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Occasional Papers of the BSG

EXPLORING THE HISTORY OF LIFE
PROCEEDINGS OF THE FIFTH BSG CONFERENCE

edited by
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Occasional Papers of the BSG

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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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Exploring the History of Life: Proceedings of the Fifth BSG Conference

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Welcome

Welcome to the 2006 conference of the BSG: A Creation Biology Study Group at Cedarville University. The theme, “Exploring the History of Life”, displays all of the positive characteristics of the BSG. Your mission to explore, discover and explain Truth (with a capital “T”) is exciting. May your tribe increase!

I trust your visit to the campus of Cedarville University will be an encouragement to you. I pray you will be mutually encouraged, spiritually refreshed and intellectually stimulated these few days.

May God bless you as you continue to serve Him.

Bill Brown
President
Cedarville University

Introduction

Science and history are usually seen as two different fields. They are separate subjects all through the American school system. Most colleges and universities have biology and history in separate departments or divisions. Why then should an ostensibly science-centered BSG conference adopt as its theme “Exploring the History of Life”?

The theme was originally intended to elicit discussion about the different ways that creationists view the history of life on this planet. Young-age creationists hold to a recent creation, an historical Fall, a global Flood, and subsequent recovery period during which the earth was re-filled with organisms (including humans dispersing from the tower of Babel). The Bible gives some details about these events, but leaves many questions unanswered. As a result, even within the creationist community, there is disagreement over what it all means.

Differences in interpreting the history of creation can be seen most clearly in geology, where there are at least four different models of earth history that approach the fossil record very differently. Within biology, there is less vocal disagreement over the history of baramins. Some creationists believe that baramins comprise many species and that biological change has been dramatic. Others are more focused on the mechanism of change and prefer a smaller baramin with less speciation. Another area of disagreement in biology is the origin of viruses. Some creationists believe that creation was finished at the end of creation week, and therefore must have included benign forms of viruses. Others see no evidence of beneficial function in viruses and prefer to put their origin at the Fall.

How creationists respond to these disagreements depends on their view of science (and to some extent on their understanding or misunderstanding of Scripture). Many creationists insist that the proper domain of science is that part of the physical world that is subject to repeated observation. Since the past cannot be subjected to repeated observations, the past is not the proper domain of science. They view hypotheses about historical geology or historical biogeography with suspicion, because of the impossibility of viewing the past to know what really happened.

An alternative view recognizes many more shades of gray in science. Like the previous view of science, this view understands the domain of science to encompass the interpretation, description, and explanation of data. Rather than insist on a strict dichotomy

between history and science, this view recognizes that scientific descriptions or interpretations can sometimes be only indirectly connected to data. For example, “this cat has splotches of color in its fur” is a description that is quite close to the data. Other claims about the same cat might be much less directly connected to the data: “this cat has a genetic allele that gives it splotches of color in its fur due to X chromosome inactivation.” The latter statement relies on many different inferences about inheritance, phenotypes, cytogenetics, etc. and it deals with entities that are not directly observable (genes). Nevertheless it is clearly a scientific claim. Compare it then with the claim “This fossilized skeleton is a cat that died in a volcanic eruption.” The claim about the volcanic eruption is an explanation of skeletal remains and the rock in which it was found, and it involves an entity that cannot be observed (a past volcanic eruption). It isn’t philosophically obvious why the claim about cat genetics is qualitatively different from the claim about the fossil cat’s death.

What could this mean for our exploration of the history of life? We have already seen that creationists differ on their views of creation’s history. We could proceed by continuing to rehash the old arguments we’ve all made for our own peculiar views. If claims about the past are “just speculation,” then there is not much more we can do. But if history is amenable to scientific investigation, then perhaps a more productive way forward would be scientific research: evaluating models, testing hypotheses, and the like.

What might creationist research look like? Let’s take the size of baramins as an example. Should we include lots of species in baramins or just a few? There are many ways of exploring this question. One way is to use the traditional hybridization criterion that Frank Marsh advocated. What kind of interspecific and intergeneric hybridization is possible? Another way would be to examine statistical baraminology techniques for many groups and many taxonomic ranks. Is there any pattern to the results, or do we find evidence of discontinuity at any taxonomic level? If we include many species in baramins, what are the genomic differences and how do we account for them? If we restrict speciation to only those mechanisms we already know about, what would this mean for evidence of broader continuity between species? All of these questions are amenable to research. None of these questions will provide decisive evidence for one view

or another, but together, a consilient view of the baramin should emerge.

Ultimately, we have to keep our disagreements in perspective. Remember that what we're doing is just science. It is a human attempt to understand the creation around us. Because humans are fallible and finite, science alone will usually contain error, even as it approaches accuracy in its depiction of creation. We are still at a very formative stage in creationism. We should critically analyze any and all extrabiblical theories and avoid viewing them as "set in stone." We must remember our own fallibilities and limitations as we do science and as we interpret others' science. Try not to take creationist theories too seriously, and be willing to change your views if something better (and consistent with Scripture) comes along. Remember that your faith is not grounded on science but on the unchanging grace of God and the redemption offered through Christ's death, burial, and resurrection. These doctrines are important truths and worth getting excited about. Whether *Geochelone elephantopus* belongs to the same baramin as *Chelydra serpentina* is exciting to some but not to most.

So let's explore the history of life, and let's use science to do it. If we keep our models consistent with the revealed truth of the Word of God, we can enjoy the freedom of doing scientific research to the glory of God. As we discover more about the history of creation, we will also discover more about the Creator, and those discoveries will make all the research worthwhile.

Todd Charles Wood
Center for Origins Research
Bryan College

Conference Schedule

Wednesday, June 7

9:00 a.m.
Registration opens

12:00 noon
Lunch

2:00 p.m.
Welcome from Cedarville University and Opening Prayer

Introductions and Announcements
Dennis Flentge
Cedarville University

2:30 p.m.
Plenary: "Baraminology and the Flood/post-Flood Boundary"
Kurt P. Wise
Bryan College

3:15 p.m.
Discussion

3:30 p.m.
Break

4:00 p.m.
Research Papers Session I

R1. Wood, "Exploration of Biological Character Space Surrounding Living and Fossil Whales (Mammalia: Cetacea)"
R2. Whitmore, "The Green River Formation and Post-Flood Diversification"

6:00 p.m.
Cookout

Thursday, June 8

8:30 a.m.
Plenary: "Are Adaptive Radiations Characteristic of the History of Life?"
Roger Sanders
Independent Scholar

9:15 a.m.
Discussion

9:30 a.m.
Break

10:00 a.m.
Research Papers Session II

R3. McGary, "Evaluating Phylogenetic Scenarios"
R5. Lightner, "The Baraminic Status of the Family Cervidae as Determined using Interspecific Hybrid Data"
R7. Kennard, "Biblical Anthropology as a Creation and Revelation Framework for Doing Bio-Ethics: With a Focus on Soul, Life and Person"
R8. Gollmer, "Design Patterns Applied to Systems Biology"

