist would accept as a test of genetic relatedness. Wood (2011) restudied the Coelurosauria matrix using taxon correlation and found morphological discontinuity between three coelurosaurian groups: Oviraptorosauria, basal birds + Deinonychosauria and a group consisting of the remaining coelurosaurs. A baraminologist could therefore infer that three baramins had been identified.

Since then, the phylogenetic data matrix used in those studies (Senter, 2010; Wood, 2011) has been enormously improved by an overhaul that included a vast number of corrections and updates, detailed later. Most of the changes resulted from examination of a large number of specimens that I had not previously had the chance to study, at the Institute of Vertebrate Paleontology and Paleoanthropology (IVPP) during a 2010 trip to Beijing. Enough changes were made to justify a new phylogenetic analysis and a new taxon correlation study with the matrix, to see whether the technique would now identify greater morphological continuity through Coelurosauria. It also seemed prudent to run taxon correlation studies on phylogenetic data matrices of other dinosaurian clades to measure morphological continuity within and between other major dinosaurian taxa. Here, therefore, I present a study incorporating taxon correlation across Dinosauria to test for morphological continuity across the group as a whole and within its subgroups.

**Methods**

**Phylogenetic analysis of Coelurosauria**

The character list (Appendix S1) and phylogenetic matrix (Appendix S2) used here for Coelurosauria are improved versions of their previously published counterparts.
(Senter, 2010), which were themselves improved versions (Senter, 2007) of a previously published matrix and character list (Kirkland et al., 2005). In each case, character state codings were updated according to new observations of fossil specimens and casts and according to insights from newly published literature. The improvements present in the current matrix and character list include the addition of new operational taxonomic units (OTUs) and characters, the arranging of all character states in anatomical order, and the updating and correction of large amounts of data for several OTUs as a result of recent personal examination of specimens (Fig. 1).

There are a few changes to previously used OTUs that deserve detailed justification. These include the splitting
of the previous OTU ‘Microraptor zhaoianus’ into four OTUs, the addition of data from NGMC (National Geological Museum of China, Beijing, China) 91 to the OTU Sinornithosaurus millenii, the addition of data from Linheraptor exquisitus to the OTU Tsagaan mangas and profound changes to the OTUs Parviceratops remotus and Shuvuuia deserti. Explanations and justifications for these changes are given in Appendix S3.

The matrix used here includes 392 characters and 102 taxa, making it the most comprehensive phylogenetic data matrix for Coelurosauria yet published. Phylogenetic analysis was performed with PAUP 4.0 for Windows (Swofford, 2001). A heuristic search with 1000 random addition sequence replicates was performed, with no limit to ‘maxtrees’. The decay index (Bremer support) of each clade was found with the same software after insertion of a command line that was created using the program MacClade 3.08a (Maddison & Maddison, 1999).

Phylogenetic analysis of Centrosaurinae

To the phylogenetic data matrix of McDonald & Horner (2010), I added Diabloceratops eatoni, using information on D. eatoni from Kirkland & DeBlieux (2010) (Appendix S4). To accommodate character states present in D. eatoni that were not included in the character list of McDonald & Horner (2010), I added a state 3 (small, conical horn) to character 2 (nasal ornamentation type in adult) and a state 4 (dorsolateral) to character 11 (orientation of supraorbital horns). Phylogenetic analysis and decay analysis were conducted as described earlier for the Coelurosauria matrix.

Taxon correlation

For taxon correlation, I used the program BDISTMDS (Wood, 2008), which is freely available for use at http://www.bryancore.org, to analyse the Coelurosauria and Centrosaurinae matrices described earlier. I used the same software to analyse several previously published phylogenetic data matrices, each emphasizing a different dinosaurian group: non-coelurosaurian Theropoda (Smith et al., 2008), basal Saurropodomorpha (Yates et al., 2010; matrix B), sauropoda (Zaher et al., 2011), Ornithischia (Butler et al., 2008), Ankylosauria (Parsons & Parsons, 2009), Stegosauria (Mateus et al., 2009), Iguanodontia (McDonald et al., 2010), Hadrosauridae (Prieto-Márquez & Salinas, 2010), Ceratopsia (Makovicky, 2010) and Chasmosaurinae (Sampson et al., 2010). For the Stegosauria matrix, I changed to ‘?’ any character state that had been coded with a letter for gap weighting in the original matrix.

BDISTMDS ignores any character with a relevance cut-off (ratio of the number of OTUs in which the state is known, to the total number of OTUs) below a value set by the researcher. Following the example of Wood (2011), I set the relevance cut-off at 75% in each analysis. For each matrix, the original number of characters and the number of characters used by BDISTMDS for taxon correlation are given in Table 1.

