

CBS Annual Conference Abstracts 2011

An ANOPA Study of Coelurosaurian Theropods

D. Cavanaugh

Independent Scholar

Recently, Senter (2010) argued that creationists ought to accept the evolution of birds from dinosaurs based on classical multidimensional scaling of a baraminic distance matrix calculated from a set of 364 characteristics of 89 theropods and Mesozoic birds. In response, Wood (2011) argued that baraminic distance correlation could be used to support a discontinuity between Mesozoic birds and theropods. The notion of gaps that isolate groups needs to be treated carefully, and one needs to look at the variation within clusters and use a judicious choice of outgroups, as well as a consideration of diversification patterns in morphospace. One also needs to be careful of the perspective of scale (distance and magnification), where statistically significant gaps and clustering may be real but misleading. I analyzed Senter's character matrix using Analysis of Patterns (ANOPA) (Cavanaugh and Sternberg 2004). Missing characters were dealt with by assigning them to the character average, which causes them to mathematically drop out of all of the ANOPA pattern distance calculations. The 2D ANOPA revealed two clouds of taxa only poorly separated. The 2? confidence ellipses between the main cloud and the second cloud have a significant overlap, suggesting that this whole assemblage of taxa is part of a single cluster. The 3D ANOPA reveals three clouds of taxa, which again overlap. When the taxa are categorized by stratigraphic first occurrence (Upper Jurassic, Lower Cretaceous, and Upper Cretaceous), there is a correlation between morphology and first occurrence. The Upper Jurassic taxa defines the core structure that is fleshed out with outward movement into Lower Cretaceous taxa and finally more outward movement to the Upper Cretaceous taxa. The Upper Jurassic *Guanlong* is almost exactly the average of the taxa assemblage, perhaps a numerical representation of this taxon being the "average" theropod. *Guanlong* and the composite taxon *Epidendrosaurus* + *Epidexipteryx* are important intermediates between two clouds of taxa. There appears to be a stratomorphic series from *Dilophosaurus* through *Allosaurus* and *Sinraptor* to *Tryannosaurus* and *Gorgosaurus*. There is also a V-shaped stratomorphic series beginning with *Protarchaeopteryx*, *Incisivosaurus*, and *Caudipteryx*, then branching to *Citipati*, IGM 100/42, *Ingenia*, and *Khaan* on one side and on the other side to *Gallimimus*, *Ornithomimus*, *Struthiomimus*, *Therizinosaurus*, *Segnosaurus*, *Erlikosaurus*, *Erliansaurus*, *Neimongosaurus*, and *Velociraptor*. There are some "significant" gaps in the taxa, but the series are nevertheless quite clear. Given the clarity of the

series, it seems at least reasonable for creationists to consider the possibility that the Jurassic "bird" *Archaeopteryx* really is related to theropod dinosaurs, not as descendant but instead as their ancestor.

- Cavanaugh, D.P. and R.v. Sternberg. 2004. Analysis of morphological groupings using ANOPA, a pattern recognition and multivariate statistical method: a case study involving centrarchid fishes. *Journal of Biological Systems* 12:137-167.
- Senter, P. 2010. Using creation science to demonstrate evolution: application of a creationist method for visualizing gaps in the fossil record to a phylogenetic study of coelurosaurian dinosaurs. *Journal of Evolutionary Biology* 23:1732-1743.
- Wood, T.C. 2011. Using creation science to demonstrate evolution? Senter's strategy revisited. *Journal of Evolutionary Biology* 24:914-918.

Editor: TCW

The Hebrew Taxonomy of Living Things

J. Daniels

Independent Scholar

There are two seemingly contradictory beliefs held by traditional Young Earth Creationists in regard to the original creation: there was no death of living organisms, and plants (biologically alive) provided the sole sustenance for both Man and animals. A common solution to this dilemma is to redefine "life" according to the Hebrew words *chay nephesh*, usually translated "living creature" (Berndt 2003; Wilson 2008). Since plants are not described as *chay nephesh*, their consumption would be allowable (Ham et al. 1990, pp. 103-112; Morris 1991; Stambaugh 1992). By building on these authors' foundations, this paper attempts to provide a definitive answer to the question of what biological organisms are included in a Hebrew definition of life through an exhaustive comparison of every Hebrew organismal classification term; their contexts, their definitions, and their associated animal groups.

No verses outside the creation account were found to include animal groups not mentioned in Genesis, and therefore Genesis 1-11 was assumed to contain a complete listing of the highest taxonomic rankings of created Hebrew animal classes. Ten words or phrases for large classes of *chay nephesh* were discovered: *tanniyn* (great sea creatures), *sherets* (swarming things), *dag/dagah* (fish), *chay erets* (beasts of the earth), *behemah* (beasts/cattle), *owph* (flying things), *remes* (creeping/moving things), *chay sadeh* (beasts of the field), *tsippor* (birds), and *owph sherets* (winged insects). For the two most difficult to elucidate categories, *remes* and *sherets*, the verbs *ramas* and *sharats* were also researched.

From this list, all Hebrew aquatic animals form two distinct

classes of *chay nephesh*: *tanniyn* and aquatic *sherets* (Genesis 1: 20-21). Within aquatic *sherets* is the subclass *dag/dagah* (Gen 1: 26). Four classes of terrestrial organisms were identified: *chay erets*, *behemah*, *owph*, and *remes* (Gen 1:21, 24-25). *Chay erets* contains the indistinct subclass *chay sadeh*. Outside Genesis, *chay erets* is used in the same way as *chay sadeh*: to describe harmful, dangerous animals. Within Genesis it occurs along with *behemah*, *remes*, and/or *owph* to distinguish between wild animals and domesticated animals (*behemah*). *Owph* is a broad term that encompasses all flying things including birds, bats and insects. Within *owph* then, is found the subclasses *owph sherets* (Leviticus 11:20-23) and *tsippor* (Gen 7:14). In regard to *remes* and *sherets*, no verse contains both words together which would identify them as two separate classes. It is my opinion that *remes* and *sherets* refer to different aspects of the same group of organisms. Both words refer to aquatic (Psalm 104:25, Gen 1:20) and terrestrial organisms (Gen 8:19, Lev 11:42) and use the verbs *ramas* (Gen 7: 14, Lev.11:44) and *sharats* (Gen 8:17, Lev 11:29) exclusively as active verbs. Additionally, they are both used in almost identical verses to describe the same animals that were destroyed during the flood (Gen 7:21,23). *Remes* refers to the locomotion of the animals (moving/creeping) and stands as a more inclusive class, with one instance being representative of all animals (Gen 9:3). Out of a total of 17 occurrences, 15 are used in construct with *behemah*, *chay erets*, and/or *owph* to define the four large classes of created terrestrial organisms. *Sherets* denotes the class's reproductive potential (bring forth abundantly KJV).

