

CBS Annual Conference Abstracts 2017

Bacteriophage Design and Maintenance of the Mammalian Microbiome; A Prediction Consistent with the Biomatrix Hypothesis

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The creation-based biomatrix theory predicts that the microbiome performs a life-supporting role in the biosphere. For instance, the mammalian microbiome has shown to be an important aspect of human health (Francis, 2003, 2008, Gruenke et al. 2004). Virus involvement in the microbiome, compared to bacteria, is more enigmatic because their lifecycle is inherently destructive to cells and tissues. In this study, our goal is a first approach to elucidate the mammalian virome and its role in the biomatrix.

Plant, animal and phage viruses live throughout the human body and all mammals. The most compelling argument for all viruses sharing common ancestry argues that viruses are remnants of cells that lived in a pre-DNA, RNA world. Because there is no compelling genetic evidence for monophyly among viruses (Holmes, 2009) and an RNA world is inconsistent with a literal reading of Genesis, each group of viruses likely developed uniquely.

Interestingly, phages are the most abundant virions and yet are largely ignored as virome members. We note in this study, that phages possess designs to help maintain the community dynamics of the microbiome in exquisite ways. For instance, one of the first phages discovered was the infamous lambda phage. It is an intestinal virus infecting *Escherichia coli*, discovered after the phage virions were released lytically from *E. coli* subjected to radiation (Luria 1978). Using the creation inference that the "good" functioning microbiome can come under threat of genetic alteration leading to pathogenesis, we postulate that the ability of lambda phage to incorporate in a benign fashion into the bacterial genome and then become lytic under stress suggests that it was designed to act as a sentinel.

If phages were designed as sentinels to maintain microbiome bacterial populations and to detect aberrant genetic alteration, then we might also expect that the phages and their first (bacteria) and second (mammal) hosts would possess designs to promote recognition of the partners in this three-partner mutualism amid a potent immune system designed to remove pathogenic microbes.

There appears to be at least two elegant design features present in this system. First, phages express proteins which recognize both mammalian extracellular matrix proteins and the surface of bacteria (Rohwer, et al., 2014). This allows the phage to be concentrated in certain tissue locations. Here, the phages interact with and eliminate potential pathogens. Additionally, phage

proteins interact with microbiome bacterial surface proteins that serve as strong ligands. We are proposing that this "cloaking" prevents the ligands from alerting the immune system. For instance, phages possess proteins, which interact with flagellin and peptidoglycan that can cause a strong immune reaction. In fact, an *E. coli* bacterium, in theory, can interact with and be simultaneously coated with phages binding its flagellum, and phages binding to the peptidoglycan in its cell wall (Luria 1973).

Second, the mammalian immune system largely detects infectious animal viruses via intracellular recognition of foreign DNA or RNA. Since phages do not invade mammalian cells, the data suggests that many are "immune" from immune system detection. This theory most likely explains the mystery regarding how the trillions of phages associated with the human body escape immune detection. It is quite possible that a few phages are recognized, but most go unrecognized and therefore do not cause a massive life-threatening inflammatory response.

We believe that this is the first creation biology study to explain the role of bacteriophages in sustaining the microbiome and enhancing the immune system as a beneficial part of the mammalian virome. We hope to try and establish laboratory protocols and experiments to extend and verify our claims.

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Editor: MAM

Inertial Laws in Population Biology: An Eulerian Perspective

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In a memoir published in 1744, the great mathematician Euler declared: "Since the fabric of the universe is most perfect, and is the work of a most wise Creator, nothing whatsoever takes place in the universe in which some relation of maximum and minimum does not appear." In this landmark work, a powerful mathematical technique called calculus of variations was founded. The variational approach, later significantly refined by Lagrange, has since then played a central role in modern physics

providing an elegant and unifying conceptual framework for the formulation of physical laws (in their classical, relativistic or quantum mechanical versions).

Biology is not physics. For some, the question of whether general laws can be expressed in mathematical terms is still widely debated (Lawton 1999, Murray 2000). While for others, evolutionary theory is essentially a “theory of forces”, (Sober 1996, Ginzburg-Colyvan 2004). Among the many mathematical approaches developed for population biology, two results have been often compared to Galileo’s principle of inertia: Malthus’ law of exponential growth in ecology and Hardy-Weinberg law of equilibrium in population genetics.

The growth principle due to Malthus says that unchecked populations grow exponentially. As it is well known, the applications that Malthus drew from this principle played a great role in the development of Darwin’s evolutionary thought.