Again following the example of Wood (2011), for each analysis I initially included only those OTUs for which ≥50% of the character states are known. In some cases in which taxon correlation identified a morphological gap between the groups of OTUs, I ran the taxon correlation analysis after adding a phylogenetically intermediate OTU in which <50% of the character states are known, to test whether its addition would result in the bridging of a morphological gap. OTUs used in this way are mentioned in the Results section.

For each analysed matrix, I ran taxon correlation analysis after deleting all taxa for which no description had been published before 1990. This was to test whether recent discoveries have filled morphological gaps in the previously known dinosaurian fossil record.

In the taxon correlation analysis of the Coelurosauria matrix, I used three suprageneric OTUs, two of which are composed of pairs of sister taxa (Protarchaeopteryx + Incisivosaurus and Epidendrosaurus + Epidipteryx) and one of which is composed of a group of four therizinosauria sister taxa (Neimongosaurus + Erlikosaurus + Erlikosaurus + Therizinosaurus). Sister taxon relationships were determined according to the results of the phylogenetic analysis described earlier. The suprageneric taxa were included so as to be able to include representatives of coelurosaurian clades for which no single genus is known.

Table 1 Number of characters used in taxon correlation analyses. O = original number of characters in the phylogenetic data matrix. N = number of characters used by the program BDISTMDS (Wood, 2008) for taxon correlation analysis. 1990 = number of characters used by BDISTMDS in the taxon correlation analysis after deletion of taxa described after 1990.

<table>
<thead>
<tr>
<th>Taxon of interest</th>
<th>O</th>
<th>N</th>
<th>1990</th>
<th>Source of matrix</th>
</tr>
</thead>
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<tr>
<td>Coelurosauria</td>
<td>391</td>
<td>229</td>
<td>300</td>
<td>This study</td>
</tr>
<tr>
<td>basalmostropoda</td>
<td>353</td>
<td>160</td>
<td>201</td>
<td>Smith et al. (2008)</td>
</tr>
<tr>
<td>+ Cryolophosaurus</td>
<td></td>
<td>144</td>
<td>n/a</td>
<td>Smith et al. (2008)</td>
</tr>
<tr>
<td>basal</td>
<td>353</td>
<td>209</td>
<td>258</td>
<td>Yates et al. (2010)</td>
</tr>
<tr>
<td>Sauropodomorpha</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>basal</td>
<td>246</td>
<td>135</td>
<td>124</td>
<td>Zaher et al. (2011)</td>
</tr>
<tr>
<td>+ Ornithischia</td>
<td>221</td>
<td>151</td>
<td>149</td>
<td>Butler et al. (2008)</td>
</tr>
<tr>
<td>basal</td>
<td>221</td>
<td>140</td>
<td>n/a</td>
<td>Butler et al. (2008)</td>
</tr>
<tr>
<td>+ Chasmosaurus</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stegosauria</td>
<td>89</td>
<td>56</td>
<td>61</td>
<td>Mateus et al. (2009)</td>
</tr>
<tr>
<td>Ankylosauria</td>
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<td>34</td>
<td>44</td>
<td>Parsons &amp; Parsons (2009)</td>
</tr>
<tr>
<td>basalmostropida</td>
<td>147</td>
<td>88</td>
<td>125</td>
<td>Makovicky (2010)</td>
</tr>
<tr>
<td>+ Zuniceratops</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Centrosaurinae</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>basalmostropida</td>
<td>148</td>
<td>103</td>
<td>103</td>
<td>Sampson et al. (2010)</td>
</tr>
<tr>
<td>+ Zuniceratops</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hadrosauridae</td>
<td>370</td>
<td>228</td>
<td>296</td>
<td>Prieto-Márquez &amp; Salinas (2010).</td>
</tr>
</tbody>
</table>
from material from which \( \geq 50\% \) of the characters in the matrix could be coded. I also combined data from the three species of Microraptor into a single OTU for taxon correlation, so as to be able to maximize utilized data from this genus.

Some of the other matrices included suprageneric OTUs with much greater taxonomic breadth. Such OTUs (Crurotarsi, Theropoda, Neotheropoda, Prosauropoda, Neosauropoda, Ornithischia, Ankyloploplexia, Centrosauria + Leptoceratopsidae, Ankylosauria and Stegosauria) were deleted from the matrices before taxon correlation so as not to introduce artefacts into the results.