All classifications were directly used in context as *chay nephesh* in at least one instance. While not biologically comprehensive or all inclusive, the Bible does display a strong semblance of hierarchy among animal groups. All animals mentioned in the Bible fall under the umbrella of *chay nephesh*. Six taxa comprise the next level, with most having one or two subtaxa, which are in turn composed of individual animals.

- Berndt, C. 2003. The pre-Fall mortality of aquatic autotrophs and other designated *nephesh* kinds. *CRSQ* 40: 85-89.
- Ham, K., A. Snelling, and C. Wieland. 1990. *The Answers Book*. Master's Books, Green Forest, Arkansas.
- Morris, J. 1991. Are Plants Alive? *Acts & Facts* 20: (9).
- Stambaugh J. 1992. 'Life' according to the Bible, and the scientific evidence. *TJ* 6(2):98-121.
- Wilson, G. 2008. Bugs, Baramins, and Beauty. *Creation* 30(3):42-44.

Editor: ID

A Just Holy War ... with Animals? Genesis 9, Deuteronomy 20, and a Conservation Ethic for a Creation under a Curse

I. Demme

Independent Scholar

In Genesis 9.1-17 God makes a covenant with Noah, all Noah's descendants, and all animals. While the focus of the covenant is the promise never again destroy all life with a flood, God also describes some differences in the way humans and animals will relate now (as opposed to the way those relationships were set up in Genesis 1.28-30).

While the immediate context is the preservation of humanity and animality through the great flood, the content of these changes suggests that they may be occasioned by the curse of

Genesis 3.14-19. (There are several indications that God had already given instructions regarding animal sacrifice prior to this point, particularly in the story of Abel's murder and the distinction made between clean and unclean animals on the ark. Not only does the Torah require consumption of flesh and proper disposal of blood in animal sacrifice, but all other ancient cultures have similar regulations, suggesting a pre-Flood origin).

In Genesis 9.3 God permits the flesh of animals to be eaten by humans as a gift in addition to plants (Genesis 1.28). Where God had prescribed human rule over animals in Genesis 1.26-28, he promises human victory over animals in Genesis 9.2. The strong parallels between the language used to describe human victory over the animal kingdom here and the texts describing military victory over Israel's national enemies ((c.f. Deuteronomy 11.25, Exodus 23.27, Deuteronomy 7.24)) has been noted by other commentators (e.g. Mathews 1996, p. 401), and it suggests that the author is drawing our attention to the parallels between these sorts of conflict.

As in the laws for Israel's warfare against other nations, God imposes specific limitations, which in Genesis 9 focus on the life-carrying blood of humans and animals. Shedding of human blood, whether by humans or animals, is to be punished by death. While animal flesh is given to humans for food, animal blood is reserved by God as sacrosanct, and is not to be eaten (Genesis 9.4, see also Leviticus 17.3-14 and Acts 15.20).

In this, as in other passages in the Pentateuch that restrict the taking of animal life (e.g. Deuteronomy 22.6), the language of warfare seems to me to suggest a parallel between an ethic of warfare against other humans and an ethic of animal treatment. This is consonant with an understanding of the curse as a degradation of cooperation, symbiosis, and peace into competition, parasitism, and hostility. While the conflict between humans and the creation is not warfare in the sense of organized conflict between nations, it is similar enough to evoke similar description and similar ethical principles.

Some of the ethical principles of just warfare seen in Deuteronomy 20 and elsewhere may thus be employed to shed light on the laws concerning the treatment of animals in the Pentateuch and also on controversies over animal treatment today. In particular, the principles of proportionality and right intention may be applied. Right intention in human-animal conflict, as in conflicts with humans, requires a focus on securing lasting peace between belligerents. While complete peace with the creation is a feature of the prophesied Messianic kingdom (Isaiah 11, 16, Hosea 2 etc.), understanding peace as a goal toward which God is moving adds a new perspective on our responsibilities as God's images. Proportionality (examining the means used to secure peace by balancing their potential to bring victory with their potential to create continued hostility) also applies to human-animal conflict. For example, when considering an experiment to be performed on animal subjects, the likelihood of knowledge gained which can bring creation into a peace which glorifies our Creator should be measured against the immediate damage done to our relationship with the experimental subjects. Likewise, when considering the modification of ecosystems for a given purpose, we should consider both the immediate and the long term effects on our relationship with the organisms which inhabit that system, and which effects help or hinder our mandate as images of God

who are to lead all creation in worship of the Creator.

Mathews, K.A. 1996. *Genesis 1-11:26, New American Commentary, Volume 1A*. Broadman & Holman, Nashville, TN.

Editor: RWS

Balancing *Imago Dei* with Dominion: A Biblical Understanding of Conservation Ethics

S. Elaine
Independent Scholar

Conservation ethics handles the issue of how humankind should manage conflicts between endangered animals and human interests, especially when people's needs are equally desperate. Typical responses range from creation dismissal (man and his needs are most important), as attributed to Christians by Lynn White (White 1974, pp. 4-5), to forms of hyper-environmentalism (creation must be protected even at the expense of man). However neither reaction is balanced as neither fully addresses the dual concepts of *imago Dei* (man created in God's image) and dominion (the divine charge for man to rule over creation). While it could be argued that man as an eternal being has more inherent worth than creation, the concept of dominion given in direct context of God's image implies humanity is to exercise its rule in a godly fashion (Genesis 1:26-28) (Gentry 2008). That is, man is to rule as God would and enable creation to fulfill its God-given purposes. Only a position which balances the eternal worth of man with his responsibility under God for creation will adequately handle the complex ethical problems of conservation. However, each solution will be specific to the conflicting species and human culture. As a working example, the case of Amur leopards and rural Russians is examined. Critically endangered, the Amur is the rarest and most genetically vulnerable of eight subspecies of leopard, with less than 30 native individuals. Its current situation developed through poor land management, poaching of it and its prey, and livestock conflicts. Today, restricted reserves support few wild ungulates, forcing Amurs to seek prey elsewhere, such as livestock penned nearby. Rural Russians protect their livelihood often by killing leopards (Uphyrkina 2002). Any solutions to this ethical dilemma must address the land, prey, and protection needs of Amur leopards, as well as the economic needs of the local people. Potential solutions include: relocating the leopards or people, fencing, livestock compensation or insurance, better livestock husbandry, tourism, or economic improvements. However, such a conservation model spawns further questions: is it valid to preserve a subspecies of leopard? At what classification level is conservation ideal-family, genus, species, or individual? Or perhaps, is it possible to genetically preserve the "created kinds"? Conservationists must also consider the ecological impact of species including whether they are keystone species, a prey base, etc. Perhaps, with our current biological understanding there can be no broad ideal. Nevertheless, the balancing model of *imago Dei* and dominion provides an ethical framework upon which conservationists may build toward a solution through the complex details of individual situations which will be not only pragmatic, but biblically sound.

