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Number Four

Occasional Papers of the Baraminology Study Group

DISCOVERING THE CREATOR
PROCEEDINGS OF THE THIRD BSG CONFERENCE

edited by
Roger W. Sanders

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Occasional Papers of the Baraminology Study Group

Editor: Roger Sanders, 1854 Greenwood Road, Weatherford, TX 76088, USA
Email: opbsgeditor@bryancore.org

Assistant Editor: Todd Wood, Center for Origins Research and Education, Bryan College, Dayton, TN 37321, USA

Editorial Board: Joseph Francis, Margaret Helder, Georg Huber, Richard Sternberg

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1. Develop a new view of biology that is consistent with the Biblical record.
2. Encourage high-quality creation biology and baraminology research.
3. Sponsor conferences and other appropriate activities to promote creation biology.
4. Develop a community of creation biologists who share these goals.

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Discovering the Creator: Proceedings of the Third BSG Conference

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Introduction

I struggle with the paintings which have within them “hidden” pictures. I’m told that to see these things I’m supposed to focus somewhere other than immediately on the canvas — in most cases to focus (somehow not explained to me) beyond the canvas. I can stand before such framed wall mounts for extended periods of time and never see anything I am “supposed” to see (wondering all the while if it’s really there and whether there is a hidden camera somewhere documenting how ridiculous I look trying to see what isn’t there). In fact, a case in point... Years ago a student left a tract on my desk which supposedly had a picture of Christ on it “if only I could see it the right way.” It laid on my desk for over seven years, I being unsuccessful in that entire period in so seeing Christ (I fear something symbolically appropriate in that!), before it burnt in a fire four years ago. The loss of that continual reminder of perceptual inadequacy was one of the few “happy” losses in that fire! Now, please don’t misunderstand. I’m not always completely unsuccessful at such perception. There have been times standing before such works that I see glimpses of the hidden picture, but the picture is fleeting. It is difficult to stay focused on it. I see something similar in creation science. For centuries the world has more or less seen science as a human endeavor to understand the physical world. Individuals here and there have been able to focus upon the God Who is behind it all, but this seems to be a fleeting picture. It is time we focus properly and clearly — not on the science, or upon the doers of it, or even upon the physical world, but rather refocus on what is beyond and within the picture. We need to focus on the One Who created the physical world and ourselves — the One for Whom all this exists.

God, man, and the creation have been intricately and purposely linked from the very beginning. God formed and sustains man and the creation to mutually interact so as to bring glory to God.

God created the earth by commanding it into being (Psa. 33:9) but He did not create without purpose. God created the earth to be inhabited (Isa. 45:18). He stretched out the heavens, but did so “as a tent to dwell in” (Isa. 40:22). God created plants to be “pleasant to the sight” and “good for food” for humans (Gen. 2:9). He created lights in the heavens, but did so “as signs, seasons, days, and years” — as time markers for man (Gen. 1:14). Ultimately, He created man from creation’s very substance (Gen. 2:7). God fashioned creation in such a way that man might

live and thrive to know God and glorify Him as God.

Man was created in the image of God (Gen. 1:26a) — optimally designed to manifest, honor, and glorify the Creator on stage before the creation. The creation was also placed in man’s care (Gen. 1:26b-27). Man was placed in the Garden “to dress it and to keep it” (Gen. 2:15), to nurture and develop the creation to maximize the glory it brings to God. On the very first day of human existence man is asked to name the animals (Gen. 2:19-20). This is probably one of the first manifestations of man’s role as steward of God’s creation. God presented man with responsibilities to the creation which were designed to bring glory to God.

God also designed the creation to teach man about Himself. Even the invisible attributes of God are “plainly evident” in those things made (Rom. 1:19-20a). This teaching is both universal and powerful. It is so powerful that God condemns “all ungodliness and unrighteousness of men” (Rom. 1:17) because God’s teaching from the creation leaves all men “without excuse” (Rom. 1:20b). The creation has been fashioned in such a way as to teach man about God and thereby glorify Him.

Not only were things created with these original purposes, but these purposes remain with us into the present. The Fall took away neither our image-bearing status nor our dominion (e.g. Gen. 9:1-7), the creation continues to sustain us, and God continues to teach us through the creation (Rom. 1:17-20). Things also persist because He continues to sustain them (Col. 1:16-17). The intimate link between God, man, and the creation was there in the beginning and continues to be there in the present.

Secular science (and even, ironically enough, some creation science) would suggest that man can study the physical world without involving God. This claim is invalid. Separating a study of the creation from its Creator is artificial at best and perhaps actually an example of human sin. The world exists and we exist because God created it in the beginning, and has purposely chosen to sustain it another nanosecond of physical time. We can interact with and understand the physical world because God created the physical world and us so that that could happen. Science is possible only because God created the physical world so we could exist, know Him, and obey Him. Science owes a great debt of gratitude not only to humans who were clever enough to devise its rules, and the physical world itself which was kind enough to

allow us to understand it, but even more so to God who created humans clever enough to understand the physical world and the physical world kind enough for us to understand it.

As its title suggests, this conference's theme is "Discovering the Creator." We would like to see science become an efficient means towards this end. Rather than only briefly glimpsing the Creator through science, we would like the Creator to be the clear focus of our science. Our desire to better know our Savior and Lord ought to then function as a powerful motivation in our science — thus the subtitle of our conference ("Knowing God as a Motivation for Science"). This will not likely happen in a single conference. I pray that our focus will be stimulated, encouraged, and perhaps in some cases initiated by this conference. While we are together, consider embracing that focus. I suspect that every presentation, discussion, and interaction of this conference will be more rewarding if we do so.

After we depart, let us also consider keeping the conference theme before us in what we do. Just as focusing on Christ was a challenge to Peter as he walked across the waves, it may prove to be a challenge to us to maintain our focus on Him as we do our science. It would be an answer to prayer if this conference can function also as an ebenezer — a reminder to us in the future — of our need to focus on Him when our attention is diverted somewhere else.

To Him Be Our Focus,

Kurt P. Wise,
Director of Origins Research and Education
Associate Professor of Science
Bryan College, Dayton, TN

Conference Schedule

All events will take place in the Rhea County Room of the Latimer Student Center

Wednesday, June 9

1:30 p.m.
Registration opens

5:30 p.m.
Dinner

6:30 p.m.
Welcome from Bryan College and Opening Prayer

Introductions and Announcements
Todd C. Wood
Bryan College

7:00 p.m.
Plenary: "Discovering the Creator: Knowing God as a
Motivation for Science"
Todd C. Wood
Bryan College

8:00 p.m.
Plenary: "Anarthrous Ordinal Numbers in Genesis 1"
David Fouts
Bryan College

Thursday, June 10

8:00 a.m.
Breakfast

8:30 a.m.
Plenary: "Design Reasoning and Discontinuity in Biology"
Paul Nelson
Discovery Institute

9:20 a.m.
Plenary: "The Multifaceted Nature of Microbially-Based
Symbiotic Partnerships: Detection of Patterns and Implications
for Creation Research"
Joseph Francis
The Master's College

10:10 a.m.
Break

10:30 a.m.
Plenary: "Theological Implications of Alternative Models:
Death before Sin and the Matter of the Atonement"
Marco Terreros
Colombia Adventist University

11:20 a.m.
Plenary: "The Origins of Natural Evil"
Gordon Wilson
New St. Andrews College

12:10 p.m.
Lunch

12:40 p.m.
Rhea County Courthouse Tour (optional)

2:00 p.m.
Plenary: “In Search of the Silver Bullet —or—God’s History Lesson for Systematics”
Roger Sanders
Editor, *OPBSG*