The principle can be stated as follows: for a population of size $N(t)$ subject to some environmental “forces”, the time evolution of its growth rate r (also known as the Malthusian parameter or fitness) obeys the differential equation:

$$\frac{d}{dt}(r) = \frac{d}{dt}\left(\frac{1}{N} \frac{d}{dt} N\right) = f$$

The analogy with the inertia principle is then clear: in the absence of “forces” (i.e. $f=0$) populations grow exponentially:

$$\frac{1}{N} \frac{d}{dt} N = r = cst$$

gives $N(t) = N(0)e^{rt}$.

This remark is also the starting point of the Galilean or inertial approach in ecology developed by Ginzburg. A similar but different approach to the Malthusian principle would use the concept of “quantity of life” introduced by Volterra in 1932.

Using the classical Euler-Lagrange equation and the formalism developed more recently by Tonti and Strang, one can show that an exponential growth model corresponds to the minimization of the following functional:

$$J(X, N) = \int (N \ln N + rX) dt$$

where

$$X(t) = \int_0^t N(\tau) d\tau$$

is the quantity of life.

Several interesting mathematical properties (duality, min/max) can be exploited using the above-mentioned formalism. Some of these properties are expected to possess interesting biological interpretation. The presence of an entropic term (Boltzmann entropy) in the functional $J(X, N)$ is especially intriguing.

The logistic growth model and simple forms of Fisher’s Fundamental Theorem of Natural Selection can also be expressed and interpreted within this approach.

Interestingly, another form of entropy plays a role in the “inertia principle” of population genetics: it can be shown that the Hardy-Weinberg equilibrium corresponds to the minimization of the Shannon entropy

$$-\sum_{i=1}^4 p_i \ln p_i$$

under some natural, built-in, linear equality constraints.

Of course, the two above “inertial” (zero force) models are biologically trivial. Their interest is chiefly theoretical as they could be a significant step in understanding the “forces” and the “dynamics” governing living organisms.

While variational principles have proved to be very fruitful in physics, the use and role of optimization remain highly debated in evolutionary theory. The very concept of optimality has a teleological overtone that seems to directly challenge the very notion of blind, unguided, evolution (see e.g. Brandon-Rausher 1996, Orzack-Sober, 2001).

The present note shows that optimization principles may play a more important role than usually recognized in population biology. This suggests that the living world can be more accurately described according to the worldview expressed by Euler rather than by the one developed by Malthus, Darwin and their followers.

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Editor: TCW

Baraminological Analysis of Phytosauria (Reptilia: Archosauromorpha): The Crocodile Look-Alikes

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There are remarkable convergences between the archosauromorph faunas of the Triassic and the dinosaur and crocodylian faunas from higher in the Mesozoic (Stocker et al., 2016). Multiple examples of animals from different created kinds show obvious morphological convergence, which suggests a possible template community in the pre-Flood world. One example of this convergence is found in phytosaurs, an unusual group of extinct archosauromorphs from the Upper Triassic (Middle Triassic if *Diandongosuchus* is a phytosaur (Stocker et al., 2017)). These animals are not crocodiles, but are similar in appearance and possibly ecology. Because phytosaurs closely resemble an unrelated group and their phylogenetic position in Archosauriformes is contentious, they are an appropriate group to study in order to better understand pre-Flood convergence.

We used statistical baraminological methods to determine if phytosaurs were discontinuous from other archosauromorphs, which would help us determine how many crocodylian-convergent created kinds exist within Phytosauria. Most species within Phytosauria are also included in the family Phytosauridae, although there are some phytosaurs (e.g., *Paleorhinus* and *Ebrachosuchus*) which fall outside Phytosauridae.

We analyzed a phytosaur dataset by Butler et. al (2014) with BDISTMDS (Wood, 2008), which had *Euparkeria* as an outgroup. The Butler et. al. dataset had 24 taxa and 46 characters. Using a 0.75 character relevance in our analysis, 19 characters were excluded from the analysis.

The BDC result reveals two blocks of positive correlation separated by either negative correlation or no correlation. The larger block of positive correlation consists only of phytosaurids. Within this larger block, there appear to be two blocks of positive correlation which are linked through a few taxa. The smaller block consists of the pseudopalatines, whereas the larger block contains the other phytosaurids. The block containing the outgroup taxon (*Euparkeria*) in the BDC plot also includes several non-phytosaurid phytosaurs and two phytosaurids (*Angistorhinus* and *Brachysuchus*); however, neither *Brachysuchus* nor *Angistorhinus* actually shares positive correlation with *Euparkeria*. The 3D MDS results do show a tight cluster of phytosaurids separated by a large gap in character space from a diffuse *Euparkeria* + non-phytosaurid phytosaurs + *Brachysuchus* + *Angistorhinus* cluster. Interestingly, the pseudopalatine cluster is also separated from the other two clusters in character space. The MDS stress in three dimensions is 0.176, and is lowest in four dimensions at 0.170.