Results

Phylogenetic analysis of Coelurosauria

Phylogenetic analysis of the Coelurosauria matrix recovered 82 most parsimonious trees with 1284 steps. For these trees, the consistency index is 0.3780, the homoplasy index is 0.6220, the retention index is 0.8119, and the rescaled consistency index is 0.3069. These measures are better for the current analysis than they were for analyses using previous versions of the matrix (Senter, 2007, 2010), indicating greater reliability of the current matrix. This is expected, because the current matrix incorporates a vast number of corrections based on observations of material that I had not previously had the chance to examine.

The strict consensus tree (Fig. 1) is similar to that produced by the previous version of the matrix (Senter, 2010). However, there are a few important differences. Therizinosauroida and Alvarezsauroidea have switched places. Caudipteryx and Microvenator are found to be sister taxa. The old OTU ‘Microraptor zhaoianus’, which formerly included data from Cryptovolans, is found to be polyphyletic. Cryptovolans clusters not with Microraptor but with Sinornithosaurus and Graciliraptor. The M. zhaoianus holotype clusters with Microraptor gui rather than with the CAGS ‘M. zhaoianus’ specimens, indicating that the latter represent an unnamed species of Microraptor. Velociraptorinæ, instead of consisting only of Velociraptor (Senter et al., 2004; Senter, 2007, 2010), includes Tsagaan and Adasaurus. Also, for many clades, decay indices (Fig. 1) are much improved over those of analyses using previous versions of the matrix (Senter, 2007, 2010). Synapomorphies uniting the various clades are given in Appendix S5.

Phylogenetic analysis of Centrosaurinae

Phylogenetic analysis of the Centrosaurinae matrix recovered a single most parsimonious tree of 43 steps (Fig. 2). In this tree, Diabloceratops is the sister taxon to all other Centrosaurinae. Otherwise the tree is identical to that found by McDonald & Horner (2010). For the tree, the consistency index is 0.9535, the homoplasy index is 0.0667, the retention index is 0.9355 and the rescaled consistency index is 0.8920. Synapomorphies uniting the various clades are given in Appendix S6.

Taxon correlation

For the Coelurosauria matrix (described under Methods, earlier), taxon correlation reveals significant, positive correlation within and significant, negative correlation between two groups (Fig. 3). One group includes Tyrannosauroidea, Compsognathidae, Ornithomimosauria, Alvarezsauroidea, Ornitholestes, and the non-coelurosaurian outgroups Sinraptor, Allosaurus and Dilophosaurus. The second group includes Oviraptorosauroida, Therizinosauria, Troodontidae and Dromaeosauridae, and all included members of Avialae (birds). Interestingly, significant, positive correlation links the three OTUs Protarchaeopteryx + Incisivosaurus, Caudipteryx and Beipiaosaurus not only with Oviraptoridae (Khaan, Ingenia, Citipati, IGM 100/42) but also with Paraves (Troodontidae, Dromaeosauridae and Avialae), but paravians do not exhibit significant, positive correlation with oviraptorosaurs. The three OTUs therefore ‘bridge’ a morphological gap between Oviraptoridae and Paraves. Also, therizinosauroids (Beipiaosaurus, Falcarius and Therizinosauridae) exhibit positive correlation with compsgnathids, Ornitholestes and Haplocheirus as well as the Oviraptorosauria + Paraves group. For the version of the Coelurosauria matrix using only taxa that had been described by 1990 (hereafter referred to in each case as ‘the 1990 version of the matrix’ for the sake of brevity), taxon correlation reveals significant, negative correlation between three groups: Oviraptorosauroida, Dromaeosauridae + Archaeopteryx; and a group composed of Tyrannosauroidea, Ornithomimosauria, Compsognathus and Ornitholestes; and the non-coelurosaurian outgroups Allosaurus and Dilophosaurus (Fig. 3).