2:50 p.m.
Research Talks Session I

Cavanaugh, “The Catarrhine Primates Revisited: An ANOPA Study”
Davis, “Baraminological Interpretation of Squirrel (Rodentia: Sciuridae) Phylogeny”
Gollmer, “Modeling Holistic Behavior for Analysis by Systems Theory”
Gruenke, “A Proposal for a Creationist Survey of Viruses”

5:30 p.m.
Dinner

7:00 - 9:00 p.m.
Poster Session

Friday, June 11

8:00 a.m.
Breakfast

8:30 a.m.
Plenary: “DNA Evidence in Basic Type Biology”
Judith Diehl
Independent Scholar

9:20 a.m.
Plenary: “Is the Equidae a Holobaramin?”
Paul Garner
Biblical Creation Ministries

10:10 a.m.
Break

10:30 a.m.
Plenary: “Pre-Flood Biogeography”
Kurt P. Wise
Bryan College

11:20 a.m.
Plenary: “Discovering the Creator - And What He Teaches Us About Teaching”
Sheila Richardson
Independent Scholar

12:10 p.m.
Lunch

12:40 p.m.
Rhea County Courthouse Tour (optional)

2:00 p.m.
Plenary: “What Happened to the Dinosaurs?”
A.V. Chadwick
Southwestern Adventist University

2:50 p.m.
Research Talks Session II

Mace, “The HybriDatabase”
Moeller, “The Effect of Design Constraints on the Plasticity of Traits within a Baramin: Echolocation, Flight and Masticatory Systems in Chiroptera”
Ross, “Mosasaurs: Baraminology, Biostratigraphy, and Boondoggle”
Sternberg, “Systematic Position of the Cetacea Revisited: A Fuzzy Sets-based Analysis of Morphological Discontinuity and ‘Transitional Forms’”

4:30 p.m.
Discussion

5:30 p.m.
Dinner

Plenary Abstracts

P1. Discovering the Creator: Knowing God as a Motivation for Science

Todd Charles Wood
Bryan College

Although personal biases and motivation form an inescapable part of science, they are very rarely the subject of discourse by scientists. As Christians, we are instructed to ‘make the most of the time’ (Eph. 5:15-16) and to do all ‘for the glory of God’ (1 Cor. 10:31). Because of these commands, it is important for all Christians in science to reflect on their underlying motives for engaging in their particular disciplines. Beginning with Hebrews 12:1-2, I developed a novel motivation for science, consisting of the following three points: 1) Science, like all Christian activity, ought to be performed in a community (‘surrounded by so great a cloud of witnesses’). Fellowship with other scientists and nurturing students should become prime goals of each scientist. 2) Scientific errors ought not be destroyed but instead ‘laid aside.’ Creationists often allow evolutionary theory to become the focus of their work and to set their research agenda. Since things that beset us are to be laid aside, we need to re-orient our research priorities with evolution as only a minor focus. 3) Jesus Christ the Creator should become the focus of our scientific activities (‘looking to Jesus as the author and finisher of our faith’). Since creation is a form of revelation (Ps. 19, Rom. 1), it must be possible to discover God’s attributes in the things He has made.

Whereas the implementation of the first two points seems straightforward, placing Jesus Christ as the central focus of science poses some obvious operational difficulties. Prominent among these difficulties is even imagining what biology might look like when focused on the Creator. I suggest a five-fold theoretical organization of biology that will allow creationists to develop a new biology based on God’s revelation in His Creation. First of these theoretical necessities is a theory of design, which must be developed together with a theory of imperfection (natural evil). The final three models of biogeography, biosystematics, and diversification (speciation) can be synthesized as specific expressions of design, tinged by the curse. Using these five theoretical models and field-specific content, creationists can re-create any field of biology with the Designer as the foundation and goal.

P2. The Anarthrous Ordinals of Genesis One

David Fouts
Bryan College

Recent attempts have been made to understand Genesis One differently from the traditional understanding of Creation by decree of God over a period of six consecutive days of 24 hours duration. One of the most recent attempts has been to understand the sequencing of the days to be different than six successive days. Instead, they are to be understood as fitting a literary framework and not to be understood as indication sequence in any normal sense of that word. To justify this position, appeal is made to the fact that the second through fifth days, though so named by the appropriate ordinal numbers in the originally written Hebrew text, are actually to be understood as simply “a second day,” “a third day,” “a fourth day,” “a fifth day,” since they are in fact anarthrous (having no article “the”) rather than articular (with the article “the” present).

This paper will demonstrate that though it is true that the ordinals second through fifth of Genesis One are indeed anarthrous, definiteness demanding a translation of “the second day” etc., may be established by other means in Hebrew than the presence of the article. Most notably, definiteness may be established by the presence of the ordinal number itself, rather than the presence of an article. In fact, the presence or absence of an article with an ordinal number is grammatically determined by the noun that the ordinal modifies. When that noun is articular, the ordinal, functioning as an adjective, is also articular. If the noun modified is anarthrous, the associated ordinal will also be anarthrous.

Since in the case of Genesis One, the term “day” modified respectively by the ordinals second through fifth is anarthrous, one expects to find the ordinals likewise anarthrous. The definiteness of the day is determined by the ordinal itself and therefore is appropriately translate “the second day,” etc.

P3. Design Reasoning and Discontinuity in Biology

Paul Nelson

Discovery Institute

“Some circumstantial evidence is very strong,” wrote Henry David Thoreau, “as when you find a trout in the milk.” Why do some patterns, such as finding a fish in a milk can, trigger the suspicion that an intelligence was involved? How do we know when an event or pattern was caused by a mind like our own? Are these inferences to intelligent causes merely intuitions, or can they be grounded in a scientifically fruitful method? This lecture answers these questions by exploring the basic logic of design reasoning. Topics covered include the history of the design argument, Dembski’s explanatory filter, the concept of specified complexity, alternative Bayesian approaches, the major criticisms of design inferences, and the relation of design reasoning to pattern detection and the significance of discontinuities in biological systematics.

P4. The Multifaceted Nature of Microbially-Based Symbiotic Partnerships: Detection of Patterns and Implications for Creation Research

Joseph W. Francis

Master’s College

Microbes are ubiquitous in nature and form a life-supporting organosubstrate prevalent throughout the biosphere (Francis 2003). Microbes readily participate in beneficial symbiotic relationships, and the number of microbial species participating in beneficial activities most likely far outnumbers the microbial species involved in pathogenesis (Francis 2003). Creationism predicts that all living organisms may benefit from symbiotic relationships with microbes and this relationship may be a remnant of a pre-Fall environment that was free of lethal parasitism and disease (Francis 2003). Since symbiosis is prevalent in nature and demonstrates the beneficial aspects of microbes, creationists should find this a fruitful area of research and exploration. However, relatively few symbiotic relationships have been extensively studied and documented. The lack of study in this area is most likely the result of a focus in contemporary biology on the concepts of competition and parasitism and a corresponding low interest in the nature of microbial symbionts. Furthermore, symbiotic relationships are complex and involve multiple partners, and this makes their study problematic because 1) biologists tend to focus on individual organisms rather than community interactions and 2) symbionts can be morphologically altered by the partnership making their detection difficult. In this paper, I will compare and contrast the functions of microbial symbionts within three different complex biological communities with the goal of detecting patterns that could be used as predictors of symbiotic relationships. Within each community, complex and possibly unique associations can be detected among the partners, but patterns common to all the communities can also be detected. Three major patterns emerge from analysis of the communities. First, dramatic changes in morphology are induced by symbiotic associations and can occur among symbionts and/or their hosts

at the molecular, cell, tissue or organismal level. Secondly, symbionts play major roles as providers of nutrition and regulators of population control within each community and in each case this may directly or indirectly influence several factors including the geographical distribution of the host and/or symbiont. It is interesting to note also that the nutritional and population control functions of microbial symbionts, in many cases, correlates directly with the morphology changes induced by the symbiotic relationships. And thirdly, many of the beneficial aspects of microbial symbionts appear pathological and destructive at the cell level when viewed apart from the symbiotic community. The results of this study suggest that creation biologists will 1) gain a better understanding of organisms if they are studied *in situ*, in the context of the complex communities in which they thrive (a “systems biology” approach) and 2) be able to predict the existence of symbiotic relationships using patterns observed among existing known symbiotic relationships.