12:00 noon
Lunch

2:00 p.m.
Research Papers Session III

R9. Francis, "The Role of Virulence Factors in the Establishment of Beneficial Ecological Relationships of *Vibrio cholera* and *Vibrio fischeri*"
R10. Fouts, "Man as the Image of God"

R11. Demme, "Toward a Biblical Theology of Creation and Curse"

4:00 p.m.
BSG Business Meeting

5:00 p.m.
Dinner

7:00 p.m.
Poster Session

Friday, June 9

8:30 a.m.
Plenary: "What Happened to the Dinosaurs?"
Art Chadwick
Southwestern Adventist University

9:15 a.m.
Discussion

9:30 a.m.
Break

10:00 a.m.
Research Papers Session IV

R12. Cavanaugh, "An ANOPA study of Arthropod morphospace represented by Cambrian and living forms"
R13. Brophy, "A Review of Interspecific Hybridization in the Order Testudines"
R14. Bartlett, "Metaprogramming and Genomics"

12:00 noon
Lunch

Plenary Abstracts

P1. Baraminology and the Flood/post-Flood Boundary

K.P. Wise
Bryan College

Consensus has not been achieved on what part of the geologic record was generated in the Noachian deluge. Ideas range from almost the entire stratigraphic record (Price, 1923) to no geologic expression at all (e.g. Buckland 1836; Robinson 2000). The Flood/post-Flood boundary has been placed in the Pleistocene (e.g. Buckland 1823; Whitcomb and Morris 1961), the top of the Tertiary (Oard 1990), top of the Mesozoic (Austin *et al.* 1994), in the Carboniferous (Robinson 1996; Scheven 1996), and even in the Hadaean (Robinson 2000). Of the criteria used to define the boundary, several are baraminological in nature. For example, the farther down the stratigraphic column the boundary is placed, the fewer baramins are represented in Flood sediments and the more biological change is evidenced in post-Flood sediments – both of which are Flood/post-Flood criteria to some (e.g. Robinson 1996: 51-54). Furthermore, burial order must be explained differently if it is in Flood versus post-Flood sediment – most commonly by ecological zonation in Flood sediments and intrabaraminic diversification in post-Flood sediments. The relative success of these explanations could constitute a third baraminological criterion for the Flood/post-Flood boundary.

Fossil sequences include (but are not limited to) mammals showing increasing hypsodonty, plant phyla through the Paleozoic, and taxa leading up to the Atdabian, to amphibians, to mammals, to birds, to whales, and to humans. Wise (2003a, 2003b) proposed that the sequence of plant phyla and the taxa leading to the amphibians and the Atdabian could be due to Flood-caused burial of pre-Flood ecological zones. At least one case of increasing hypsodonty has been explained as post-Flood intrabaraminic diversification (Cavanaugh *et al.* 2003) and the ape-human sequence has been explained as an artifact of post-Flood biogeography (Wise 1994). Explanations of fossil sequences have thus far been done in a *post hoc* fashion and run the risk of becoming *ad hoc* in nature.

Cavanaugh *et al.* (2003) interpreted the horse sequence as post-Flood intrabaraminic diversification partly because the containing sediments were thought to be post-Flood. However,

intrabaraminic diversification could have been postulated for it because 1) there was a clear intra-familial (likely intrabaraminic) morphological sequence; 2) the morphological sequence followed a stratigraphic trend; and 3) the morphological sequence paralleled a vegetational shift and a climatic trend which together made sense of the morphological pattern. At this point in time, none of these three criteria are true of the other fossil sequences, so this criterion gives us no good reason to assume that the other fossil sequences are due to intrabaraminic diversification.

A curious characteristic which *is* in common between the horse sequence and a couple of the other sequences is trans-familial convergence. Just as a variety of mammal families show increased hypsodonty and size in the same stratigraphic interval, so also a number of reptile families show an increase in mammal-likeness in Triassic sediments (cynognathids, tritylodontids, trithelodontids, chiniquodontids, traversodontids, diademodontids) and bird-likeness in Cretaceous sediments (pterosaurs, dromaeosaurids, troodontids, ornithomimids: Feduccia 1999). The fact that these Mesozoic sequences lack an explanatory environmental trend suggests that the convergences may be due to transitional ecologies in the pre-Flood world rather than intrabaraminic diversification in the post-Flood world. This in turn has interesting implications for pre-Flood biogeography. If valid, this criterion implies that the Flood/post-Flood boundary should be placed between the Upper Cretaceous and the Eocene.

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P2. Are Adaptive Radiations Characteristic of the History of Life?

R.W. Sanders

Independent Scholar

The concept of adaptive radiation has developed in the context of groups of closely related species resulting from a rare colonization events to “recently” exposed, isolated territories. This concept comprises two aspects of evolutionary theory: 1) **radiation** – the near-synchronous divergence from a common ancestor (the colonist) into many species of divergent form, and 2) **adaptation** – natural selection by the environment to fit each divergent form to a specifically different ecological niche (Carlquist 1974, pp. 97-118). Evolutionary theory implicates diversification by sympatric or parapatric speciation in juxtaposed, divergent habitats within geographically restricted areas, e.g., newly exposed islands, lakes, or mountain peaks. (The term is also used in paleontology to describe the “sudden appearance” of disparate lineages and body plans, e.g., Cambrian “explosion”, Cretaceous flowering plants, and Cenozoic mammals, an origins issue needing detailed creationist evaluation and not considered here further). What value is the concept within the creation model? The hypotheses presented here are that 1) recent diversifications may be radiations but are not adaptive, and 2) the pattern of radiations may be related to the Flood and post-Flood geologic and climatic models being developed.

Demonstrating radiations is straightforward by applying cladistic methods (for the sake of the argument), as synchronous origins should result in irresolvable polytomies. Such polytomies may be the result of the presence of only unique traits in the related but divergent species, mosaics of homoplastic traits among these species, or a combination of the two character patterns. Deducing adaptation requires a (more or less) one-to-one correspondence between environmental factors and observable traits in the organisms in which the adaptation is supposed to exist. Island environments are best suited to such study as the number of variables (especially biotic factors) is limited and correlations are much easier to discern.

Three cases, which have been proposed as some of the best examples of adaptive radiation in plants—the rosette-tree dandelions and daisies of the Robinson Crusoe Islands and the tree-sunflowers of the Galápagos Islands (Carlquist 1974, pp. 202-211), are studied. Morphological cladistic analyses by

the author (Sanders et al. 1987; data from Eliasson 1974) and published molecular cladistic studies (Crawford et al. 1992; Sang et al. 1995) demonstrate radiations in these plants of both archipelagos. Principal components analysis of soil, topographic, and vegetational factors in the Robinson Crusoe Islands showed strong overlap of the related species. Although these species are often closely juxtaposed, the data failed to demonstrate adaptation and nonallopatric speciation in these species. A scenario of geographic isolation of founder populations followed by migration into increasingly restricted shared territory is a better hypothesis. The Galápagos plants are, with one exception, geographically isolated, and a one-to-one correspondence of species-to-habitat remains to be demonstrated. Thus, adaptation cannot be deduced as primary in these plants, as well (see also Wood 2005).