For the non-coelurosaurian Theropoda matrix (Smith et al., 2008), taxon correlation reveals significant, positive correlation within three groups: Paraves, coelophysoid theropods + Elasmosaurus + Herrerasaurus + Plateosaurus + Silesaurus and a group composed of other Tetanurae
Fig. 3 Results of taxon correlation analysis of Coelurosauria. Filled squares represent positive correlation between taxa, and open circles represent negative correlation between taxa. (a) Results of taxon correlation using taxa described before and since 1990. (b) Results of taxon correlation using only taxa described by the end of 1990. (c) Phylogenetic relationships (as found here) of taxa used in the taxon correlation.
Fig. 4 Results of taxon correlation analysis of Theropoda. Filled squares represent positive correlation between taxa, and open circles represent negative correlation between taxa. (a) Results of taxon correlation using taxa described before and since 1990, without Cryolophosaurus. (b) Results of taxon correlation using taxa described before and since 1990, with Cryolophosaurus. (c) Results of taxon correlation using only taxa described by the end of 1990. (d) Phylogenetic relationships (Smith et al., 2008) of taxa used in the taxon correlation analysis, with each boxed group of silhouettes indicating a group for which taxon correlation found within-group morphological continuity; for silhouette groups in different boxes, taxon correlation found morphological discontinuity between the groups. It should be noted that the boxing of silhouettes in part c of this figure is per the results of the more taxonomically inclusive correlation analysis illustrated in part b, not the less inclusive analyses illustrated in parts a and c. Silhouettes are not drawn to scale.

Fig. 3 (continued) analysis, with each boxed group of silhouettes indicating a group for which taxon correlation found within-group morphological continuity; for silhouette groups in different boxes, taxon correlation found morphological discontinuity between the groups. It should be noted that the boxing of silhouettes in part c of this figure is per the results of the more taxonomically inclusive correlation analysis illustrated in part a, not the less inclusive analysis illustrated in part b. Silhouettes are not drawn to scale.
(Ceratosaurus, Abelisauridae, Baryonyx, Carnosauria, Tyranosauroida, Ornithomimosauria and Ornitholestes) (Fig. 4). Significant, negative correlation exists between the three groups, except that Paraves is positively correlated with Tyrannosauridae, Ornitholestes and Ornithomimosauria (represented by Sinornithomimus). The 1990 version of the matrix yields similar results except that Ornitholestes is positively correlated only with Paraves (Fig. 4).

When Cryolophosaurus (for which 47.9% of the character states are known) is added to the matrix, it and Ceratosaurus and Dilophosaurus are positively correlated both with the group containing Coelophysoidae and with the group containing basal Tetanurae (Fig. 4). The morphological gap between the two groups is thus bridged.

For the basal Sauropodomorpha matrix (Yates et al., 2010, matrix B), taxon correlation reveals significant,
negative correlation between two groups. One includes Tazoudasaurus and Eusauropoda. The other includes the remaining sauropodomorphs, the basal saurischians Herrerasaurus and Eoraptor, the basal ornithodirans Marasuchus and Silesaurus and the basal archosauriform outgroup Euparkeria. Significant, positive correlation is present among the members of each of the two groups (Fig. 5). The morphological gap between the two groups was not bridged by the addition of any phylogenetically intermediate taxon (Antetonitrus, Lessemsaurus, Gongxianosaurus, Vulcanodon and Barapasaurus). The 1990 version of the matrix yields similar results (Fig. 5).

For the Sauropoda matrix (Zaher et al., 2011), taxon correlation reveals significant, positive correlation across advanced titanosaurs (Tapuiasaurus, Rapetosaurus, Saltasaurus and Opisthocoelicaudia) and across a group composed of the rest of Eusauropoda (Fig. 6). It reveals significant, negative correlation between several members of the two groups. However, the basal titanosaur Phuwiangosaurus is positively correlated with both groups, thus bridging the morphological gap between them. For the 1990 version of the Sauropoda matrix, taxon correlation reveals significant, positive correlation within each of the same two groups and significant, negative correlation between the two, with no taxon bridging the gap between them (Fig. 6).

For the Ornithischia matrix (Butler et al., 2008), taxon correlation reveals significant, positive correlation across nearly all included ornithischians and between ornithischians and Herrerasaurus and Euparkeria (Fig. 7). Pachycephalosaurs and basal ceratopsians are exceptions; the former are correlated negatively with other ornithischians, and the latter are neither positively nor negatively correlated with other ornithischians. The 1990 version of the matrix yields similar results, except that Herrerasaurus and Euparkeria are not correlated with ornithischians (Fig. 7).