Francis JW. 2003. The organosubstrate of life: a creationist perspective of microbes and viruses. In Ivey RL, ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 434-444.

P5. Theological Implications of Alternative Models: Death before Sin and the Matter of the Atonement

Marco Terreros

Colombia Adventist University

Charles Darwin established theoretically that evolution cannot operate without struggle and death. Therefore, evolution presupposes the presence of death on earth for aeons prior to the appearance of *Homo sapiens*. This means, for theistic evolution, that a long history of death preceded the appearance of Adam, implying that death is not connected to Adam’s sin. But this disconnection conveys serious consequences for Christian theology in several areas.

First of all, it affects the theology of salvation by undermining the validity of Christ’s work of atonement understood in a substitutionary sense. Theologically, as well as historically, Fall and redemption correspond to each other. The historical reality of the first made the second necessary. Redemption history begins with the sin of man; it was at the Fall that the *proto-euangelion* was announced (Gen. 3:15). If man’s voluntary, free decision is removed or severed from death, sin as a cause of death disappears from the story of redemption. Such separation of death from sin implies that if death entered the world through any other means than by human sin, then the solution to the problem of death can be found without having first to solve the problem of human sin. This would mean that Christ did not really have to die because death is not the wages of sin. Thus Christ’s death loses its atoning value.

Reaching this conclusion means that God could have solved the death problem in a better way than He chose. If this is true, then Jesus’s sinless life and sacrificial death were, in reality, unnecessary. But this recognition makes God’s salvific plan a faulted one instead of a perfect one, jeopardizing His wisdom in designing it and affects His love in setting the plan in motion.

In short, the admission of no cause-effect connection between sin and death renders the whole plan of salvation useless. Other areas of Christian belief besides atonement theology—though certainly not disconnected from it—are also negatively impacted by the concept that death anteceded sin. These include:

The goodness of God and the goodness of creation. Conditions where struggle and death are common due to the scarcity of resources, as posed by evolutionary theory, do not match the biblical picture of a creation originally pronounced “very good” (Gen. 1:31), nor do they speak of a good Creator.

The authority of Scriptures. The claim that innumerable living forms died for long ages preceding Adam undermines confidence in the Genesis record. Thus, by the concept of death before the Fall, the Genesis account is not only reinterpreted, but its historical validity is denied, for both Old and New Testaments point to all kinds of death as brought about into the world by the sin of Adam.

The doctrine of humanity. Bible evidence indicates that brutish forefathers could not have preceded Adam in a line of unbroken continuity. This means that belief in the organic evolution of man, entailing hominids dying for ages long before man reached the state of consciousness, degrades humanity from the high position given them by God himself in creating man and woman in His own image and likeness (Gen. 1:26-27).

The doctrine of eschatology. Theistic evolution presupposes death to be good and, as such, as having been originally placed into the process of nature by God himself. But, if death is something good, or natural, and originally intended by God himself for His creatures, there is little reason to believe that death will ever be eliminated from the world as suggested by biblical texts (e.g. 1 Cor. 15:26; Rev. 21:4). For if death was present on earth long before sin, the prospect is that death will remain long after sin is eradicated from the world.

P6. The Origins of Natural Evil

Gordon Wilson

New St. Andrews College

In a cursory survey of life it is obvious that a vast number of species spanning most kingdoms and phyla have features that are teleologically designed to deal out disease and/or death. Many pathogens, parasites, and predators have sophisticated genetic, morphological, and behavioral arsenals (natural evil) that clearly testify to the God’s eternal power and divine nature (Romans 1:20), i.e. they are not the result of mutation and natural selection. These range from the bacterial type III secretion systems, the cnidarian nematocysts, the toxoglossate radula and apparatus of *Conus*, the parasitic physiology of *Wuchereria bancrofti*, the piercing/sucking mouthparts of predaceous insects, and the solenoglyphous skull, pit organs, and venom apparatus of pit vipers. Scripture states that: 1) every green plant was given for food (Genesis 1:30), 2) death and disease are a consequence of sin (Genesis 2:17), and 3) creation was completed on the sixth day (Genesis 2:1). The following six scenarios attempt to explain the presence of natural evil in the biological world from a young earth creationist framework. I will then assess them in light of these aforementioned biblical truths.

At creation creatures that were to become pathogens, parasites,

and predators:

- 1) had dual gene sets: (such as in holometabola: larva, pupa, and adult) one gene set for benign morphology and behavior (sinless contingency) and one for malignant morphology and behavior (Fall contingency) with only the benign gene sets expressed prior to the Fall.
- 2) had malignant morphological gene sets expressed for an imminent preordained (or fore-known) Fall, with no usage prior to the Fall. Malignant behavioral gene sets expressed after the Fall.
- 3) had the same malignant morphology before and after the Fall, however benign usage was normative before the Fall. After the Fall micro-evolutionary factors altered benign behavior into malignant behavior.
- 4) were morphologically and behaviorally benign and then subsequent to the Fall malignant genes were designed, created, and incorporated into the genome of certain creatures transforming them into pathogens, parasites, and predators.
- 5) were subject to random mutation and natural selection after the Fall transforming their benign gene sets into malignant gene sets. The latter were not designed by God.
- 6) were completely benign in all respects but at the Fall the enemy (Satan, et. al.) engaged in post-Fall genetic modification and/or bestiality that resulted in creatures with malignant behavior and morphology.

I will argue that the two scenarios that are the most harmonious with both scripture and the scientific data are 1) and 2). Any scenario attributing the presence of these highly complex morphological and behavioral arsenals to random mutation and natural selection is granting creative powers to mindless processes (this is no better than atheistic evolution). Any scenario that attributes these complex arsenals to God’s creative power yet shifts their time of origin to a post-Fall creative act, contradicts the finished creation on day six. Finally, any scenario that attributes these complex arsenals to Satan et. al., attributes too much creative power and intelligence to the powers of darkness.

P7. In Search of the Silver Bullet—Or—God’s History Lesson for Systematics

Roger W. Sanders

Independent Scholar

Following biologists’ acceptance of Darwinian evolution, the history of systematic biology has been marked by a parade of mutually exclusive, contradictory, and competitive phylogenetic classifications and by a myopic search for the Silver Bullet—the one new method of obtaining sets of character data or analyzing character data that would unambiguously resolve the conflicting data into a single unified non-contradictory classification. Technical advances brought chromosome and breeding studies; then came elucidation of secondary metabolites, ultrastructure revealed by transmission and scanning electron microscopy, computer-assisted phenetic analyses, and protein structure; and now the bandwagon is computer-assisted cladistic analyses dovetailed with nucleotide sequences of DNA.