Gentry, P.J. 2008. Kingdom through covenant: Humanity as the divine image. *Southern Baptist Journal of Theology* 12(1):16-42.

Uphyrkina, O., D. Miquelle, H. Quigley, C. Driscoll, and S.J. O'Brien. 2002. Conservation genetics of the Far Eastern Leopard (*Pantera pardus orientalis*). *Journal of Heredity* 93(5):303-311.

White, L. 1974. *The Historical Roots of Our Ecological Crisis*. Harper and Row, New York.

Editor: RWS

Does Biblical Similarity Inform Biological Similarity?

J. Francis, A. Chou
The Master's College

Biological similarity is a major observable phenomenon in the living world. Living things resemble other living things at the gross morphological level and at the cellular and genetic level. Theories in evolutionary biology propose that biological similarity can result from common ancestry (homology) or evolutionary processes working in common environments to produce similarity (homoplasy). In contrast, a creationist model of biological similarity is virtually non-existent. Creationists have argued that similarity is derived from common design. Yet, at the same time, creationists infer that discontinuity or dissimilarity arises from common design. Furthermore, there has been little to no explanation for why some organisms which were created as separate baramins express a high degree of similarity genomically and morphologically. Evolutionary creationists insist that this high degree of similarity implies common ancestry of what some creationists argue are separately created kinds.

In this study we investigate the concept of biblical similarity to determine if it informs biological similarity. We begin with the premise that God has intentionally designed creation in wisdom. Psalm 104 provides textual grounds for this assertion as well as a paradigm for its application. For instance, the psalmist praises the Lord for creating water in its ability to both flood the world (Ps 104:6-7) in addition to quench the thirst of animals (v. 11). The sun, moon, and stars not only provide light but also regulate time (vv. 19-23). God has intentionally created the world to illustrate His wisdom (v. 24). Based upon this foundation, one may observe biological similarity in terms of its theological purpose; does the Scripture appeal to biological similarity in any fashion and if so, to what end? Some of the clearest examples of biological similarity are found in prophetic and wisdom literature. The biblical writers make comparisons using similes and metaphors using body parts common to animals and man. Joel discusses the locust plague in terms of the teeth of a lion (Joel 1:6). The tongue of a serpent is compared to the tongue of man (Ps 140:3). Metaphors (and analogies) take concrete and tangible concepts to illustrate or point to abstract characteristics. It presumes the audience grasps fundamental correspondences in hope of comprehending more complex relationships. Thus, the metaphor of a serpent's tongue could break down if humans or other creatures lacked tongues. It appears that biological similarity is used by biblical writers to instruct the people of God. The commonality in creation creates the foundation by which helpful comparisons can be made to illustrate certain theological truths in the Bible. God, in part, intentions biological similarity for this purpose.

At the same time, we are hard pressed to find many examples of where animal and human body parts are precisely equated in the same context. Instead, the biblical writers tend to compare man

with animals holistically and usually in a derogatory manner (Ps 22:13; Ecc 3:18; Job 18:3; counter examples Gen 49:9; Ezek 19:1-6). This dissuades the reader from reading relationally-derived biological homology into biological similarity. Similarly, animal behavior is compared more often with human behavior than with body parts (Ps 17:12; Prov 19:12; 30:19, 24-31). Along this line, the metaphors comparing man directly with the parts of plants (Ps 1:3; Is 11:1; Ezek 19:10; Dan 4:20-22) are seemingly more plentiful than comparisons of man directly with animal parts. These observations appear to qualify analogies of similarity; the emphasis of comparisons rest more on non-biological overlap as well as on the distinctiveness of man from creation. Such attention affirms the creation paradigm in Genesis 1:26-28 where man is distinguished from the rest of creation. Therefore, while man's body parts do have similarity with animals, this is strictly a function of God's didactic wisdom in creation. Any further conclusions (i.e., biological homology) are most likely excluded by Scripture's portrayal of categorical differences between man and beast. Thus, in conclusion, scripture utilizes similarity but puts an emphasis on distinctiveness; this can serve as a theological model for studies of biological similarity which can be viewed as a relevant concept within a larger creation model of biology.

Editor: TCW

A Biblical View of Australopithecines and Paleoanthropological Data

J. Klenck

Paleontological Research Corporation

A theory is proposed that Genesis provides a scriptural context for australopithecines as a potential helper or *ezer* [עֵזֶר] for Adam before the formation of Eve (Genesis 2:18-20). This view counters evolutionary theories claiming that australopithecines are ancestral to human populations. Many creationists proffer that australopithecines resemble great apes. Evolutionists respond exhibiting human-like features in australopithecines such as morphological evidence for bipedal locomotion.

Possible definitions of *ezer* include helper, companion, or attendant. The creation of an *ezer* before Eve cannot be viewed as an experiment since God is omniscient; however, scriptures provide no reasoning for their formation before Eve. Can animals be an *ezer*? Scriptures outside Genesis 2:18-20 are lacking and Biblical support or lack thereof for this assertion is equivocal. Was Eve created as an *ezer*? Wording in Genesis suggests that Eve was equal to Adam in the Garden before the Fall, and there is no mention by Adam of Eve being an *ezer*. Instead, Adam describes Eve as "bone of my bones and flesh of my flesh." Genesis 2:18-20 suggests *ezer* animals were created prior to Eve. Potential *ezer* entities were created by God, reviewed during the animal naming event, however, Adam considered these animals as not being suitable, parallel, or corresponding to him [כַּנְגִידוֹ].

Regarding the paleoanthropological contexts of australopithecines, archaeological data evidences their associations with the earliest stratigraphy containing human remains and that these associations preceded human interaction with other animal domesticates such as sheep (*Ovis aries*), goat (*Capra hircus*), and dog (*Canis familiaris*). Furthermore,

australopithecine cognitive abilities may have exceeded those of apes, as evidenced by an enlarged cerebral cortex in *A. afarensis*; but not humans as archaeological assemblages provide little evidence for their tool making ability.