The conclusion is drawn that non-adaptive radiations have occurred when latent, created information was expressed in small, fragmenting populations that colonized newly exposed habitats. Furthermore, cycles of stochastic radiations should be correlated with the cycles of increasingly dampened catastrophes from the Flood into post-Flood times. As such, stochastic (but not adaptive) radiations are viewed as common to the history of diversification within baramins.

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P3. What Happened to the Dinosaurs?

A.V. Chadwick

Southwestern Adventist University

One of the most popular subjects among young people and one of the great unanswered curiosities of all time concerns the origin and fate of the dinosaurs. The standard model suggests that dinosaurs as a group first evolved in the Late Triassic and died out suddenly in the uppermost Cretaceous 65 million years ago. This scenario is very different from a model consistent with the most straightforward reading of the Bible and thus provides numerous opportunities for testing the explanations of the standard model against the model of earth history suggested by Genesis. One remarkable occurrence in the fossil record that may provide a point for model testing is extensive accumulations of fossil remains of animals such as dinosaurs in deposits called “bone beds.” The deposits are generally attributed to shallow water processes such as rivers because the enclosing sediments often preserve features consistent with fluvial origin. The bones themselves are typically thought to have accumulated over many

years.

We have conducted research on an extensive bone bed on the Hanson Ranch in eastern Wyoming since 1997 continuing up to this present year. The results have provided us with a source of data to test whether the bones accumulated over an extended period of time or whether they may have accumulated rapidly. We have studied the deposits using modern technological methods that have enabled us to precisely record the positions of every bone. The assemblage we have found includes in addition to bones, components of freshwater molluscs and other forms from fresh or brackish water along with components typical of marine environments such as acritarchs and dinoflagellates. Our bone bed, one of the largest in the world, did not result from accumulation over time. Instead, a huge number (estimated to be 10,000 to 25,000 animals on the basis of 165 meters of excavation at 8 quarry sites) of *Edmontosaurus* and minor numbers of other ornithomimid and theropod dinosaurs were killed catastrophically and subsequently rotted, leaving a massive accumulation of bones, flesh and theropod teeth in what was apparently a swampy freshwater nearshore environment. Subsequently these bones were remobilized and transported, again catastrophically, in a matrix of clay and mud into deeper water where they formed a graded bed. Finally, burial, uplift and modern erosion has exposed the bones again for our study.

Research Abstracts

R1. Exploration of Biological Character Space Surrounding Living and Fossil Whales (Mammalia: Cetacea)

T.C. Wood
Bryan College

Wise (1995) argued that “transitional forms” are not a high priority for creationist research, but intermediate forms constitute a lesser research priority in the area of biological similarity. Archaeoceti are cited as stratomorphic intermediates between extant cetaceans and artiodactyls. I performed classical 3D multidimensional scaling (MDS) on baraminic distances from three datasets containing archaeocetes. The first dataset from O’Leary and Geisler (1999) contains 40 taxa and 123 characters. The taxa consist of two extant cetaceans (*Tursiops* and *Balaenoptera*), seven archaeocetes, and 31 outgroup taxa largely representing ungulates. After filtering at 0.85 relevance, 34 characters remained for calculating baraminic distances. In the MDS results, the cetaceans were clearly separated from other taxa at an average distance of 0.477 (total average 0.397). The archaeocetes are adjacent to extant cetaceans but are not intermediate between them and land mammals. The cetacean group is diffuse, with notable spacing between all taxa. The second dataset from O’Leary et al. (2004) contains 68 taxa and 186 characters. The taxa consist of four extant cetaceans, six archaeocetes, and 56 outgroup taxa largely representing ungulates. After filtering at 0.85 relevance, 50 characters remained for calculating baraminic distances. MDS of the baraminic distances revealed no specific groups, but did show an average distance of 0.371 between extant cetaceans and archaeocetes (total average 0.326). As with the O’Leary and Geisler dataset, cetaceans were widely spaced, and archaeocetes were adjacent to extant cetaceans but not intermediate between them and outgroup taxa. The closest taxa to the archaeocetes were the mesonychids *Harpagolestes* (0.09 to *Basilosaurus*) and *Dissacus praenuntius* (0.07 to *Pakicetus*). The closest taxa to the extant cetaceans were *Hippopotamus* (0.209 to *Tursiops*) and *Orycteropus* (0.109 to *Delphinapterus*). Because molecular analysis (e.g. Ursing and Arnason 1998) suggested a close affinity between cetaceans and hippopotamids, I examined a dataset of

extant and fossil Hippopotamidae from Boisserie et al. (2005). The dataset consists of 32 taxa, including eight extant and fossil hippopotamids, two archaeocetes (*Artiocetus* and *Pakicetus*), and 22 outgroup taxa. To increase the number of characters in the dataset, I eliminated the outgroup taxon *Xenohyus venitor*, which had only 36.2% known character states. After filtering at 0.9 relevance, 50 characters remained for calculating baraminic distances. Baraminic distance correlation revealed two groups connected internally by positive correlation and separated by negative correlation. The two groups are the Hippopotamidae + *Merycopotamus* + *Libycosaurus* (hippopotamid group) and the remaining outgroup taxa. The groups were connected by positive correlation between *Elomeryx* and *Merycopotamus*. MDS revealed an average distance of 0.529 between hippopotamid group and the remaining outgroups (total average 0.386). *Elomeryx* was the closest outgroup taxon to the hippopotamid group (0.242 to *Merycopotamus*). The archaeocetes are not close to the hippopotamid group (average distance 0.439). Based on these results, I conclude the following: (1) Archaeocetes are adjacent to modern whales but are not morphological intermediates between extant cetaceans and artiodactyls. (2) My results confirm the results of Cavanaugh and Sternberg (2005) and are consistent with Mace and Wood’s (2005) finding of discontinuity between archaeocetes and extant cetaceans. (3) Family Hippopotamidae + *Merycopotamus* + *Libycosaurus* is a holobaramin.