To test the success of the search for the Silver Bullet, the five major contemporary “morphological” classifications of flowering plants systematics are compared via a consensus classification and deviations from that consensus. These classifications are not cladistic because no higher-level cladistic-based systems using characters other than DNA sequences have ever been proposed. This is because convergence among these “morphological” characters at higher taxonomic levels is believed to be pervasive “noise” that swamps the taxonomic “signal” of the few nonconvergent characters. However, the evolutionary community considers the sequenced genes to be nonconvergent, “low noise” characters, homologous across all angiosperms and reflecting the true evolutionary history of the group. Thus, the consensus classification presented here is also compared to the single DNA or molecular classification proposed by the Angiosperm Phylogeny Group (APG). In the consensus classification, the major family-level groups that are recognized by all classifications (including the APG classification) are designated as core groups and grouped into larger hierarchical groups by majority rule consensus. Smaller groups (segregate families and genera), for which there is no consensus on their taxonomic placement, are listed with each core group with which each classification associates them. These groups form links between the core groups and are called “boundary groups”. Although the APG classification is touted as a resolved molecular classification, it is actually a majority rule consensus of the conflicting dendrograms for the three genes on which it is based. The positions of a sample of the core groups on these dendrograms are compared.

Conflict among the five “morphological” classifications, between the “morphological” consensus and the APG classification, and among gene dendrograms shows clearly that no single classification reflects true relationships. Although molecular data are sophisticated, systematists actually are regressing to “one-character taxonomy” when basing classifications on these data. There is no Silver Bullet.

Both the Bible and the conflicting classifications suggest that God designed life to be classified in multiple ways—a netted pattern of relationships (Wise 1998). Sanders and Wise (2003) developed this implication further with the introduction of the cognitum concept, which is reviewed here. Since God communicates general revelation through the cognitive senses, creationists should develop biosystematic research that explores God’s design of biodiversity rather than forcing the data into a pre-conceived single pattern. It is of great interest that the pattern of core groups surrounded by their boundary groups coincides with the concept of groups as cognita. The interconnectedness of the core groups is further evidence that to develop classifications that reflect multiple, simultaneous patterns of designed similarity would bring glory to Him.

Wise, K.P. 1998. Is life singularly nested or not? In R.E. Walsh, ed. *Proceedings of the Fourth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 619-631.

Sanders, R.W. and K.P. Wise. 2003. The Cognitum: A Perception-Dependent Concept Needed in Baraminology. In R.L. Ivey, ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 445-455.

P8. DNA Evidence in Basic Type Biology

Judith Diehl

Independent Scholar

Basic types and baramins are two approaches to one and the same goal: to possibly identify the units of creation. Whereas baraminology concentrates on gaps between groups emerging from a compilation of overall evidence, the basic type approach uses the criterion of hybridization as an indication of a deep-rooted similarity between organisms which cannot be attributed to mere coincidence. The strength of this approach is to unequivocally identify members of a basic type whereas no conclusions can be drawn from the lack of hybridizations. However, basic types are believed to be larger than actually hybridizing species groups, and the concept is not applicable anyway to e.g. asexual or fossil organisms. In studying well-described basic types by molecular methods, we can learn something about their potential to identify them, to possibly stretch their limits and to gain insights from congruence of clusters as well as from the lack of it.

Several examples from different groups of organisms and different kinds of markers will be given to show the potential as well as the limits of molecular approaches to elucidate the origin of created units. Apart from the general lingering problem of confusing (sequence) similarity with homology, (i) coding genes have often been shown to produce misleading results about relationships. This is partly explained by selection pressure for the maintainance of function. On the other hand, there is increasing evidence from multiple-gene studies that the results obtained from different molecular markers are often getting more and more incongruent instead of converging to the ‘real’ relationships. (ii) Non-coding DNA is generally giving better results (i.e., more congruent to morphology and other evidence), not only because it is more or less selectively neutral, but probably also because it is much more variable and therefore usually applied to lower taxonomic levels. The idea that it works better because close to the species level we are dealing with actual relationships (instead of biologically meaningless similarity thought to occur at higher taxonomic levels) is tempting, but entirely concept-based. While congruence of hybridizations, molecular, morphological and other evidence might be reassuring, it is probably unrealistic to expect it to be generally found for basic types or baramins. (iii) Alignability of non-coding sequences and (iv) congruence of genomic maps could in some cases also be good criteria for organisms to be of common origin. None of these criteria should however be generalized or applied in an uncritical way.

Molecular methods do have a high potential to exclude particular taxa from a group or to include unexpected members whose morphological similarity was not immediately obvious before. Also, there are now methods available for addressing the hybridization criterion directly with molecular approaches. E.g., it became possible to identify genes from both parents stemming from past hybridization events; and incongruences between gene trees of uniparentally and biparentally inherited markers can provide evidence for unexpected hybridizations in the past for which no other traces are left nowadays. This is especially frequently observed in plants in which hybrid speciation is believed to have been played a major role in their diversification.

P9. Is the Equidae a Holobaramin?

Paul Garner

Biblical Creation Ministries

Horses are well-represented in the fossil record, especially in North America, and appear to form a convincing, though complex, phylogenetic sequence. This sequence has been cited as important evidence in support of evolutionary theory, while creationists have attempted to debunk it as artificial and composed of non-equivalent parts. The status of *Hyracotherium* as the ancestral horse has been particularly controversial in the creationist literature. A common, but erroneous, claim is that *Hyracotherium* is actually a hyracoid. Although Owen (1841) named *Hyracotherium* for its resemblance to a hyrax, he also likened it in other respects to entelodonts, pigs, and hares. Cladistic analyses based on new and previously known specimens suggest that the taxonomy and relationships of Eocene perissodactyls – including *Hyracotherium* – are much more complex than previously recognised (Hooker 1989, 1994; Froehlich 1999, 2002). The genus *Hyracotherium* is now regarded as a paraphyletic ‘wastebasket’ taxon. A number of species attributed to this genus are not equids, but are thought to have given rise to other perissodactyl clades. The type species *Hyracotherium leporinum* Owen (1841) appears to nest within the Palaeotheriidae. The claim that *Hyracotherium* was a hyrax originated with Cousins (1971), citing a German-language publication by Nilsson (1954). Its persistence in the creationist literature reminds us of the dangers of uncritical reliance on secondary sources.

Recently, some creationists have taken a more positive approach to the horse series. Cavanaugh *et al* (2003) concluded that nineteen fossil equids – including *Hyracotherium* – belonged to a single monobaramin. However, their analysis did not include a non-equid outgroup and was thus unable to detect any discontinuity surrounding the equids. This paper reports a baraminic distance correlation analysis of a morphological dataset obtained from Hooker (1994). The dataset consists of 35 characters for 13 fossil taxa. *Propachynolophus levei* was excluded from the analysis because 17 of the 35 characters were missing for this taxon. Included in the analysis were ten fossil perissodactyls, including equids and non-equids, and two phenacodontid condylarths. Baraminic distances were calculated according to the formulae described by Robinson and Cavanaugh (1998) and all characters with less than 90% relevance were eliminated. This excluded the three non-dental characters. Correlations of baraminic distances were calculated. The analysis reveals four clusters of taxa united by significant positive correlation: (1) *Cymbalophus cuniculus* plus ‘*Hyracotherium sandrae*’; (2) *Phenacodus* plus *Ectocion*; (3) *Cardiophus* plus *Hallensia louisii* plus *Pachynolophus hookeri*; (4) *Hyracotherium leporinum* plus *Propachynolophus gaudryi* plus ‘*Propachynolophus maldani*’. This group in turn appears to correlate with *Pliolophus pernix* plus *Pliolophus vulpiceps*. However, overall there is poor negative correlation between these clusters. The exception is the significant negative correlation between the phenacodonts and the remaining taxa – consistent with their status as outgroup taxa. The major limitation of this study is that all the included characters are dental, so the dataset is not holistic. For this reason, strong conclusions cannot be

drawn and the question of whether the Equidae is a holobaramin remains unresolved.