Theoretical correlations between the *ezer* from Genesis 2:19-20 and australopithecines appear warranted since australopithecines most closely resembled humans (made in the image of God), their cognitive and physical abilities were more similar to humans compared to other fauna, and their remains are associated with early human assemblages. Despite these similarities, however, Adam still recognized that they were not suitable or corresponding to him [כַּנְגִידוֹ], indicating that they were a separate creation. In conclusion, although scriptural support is equivocal regarding correlations between animals and *ezer*, in Genesis 2:18-20 this association is possible and warrants future discourse and consideration.

Editor: TCW

Biological Origins in Christian Textbooks: Problems and Suggestions for Improvement

E. Lantzer, A. Daniels

Independent Scholars

In order to equip future scientists to further the development of a scientific model of creation, curriculum is needed that adequately prepares Christian high school students for the rigor and scientific realities of the academic world. This study is intended to inform the members of the creation community about the problems of current curricula and provide suggestions for improvement. The treatment of biological origins was evaluated in several biology textbooks from major Christian publishers. We developed a rubric of topics, and evaluated each textbook's origins section by paragraph, evaluating their position on each topic. In the process, four general problems emerged across all the textbooks. In addition to evaluating the textbooks, we designed a survey to quantify students' beliefs about origins issues with the purpose of providing a framework for evaluating students' preparedness. It was given to seniors at five Christian high schools with a total of 114 participants. The survey results show that the majority of seniors were well versed in a dogmatic version of creationist thought, but unaccustomed to thinking about the issues in more complex ways. They were nearly unanimous in their affirmation of a Divine creation in six literal days with man as a separate creation. However, only 22% agreed with the statement, "A single species can diversify over time to create many different species," which falls within the consensus of both standard evolutionary and YEC scientific thought. Though the survey covered only a small cross-section of students in one area of the U.S., these answers are consistent with the results we would expect after evaluating the curricula.

The following are the observed problems with the curricula. First, creationists have traditionally focused on apologetics, which is reflected in the textbooks' preoccupation with anti-evolution arguments. This creates an unintentional problem when students discover post-high school that evolution issues are broader than the apologetic arguments they have been taught. Second, specific interpretations of scientific evidence are linked too closely to Christian beliefs. When they discover that specific interpretations

are more complex than they realized, students can either discard the creation account, or, unable to disassociate specific doctrines of creation from their understanding of faith, they can reject Christianity altogether. Third, the texts do not teach the students how to think critically about origins issues. They present conclusions, largely focusing on tearing down the evolutionary model, instead of guiding students through the thinking process. When students are confronted with new and conflicting evidence, they do not have the training to evaluate it in light of their belief system. Finally, Christian textbooks sometimes use outdated research in refutation of evolution and support of YEC. This is an obvious shortcoming in light of academic and biblical principles, and in giving students an understanding of current scientific thought.

The hope is not to keep students from becoming evolutionists at college but rather to equip them to be creationists who do good science. We thus offer these suggestions for curriculum improvement. First, the appropriate focus of a Christian biology textbook should be science, not apologetics. It must teach current creationist thought and evolutionary theory. Students learn to think by exposure, not ignorance. The concepts presented to students in college should not be a surprise. Second, the high school biology course should be a safe place for exploring doubts and examining conflicting evidence. Accordingly, the curriculum should fairly present more than one Biblical and scientific interpretation. Third, it is crucial to teach critical thinking skills. Students need to be provided with the necessary schema to explore creation at the college level and trained to evaluate evidence and draw their own conclusions. Fourth, while biology textbooks can and should address origins topics, we feel they are inadequate to bring about the needed paradigm shift to constructive creation research. A better alternative is a resource created by YEC researchers and educators to serve as curriculum for a separate class on origins or supplement existing courses. An internet resource would provide the flexibility of easy revisions and low-cost access. It also allows for expansion as nearly-unlimited resources can be linked together, allowing exploration of topics in greater depth than printed textbooks allow.

Editor: RWS

Survey of Microbial Composition and Mechanisms of Living Stromatolites of the Bahamas and Australia

G. Purdom, A. Snelling

Answers in Genesis

Stromatolite definitions, although varied, typically refer to a laminated and lithified structure that is the result of microbial activity over the course of time. Fossil stromatolites are abundant; however, modern living stromatolites are rare.

Two well-studied examples include those found in the Exuma Cays of the Bahamas and Shark Bay in Australia. Although the stromatolites in these locations share similar appearances at both the macroscopic and microscopic levels, the environment in which they form is quite different. The stromatolites in the Bahamas form in normal saline seawater whereas those in Australia form in a hypersaline environment (double the salinity of normal seawater in the secluded Hamelin Pool in Shark Bay).

Stromatolites consist of “guilds” of bacteria that perform different functions such that the end metabolic products produced by one bacterial guild provide the starting metabolic products for a different guild. This distribution of functions benefits the microbial community and effectively builds the stromatolite. Microbial composition varies but typically consists of three major bacterial types. The top layer of the stromatolite consists of cyanobacteria (or other phototrophs) that are active in photosynthesis. Cyanobacteria play a major role in the overall growth of the stromatolite as they are the primary producers converting carbon dioxide to sugars. These sugars are the primary source of nutrients used by heterotrophic bacteria located lower in the stromatolite. Endolithic cyanobacteria are also common in lower layers where they bore through lithified layers of the stromatolite. The boring activity aids in welding together calcium carbonate grains that have been precipitated by the heterotrophic bacteria. Bahamian and Australian stromatolites have similar microbial compositions; however, there are some differences. Australian stromatolites tend to have a greater diversity of heterotrophic bacteria, less cyanobacteria (more anoxygenic phototrophs), and some archaea (mainly halophiles) compared to Bahamian stromatolites.

Lithification (the process of sediments becoming solid rock) results directly from microbial activity performed mainly by heterotrophic bacteria. However, cyanobacteria are responsible for accretion (addition) of sediment. Bacteria actively precipitate and/or trap and bind calcium carbonate in secretions such as extracellular polymeric substance (EPS). Microbial activity consists of a complex set of chemical reactions that result in both the dissolution and precipitation of calcium carbonate. The following processes are involved: photoautotrophy, aerobic respiration, anaerobic respiration (nitrate and sulfate reduction), and chemolithoautotrophy (sulfate oxidation). When these processes result in net precipitation of calcium carbonate, lithification occurs.