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R2. The Green River Formation and Post-Flood Diversification

J. Whitmore¹ & K.P. Wise²

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The Green River Formation (GRF) is an aerially discontinuous sedimentary unit in Wyoming, Utah, and Colorado, famous for Eocene fossils. The Flood versus post-Flood status of the GRF has been debated (Oard and Whitmore 2006), but its post-Flood lacustrine origin is strongly evidenced by: 1) The GRF is a *local to regional* deposit containing *terrestrial* fossils which is underlain by *continent-wide* deposits containing *marine* fossils (Dickinson et al. 1988). 2) The flat-lying GRF rests unconformably on folded Paleozoic and Mesozoic rocks (Lamerson 1982) indicating they were probably deposited after the uplift described in Psalm 104:8 (Whitmore 2006a). 3) Sedimentology, paleontology, taphonomy and geochemistry are all consistent with lacustrine deposition (Whitmore 2006b).

Because of large differences in numbers in the Samaritan, Septuagint, and Masoretic texts of Genesis 11 combined with uncertainty about Babel's location in Genesis 11 chronology, creationists have not agreed upon a post-Flood time scale. In a short chronology Babel post-dates the Flood by 1-3.5 centuries; in a long chronology 5.3-12 centuries. Pleistocene sediments document the oldest post-Flood evidence for wide geographic distribution of humans (Lubenow 2004) – thus the oldest sediments definitely post-dating the confusion of tongues at Babel (Wise 2005). The GRF is at the bottom of a thick stack of Eocene through Pliocene sediments – all of which may be pre-Babel. Depending upon the post-Flood timescale used, the GRF was deposited probably somewhere in the range of 25 to 300 years after the Flood. Its early post-Flood date is confirmed by *Hyracotherium*, the first animals in an intrabaraminic biological trajectory (Cavanaugh et al. 2003). Combined with excellent fossil preservation, the low stratigraphic position and great distance from the mountains of Ararat makes the GRF a spectacular window into early post-Flood biogeography and intrabaraminic diversification.

The GRF (Grande 1980; Feduccia 1999) demonstrates remarkable disparity with over 500 fossil species in about 230 families (proxies for baramins) in about 104 orders, representing every kingdom of organisms. The vertebrates and plants, as examples are represented by at least 42 and 29 orders and 68 and 46 families respectively. It seems that even at this great distance from Ararat at such a short time after the Flood a tremendous range of terrestrial and fresh-water baramins had made it most of the way around the world. After the Flood, baramins spread across the globe very rapidly.

Species diversity within families (as a proxy for intra-baraminic diversity) is very low. In non-insect families there is an average of 1.2 species/genus and 1.7 species/family (vertebrates and plants have 1.2 and 1.1 species/genus and 1.6 and 1.7 species/family respectively). Insects show a higher diversity at >3.3

species/family. Somewhat expectedly, species diversity in baramins seems to have been very low soon after the Flood, suggesting that first-order intrabaraminic diversification may be modeled *following* low diversity biodispersal. This suggests baramins dispersed at low diversity and diversification occurred at the termini of post-Flood dispersion paths.

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R3. Evaluating Phylogenetic Scenarios

K. McGary

Independent Scholar

Many comparative studies report molecular phylogenetic trees that have been generated under the assumption of common ancestry. These studies will be more easily interpreted within a baraminology framework when we understand how modern tree-scoring algorithms treat various initial conditions that are plausible within a framework of common design with discontinuous ancestry. I propose to generate simulated molecular datasets under various scenarios and evaluate them using modern phylogenetic tools. I propose to generate simulated gene datasets using standard likelihood models of evolution using model parameters derived from real genes. The simulated datasets will be evaluated under Maximum Parsimony and Maximum Likelihood models. I will study two types of scenarios. First, I will examine the effects of various levels of initial sequence divergence between baramins. In this analysis, mono-baraminic trees will be compared to polybaraminic trees. Second, the potential effects of environmental convergence will be studied by co-varying the evolutionary rate of polybaraminic groups of organisms and looking for distortions in the estimated topology. The topology and branch lengths of estimated phylogenetic trees will be compared with the originally simulated tree manually and using weighted Robinson-Foulds distance. Increased initial sequence divergence between baramins is anticipated to improve the correct identification of baramins from phylogenetic trees. Specifically, long branches resulting from long initial divergence

will indicate boundaries of baramin. Conversely, monobaramins separated by less initial sequence divergence will not be identifiable using sequence data. Co-varying evolutionary rates between members of different baramins is expected to positively mislead baraminologists by causing unrelated organisms to cluster in the tree. Research of this nature will facilitate interpretation of phylogenetic trees and may clarify the conditions that allow discontinuities between monobaramins to be inferred. In addition, the effects of variation in evolutionary rate may allow baraminologists to explain instances of consilience between morphological and sequence data when polybaraminic clades are placed together in phylogenetic trees. Recent work has suggested that the evolutionary rate of a gene is tied to its level of expression, which may provide a mechanism for unrelated organisms to group together in phylogenetic studies.

R4. Do New Molecular Functions Arise by Gene Duplication?

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Gene duplication is a special type of mutation that increases the DNA content of genomes. The major mechanisms of gene duplication include polyploidy, polysomy, unequal crossing-over, and transposition. Here we explore the fate of duplicated genes in the light of recent discoveries on genome stabilizing mechanisms, namely, gene silencing, as well as empirical findings about the function and regulation of well known gene families, and argue that: 1. Most gene duplications are aberrations of cell division processes that (except for polyploidy) disrupt genes or the delicate balance between genes, causing malformations, diseases, or sterility. 2. No new molecular functions have been documented in engineered gene duplications such as synthetic polyploidy, although superior vigor and separate hybrid phenotypes are common. 3. Duplicated genes are usually silenced epigenetically, followed by degenerative mutations, ending up in nonfunctionalization. 4. Regulation of many supposedly duplicated gene clusters or gene families is irreducibly complex, and demands simultaneous development of fully functional multiple genes and switching networks, which have no counterparts in lower organisms.

To further develop the hypothesis that gene duplication cannot provide the raw materials in which novel molecular functions diverge, the factor of interbaraminic vs. intrabaraminic genetic variation must be integrated. Therefore, we propose the following criteria to distinguish DNA sequences that were duplicated in history and paralogous genes that were created individually. 1. Copy-number polymorphisms among individuals of the same species (or related species within a baramin) obviously demonstrate recent duplications. 2. Elements of irreducibly complex systems are not likely products of gene duplications. The more genes required to arise simultaneously by duplication-neofunctionalization events, the lower the possibility. These include genes with complex regulation hierarchies. 3. Degree of sequence homology is not a good indicator in determining whether the genes are duplicates or not. Frequently, multiple

identical copies of a gene are required during certain stages of the cell cycle. These genes may require complicated mechanisms such as gene conversion to prevent diversification. 4. Duplication by transposition is possible but is normally suppressed.

In-depth studies of copy-number polymorphisms within species will certainly shed more light on this topic. Observation of any new molecular functions in individuals with extra copies of a gene will nullify the above argument. Further investigation of the function of transposable elements and their copy number polymorphism may clarify the interplay between transposition and genome stabilizing mechanisms. At least theoretically, long-term observation of congenitally engineered organisms with multiple copies of a transgene will yield an even more definitive answer.