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P10. Pre-Flood Biogeography

Kurt Wise

Bryan College

According to Romans 1:18-20, the physical creation visually demonstrates the nature of God. This is done through a mechanism I call theiscience. The biological world, as part of the physical creation, and more specifically, biogeography, as part of the biological world, should demonstrate attributes of God. As examples, biogeography manifests diversity (reflective of His triune nature), complexity (reflective of His omniscience), interdependence (reflective of His care and provision), and beauty (reflective of His glory). The universality of the Romans passage suggests that the biogeography of the pre-Flood world fulfilled the same function. One might go so far as to infer from this that the pre-Flood world possessed a comparable amount of biogeographic diversity, complexity, interdependence, and beauty to the present – what I will here call “theiscient intensity” (TI).

On the other hand, several phenomena should have reduced inter- and intra-community TI through time: 1) the Fall and its cumulative effects through time; 2) the community bottleneck of the ark (where all ark-born organisms – regardless of environment – were placed in the singular ‘environment’ of the ark during the Flood); 3) the community homogenization of the Flood (where all non-ark-born organisms – regardless of environment – were mixed together and transported in Flood waters for the many months of the Flood event); 4) the dispersal bottlenecks following the Flood (where – unless relocated by a mechanism unknown to us – organisms were forced to begin their dispersal from their respective landing points); 5) baraminic extinction – inferred because of the many extinct groups of organisms classified at the taxonomic level of the family and above. Any one or more of these factors would be expected to result in a pre-Flood world with a lower TI than the present world.

Although the author knows of no studies that measure and/or predict relative levels of TI in pre-Flood and modern worlds, his qualitative sense is that there may be little or no difference. If this is true, it would suggest that there is not only a mechanism of intrabaraminic diversification built into God's biological creation, there are also mechanisms which develop biogeographic diversity, complexity, interdependence, and beauty.

Modern communities can be identified by complete trophic level representation, high disparity, and sub-global diversity levels. These same features seem to characterize fossil assemblages in many sedimentary layers, suggesting they may represent communities – many of them pre-Flood communities. This in turn suggests that communities were somehow transported en masse during the Flood. If this is true, then the uniqueness of fossil biotas suggests the pre-Flood world possessed a large diversity of communities unknown in the present (with the interesting caveat that there is also a rather large diversity of modern communities unrepresented in Flood sediments). The trans-continental to global distribution of some of these fossil biotas suggests that many of these communities were geographically extensive (linear dimensions on the order of 10^3 miles) in the pre-Flood world and may be more properly labeled as biomes. Unique pre-Flood biomes which have so far been inferred from the fossil record include a stromatolite-dominated fringing hydrothermal reef biome, a floating lycopod/sphenophyte forest biome, an epeiric sea biome containing Sepkoski's 'Paleozoic Fauna', and a dinosaur/gymnosperm biome. Postulating such pre-Flood biomes has allowed explanation of much of the fossil record order as well as the reduced diversity and biogeographic distribution of component organisms in the present. If Flood sediments are limited to Primary and Secondary sediments as Flood modellers have suggested, angiosperms, mammals, and humans are virtually unrepresented in Flood sediments. Even so, the abundance of these organisms in the present suggests there was probably also a pre-Flood angiosperm/mammal/human biome.

Continental configuration of the pre-Flood world is inferred from paleomagnetism, paleocurrents, matching geology, and continental-margin-defining Uppermost Proterozoic diamictites. At this point it looks most likely that the present continents were arranged in a slightly-broken-up Rodinia configuration, with connected, or near-connected continents spread from the South Pole (Gondwana continents) to the Equator (Laurentia and Eurasia). The hydrothermal reef seems to have fringed the entire continental mass and the floating forest seems to have occupied an equatorial position. The epeiric seas seem to cover most of the present continental land mass. The greatest mystery at this point is where the terrestrial biotas were located, as shield areas seem of insufficient area to house the inferred terrestrial diversity.

P11. Discovering the Creator—and What He Teaches Us About Teaching

Sheila Richardson

Independent Scholar

In the exciting world of scientific research, the subject of education often slips quietly to the background. All too often the educator is regarded as one who "can't do, so he teaches." The prevalent attitudes are reflected in salaries, in prestige, in priorities. In contrast, God's Word makes it clear that teaching is clearly a priority of the Creator (Deut. 4:1, 6:6-7; Job 12:7-9; Matt. 4:23; John 14:26; Rom. 1:20, 12:6-7; Col. 3:16; I Tim. 5:17). Since education is rarely considered at science conferences, it is imperative for us as Christians to focus on the issue of education as we 'discover the Creator.'

While origins education should begin with the very young (as soon as a child is able to touch, taste, smell, hear, and see created things), the target age for more intense instruction should be the early teens. The emotional and physical development of this group provides challenges to the educator. Once the educator meets these challenges, however, he will discover that the principles and strategies utilized are equally successful in reaching older teens and adults.

Educational principles for all ages can be identified as we 'discover the Creator.' God as the Supreme Communicator illustrates the need for clarity, for simplicity, for defining terms in alternate ways, and for repetition. His love of variety is evidenced by the varied learning styles of His creatures, suggesting different requirements for auditory, visual, and kinesthetic learners. Jesus' teaching illustrates how teachers can use simple analogies to explain complex concepts. For example, the structure of DNA can be taught using marshmallows, gumdrops and toothpicks. Continuity, discontinuity, and baraminology can be clarified through the use of clip art cut outs, and mediated design can be explained through Mr. Potato Head.

Finally, one of the greatest challenges in origins education today is teaching the teachers. A great wall seems to stand between those who are the model builders and researchers and those who teach, especially at the lay level. The researchers do not have the time or sometimes the skill to communicate on a popular level. The teachers do not have the most recent and accurate data or the time to stay current in the many disciplines related to origins. If opportunities could be provided for the presentation of accurate and timely data plus continuing education to the best teachers available, the teachers then could use their particular expertise to write age appropriate curricula and to communicate the message on the popular level. The barriers between the two groups must be broken down.

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Wise, K.P. and S.A. Richardson. 2004. *Something from Nothing*. Broadman and Holman Publishers, Nashville (mature youth, college age focus).

Richardson, S. *It All Begins with Genesis*. Answers in Genesis, Florence, KY (youth curriculum).

Wood, T.C. and M.J. Murray. *Understanding the Pattern of Life*. Broadman and Holman Publishers, Nashville.

P12. What Happened to the Dinosaurs?

A.V. Chadwick

Southwestern Adventist University

The demise of the dinosaurs is a topic of continuing discussion and debate, as well as widespread interest. The various theories for the fate of the dinosaurs make interesting reading. How much is fiction, how much is fact? The answers are of great interest to those of us seeking to understand the past history of the earth.

We have had the privilege of being involved in excavation and study of one of the largest dinosaur bone beds in the world from the Upper Cretaceous Lance Formation in eastern Wyoming. These bones represent the remains of as many as 10,000 dinosaurs and other animals. The fauna we have recognized up until now includes mammal genera represented by teeth: *Cimolodon*, *Cimolestes*, *Multituberculata* sp. indet., *Gypsonictops*, *Mesodma*; dinosaur genera represented by bones or teeth: *Edmontosaurus*, *Triceratops*, *Nanotyrannus*, *Tyrannosaurus*, *Pachycephalosaurus*, *Saurornitholestes*, *Troodon*, *Ricardoestesia*, *Thescelosaurus*, *Aublysodon*, *Nodosaurus*?; other reptiles: *Leptochamops*, *Brachychampsa*, *Leidyosuchus*, various species of turtles; fish genera represented by teeth: *Placodon*, *Kindleya*, *Lepisosteus*, *Myledaphus*, *Lissodus*, *Squatirhina*, *Ischyrrhiza*, *Lissodus*, as well as several genera of bivalves and gastropods and many plant families.