When the recently described basal ceratopsian Chaoyangsaurus (for which 36.7% of the character states are known) is included in the taxon correlation analysis, Pachycephalosauria and Ceratopsia join the rest of Ornithischia with positive correlation (Fig. 7).
Fig. 7 Results of taxon correlation analysis of basal Ornithischia. Filled squares represent positive correlation between taxa, and open circles represent negative correlation between taxa. (a) Results of taxon correlation using taxa described before and since 1990, without Chaoyangsaurus. (b) Results of taxon correlation using taxa described before and since 1990, with Chaoyangsaurus. (c) Results of taxon correlation using only taxa described by the end of 1990. (d) Phylogenetic relationships (Butler et al., 2008) of taxa used in the taxon correlation analysis, with box around silhouettes indicating that taxon correlation found morphological continuity within the group. It should be noted that the boxing of silhouettes in part c of this figure is per the results of the more taxonomically inclusive correlation analysis illustrated in part b, not the less inclusive analyses illustrated in parts a and c. Silhouettes are not drawn to scale.
For the Ankylosauria matrix (Parsons & Parsons, 2009), taxon correlation reveals significant, positive correlation within Ankylosauridae and within a group composed of Nodosauridae, *Scelidosaurus* and the stegosaur *Huayangosaurus* (Fig. 8). It reveals significant, negative correlation between the two groups. *Cedarpelta* does not correlate with either group. Addition of the phylogenetically intermediate OTU *Minmi* does not result in a bridging of the morphological gap. The 1990 version of the matrix yields similar results (Fig. 8).

For the Stegosauria matrix (Mateus et al., 2009), taxon correlation reveals significant, positive correlation within three groups: Stegosauria, Ankylosauria and *Scelidosaurus + Scutellosaurus + Lesothosaurus* (Fig. 9). It
reveals significant, negative correlation between the last group and Stegosauria. Addition of the basal stegosaur *Gigantosaurus* does not result in a bridging of the morphological gap between stegosaurs and either other group. The 1990 version of the matrix yields similar results except that no correlation is found among stegosaurs (Fig. 9).

For the Iguanodontia matrix (McDonald et al., 2010), taxon correlation reveals significant, positive correlation across the advanced iguanodontian clade Hadrosauriformes (Fig. 10). It also reveals significant, positive correlation in a group composed of basal Iguanodontia plus *Hypsilophodon* and *Lesothosaurus*. There is significant, negative correlation between the two groups. The morphological gap between the two groups was not bridged by the addition of any phylogenetically intermediate taxon (*Cumnornia*, *Cantopsaurus* aphanoecetes, *Hippodraco*, *Theiophytalia* and *Iguanacolossus*). The 1990 version of the matrix yields similar results (Fig. 10).

For the Hadrosauridae matrix (Prieto-Márquez & Salinas, 2010), taxon correlation reveals significant, positive correlation within Hadrosauridae and within non-hadrosaurid hadrosauriforms (Fig. 11). It reveals significant, negative correlation between the two groups. It also reveals significant, positive correlation between the non-hadrosaurid hadrosauriform *Lophorhothon* and several hadrosaurine OTUs. The 1990 version of the matrix yields similar results except that *Lophorhothon* is positively correlated with only one hadrosaurine OTU: *Kritosaurus* (Fig. 11).

For the Ceratopsia matrix (Makovicky, 2010), taxon correlation reveals significant, positive correlation within Neoceratopsia, except that the two included members of Ceratopsidae (*Triceratops* and *Centrosaurus*) are not positively or negatively correlated with any other neoceratopsian taxon (Fig. 12). It reveals significant, positive correlation within a group composed of the ornithopod *Hypsilophodon*, the pachycephalosaur *Stegoceras* and the basal ceratopsians *Yimelong*, *Psittacosaurus* and *Chaoyangosaurus*. It also reveals significant, negative correlation between that group and all Neoceratopsia. The 1990 version of the matrix yields similar results (Fig. 12).

For the Centrosaurinae matrix (described under Methods, earlier), taxon correlation reveals significant, positive correlation across Centrosaurinae (Fig. 13). It reveals significant, negative correlation between *Leptoceratops* and Centrosaurinae and between *Leptoceratops* and the suprageneric taxon Chasmosaurinae. It reveals neither positive nor negative correlation between Chasmosaurinae and Centrosaurinae. The 1990 version of the matrix yields similar results (Fig. 13).

For the Chasmosaurinae matrix (Sampson et al., 2010), taxon correlation reveals significant, positive correlation across Ceratopsidae and between the basal neoceratopsians *Protoceratops* and Centrosaurinae and between *Leptoceratops* and the suprageneric taxon Chasmosaurinae. It reveals neither positive nor negative correlation between Chasmosaurinae and Centrosaurinae. The 1990 version of the matrix yields similar results except that Chasmosaurinae and Centrosaurinae are neither positively nor negatively correlated (Fig. 14).