Depending on dominant chemical reactions by bacteria, accretion and lithification of the stromatolite occurs at intervals. Each layer or lamina of a stromatolite represents a former surface mat of bacteria. As long as cyanobacteria (or other phototrophs) colonize the top surface of the stromatolite growth is likely to continue. Although several studies have been done to estimate the growth rate of stromatolites, no consensus has been reached. However, most living stromatolites are considered to be no more than several thousand years old.

Understanding microbial composition and mechanisms of living stromatolites is crucial to determining the biogenicity of fossil stromatolites. Although there is a paucity of fossilized bacteria in fossil stromatolites, their structural features closely resemble those of living stromatolites. This and other evidences leave little doubt as to the biogenicity of many fossil stromatolites. Fossil stromatolites have been found mainly in the Archean and Proterozoic strata with greatly diminished numbers in Phanerozoic strata. The biogenicity of the “oldest” Archean stromatolites has been highly questioned due to the 3.5 billion year age assigned to their host rock layers. This leaves only a scant one billion years for the evolution of cyanobacteria and their major metabolic process of photosynthesis from non-life. However, there appears to be little difference structurally between

Archean and Proterozoic stromatolites leading to the conclusion that Archean stromatolites are likely biogenic as well.

It is hoped that this study of living stromatolites will assist creation geologists in determining the biogenicity of fossil stromatolites. Discernment of genuine stromatolites in the geological record may help in determining boundaries between Creation Week, pre-Flood and Flood strata. In addition, understanding how living stromatolites form in different environments and comparing their structures to fossil stromatolites may provide a window on pre-Flood environments. A pre-Flood stromatolite reef biome has already been recognized, but stromatolites may have also grown in other pre-Flood biological communities.

Editor: MR

Application of the Post-Flood Continuity Criterion to Flowering Plants

R.W. Sanders
Bryan College

As baraminology has developed, various criteria have been proposed to evaluate the existence and inclusivity of baramins. Wise (2008, 2009) proposed the Post-Flood Continuity Criterion (PFCC) to estimate the baramins of mammals. For each Paleogene subseries, he calculated the probability that fossils represent pre-flood taxa and, thus, considered taxa occurring in the Lower Eocene or lower strata to have a continuous fossil record with the Flood (CFR). The PFCC identifies as baramin the taxon of which some but not all of its included taxa of next lower rank have a CFR. Because flowering plants have an extensive fossil pollen record in the Upper Cretaceous and Cenozoic strata, I investigated the applicability of the PFCC to this group, even though most of its baramins would survive the Flood outside the ark. Based on results of statistical baraminology, the lowest rank considered as PFCC candidate was family; subclass was considered too inclusive to be consistent with biblical data. The data were tabulated from the only available compendium that identifies fossil pollen with modern angiosperm genera and families (Muller 1981). The PFCC provides a minimum number of more inclusive baramins and was calculated for four different classification systems. The maximum number of baramins (i.e., least inclusive) was calculated as the number of families with a CFR without regard to whether other families sharing the next higher rank also have a CFR; this number is 58 (18% of the 316 traditional living families), including three disparate families that Wood (2008) identified as holobaramins: Poaceae (grasses), Nymphaeaceae (waterlilies), and Olacaceae (tallow-woods). Within the 58 families, 90 genera (or groups of genera with indistinguishable pollen) have a CFR. The number of baramins determined by the PFCC was 40 for Cronquist's system (14 at the family level, 26 at ordinal), 23 for Takhtajan's system (3 at the family level, 6 at ordinal, 14 at superordinal), 22 for Dahlgren's system (6 at the family level, 2 at the ordinal, 14 at the superordinal), and 18 for the Angiosperm Phylogeny Group molecular classification (2 at the family level, 8 at the ordinal, 8 at the superordinal). Because these classifications are not finely divided hierarchies with multiple intercalary ranks as in Wise's study of mammals, numerous families (161, 59, 87, and 16 respectively) were left without placement in potentially more inclusive baramins. It is

clear that both the maximum and minimum values are highly dependent on the quality of the fossil record. Although Wise (2009) argued for a high quality mammalian record, this is not yet documented for angiosperms. Likewise, the PFCC baramins are highly dependent on the particular classification and the number of ranks in its hierarchy. Only 10 mammal families (all extinct) were among Wise's PFCC baramins, and only 12 living families have a CFR; no extant mammal genera have a CFR. Thus, it appears that modern mammals diversified predominantly after the Flood. However, modern angiosperm diversity likely was higher prior to and was preserved through the Flood. Therefore, with the available data the CFR may possibly serve as estimator of baramins in angiosperms, but the PFCC does not. Indeed, the PFCC method needs more critical discussion and evaluation by the young-age creationist community before broad conclusions are drawn. Future work will focus on documenting 1) literature updates to add macrofossils and extend the pollen records to lower strata, 2) the completeness of the angiosperm fossil record, and 3) the finer-scaled hierarchy implied in published traditional and molecular systems in order to place "orphaned" families. Also, the fossil genera will be placed in their subfamilial and tribal taxa to determine whether the PFCC would identify any group below the rank of family as baramin.

Muller, J. 1981. Fossil pollen records of extant angiosperms. *Botanical Review* 47: 1-142.

Wise, K.P. 2008. Baraminology and the fossil history of the mammals. *Occasional Papers of the BSG* 11:10.

Wise, K.P. 2009. Mammal kinds: How many were on the ark? *Center for Origins Research Issues in Creation* 5: 129-161.

Wood, T.C. 2008. Animal and plant baramins. *Center for Origins Research Issues in Creation* 3: 1-258.