R5. The Baraminic Status of the Family Cervidae as Determined Using Interspecific Hybrid Data

J.K. Lightner

Independent Scholar

Cervidae, the deer family, is one of six families within the suborder Ruminantia. It contains over 40 species divided among four subfamilies. Internet databases and search engines were used to find interspecific hybrid data to determine baraminic relationships.

Within the subfamily Cervinae, all four genera were linked by hybrid data. *Axis axis* has formed hybrids with *A. porcinus*, *Cervus duvaucelii*, *C. elaphus* (Gray 1972), which now includes *C. canadensis*, and *C. nippon* (Asher, et. al. 1999). *A. porcinus* has hybridized with *Dama dama*. *C. elaphus* has hybridized with *Elaphurus davidianus* (Gray 1972). Further hybrids include *C. elaphus* with *C. unicolor* (Muir et. al. 1997); *C. unicolor* with *C. timorensis*; and *D. dama* with *D. mesopotamica* (Mackay 1997). Prior to 1983, most taxonomists included *C. alfredi* as a subspecies of *C. unicolor*, although some authors classified it as a subspecies of *C. mariannus* with which it has been documented to hybridize (Huffman).

The subfamily Cervinae is also linked with several of the nine genera in the subfamily Odocoileinae. *A. axis* has hybridized with *Odocoileus virginianus*, and *A. porcinus* has hybridized with *Capreolus capreolus*. A presumed hybrid has been reported between *C. canadensis* and *Alces alces*. Further hybrids within this subfamily include *O. virginianus* with *O. hemionus* (Gray 1972) and *C. capreolus* with *C. pygargus* (Danilkin 1995).

There is no hybrid data linking the above two subfamilies with Hydropotinae (consisting of one species) or Muntiacinae (consisting of about 10 species depending on the source). There is a reported hybrid within the genus Muntiacus between *M. muntjak* and *M. reevesi* (Gray 1972).

There are two alleged hybrids between deer species and species of the family Bovidae, a second family in Ruminantia. One is between European roe deer (*Capreolus capreolus*) and sheep (*Ovis aries*). The second is between moose (*Alces alces*) and domestic cattle (*Bos taurus*). Mating has been observed between wapiti (*Cervus elaphus*) and domestic cattle, but no progeny have been reported (Gray 1972).

Well documented hybrids indicate that at least two of the four

Cervidae subfamilies are monobaraminic. The alleged hybrids indicate the family Bovidae may be monobaraminic with deer as well. While no hybrid data presently exists, some of the other families in this suborder could also be monobaraminic with deer. The other families are Tragulidae (mouse deer), Moschidae (musk deer), Giraffidae (giraffe, okapi), and Antilocapridae (pronghorn).

Future research directed toward forming interfamilial hybrids within this suborder would be helpful. Several species of deer are farmed, making it more practical to attempt crosses between these species and cattle, sheep, or goats. Sometimes differences can form between animals of the same kind so that hybrids are very rare or impossible to produce. Therefore, *in vitro* studies to determine the amount of early embryonic development would be valuable as well.

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R6. The Origin of Viral Disease: A Foray into Creationist Virology

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Bergman (1999) suggested that God did not make viruses to be pathogenic and that viruses may have been created to fill a harmless or even beneficial role. Gruenke et al. (2004) initiated a survey to evaluate the virulence of viruses. They hypothesized that if pathogenic viruses arose by degeneration from nonpathogenic forms, pathogenic viruses must be only slightly different from nonpathogenic forms. These differences might be manifest as hosts or vectors infected by a pathogenic virus but that exhibit no symptoms or as closely-related viruses that do not cause disease. Gruenke et al. (2004) therefore recommended a survey of viruses to identify hosts or vectors that exhibit no symptoms and viruses that do not cause disease. To implement a first step in this project, we surveyed the 226 viral genera listed in the internet version of the VIIth report of the International Committee on Taxonomy of Viruses (ICTV) published in 2000 (<http://www.virustaxonomyonline.com>). Using a simple spreadsheet, we recorded host range, pathology, transmission vectors, and tissue specificity. We also tried to score each viral genus as pathogenic, nonpathogenic, or both (having pathogenic and nonpathogenic species). Overall, we found nonpathogenic virus species in 53 genera (23.5%). The ICTV report categorized viruses as dsDNA, ssDNA, dsRNA, negative sense ssRNA, positive sense ssRNA, and reverse transcribing viruses. Of these six categories, the ssDNA viruses were the most

virulent, with no record of any nonpathogenic forms. The dsRNA viruses had proportionally the most genera with nonpathogenic forms (50% of 22 genera). The greatest number of genera with nonpathogenic forms was 19 in the positive sense ssRNA viruses, but this was only 24% of the genera in the category. These low percentages might indicate that known viruses are largely pathogenic, but the inherent bias present in virus discovery and description prevents a firm conclusion on this. Viruses are sought and studied only when a pathology is present, and this could lead to an under-representation of nonpathogenic viruses in the database of known viruses. We also found it challenging to classify viruses as virulent or pathogenic when a spectrum of pathogenicity is present. Some viruses, like cytomegalovirus, produce symptoms in humans, but the symptoms are so mild that CMV infections can go completely unnoticed. Other viruses dangerous to one species, like HIV in humans, can be harmless in another, like chimpanzees. These examples would support our initial hypothesis, that viral virulence can vary widely, which is consistent with degeneration from harmless ancestors. Since the 2000 ICTV report has since been supplanted by the 2005 ICTV report (which still has 3142 unassigned virus species, see Fanquet and Fargette 2005), we recommend continuing this research with a more recent database. We also recommend surveying additional resources, such as *Fields Virology*.

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R7. Biblical Anthropology as a Creation and Revelation Framework for Doing Bio-Ethics: With a Focus on Soul, Life and Person

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An integrated model of the nature of humanness with specific emphasis on “soul” is developed through an analysis of Biblical texts. This results in a *functionalism*, which I call a *multi-faceted unity* (of: image of God, soul, spirit, body, heart, mind, will, and conscience). This approach is in contrast to Christian bio-ethicists who start from the field of philosophy or biology and tack some devotional elements of the Bible on the rafters of their view.

The Biblical concept of Soul has a holistic meaning of “complete living being” in a non-microbial pre-modern manner (i.e. fish, fowl, insect, reptile, amphibian, and mammal; e.g., Gen 1:20, 24, 30; 2:7; 9:4-5, 10). Thus, animals have certain privileges against extremes of bio-ethical abuse under the ruling image-of-God [Gen. 9:4-6; Ex. 21:28-29; Deut. 25:4; Mt. 12:11-12]. Furthermore, the word for soul is the best Biblical term for a concept of person, thus raising the Christian ethical impact from orthodox trinitarian concepts of person (namely, “an instance of a spiritual being as a moral end in itself in relation to others”) in contrast to modern philosophical ones (e.g., self-aware individual). Thus, “soul” as a concept for life and “soul” as a

biological definition for life are not identical. When biological definitions of life aren't used to ignore the Biblical concept and implications of soul/life, they need not threaten these points made from the concept of soul.