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Fig. 9 Results of taxon correlation analysis of Stegosauria. Filled squares represent positive correlation between taxa, and open circles represent negative correlation between taxa. (a) Results of taxon correlation using taxa described before and since 1990. (b) Results of taxon correlation using only taxa described by the end of 1990. (c) Phylogenetic relationships (Mateus et al., 2009) of taxa used in the taxon correlation analysis, with each boxed group of silhouettes indicating a group for which taxon correlation found within-group morphological continuity; for silhouette groups in different boxes, taxon correlation found morphological discontinuity between the groups. It should be noted that the boxing of silhouettes in part c of this figure is per the results of the more taxonomically inclusive correlation analysis illustrated in part a, not the less inclusive analysis illustrated in part b. Silhouettes are not drawn to scale.
Discussion

At first, the results of the taxon correlation analyses appear to imply good news for the creationist world view, on several fronts. First, seven major dinosaurian groups (birdlike coelurosaurs, *Tazoudasaurus* + Eusauropoda, Stegosauria, Ankylosauridae, Neoceratopsia, Hadrosauridae and basal Hadrosauriformes) are separated from the rest of Dinosauria by morphological gaps (Fig. 15). Creationist inferences that variety within Eusauropoda (Morris, 1999) and Ceratopsidae (Ham, 2009) represent diversification within separately created kinds are congruent with these results. Second, each morphologically continuous group found by taxon correlation includes at least some herbivores. This is congruent with the creationist assertion that all carnivorous animals are descendants of originally herbivorous ancestors (Unfred, 1990; Gish, 1992; Ham, 1998, 2006, 2009; Larsen, 2001; McIntosh & Hodge, 2006). Third, although creationists have answered the problem of room on Noah’s ark for multiple pairs of gigantic dinosaurs by asserting that only about 50 ‘created kinds’ of dinosaurs existed (Ham, 1998, 2001, 2006, 2009; Morris, 1999), the problem is solved even better by the results of this study, in which only eight dinosaur ‘kinds’ are found.

However, a second look reveals that these results are at odds with the creationist view. Whether there were...
Fig. 11 Results of taxon correlation analysis of Hadrosauridae. Filled squares represent positive correlation between taxa, and open circles represent negative correlation between taxa. (a) Results of taxon correlation using taxa described before and since 1990. (b) Results of taxon correlation using only taxa described by the end of 1990. (c) Phylogenetic relationships (Prieto-Márquez & Salinas, 2010) of taxa used in the taxon correlation analysis, with each boxed group of silhouettes indicating a group for which taxon correlation found within-group morphological continuity; for silhouette groups in different boxes, taxon correlation found morphological discontinuity between the groups. It should be noted that the boxing of silhouettes in part c of this figure is per the results of the more taxonomically inclusive correlation analysis illustrated in part a, not the less inclusive analysis illustrated in part b. Silhouettes are not drawn to scale.
eight dinosaur ‘kinds’ or 50, the diversity within each ‘kind’ is enormous. Acceptance that such diversity arose by natural means in only a few thousand years therefore stretches the imagination. The largest dinosaurian baramin recovered by this study includes *Euparkeria*, basal ornithodirans (*Silesaurus* and *Marasuchus*), basal saurischians, basal ornithischians, basal sauropodomorphs, basal thyreophorans, nodosaurid ankylosaurs, pachycephalosaurs, basal ceratopsians, basal ornithopods and all but the most birdlike theropods in an unbroken spectrum of morphological continuity. The creationist viewpoint allows for diversification within baramins, but the diversity within this morphologically continuous group is extreme. Also, the inclusion of the Middle Triassic non-dinosaurs *Euparkeria* and *Marasuchus* within the group is at odds with the creationist claim that fossil representatives of the predinosaurian, ancestral stock from which dino-

Fig. 12 Results of taxon correlation analysis of Ceratopsia. Filled squares represent positive correlation between taxa, and open circles represent negative correlation between taxa. (a) Results of taxon correlation using taxa described before and since 1990. (b) Results of taxon correlation using only taxa described by the end of 1990. (c) Phylogenetic relationships (Makovicky, 2010) of taxa used in the taxon correlation analysis, with each boxed group of silhouettes indicating a group for which taxon correlation found within-group morphological continuity; for silhouette groups in different boxes, taxon correlation found morphological discontinuity between the groups. It should be noted that the boxing of silhouettes in part c of this figure is per the results of the more taxonomically inclusive correlation analysis illustrated in part a, not the less inclusive analysis illustrated in part b. Silhouettes are not drawn to scale.
saurs arose have never been found (DeYoung, 2000; Ham, 2006; Bergman, 2009).