Editor: MR

Creationist Interpretation of Fossil Pollen Assemblages of the K-Pg Boundary

R.W. Sanders
Bryan College

Creation geologists have documented strong evidence that the Cretaceous-Paleogene (K-Pg) boundary marks the end of Noah's Flood. Because pollen is the most resistant and likely organ of plants to be fossilized and occurs across the K-Pg boundary, a study of fossil pollen should aid in interpreting the late Flood and post-Flood events. Two fossil pollen assemblages dominate Upper Cretaceous strata of the Northern Hemisphere (Nichols & Johnson 2008, pp. 46-66). The Normapolles assemblage is composed of several extinct genera unplaced in extant families but similar to the wind-pollinated walnuts. The Normapolles Province covers southern Europe and eastern North America. Above the K-Pg boundary, this assemblage began declining, especially above the Upper Paleocene, disappearing by the Lower Oligocene. The Triprojectate assemblage includes several unrelated extinct genera without clear affinities to extant families. However, these probably wind-pollinated genera were once thought to be related because all samples exhibit three equatorial projections. The Triprojectate Province extends from northern Europe and northern Asia to northern and western North America. It disappears abruptly at the K-Pg boundary, but isolated species occur sporadically into Eocene strata. Immediately above this

extinction is a thin stratum with a peak in iridium concentration and replacement by nearly 100% concentration of a single fern species. Subtropical and tropical forest angiosperms (Normapolles plus diverse extant tropical families) gain dominance about 10 cm above the K-Pg boundary. The conventional interpretation is that the two provinces developed in isolation during the Cretaceous with the Triprojectate assemblage nearly decimated by the terminal Cretaceous bolide impact. Primary succession led to dominance by ferns (considered better adapted to reduced sunlight and rapid colonization by wind-borne spores) some thousands of years until the remnant Normapolles assemblage immigrated and newly evolving genera replaced both. This derives from the conventional geological model of epicontinental sea barriers in central North America and Eurasia, with migration across the embryonic North Atlantic and subaerial Beringia. The following interpretation within a creation-diluvial framework is proposed: 1) The Normapolles assemblage may represent a single wind-pollinated baramin. The Triprojectate assemblage more likely represents several baramins with analogous morphologies related to the environmental factors of a shared biome. 2) Both assemblages were the dominant wind-pollinated taxa in pre-Flood upland poleward areas inundated late in the Flood and were associated perhaps more closely with the dinosaur biogeographic province than with the mammal province as were many other angiosperms (Wood & Murray 2003, p. 190). 3) The fossils are probably allochthonous, not representing *in situ* floras. The macroscopic organs of these fossils and any associated insect-pollinated plants were separated and/or, when waterlogged, destroyed due to Flood actions. 3) The distributions of the fossils may be related to gyres developing in the flooded continental areas (Barnette & Baumgardner 1994). Alternatively, the assemblages were deposited by concentrically parallel circumpolar currents with marginal gyres. 4) As the flood abated, primary succession led to a few years of fern dominance that quickly transitioned to early successional, low diversity, open woodland regenerating first from buoyant and/or raft-transported propagules originally from pre-flood forests associated with Normapolles taxa. Over decades, diverse, late successional tropical forest developed as unrelated baramins, which survived the Flood in low numbers, increased and diversified in the forests as the high rainfall and temperatures persisted. Triprojectates failed to propagate adequately in post-Flood environments to regain dominance, and their meager Lower Paleocene remnant assemblage is largely due to redeposition. The feasibility of the above creationist interpretation depends largely on its congruence with yet underdeveloped creationist models of the geology of the Northern Hemisphere. Still problematic are the location and demise of the mammal (*viz.*, the human-mammal-bird-food plant) pre-Flood biogeographic province, a lack of a well-defined progression of geological processes for Secondary strata, and configuration of continents, shore lines, and ocean circulation during the late Flood/post-Flood transition.

Barnette, D.W. and J.R. Baumgardner. 1994. Patterns of ocean circulation over the continents during Noah's Flood. In: Walsh, RE, ed. Proceedings of the Third International Conference on Creationism. Creation Science Fellowship, Pittsburgh, pp. 77-86.

Nichols, D.J. and K.R. Johnson. 2008. Plant and the K-T Boundary. Cambridge University Press, Cambridge, UK.

Wood, T.C. and M.J. Murray. 2003. Understanding the Pattern of Life: Origins

and Organization of the Species. Broadman & Holman Publ., Nashville, TN.
Editor: MR

The Chimpanzee Genome is Nearly Identical to the Human Genome

T.C. Wood

Bryan College

The completion of the draft genome of chimpanzee (*Pan troglodytes*) should have settled the question of the similarity of the chimpanzee and human genomes, but doubts among creationists persist. For example, Tomkins (2009) and Rana (2011) claim that the actual similarity of the chimpanzee and human genomes could be as low as 90%, rather than the reported >98% identity (Chimpanzee Sequencing and Analysis Consortium). To address the hypothesis that the chimp and human genome are >98% identical, I used a random sampling method which allowed for an accurate estimate of the similarity by accounting for both nucleotide mismatches and missing sequences. To randomly sample the genomic sequences of chimpanzees and humans, 40,000 sequence traces from each species were obtained from GenBank and compared to the finished human genome (build 37) using BLASTN (Altschul et al. 1990). The trace sequences were not processed in any way and should therefore represent a truly random sample of the two genomes. For each species, the most similar human genomic sequence to each sequence trace was recorded. As expected, the sequence traces aligned to uniformly random locations throughout the human genome. For the human trace sequences, 39,655 sequences aligned with a mean percent identity of 99.2% and a total alignment length of 9.75 Mb. For the chimpanzee trace sequences, 38,855 sequences aligned with a mean percent identity of 97.4% and a total alignment length of 24.8 Mb. Given a sample size of 24.8 Mb, the percent identity of a complete chimpanzee/human genome comparison should be greater than 97.4% with a 99% confidence interval of 97.39% - 97.41%. Since the error rate in the trace sequences is approximately 0.8% (based on BLASTN comparisons of human trace sequences to finished sequence), the actual similarity of finished chimpanzee and human genome sequences should be closer to 98.2%. Sequence traces that do not align in BLASTN searches of the finished human genome result from failed sequencing reactions, nonhuman sequence contamination, short or low complexity sequences that BLASTN will not align for computational reasons, as well as sequences that are genuinely absent from the human genome. Since three times as many chimpanzee traces than human traces failed to align (1145 vs. 345), it is likely that some chimpanzee trace sequences are truly absent from the human genome, but the fraction of missing chimpanzee traces ($1145/40,000 = 2.9\%$) is still very small. To test whether the chimpanzee genome could be much less similar than these estimates, the finished human genome sequence (build 37) was artificially modified by randomly altering nucleotides to create simulated genomes of 95%, 90%, and 85% identity to the actual human genome sequence (referred to as sim95, sim90, and sim85 respectively). BLASTN was then used to compare the 40,000 human traces to the modified genome sequences. Compared to sim95, 39,561 human trace sequences aligned with a mean percent identity of 94.7% and a total alignment

length of 9.61 Mb. Compared to sim90, 37,126 human trace sequences aligned with a mean percent identity of 90.4% and a total alignment length of 8.71 Mb. Compared to sim85, 32,540 human trace sequences aligned with a mean percent identity of 84.8% and a total alignment length of 6.02 Mb. The probability of the chimpanzee genome being less than 95% identical to the human genome is therefore $<2.2 \times 10^{-16}$ (Wilcoxon Rank Sum Test, $W = 1360474665$). The estimates presented here are superior to previous estimates because (1) confidence intervals for the similarity of the entire genomes based on the sample size are reported and (2) controls that allow accurate estimation of similarity for genomes that are much less similar than 99% identical are utilized. By all these estimates, the chimpanzee genome is nearly identical to the human genome.