A human holistic soul has continuity from conception to death (and even into the afterlife), and thus soul/person is legally protected in the Bible, and those who kill a fetus are then culpable of murder and were to be killed by capital punishment (especially, Gen. 4:1, 25; Ex. 21:22-24; Pss. 51:5; 139:13-15; Rev. 6:9). Thus, such an orthodox trinitarianly informed concept of person fosters a right to life commitment within the context of discussions about abortion and euthanasia, whereas, modern philosophical concepts of person tend to be biased toward a pro-choice commitment. That is, a combined view of soul (life and person) encourages a reflective engagement on behalf of souls.

A soul knows, wills, and feels. Thus, 1) experimentation and treatment on souls should respect informed consent of the soul affected (if possible) or the responsible souls who retain relational oversight for this soul's well-being. 2) Though the choices and emotions and abilities of a person change through impairing diseases (MS, Alzheimer's, dementia) and brain injury, and social presentation of self, there is continuity of the person through such losses and variety. 3) A gradated absolute ethic is to be implemented, preferring the fostering of maximizing personhood (spirituality, reflective thought and choices, relationship, and respect), which loves God supremely and then others to the extent that such love consistently maximizes personhood within the framework of God's absolutes.

R8. Design Patterns Applied to Systems Biology

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Upon completion of the sequencing of the human genome, a shift has occurred in genomics research. Although there is an ongoing effort to sequence the genomes of many organisms; there is a growing effort to understand the functional relationships between the proteins coded in the genome and the maintenance, response, and activities of an organism. A subgroup of bioinformatics research, Systems Biology, attempts to make sense of these relationships.

Current thinking in Systems Biology attributes biological order to the deterministic outcome of biochemical interactions and to the chance convergence of fortuitous variations. Within an evolutionary paradigm, the order in biochemical networks is of a rudimentary level and the search for higher levels of order is unproductive. Others feel that due to self-organizing principles, a higher level of order does exist. Although not deterministic in the sense of the lawful nature of chemical reactions, self-organization is seen as an inevitable result of complex interactions. Neither of these approaches considers the possibility of choice to explain the order present in biological systems.

It is proposed that choice, in the context of biology, is the selection of one option among a set of viable implementations of a biological function. In mammals, hemoglobin is used to transport oxygen; however, hemocyanin in many arthropods and chlorocruorin in many annelids serve the same purpose. There

are reasons why one implementation is superior to the other in the context of the whole organism; however, this does not negate the premise that a choice is made between multiple viable options.

To provide a context for studying choice in biological systems, the analogy of computer programming will be used. Biological systems, as well as computer programming, must operate within a physical context and produce a set of well defined outcomes. With a living cell, the physical context is the nature of chemical reactions and the spatial and temporal separation of reactions. In a computer, it is the definition of logic circuitry and the spatial and temporal separation of instructions or commands.

Using accepted methods for defining relationships between low-level components, a comparison is made between biological and computational systems. Systems Biology Markup Language (SBML) is used to define biological relationships and a number of SBML models for signal transduction, metabolic pathways, and cell division are available through the world-wide-web. The model used for defining computational relationships is the Unified Modeling Language (UML). A number of design patterns are defined using UML and these represent patterns of best practice for solving specific computational problems.

This comparison between biological and computational systems provides a basis for a cross-fertilization of ideas between the two disciplines. By carefully defining how the physical context dictates the behavior of a system's components, it is possible to evaluate the range of possible choices available to implement a particular system-level function. Although there will not be a one-to-one correspondence between best practices in biology and computer science, there is an opportunity to expand the number of options from which to choose.

R9. The Role of Virulence Factors in the Establishment of Beneficial Ecological Relationships of *Vibrio cholera* and *Vibrio fischeri*

J. Francis

The Master's College

Creationists predict that pathogenesis did not exist prior to the Fall. Therefore, many disease causing bacteria may have originally played strictly beneficial roles within living organisms and ecosystems. Several ideas and theories have been postulated for how virulence mechanisms arose after the Fall. However, the origin of some virulence factors is difficult to determine since the factors are complex and appear designed to interact intricately with cell components. *Vibrio cholera*, the causative agent of cholera, possesses several virulence factors that appear to be derived from genes subsequently added to the bacterial genome via transduction and transformation, which is consistent with a post-Fall modification view. Recently it has been shown that *V. cholera* plays an important role in the decay of chitin in aquatic environments. Interestingly, several of the virulence factors produced by *V. cholera* are postulated to also play a role in chitin degradation. Chitin is the most abundant polysaccharide in aquatic environments. *Vibrio cholera* appears to be more fit in its aquatic environment than in the lumen of the human intestine where it can cause severe acute and sometimes lethal disease conditions. Furthermore, *Vibrio fischeri* (a bacterium similar to

V. cholera) also uses virulence factors, similar to several found in *V. cholera* and other pathogens, to establish a beneficial symbiotic relationship with the Bobtail squid (*Euprymna scolopes*). In this symbiotic relationship, virulence factors are involved in tissue remodeling and morphogenesis of an elaborate light-producing organ. Interestingly, not only do these bacteria appear to be more fit for their beneficial ecological roles, but inflammation, tissue degradation and toxin production that cause pathogenesis in some ecological settings play beneficial roles in other ecological settings. Furthermore, it has also been recently documented that genomic modification (which is often postulated to play a role in the formation of a pathogenic bacterium) has been shown to be induced by the ecological setting and not the pathogenic setting of this bacterium. An example of this is *V. cholera*, whose genome shows evidence of modification by transformation when the bacteria are in its aquatic setting in the presence of chitin, yet transformation competence of this bacterium has not been observed in 60 years of laboratory studies. This suggests that the natural setting triggers the pathogenic abilities of *V. cholera*, and the toxic detrimental aspects of these abilities are not expressed if the bacterium is confined to this setting.

Thorough documentation of beneficial activities of microbes, prompted by a creationist perspective and research, will not only help us understand ecological relationships, but should aid in understanding the derivation of disease processes and pathogenesis. For instance, it appears that in many ways the disease process caused by pathogenic vibrio may not necessarily be due to genomic or proteomic modification but may result from environmental factors that promote the spread of bacteria beyond their niche. Interestingly, this is supported by studies showing *V. cholera* can be detected in many aquatic systems but tend to cause human disease only after changes in ocean temperature and monsoons cause an increase of the *Vibrio* population along with a corresponding decrease in the numbers of population-controlling bacteriophages.