Because *Euparkeria*, *Silesaurus* and *Marasuchus* are used as outgroups, one could reasonably argue that the positive correlation between them and basal members of dinosaurian lineages is an artefact of character coding. It is possible that if more characters relevant to non-dinosaurs were included, taxon correlation would have found negative correlation between the outgroups and the dinosaurs. However, even so, the results of the taxon correlation analyses show that dinosaur-relevant characters still link basal saurischians (e.g. *Herrerasaurus*) with basal ornithischians (e.g. *Heterodontosaurus* and *Agilisaurus*). Morphological similarity between the basal members of both groups is therefore arguably real.

Furthermore, taxon correlation did not unambiguously separate theropods into separate baramins. When the Coelurosauria matrix was used, positive correlation was found between therizinosaurs and Paraves + Oviraptorosaurus and also between therizinosaurs and the more basal coelurosaurian taxa Compsognathidae, *Ornitholestes* and *Haplocheirus* (Fig. 3). One could therefore reasonably argue that therizinosaurs bridge the morphological gap between the more birdlike theropods and the rest of Theropoda. Also, taxon correlation with the basal Theropoda matrix found significant, positive correlation between Paraves and basal coelosaurs such as *Ornitholestes* and tyrannosaurs (Fig. 4).

Another apparent gap between taxa that could be interpreted as having been bridged is the one between Hadrosauridae and basal Hadrosauriformes. *Lophorhothon*, which occupies a phylogenetic position immediately outside Hadrosauridae (Prieto-Márquez & Salinas, 2010), is positively correlated both with Hadrosauridae and with basal hadrosauriforms (Fig. 11). It therefore can be considered to bridge the morphological gap between the two groups.

Another possibly bridged gap is the one between basal ceratopsians and Neoceratopsia. When the Ornithischia matrix was used, no such gap appeared; the basal ceratopsian *Chaoyangsaurus* was positively correlated with the neoceratopsians *Archaeoceratops* and *Liaoceratops* (Fig. 7). Another apparent gap is present between Ceratopsidae and *Leptoceratops* when the Centrosaurinae matrix is used (Fig. 13) and between Ceratopsidae and *Leptoceratops + Protoceratops* when the Chasmosaurinae matrix is used (Fig. 14). However, in both cases, the apparent gap could be an artifact of noninclusion of *Zuniceratops*, which bridges the gap when the Ceratopsia matrix is used (Fig. 12).

If the apparent morphological gaps within Theropoda, Hadrosauriformes and Ceratopsia are truly bridged, then only four dinosaurian taxa are set apart from the rest of Dinosauria by morphological gaps: Eusauropoda + Tazoudasaurus, Hadrosauriformes, Stegosauria and Ankylosauridae (Fig. 15).

The most comprehensive creationist review of dinosaurian taxa is that by Duane Gish (1995). Therein, he argues that no transitional forms link *Stegosaurus*, *ankylosaurs*, *Triceratops*, *Centrosaurus*, *Saurolophus*, *Parasaurolophus*, *Lambeosaurus*, *Corythosaurus*, *Struthiomimus*, *Allosaurus*, *Tyranosaurus*, *Apatosaurus*, *Diplodocus* or *Brachiosaurus* to any other dinosaur. This study tests this claim for each of these genera and falsifies it on all...
counts. Each of these taxa is part of a morphological continuum that includes several other genera and in most cases, several families. Moreover, the results of the taxon correlation analyses with the 1990 versions of the matrices show that, even before 1990, it should have already been apparent that these genera were not separately created.

Gish (1995) also states that no fossil transitions linking small bipeds to the large, quadrupedal sauropods are known. The results of this study are congruent with that statement, because a persistent morphological gap separates Eusauropoda from bipedal dinosaurs. However, the results of this study reveal an unbroken morphological continuum uniting small, bipedal basal saurischians with large, quadrupedal sauropodomorphs such as *Melanorosaurus*; small, bipedal ornithischians with large, quadrupedal thyreophorans such as *Scelidosaurus* and *Nodosauridae*; and small, bipedal neoceratopsians with medium-sized quadrupeds such as *Protoceratops* and the large quadrupeds of the family Ceratopsidae. Therefore, even by the creationist standard of taxon correlation, at least three groups of large
dinosaurian quadrupeds evolved from small, bipedal dinosaurs.