Altschul, S.F., W. Gish, W. Miller, E.W. Myers, and D.J. Lipman. 1990. Basic local alignment search tool. *Journal of Molecular Biology* 215:403-410.

Chimpanzee Sequencing and Analysis Consortium. 2005. Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature* 437: 69-87.

Rana, F. 2010. DNA comparisons between humans and chimps: a response to the Venema critique of the RTB human origins model, part 2. <http://www.reasons.org/dna-comparisons-between-humans-and-chimps-response-venema-critique-rtb-human-origins-model-part-2>, accessed April 19, 2011.

Tomkins, J. 2009. Human-chimp similarities: common ancestry or flawed research? *Acts & Facts* 38(6):12.

Editor: JWF

The Platypus (*Ornithorhynchus anatinus*) is a Mammal

T.C. Wood
Bryan College

Recently, some creationist writers have begun to distinguish between “intermediate” or “transitional” forms and “mosaics.” Whereas the former might evidence the evolution of one group of organisms to another, the latter allegedly represents a chimeric creation from parts derived from different groups of organisms. Creationists cite the platypus (*Ornithorhynchus anatinus*) as a mosaic (e.g., Huse 1983, pp. 109-110), sometimes drawing an explicit analogy to *Archaeopteryx*, *Tiktaalik*, or other fossil forms which are alleged to represent evolutionary transitions (Wise 2008). I tested the mosaic nature of the protein sequences of the platypus genome (Warren et al. 2008) using three methods. First, I identified the most similar proteins to the platypus proteome in FASTA searches of a version of SwissProt with platypus protein sequences removed. If the platypus proteome is mosaic, the most similar proteins to platypus proteins should come from a variety of taxonomic sources. Instead, I found that 85% of the platypus proteins were most similar to proteins from one of four mammals: human, mouse, cow, or rat. Only 2.53% and 0.03% of platypus proteins were most similar to proteins from birds and lepidosaurs respectively. Second, I used FASTA to compare platypus proteins to human and chicken proteins, recording the best match for both species. If the platypus is a mosaic of avian and mammalian genes, I would expect that many platypus proteins would be significantly more similar to avian than to mammalian proteins. The 24,515 platypus proteins that had significant ($E < 10^{-5}$) matches in both humans and chickens are significantly more similar to human proteins than to chicken proteins, as measured by percent identity

(Wilcoxon rank sum test, $p < 2.2 \times 10^{-16}$). Further, although 6509 platypus proteins (26.6%) were more similar to chicken proteins than to human proteins, the average difference in percent identity was only 5.2%. For my third test, I used FASTA to identify reciprocal best matches (RBMs - approximate orthologous sequences) to platypus proteins from six other species: chicken, possum, dog, horse, mouse, and human. If the platypus is a mosaic, I would expect to see a significant number of proteins shared exclusively with chicken but not with other mammals. Of the total 26,836 platypus proteins, 36% had RBMs in no other species, and 25% had RBMs in all other species. Of the remaining 10,575 informative proteins, 1383 (13%) had RBMs in all mammals but not in chicken, and 982 (9%) had RBMs in four of the five other mammals but not in chicken. Only 2% (496) of the informative platypus proteins had RBMs exclusively in chicken. All three of these tests indicate that the mosaic character of the platypus proteome is negligible. Consequently, the platypus can only be classified as a mosaic by overemphasizing a handful of peculiar traits (e.g., presence of a bill and cloaca, oviparity, sex chromosomes, etc.). The platypus is a mammal.

Huse, S.M. 1983. *The Collapse of Evolution*. Baker Book House, Grand Rapids, MI.

Warren et al. 2008. Genome analysis of the platypus reveals unique signatures of evolution. *Nature* 453:175-183.

Wise, K.P. 2008. Mystifying mosaics. *Answers* 3(3):56-59.

Editor: JWF

Preliminary Baraminological Analysis of Jurassic and Cretaceous Avialae

T.C. Wood¹, M. Ross², and P.A. Garner³

¹Bryan College

²Liberty University

³Biblical Creation Ministries

In 1868, Huxley suggested that dinosaurs and birds shared anatomical affinities that could indicate an evolutionary relationship. The evolution of birds from dinosaurs is now widely accepted, especially after recent discoveries of theropods with feathers and feather-like integumentary structures (Norell and Xu 2005). Recently, Senter (2010) argued that even creationists should accept the evolutionary relationship of birds and dinosaurs based on multidimensional scaling (MDS) studies of coelurosaurs, but Wood (2011) found evidence of discontinuity between Avialae and Deinonychosauria and between Avialae and Oviraptorosauria.

Here, we examine three additional Avialae character matrices from Chiappe (2001), Zhou et al. (2008), and O'Connor et al. (2009). Chiappe's matrix consists of 24 taxa and 169 characters. For our calculations, we used 13 taxa with >40% character states known. After filtering at 0.75 character relevance cutoff, we used 76 characters to calculate baraminic distances. We found negative BDC between the Alvarezsaurids and the Avialae. Positive BDC was limited to three groups of avialans: Ornithuromorpha (*Patagopteryx*, *Ichthyornis*, and *Anas*, but not *Hesperornis*), Euenantiornithes (*Sinornis* and *Concornis*), and other Avialae (*Archaeopteryx*, *Rahonavis*, *Changchengornis*, and *Confuciusornis*). *Hesperornis* was not positively or negatively correlated with any other taxa. Zhou et al.'s (2008) matrix consisted of 205 characters and 29 taxa. For

our calculations, we used 23 taxa with >40% character states known and 107 characters (character relevance cutoff: 0.75). We found positive BDC within two groups corresponding to the Ornithuromorpha (except *Patagopteryx*) and the remaining Avialae plus the Dromaeosauridae outgroup. Negative BDC was observed between the two groups, except for positive BDC between *Archaeorhynchus* and three ornithuromorph taxa, *Yixianornis*, *Yanornis*, and *Hongshanornis*. O'Connor's (2009) matrix consisted of 242 characters and 29 taxa. We used 22 taxa with >40% of their character states known. After filtering at a character relevance cutoff of 0.75, we used 87 characters to calculate baraminic distances. We found three groups of taxa corresponding to the Enantiornithes, Ornithuromorpha, and Avialae plus the Dromaeosauridae outgroup. Within each group, only positive BDC was observed, and negative BDC was observed between Ornithuromorpha and Enantiornithes and between Ornithuromorpha and other Avialae. Between Enantiornithes and other Avialae, we found no negative BDC and one instance of positive BDC (between *Sapeornis* and DNHM D2522).