R10. Man as the Image of God

D. Fouts

Independent Scholar

Traditional translations of the term בצלמנו (*b^ešalmēnū*) and כדמותנו (*kidmūtēnū*) in Genesis 1:26 have been understood that God purposed to make man “in our image” and “according to our likeness.” Thus the outward appearance of man is perhaps over-emphasized. Unfortunately, this rendering causes some confusion concerning issues of the nature of God in that if man is made in the image of God, i.e., as reflecting Him, then what does God look like? Are anthropomorphisms figures of speech, or simply descriptions of God’s appendages? Does God look male or female? Can men claim to be more Godlike than women, or vice-versa? Is He black, brown, red, yellow, or white? Can any race claim to be closer in appearance to God than another?

Another possibility exists when one renders the Hebrew terms in this traditional manner, and that is that the terms may refer instead solely to the communicable attributes of God. So, being in the image of God or after His likeness involves characteristics such as creativity, intelligence, kindness, justice, love, reason, and

emotion, to name but a few. This understanding also leads to an element of confusion in that if a given human lacks any of these qualities, then their humanity may be considered as diminished. Do they therefore fall short of the standard of God-likeness intended in the original creation? Do the gifted in intellect have a claim to be closer to God? Too, how does the introduction of sin into the created order in general, and into mankind specifically, affect the image of God in man?

Many Hebrew scholars prefer to see in these terms the understanding that *b^ešalmēnū* and *kidmūtēnū* actually refer to mankind being made not in the image of God, but rather “as” the image of God, with the ב (*bêt*) preposition serving as a *bêt essentiae*, or, *bêt* of essence. Thus God intended man to be His representative on earth to the created order. This understanding is very consistent with the use of the terms צלם (*šelem*), דמות (*d^emūt*) and רדה (*rādā*) elsewhere in the Scriptures. Too, it is very consistent with other analogies, such as Exod. 4:16; Ps. 8: 5-8; and 2 Cor. 4:4; Col. 1:15. The emphases then are not on the outward physical appearance of man, nor on the various attributes that he/she may manifest to a greater or lesser degree, but rather on the role of mankind as being God’s representatives on the earth that contains His creation. As such, to adequately represent God, mankind must be male and female, multi-racial, and reflect the attributes and characteristics of God, appropriate to that representation.

This understanding has ramifications for many current issues. For instance, as representatives of God commanded to subdue the created order and rule over it, mankind is of necessity a steward of that created order. Mankind therefore must be involved with proper environmental issues of conservation and preservation. Mankind must also recognize the equal value of other races (true light is a combination of all the colors of the rainbow). However, the presence of sin in mankind has diminished his ability to function well in the role of representative of God. It is only in Christ, the one who truly functions as God on earth (2 Cor. 4:4; Col. 1:15), that a humanity thus restored can fully function as God intended.

R11. Toward a Biblical Theology of Creation and Curse

I. Demme

Independent Scholar

It is the contention of this author that purpose and design in modern organisms cannot be understood apart from the biblical framework of creation, curse, and new creation. All other biblical theology assumes this redemptive-historical framework.

The biblical account of creation tells us that all living things were created to live together in harmony for the purpose of glorifying God. The biblical authors depict creation as a temple for the worship of God, with humans as the central image of God, and as his priests. In fact the very significant biblical (and extrabiblical) concepts of sacred time and sacred space – of temple/tabernacle and Sabbath are intended as signs and shadows of both the initial creation and the eventual redemption of creation.

The curse is in its essence a dysfunction in the natural order of

creation, and one which sets the various parts of creation against each other and disrupts the worship of God. Plants and animals are placed at enmity with each other, men and women are put at odds, and animals and plants are placed in conflict with each other. The world in which we now live is in a state of anarchy and civil war, in which parts of the creation can only survive at the expense of other parts. This necessitates a change in the behavior and morphology of living organisms as they can no longer depend on cooperation from other living things, but must themselves struggle to survive. That is, further designs must be initiated (perhaps revealed for the first time) at the Fall (e.g. overproduction, natural selection, carnivory, thorns, toxins and tannins).

We can distinguish then between different types of design. On the one hand we have systems designed to work in concert with the remainder of creation in a complex and unified system that brings worship and glory to God (direct or unmediated design, sensu Wood & Murray 2003). On the other hand we have systems which are designed primarily to maximize the goodness/cooperation/worship in a fallen world and (in order to achieve this) effectively preserves created kinds (mediated design, sensu Wood & Murray 2003). In addition there are also features in living things which come about as a result of God's curse on creation which do not have value either for survival or worship, and which illustrate the effects of sin and death.

Both the biblical texts and early Jewish and Christian literature make it abundantly clear that the immortality of the new creation is a return to the immortality of the original creation. This does not necessitate an unchanging or nonphysical state as many theologians have implied, but rather a sabbatic state of resting in the provision of God (sensu Hafemann 2001) in harmony with the whole of creation in communal worship and obedience. A systems view of biology and ecology in concert with a robust biblical theology of the curse (cf. Romans 8.18-25) are necessary to help us understand the divine intentionality behind those designs in our present environment, both direct and mediated.

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R12. An ANOPA study of Arthropod morphospace represented by Cambrian and living forms

D.P. Cavanaugh
Independent Scholar

An ANOPA (Cavanaugh & Sternberg 2004) analysis of Cambrian and living the aquatic arthropods was conducted based on published data (Wills 1997; Wills et al. 1994, 1998). The ANOPA analysis was supplemented by Principal Component Analysis, Multi-dimensional Scaling, Cladistics, and Basis Vector Factor Analysis. Out-group taxa were *Waptia* and *Lepidocaris*.

ANOPA results reflect a clearly constrained, albeit highly unusually shaped morphospace. 1D, 2D, and 3D projections all reveal two major sections of the morphospace, representing relatively symmetrical shapes (i.e. a crescent and an ovaloid) with sharp outer boundaries. Plots of rank order versus of both

T0 and A0 distances have significantly linear sections within the resulting curves, which reflect distinct statistical populations. Analysis recovered 5 groups, each seemingly partitioned into subgroups of 4 (8 taxa), 7 (21 taxa), 5 (8 taxa), 7 (14 taxa) and 4 (13 taxa) subgroups respectively for a total of 27 sub-groups and a total of 64 taxa. While there are some gaps within the boundaries of the basic two sections resulting from sub-groups, these gaps do not detract significantly from a reasonably uniform filling of taxa (subject to the limitation of the number of taxa sampled in the data set) within section boundaries. Results of the basis vector factor analysis suggest that there are not only distinct boundaries to the Arthropod morphospace, but there is also significant structure (particularly the linear structure) within this morphospace as well, with respect to the distribution of taxa.