We have developed new techniques for preserving the information from our excavations using digital photographs, high-resolution GPS, and GIS software. This enables us to recreate in the computer, precise virtual photographic maps of the distribution of all bones, bone fragments, teeth and ossified tendons found in the quarry. We have used the same technology to determine accurate maps of the bone distribution in outcrop and the extent of the bed.

The study is on-going and we are in the midst of our fifth season of excavation. While our results at this point are still tentative, we have established some points to conclusion. The bones are preserved in a bed less than one meter thick in a poorly cemented mudstone. Most of the bones are preserved in pristine condition, and do not appear to have been exposed to weathering subsequent to death. Most bones are also disarticulated and skeletal elements are dispersed in a random fashion. However the bones occur in a clearly defined normally graded bed within the mudstone interval. There is also a consistent sorting by bone type within the graded interval such that certain bone types appear, independent of size, at well-defined positions within the bed. At this time it is clear that the dinosaurs did not die where the bones now lie, but they must have died in close proximity elsewhere, and subsequently been remobilized within the mudstone and catastrophically transported as a unit to their present location. Apparently there was some scavenging of the remains prior to transport, as the teeth of carnivores are associated with the transported remains. Some bones bear tooth marks that could relate to cause of death or to subsequent scavenging.

A conceivable scenario for the bone bed is the following: A huge number of dinosaurs, perhaps as many as 100,000 *Edmontosaurus* and other forms, drown during a megacatastrophic flood. Some dinosaurs are still alive, perhaps mostly carnivorous forms. The dead dinosaurs are washed out across an extensive flood plain

or transported across open water to a leeward shore where they accumulate as a gigantic lag on an oversteepened delta front. There, the rotting carcasses are scavenged by carnivores. During the process of decomposition and scavenging, the bones become disarticulated and separated. With continued accumulations of sediment, the delta front becomes unstable, and finally, perhaps triggered by seismic activity, the delta front gives way, remobilizing the now disarticulated dinosaur remains along with the suspending muddy matrix. As the mass continues moving downslope, the bones are sorted during transport into a normally graded bed. The flow slows, losing energy until it finally comes to rest in what is now an eroded landscape in eastern Wyoming where the bones are once again coming to life.

Research Abstracts

R1. Physio-Chemical properties of Amino-Acids, a New Class of Metrics for Numerical Baraminology and Biosystematics

David Cavanaugh
Independent Scholar

Traditionally, character and distance metrics used in Biosystematic studies, using analytical procedures from either Phenetics or Cladistics, are based upon encoding molecular states (e.g. DNA bases) as discrete, or state characters. Establishing a link between physio-chemical properties of amino-acids and the genetic code has been elusive despite considerable effort. DNA state characters have become the dominant basis for Biosystematics studies that rely upon molecular characters. DNA characters enjoy wide acceptance as they are readily analyzable within a Darwinian Evolutionary framework. DNA characters have an advantage in that mutations readily distinguish between closely related taxa. However, such information is lost when codons are converted into their amino-acid equivalent characters. Despite the seemingly obvious advantages of DNA characters, significant information is lost regarding the structure and function of the particular proteins that are encoded by their corresponding DNA gene sequences. This paper shows a link between the standard genetic code and physio-chemical metrics of the standard 20 amino-acids. Specific physio-chemical properties of the 20 standard residues in this study are reported as normalized proclivities. Proclivities are reported for residue hydrophobicity, beta sheet conformation and double bends, and are the metrics used with reported applications. Thus, the utility of the reported amino-acid metrics (proclivities) are illustrated by the analysis of several biologically meaningful examples with their associated numerical and semi-numerical procedures. Applications explored include a derived proclivity metric for secondary structure prediction and protein classification, Fast Fourier Transform (FFT) analysis of proclivities to produce “energy” spectra useful for secondary structure analysis and protein classification, proclivity metrics used in protein primary structure alignments as a first step for extracting molecular characters for taxonomic analysis.

R2. The Cataharrine Primates Revisited: An ANOPA Study

David Cavanaugh
Independent Scholar

The 1998 *CRSQ* Robinson and Cavanaugh study of the Cataharrine primates was conducted with first generation Numerical Baraminology methods analyzing characters sampled from morphological, ecological, chromosomal and molecular criteria. Analysis Of PATterns (ANOPA) is a second generation Numerical Baraminology method which has been used in a number of Baraminological studies in recent years. This paper uses ANOPA to reanalyze the data set used from the Robinson and Cavanaugh study. The current study results demonstrate excellent resolution of homo sapiens from both the great apes and the old world monkeys, the latter two groups forming distinct and well separated statistical populations. These results suggest the Cataharrine primates to be an apobaraminical assemblage of taxa, and suggest the monobaraminical status of both the old world monkeys and great apes. These findings illustrate the continuing importance of the Cataharrine primates to theoretical biology and to Baraminology in particular. The Cataharrine primates serve as an excellent assemblage of Taxa for the investigation of the properties and reliability of Numerical Baraminology procedures and algorithms.

R3. Baraminological Interpretation of Squirrel Phylogeny

Allen H. Davis
Independent Scholar

The squirrels (Family Sciuridae) are mammals sharing certain easily identifiable characteristics. Three subdivisions of the family are recognized, corresponding to the ground squirrels, tree squirrels, and the flying squirrels. Various fossil rodents are classified in Sciuridae, and extant species have been subjected to DNA sequencing and other biochemical analyses. Using these data, phylogenetic trees have been proposed for the family, but these trees leave a number of unanswered questions and certain inconsistencies with the data.

I am engaged in an ongoing study to evaluate squirrel taxonomy from the perspective of young earth baraminology. Data to be considered include interspecific hybridization of sciurids and morphological characters evaluated by baraminic distance and Analysis of Patterns (ANOPA) methods. As in other baraminology studies, the results of these analyses will aid in the re-interpretation of sciurid phylogeny within the young-earth creation framework. Also of significance to the creationist is the biogeography of the squirrels, which is constrained by dispersal from Ararat since the squirrels must have been on the Ark. This paper presents the preliminary results of my work with recommendations for future research and interpretation.

R4. Modeling Holistic Behavior of Biological Systems for Analysis by Systems Theory

Steven Gollmer
Cedarville University

Due to the complexity of biological systems it is not possible to capture the richness of their interactions by purely studying the individual parts. Only a subset of all possible interactions between individual parts results in functional behavior. This restriction of functional possibilities is sometimes described as an emergent property of the system and emphasizes a holistic approach to the study of biological systems.

By using concepts from systems theory a systemic approach to modeling biological systems is possible. This approach is currently used successfully in such areas as niche theory and organism biology. This presentation looks at a framework for modeling biological systems as Complex Functional Units (CFU's). With this level of abstraction it is possible to model systems from intracellular processes to ecological environments.

Focusing on the number and quality of interactions between CFU's it is possible to determine criteria for the interchangeability of CFU's with similar functionality, but different implementation. Adaptability of CFU's to changing conditions can also be studied to evaluate possible limits to variation.