These results add to Wood's (2011) suggestion of discontinuity between Avialae and dinosaurs by suggesting additional discontinuities within the Avialae. Minimally, we find no evidence of continuity between modern birds and dinosaurs. Our analysis of O'Connor et al.'s data matrix suggests the presence of three apobaramins: (1) Ornithuromorpha, (2) Enantiornithes, and (3) other Avialae plus Dromaeosauridae. Analysis of Zhou et al.'s larger data matrix supports the ornithuromorph apobaramin but combines the enantiornithes with the other Avialae and dromaeosaurids. While Chiappe's data matrix does not support a conclusion of discontinuity within the Avialae (due to a lack of negative BDC), it does not contradict it either (due to a lack of positive BDC). These results suggest that Senter's (2010) confidence that statistical baraminology supports the evolution of birds from dinosaurs is misplaced.

- Chiappe, L.M. 2001. Phylogenetic relationships among basal birds. In: Gauthier, J. and L.F. Gall, eds. *New Perspectives on the Origin and Evolution of Birds*. Yale University Press, New Haven, pp. 125-142.
- Huxley, T.H. 1868. On the animals which are most nearly intermediate between birds and reptiles. *Annals and Magazine of Natural History*, 4th series. 2: 66-75.
- Norell, M.A. and X. Xu. 2005. Feathered dinosaurs. *Annual Review of Earth and Planetary Sciences* 33:277-299.
- O'Connor, J.K., X. Wang, L.M. Chiappe, C. Gao, Q. Meng, X. Cheng, and J. Liu. 2009. Phylogenetic support for a specialized clade of Cretaceous enantiornithine birds with information from a new species. *Journal of Vertebrate Paleontology* 29:188-204.
- Senter, P. 2010. Using creation science to demonstrate evolution: application of a creationist method for visualizing gaps in the fossil record to a phylogenetic study of coelurosaurian dinosaurs. *Journal of Evolutionary Biology* 23:1732-1743.
- Wood, T.C. 2011. Using creation science to demonstrate evolution? Senter's strategy revisited. *Journal of Evolutionary Biology* 24:914-918.
- Zhou, Z., J. Clarke, and F. Zhang. 2008. Insight into diversity, body size and morphological evolution from the largest Early Cretaceous enantiornithine bird. *Journal of Anatomy* 212:565-577.

Editor: JWF

Detecting Discontinuity in the Dinosauria using Baraminic Distance Correlation

T.C. Wood¹, M. Ross², and P.A. Garner³

¹Bryan College

²Liberty University

³Biblical Creation Ministries

The past decade has seen a growth of baraminological research based on the baraminic distance correlation (BDC) test introduced by Robinson and Cavanaugh (1998), but there has been little serious assessment of the value of the BDC test itself. Here we attempt to evaluate the utility of BDC for detecting putative discontinuities among fossil groups, where discontinuity is recognized by significant, negative BDC between two groups of taxa. Assuming that the rank of family is an approximation of the holobaramin, the BDC test should detect discontinuity when more than one family is present in the set of taxa and characters being evaluated. For our evaluation, we selected nineteen character sets derived from Weishampel et al. (2004), Williamson and Carr (2002), and Sullivan (2003), all of which focus on high-level classification of dinosaurs and consequently contain multiple families. By focusing exclusively on taxa known only from fossils, all character matrices also contained many unknown character states (mean fraction of unknown character states: 0.34, range 0.11-0.54), which could hamper efforts to detect discontinuity using BDC. We performed all BDC calculations using BDISTMDS (Wood 2008). To maximize the number of characters used in BDC calculations, we eliminated taxa with less than 0.4 taxic relevance and characters with less than 0.75 character relevance. The filtered character matrices contained 22-515 characters (average 128) and 7-31 taxa (average 13.9). The fraction of unknown character states in these filtered character matrices ranged from 0.11 to 0.43 (average 0.26). We found evidence of discontinuity in thirteen of the nineteen character sets (68.4%). Six character sets failed to produce evidence of discontinuity, despite the presence of more than one family of taxa in each set. The sample of characters for matrices where discontinuity was detected was 28-515 (average 100.9), whereas the sample of characters for matrices where discontinuity was not detected was 22-505 (average 186.7). Thus, it would seem that in terms of number of characters, the failed matrices appear to be more holistic than the successful matrices. The major difference between the successful and failed matrices was the fraction of total character states still unknown, which averaged 0.233 for the successful matrices and 0.305 for the failed matrices, although the difference was not significant ($p = 0.136$, Wilcoxon rank sum test). Thus, it appears that unknown character states may inhibit detection of discontinuity by the BDC test. Based on BDC analysis of the thirteen successful matrices, we suggest the following apobaramins could be recognized: Coelophysoidea, Neoceratosauria, Tyrannosauroidea, Oviraptorosauria, Prosauropoda, Ankylosauridae, Nodosauridae, certain Iguanodontoidea (*Ouranosaurus*, *Iguanodon*, *Probactrosaurus*, *Protohadros*, *Eolambia*, and *Altirhinus*), Hadrosauridae, Pachycephalosauridae, and Ceratopsidae. To further clarify dinosaur baramins, future studies should expand this research to additional character matrices and techniques such as multidimensional scaling.

- Robinson, D.A. and D.P. Cavanaugh. 1998. A quantitative approach to baraminology with examples from the catarrhine primates. *CRSQ* 34:196-208.
- Sullivan, R.M. 2003. Revision of the dinosaur *Stegoceras lambe* (Ornithischia, Pachycephalosauridae). *Journal of Vertebrate Paleontology* 23:181-207.
- Weishampel, D.B., P. Dodson, and H. Osmólska, eds. 2004. *The Dinosauria*. 2nd ed. University of California Press, Berkeley.
- Williamson, T.E. and T.D. Carr. 2002. A new genus of derived pachycephalosaurian from western North America. *Journal of Vertebrate Paleontology* 22:779-801.
- Wood, T.C. 2008. Baraminic distance, bootstraps, and BDISTMDS. *OPBSG* 12:1-17.

Editors: JWF & GP