There are certain features/motifs which are diagnostic of the basic arthropod body plan, such as bilateral symmetry, metamerism (segmentation), fusing of segments (tagmosis), hard exoskeleton, jointed appendages and a strong tendency for adaptation and specialization of segments and attached appendages). It is reasonable to observe that there is a large, but certainly a finite number of ways that a body plan based upon segmentation, structural specialization and tagma may be structured, hence one of the fundamental reasons for the highly constrained morpho-space within the Arthropods. The possible variations about the basic arthropod (segmented) body plan may also reasonably be expected to introduce a structure upon the Arthropod morphospace itself in how taxa are distributed within the morphospace. Given the inter-taxon distances involved, it is clear that there is an underlying design relationship with the Arthropod group. It should not be concluded that *Peripatus* and *Echiniscus* are not allied with the Arthropods, as they occupy a position analogous in distance and geometry at the apex of the right arm of the symmetric crescent section. It may be that within the Arthropods there are 2 (crescent section and ovaloid section) or three apobaraminic assemblages (where the ovaloid is split about in half between left and right). Based upon the large gap separating Annelida and Mollusca, the Out-group taxa in the Wills et al (Wills 1998) study, from Arthropoda and the symmetry of the crescent section of Arthropod morphospace, the evidence is very strong that an apobaraminic boundary/gap exists at this point. Several studies to date suggest that the baraminic boundaries may be expected to lie around the family to ordinal/sub-ordinal level (Robinson 1997, Robinson & Cavanaugh 1998a, 1998b; Cavanaugh & Wood 2002; Cavanaugh et al. 2003; Cavanaugh 2004, which is a principal expected to aid in the understanding the baraminological structure of Arthropoda.

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R13. A Review of Interspecific Hybridization in the Order Testudines

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Turtles (Order Testudines) have been the subject of more baraminological research than any other single group (see Wood, 2005 for review). Nevertheless, a thorough review of interspecific hybridization, with baraminological interpretations, has yet to be reported. We found evidence of interspecific hybridization in eight of the thirteen extant turtle families. Four of the remaining families are represented by a single species each (Ernst et al., 2000). These include crosses between 74 unique species pairs, approximately 1/3 of which are intergeneric. Eighteen small monobaramins (2-4 species) were identified within the families Pelomedusidae, Chelidae, Kinosternidae, Trionychidae, Emydidae, Geoemydidae [=Bataguridae], and Testudinidae. We also reviewed several recent reports of hybridization in the family Cheloniidae (some with molecular verification) published since the release of Robinson's (1997) paper on turtle baraminology (Barber et al., 2003; Seminoff et al., 2003; Witzell and Schmid, 2003). The family Cheloniidae forms a single monobaramin, as suggested by Robinson (1997), with five of the six species connected by hybridization (hybridization between seven unique species pairs). In addition, a large monobaramin (hybridization between 17 unique species pairs, implicating at least 13 species in this monobaramin) was discovered within the family Emydidae that includes several members of the genera *Pseudemys*, *Trachemys*, *Chrysemys*, and *Graptemys*. There are eight instances of intergeneric hybridization within this monobaramin, connecting the following genera: *Emys* x *Glyptemys*, *Graptemys* x *Trachemys*, *Pseudemys* x *Chrysemys*, and *Pseudemys* x *Trachemys*. Finally, a large monobaramin (hybridization between 19 unique species pairs, implicating at least 14 species in this monobaramin) was discovered within the family Geoemydidae that includes members of the genera *Mauremys*, *Cuora*, *Sacalia*, *Cyclemys*, *Geoemyda*, *Chinemys*, and *Heosemys*. There are 12 instances of intergeneric

hybridization within this monobaramin, connecting the following genera: *Mauremys* x *Chinemys*, *Mauremys* x *Cuora*, *Mauremys* x *Cyclemys*, *Mauremys* x *Heosemys*, *Mauremys* x *Sacalia*, *Cuora* x *Geoemyda*, and *Cuora* x *Sacalia*. Hybridization was not found to connect any of the turtle families or Wood's (2005) proposed holobaramins, so we are unable to reject his hypothesis of five turtle holobaramins. Future attempts will be made to increase the membership of the aforementioned monobaramins through the examination of similarity indices (i.e. non-hybridizing turtles will be included in a monobaramin if they fall within the range of variation of hybridizing turtles).

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R14. Metaprogramming and Genomics

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V(D)J (Variable, Diversity, and Joining segments) recombination allows the genome to encode billions of useful, complex immunoglobulin proteins in a small number of germ-line DNA sequences. Immune cells can rearrange a small number of DNA segments into millions or billions of sequences, which are then used as templates for proteins. As opposed to alternative splicing, the DNA physically rearranges itself during cell maturation (Market and Papvasiliou 2003). This is similar to the behavior of metaprograms in computer science which perform source code rearrangements before compilation. The proteins which cut and rearrange the template DNA is a metaprogramming system, and the DNA sequence that is rearranged is a metaprogram.

Metaprogramming is a computer programming technique where a new programming language is defined which is translated into an existing language. The new language only contains constructs that apply to specific sets of tasks. This allows the programmer to operate more directly on specifications, while the complexities of integrating those specifications together into a workable system are in the metaprogramming system itself. The metaprogramming system is tasked with keeping the metaprogramming rearrangements meaningful and consistent (Bartlett 2005).

Similarly, genetic codes for V(D)J segments do not have to

rely on specific knowledge of the interactions, just of the basic specifications. The metaprogramming system is responsible for integrating the specifications in a way that functions properly. This allows for complex integrations using simple components. In mice, for instance, arginine is essential at the V/J intersection, but not all combinations of V/J segments would generate an arginine based on the segment sequences alone. However, the recombination mechanism can generate the needed arginine if neither the V nor J codes for it (Sanz and Capra 1987). Thus, the metaprogramming system is “smart” in that the interactions between components is taken care of by the metaprogramming system.

Recently, the addition of N and P (non-templated and palindromic) elements and nucleotide deletions at the junction of segments has been detected, and is non-random (Gauss and Lieber 1996). According to the metaprogramming model it is predicted that the constraints under which they occur follow a similar pattern of “smart” joining, with the changes occurring for structural or other functional considerations. This allows hypermutation of segment regions without adversely affecting the final immunoglobulin’s integrity.

A new type of metaprogramming, termed “enterprise metaprogramming”, allows a single metaprogram to serve for multiple related metaprogramming systems. For example, a single metaprogram describing data entities may be read by separate metaprogramming systems to generate a database design, a C++ class specification, and a data-entry tool, each integrating with the other (Bartlett 2006).

It is the recommendation of this author that biologists be on the lookout for such multi-system metaprograms in the genome. This would be characterized by a DNA template sequence which was recombined in multiple ways for multiple, interacting subsystems, so that the organism’s metaprogramming system would cause a change at one locus to affect multiple systems, perhaps in different but related tissues. The metaprogram would act as a multisystem specification, and each differentiated tissue would act on that specification in unique ways, resulting in uniquely recombined DNA that worked together system-wide.

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