It is also noteworthy that several morphological gaps in the known dinosaurian fossil record prior to 1990 have been filled by subsequent discoveries. Post-1990 dinosaur discoveries have bridged morphological gaps within basal Theropoda (via Cryolophosaurus), between basal coelurosaurs and Paraves + Oviraptorosauria (via Beipiaosaurus, Caudipteryx, Incisivosaurus and Protarchaeopteryx), between Paraves and Oviraptorosauria (via Therizinosauroidea), between Titanosauria and other eusauropods (via Phuwiangosaurus), between Ornithischia and Herrerasauridae, within Stegosauria, between Marginocephalia (Pachycephalosauria + Ceratopsia) and other ornithischians (via Chaoyangosaurus), between Ceratopsidae and other Neo- ceratopsia (via Zuniceratops), and between Centrosaurinae and Chasmosaurinae (via Albertaceratops and Diabloceratops). Even if pre-1990 gaps within Stegosauria are ignored, this series of discoveries alone has collapsed 15 potential dinosaur baramins into four in little more than two decades. Therefore, although results of this study identify seven potential morphological gaps that persist within Dinosauria, any creationist celebration of the persistence of such gaps is premature because of the general trend for such gaps to be filled by continued discovery.

It is important to note that the gap-filling trend is not limited to Dinosauria; for example, recent fossil discoveries have filled major morphological gaps in the early evolution of synapsid vertebrates (Laurin & Reisz, 1990), mammals (Ji et al., 1999, 2002; Luo et al., 2003), chordates (Shu et al., 1999; Mallatt & Chen, 2003), arthropods (Lin et al., 2006) and plants (Meyer-Berthaud & Decombeix, 2009), among other taxa.

It is also noteworthy that although Wood’s (2011) study found a morphological gap between Paraves and Oviraptorosauria, this study did not. The filling of that gap was accomplished not by the addition of new fossil discoveries but by updating the matrix with new observations of fossils. This raises the possibility that at least some apparent morphological gaps found by this study could be artifacts of gaps in observation of museum specimens by the creators of at least some of the phylogenetic data matrices used here.

To be fair, it should be acknowledged that within the creationist paradigm, it is possible to explain extreme morphological diversity within genetically related dinosaur groups, by invoking artificial selection. Selective breeding of domesticated animals by humans can result in pronounced morphological changes in very few generations (Ratliff, 2011). Such an explanation for the wide morphological variety across morphologically continuous spectra of dinosaur taxa would be consistent with previous creationist assertions that (1) ancient humans used dinosaurs for beasts of burden (Taylor, 1987; Ham, 2008) and (2) the amount of variation within today’s domesticated animals demonstrates that much variation is possible within a ‘created kind’ (García-Pozuelo-Ramos, 1999, 2002). If artificial selection is invoked, the creationist camp will no doubt be asked to explain why ancient humans would want to breed gigantic, toothy monsters such as Allosaurus and Tyrannosaurus into existence from small, docile, herbivorous ancestral stock. However, potential rejoinders are myriad. Huge theropods could have been bred as weapons of war, fighters for human entertainment.
(like dog breeds that are bred for dog fights), or—as some creationist authors have suggested (Unfried, 1990; Ham, 2009)—simply misunderstood pumpkin- and melon-eating herbivores. Of course, within the evolutionary paradigm, artificial selection of dinosaurs is nonsensical, because dinosaurs and humans are separated by over 60 million years.

In any case, to use artificial selection to explain dinosaurian diversity without discarding the baraminological method of taxon correlation, the creationist camp will have to acknowledge the genetic relatedness of a very broad morphological spectrum of dinosaurian species. It will also have to acknowledge that the assertion that Dinosauria can be divided into dozens of ‘created kinds’ (Ham, 1998, 2001, 2006, 2009; Morris, 1999) is untenable even within the creationist paradigm.

The results of this study indicate that transitional fossils linking at least four major dinosaurian groups to the rest of Dinosauria are yet to be found. Possibly, some creationist authors will hail this finding as evidence of special creation for those four groups. However, such enthusiasm should be tempered by the finding here that the rest of Dinosauria—including basal members of all major lineages—are joined in a continuous morphological spectrum. This confirms the genetic relatedness of a very broad taxonomic collection of animals, as evolutionary theory predicts, ironically by means of a measure endorsed and used by creation science.

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References


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Supporting information

Additional Supporting Information may be found in the online version of this article:
Appendix S1 Character list for phylogenetic analysis of Coelurosauria.
Appendix S2 Phylogenetic data matrix of Coelurosaui.
Appendix S3 Explanations and justifications for major changes to OTUs in the phylogenetic data matrix.
Appendix S4 Diabloceratops eatoni data for phylogenetic data matrix of Centrosaurinae.
Appendix S5 Coelurosauria synapomorphy list.
Appendix S6 Centrosaurinae synapomorphy list.

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