In order to demonstrate the applicability of CFU's to biology, several examples will be presented. The first is a comparison of C_3 and C_4 photosynthetic processes. Both perform similar functions, but have differences in their implementation. Modeled as CFU's the degree of difference in implementation will be evaluated and applied to C_3 - C_4 intermediates. The second example looks at immunology in light of CFU's. This is a preliminary exploration with the goal of evaluating the benefit of a more detailed study in the future.

R5. A Proposal for a Creationist Survey of Viruses

Jennifer Gruenke¹, Joseph W. Francis², Todd Charles Wood³

¹*Patrick Henry College*

²*The Master's College*

³*Bryan College*

Viruses are ubiquitous and affect biological life at the ecosystem, organismal, cellular, and biochemical/molecular level. The study of viruses and their classification has been influenced largely by the destructive parasitic nature of viruses. According

to most young-earth creationist (YEC) thinkers, the pathogenic nature of viruses arose as a consequence of the Fall (e.g. Bergman 1999). Recently, two YEC theories (Wood 2002; Francis 2003) have proposed possible beneficial functions viruses may have performed before the Fall. Each theory predicts that remnants of these pre-Fall functions may be observable in extant viral lifestyles and that viral pathogenicity will be limited to special circumstances. Based on a preliminary survey of viruses, we find that some viruses can infect multiple host species but may cause pathology in only one or few hosts. We therefore hypothesize that viruses may be providing beneficial functions in hosts and that these functions may be detectable and amenable to study. At the cellular level, viruses interact specifically with a remarkably large number of cell-surface and soluble receptors and can affect many aspects of cell structure and function, including changes at the membrane and organelle level as well as alteration of biochemical pathways and gene expression at the genome level. Thus it appears that viruses not only modulate organisms at the genome level but have the potential to promote non-genetic based phenotype changes. At the tissue level, viruses display an ability to remodel tissues by promoting apoptosis or influencing the manner in which populations of cells interact with one another. We hypothesize that viruses may have been created as "mobile" extraorganismal agents of gene, cell and tissue regulation and/or modification. Viruses also play beneficial roles within ecosystems in multiple ways including participation in mineral cycles and protection of some species from microbial-based pathology. Because viruses appear to have the potential to influence species composition and diversification within ecosystems we hypothesize that viruses may have been created as modulators of such systems. To evaluate these hypotheses further, we propose a systematic literature survey of known viruses to identify all potential beneficial functions and asymptomatic hosts. The survey will serve as the basis for planning future creationist research in virology.

Bergman J. 1999. Did God make pathogenic viruses? *CENTJ* 13(1):115-125.

Wood TC. 2002. The AGE-ing process: rapid post-Flood intrabaraminic diversification caused by Altruistic Genetic Elements (AGEs). *Origins (GRI)* 54:5-34.

Francis JW. 2003. The organosubstrate of life: a creationist perspective of microbes and viruses. In Ivey RL, ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 434-444.

R6. The HybriDatabase

Stephanie R. Mace, Kurt P. Wise, Todd Charles Wood
Bryan College

Interspecific hybridization has long been regarded as important data in creationist systematics (e.g. Marsh 1941). To facilitate research in hybridization, the Center for Origins Research and Education created a computerized database of hybridization information, the HybriDatabase (HDB). The HDB is implemented in MySQL with perl CGI scripts and is hosted on a linux server running RedHat 8.0. Hybridization records are digitized by student volunteers and are checked by CORE staff before entry into the HDB. Currently, the HDB contains 4437 hybrid records from 36 different published sources. The majority of these records

(4159, 93.7%) come from four references, Knobloch's *A Check List of Crosses in the Gramineae* (1726 records), Gray's *Bird Hybrids* (1500 records) and *Mammalian Hybrids* (514 records), and Scherer and Hillsberg's 1982 review of anamid hybrids (419 records). The database presently covers species from 106 different families, the top ten of which are Poaceae (1734 records), Anatidae (826 records), Fringillidae (198 records), Ploceidae (217 records), Psittacidae (162 records), Phasianidae (170 records), Bovidae (104 records), Cercopithecidae (86 records), Columbidae (75 records), and Equidae (67 records). Of these ten, the systematics of eight have been evaluated in a creationist context. Bovidae and Ploceidae have not been studied by creationists, but the number of hybrid records in the HDB suggests opportunity for fruitful baraminology research. Presently, development of the HDB web interface is underway to simplify the hybridization report, grouping the hybrid records by species. We are also developing a new database design that will allow for the recording of hybridization involving fertile hybrids as one or more of the parent organisms, which occurs frequently in cultivated plant hybridization (e.g. orchids). Ongoing work to collect hybridization records for entry in the HDB has resulted in the acquisition of 673 published papers referring to interspecific hybridization and all hybridization abstracts from 19 volumes of *Animal Breeding Abstracts* and 28 volumes of *Plant Breeding Abstracts*. These papers and the hybridizations they report will eventually be entered into the HDB. As development continues, the HDB is becoming a very valuable tool for the baraminologist, and we encourage creationists to utilize this important resource.

Marsh, F.L. 1941. *Fundamental Biology*. Self-published, Lincoln, NE.

R7. The Effect of Design Constraints on the Plasticity of Traits within a Baramin: Echolocation, Flight and Masticatory Systems in Chiroptera

Don Moeller

Independent Scholar

The oldest known fossil bat is found in Eocene sediments. Evidence indicates that the very earliest fossil microbats had well designed echolocation and flight systems. The absence of claimed intermediates between bats and non-bats in either echolocation or flight designs may justify an apobaraminic status for the bats. As many baraminologists have defined the Flood/post-Flood boundary, all known bats, fossil and living, are post-Flood. As seems to be the case for horses (Cavanaugh, et al., 2003), changes up the stratigraphic column in bats may reflect actual intrabaraminic changes in bats in the post-Flood world.

Whereas the fossil record of bats shows very little change in flight and echolocation systems, substantial changes are seen in skull and dento-maxillary systems. Differential change in different systems in the same organisms may provide useful models for evaluating the immutability of particular characters and the plasticity of others within baramins in general.

The specific parameters necessary for flight and sonar (echolocation) have been nicely quantified in mathematical terms - e.g. aspect ratio, mechanical efficiency of flight, frequency modulation, sound transmission energies, etc. Physiological

modifications such as hematocrit, heart rate, hemoglobin content, oxygen transport and extraction have also been quantified. Not surprisingly, these mathematical models suggest there are substantial design constraints in the echolocation and flight systems of bats. They also indicate that the survivability of intermediate forms is severely limited. The fact that the constraints are probably not as severe in the masticatory system, may well explain why there is more variability in the masticatory system than is seen in the flight and echolocation systems. Interestingly, however, not only do the flight and echolocation systems show less variability than the skull and masticatory systems, they also show fewer mutational variants. This may also be due to the design constraints of echolocation and flight, as mutations in a more constrained system may be expected to have more catastrophic effects on organismal survival and reproduction.

This suggests that highly constrained design systems may be identified by the combined observations of fewer mutational variants and limited morphological variation. Conversely, the discovery of systems with fewer mutational variants and limited morphological variation may suggest a high level of design constraints in the system.

Cavanaugh, D.P., T.C. Wood, and K.P. Wise. 2003. Fossil equidae: a monobaraminic, stratomorphic series. In: Ivey, R.L. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 143-153.

R8. On the Limited Role of Fossil Sequence Data for Identifying Lineages

Walter ReMine

Independent Scholar

This paper examines the role of fossil sequence data in our study of nature. Evolutionists have six ways for explaining-away 'out-of-sequence' fossils – three of those are powerful and available under the widest circumstances. Those are identified and discussed. It is shown that we must carefully apply fossil sequence data; otherwise we end up fostering various evolutionary illusions. In particular, I argue that lineages must *first* be clearly identified without use of the fossil sequence, and *then* compared with the fossil sequence for testing. (That is, a lineage is first identified by a clear-cut, long-narrow trajectory through morphology-space, with a large *void* orthogonal to the trajectory.) It happens that nature rarely meets this fundamental requirement (particularly over large macro-evolutionary scales), and therefore we rarely get to the step where the fossil sequence is usefully tested – the key disputes occur earlier in the chain of reasoning. In short, fossil sequence is important data, but it happens to play relatively little role in identifying clear-cut lineages.

Some baraminologists give the impression that our study of nature uses all the useful methodologies simultaneously, and values all data equally – in other words, that our study of nature is structureless. The idea seems to be: Go forth, study nature, and explain it by creation. I urge a more refined view. Baraminology accounts the results from various *distinct* systematic methodologies – *separate* studies of nature. Each

one is structured for studying a *specific* type of pattern – and some data-types have greater utility for discerning certain types of patterns – not all data are equal. This paper brings the role of fossil sequence into perspective, while clarifying the structure and comprehensibility of our study.

R9. Mosasaurs: Baraminology, Biostratigraphy, and Boondoggle

Marcus R. Ross
Independent Scholar

Mosasaurs were large (5-17 m) marine-adapted squamates whose remains are known around the globe from uppermost Flood sediments (Late Cretaceous: Turonian through latest Maastrichtian; Austin et al. 1994). While their biology and systematics have received adequate attention from traditional (Russell 1967) and cladistic (Bell 1997) evolutionary methods, their baraminological relationships and biostratigraphy suffer from lack of refinement.

This study attempts to refine mosasaur biostratigraphy by evaluating mosasaur generic richness among novel Stratigraphically Correlated Assemblages (SCAs). Comparison of global mosasaur richness among disparate locations is feasible assuming biostratigraphic correlation among Flood deposits is possible. Rarefaction is the primary statistical method available to test for differences in richness among the SCAs, which are thus employed as sampling units. Rarefaction calculates 1) the expected number of taxa for a given sample, and 2) the confidence intervals with which to bracket statistical expectations of mosasaur richness.

A sample data set from three mosasaur-bearing Maastrichtian deposits of the East Coast of North America demonstrates the utility of this method. Preliminary analysis indicates that mosasaur richness is not significantly different among three biostratigraphic zones within the Maastrichtian. Furthermore, the stratigraphically highest mosasaur remains in these and other locations are co-incident with impact-derived materials (consisting of a spherule layer and an iridium spike), presumably from the Chixulub impact event in Yucatan, Mexico (Olsson et al. 1997, 2002). Combined, these data suggest that mosasaur extinction was not directly related to the Flood's geological and hydrological effects. Indeed, the correlation of the mosasaurs' stratigraphic last appearance with evidence for a catastrophic impact event raises questions about auxiliary agents of extinction in effect both during and after the Flood.

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R10. Systematic Position of the Cetacea Revisited: A Fuzzy Sets-based Analysis of Morphological Discontinuity and 'Transitional Forms'

Richard Sternberg
Independent Scholar

A spate of new fossil taxa has seemingly closed the morphological chasm once thought to exist between the Cetacea and proposed sister groups (Mesonychidae and Artiodactyla). to date, cladistic analyses of morphological data from fossil and extant cetaceans, numerous artiodactyl and mesonychid representatives, and a range of outgroups support three alternative hypotheses. These three hypotheses are: 1) an Artiodactyla-Cetacea sister group relationship (Cetartiodactyla), 2) Mesonychidae as the sister taxon of the Cetacea, and 3) a paraphyletic Artiodactyla with Hippopotamidae as the closest relation of cetaceans. All three hypotheses unambiguously support the position of various 'walking whales' (e.g., pakicetids) at the base of the Cetacea. A test of the three competing hypotheses, in addition to the placement of pakicetids, ambulocetids, and other taxa as 'transitional forms' connecting groups like the basilosaurids with artiodactyls (or mesonychids), was conducted. The analysis consisted of computing degrees of relatedness based on the apomorphies shared between two taxa. For example, if two taxa have all apomorphies in common, they are related to a degree of 1.00; if no apomorphies are shared then they are related to a degree of 0.00 (discontinuity); otherwise the two forms will have a fuzzy apomorphy-compatibility value somewhere on the interval (0.00, 1.00). Since the method used does not involve the transitivity constraint (as in cladistics), the homoplasy-synapomorphy distinction is collapsed: all apomorphies are of equal significance. The results obtained support two conclusions. First, hippopotamids, mesonychids, and the "walking whales" constitute a network of forms due to combinations and permutations of apomorphies. So-called terrestrial and amphibious whales are allied with *both* mesonychids and hippopotamids to various degrees. Second, whereas the basal cetaceans are arranged in a complex map-like way to each other, they are only weakly connected to the basilosaurids-dorudontids, and strictly discontinuous with Mysticetes and Odontocetes. Serious logical problems with the interpretation of "Pseudocetes" as transitional forms are briefly presented.

R11. Distinct Phases in the Intellectual History of Comparative Biology

Todd Charles Wood
Bryan College

Comparative biology seeks to analyze and explain patterns of similarity between organisms, at the anatomical, developmental, cellular, and genetic organizational levels. Charles Darwin utilized a pattern of similarities between organisms to argue for

common ancestry (Gould's 'fact of evolution'), but creationist response to his claim has been *ad hoc*. Creationists frequently claim that similar (homologous) structures indicate a common designer at least as well as they indicate a common ancestor. This claim misses Darwin's point that the particular pattern of similarity resembles one that would arise from an evolutionary origin of organisms. His claim specifies a scheme of similarities, whereas the creationist response deals only with the fact of similarity. In order to understand the history and development of Darwin's argument, I am conducting a philosophical-historical survey of comparative biology. My initial work suggests three distinct periods in the development of the comparative approach. The first period (pre-1780s) is characterized by the observation of similarity with little speculation as to its cause or meaning. Linnaeus typifies this phase. Linnaeus used similarity to construct his classification scheme, which was little more than a mnemonic device for organizing and recalling information about any particular organism. I mark the beginning of the second phase (1780s to 1859) with Goethe's discovery of the human intermaxillary bone. As Richards argues, anatomy prior to Goethe focused on the adult, resulting in a static view of organismal form. Goethe analyzed skeletal remains from a range of developmental stages, thereby discovering the intermaxillary bone, which in the static view did not exist. Although Goethe's discovery elicited little enthusiasm from the established scientists of his day, his discovery heralds an important intellectual shift in anatomy. For the first time, comparative biology was seen not to be merely descriptive but also predictive. Thus, one could predict anatomical details of one species based on comparative studies of other species; the intermaxillary bone is found in many animals, and therefore must be present in some form in the human cranium. In France, Geoffroy would repeat Goethe's feat with his discovery of the much-reduced styloid process of the howler monkey hyoid bone (which existence was thought by the functionalists to be impossible). The third period begins with Darwin's *Origin*, which offers for the first time a widely-accepted and compelling mechanism to explain similarity. His theory of evolution explains a variety of similarity-based observations, including the nested hierarchy of classification and vestigial structures. After Darwin, comparative biologists began to subsume all evidence of similarity into the evolutionary model. So complete was the takeover of comparative biology by evolutionists that by the Darwin centennial, Owen's typological concept of homology had been re-defined as 'structures that share a common ancestor.' The discovery in the 1960s of similarity between DNA and protein sequences from different organisms further reinforced the evolutionary interpretation of biological similarity. I conclude from my preliminary research that the key to providing a compelling alternative to evolution is explaining comparative biology and its predictive power.