We interpret these results to show shared continuity within Phytosauridae and discontinuity between Phytosauridae and non-phytosaurid phytosaurs along with *Angistorhinus* and *Brachysuchus*. As a result, we suggest the family Phytosauridae (minus *Angistorhinus* and *Brachysuchus*) is a holobaramin. We also detect what we believe to be two phytosaurid monobaramins, one corresponding to Pseudopalatinae and the other consisting of the rest of the holobaraminic phytosaurids. We could not detect discontinuity surrounding Phytosauria, but we suspect that the shared positive correlation between *Euparkeria* and the non-phytosaurid phytosaurs is most likely not true continuity, but a result of the character selection biased toward more “derived” phytosaurs.

We were surprised to find evidence for multiple holobaramins of phytosaurs, which may suggest even more independent examples of convergence with the crocodylian-like body plan. We suspect that multiple kinds were designed to take on crocodylian-like niches in the pre-Flood world, although we do not yet know why. Further study of these patterns will hopefully illuminate our understanding for the pre-Flood world and post-Flood world where we see similar phenomena (e.g., Australian marsupials resembling placental mammals from other continents).

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Has Parasitism Developed in Free-Living Forms?

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Few studies of parasitology exist in creation literature, and parasitic lifestyles often seem inconsistent with a “good” design. Ingle (2015) argued that God created many organisms in symbiotic lifestyles, and requirements to maintain those relationships evidence design. Considering only species that make their living in or on a single individual of a separate species, nearly half (39%) of all animals live as parasites during some portion of their life history, with evidence of over 200 instances where parasitism developed from free-living forms (Weinstein and Curis, 2016). Many mite taxa have both free-living and parasitic forms, including taxa at the superfamily level and below. As far as we know, no study demonstrates free-living and parasitic forms within the same created kind. Ingle and Aaron (2015) demonstrated that schistosomatids (blood flukes) showed significant continuity among species, and significant discontinuity with other parasitic groups. For this research, a survey of the literature on parasite origins was conducted to determine the number of proposed origins of parasitism. We used subclass Acari, containing mites and ticks, and developed a character matrix for 16 families of Superfamily Dermanyssoidea using 22 characters obtained from a dichotomous key for the superfamily. The characters were biased towards separating each family from the rest, and include 18 morphological (from various parts of the mite external anatomy) and four behavioral characters. In order to decipher if using an outgroup was grouping unrelated taxa into the same holobaramin, two baraminic distance correlations (BDCs) and two multidimensional scaling (MDS) analyses were used: one without an outgroup, and one with a parasitic family (Demodicidae) of mites as an outgroup. Weinstein and Curis (2016) found evidence in the literature of at least 31 instances of parasitism developing within Acari, including 16 instances below the level of family. All families of Dermanyssoidea without any free-living forms showed significant positive correlation with each other and with Family Laelapidae, which contains both free-living and parasitic forms, regardless of the outgroup. The purely parasitic families showed significant negative correlation with the purely free-living families when we used no outgroup, and no correlation (positive or negative) with the purely free-living families with Demodicidae as an outgroup. The purely free-living families show significant negative correlation with the parasitic outgroup family Demodicidae. The MDS analyses confirmed the results of the BDCs, and demonstrated that the purely free-living families do not cluster together with the parasitic families regardless of the outgroup. As a result, we suggest that there is continuity among the purely parasitic families of Dermanyssoidea and Laelapidae, and that these taxa may represent a monobaramin. Additionally, these families appear to be discontinuous from the free-living dermanyssoid families and the parasitic non-dermanyssoid family Demodicidae, which would make Laelapidae + totally parasitic dermanyssoids a holobaramin. These results are tentative due to the small number of characters used, and could be revised with more characters. If created kinds tend to be at taxonomic rank of family, parasitism developed in 16 kinds of mites. If, however, multiple families of mites belong to the same kind as

our data suggest, this number could be different. Most research done on parasites assumes that parasitism developed from free-living lifestyles. However, if some created kinds contain only parasitic forms, the kind was likely always symbiotic (Ingle and Aaron, 2015). Since all parasitic families of Dermanysoidea show continuity with a family that contains both free-living and parasitic forms, parasitism may have developed from free-living forms in this kind. More research is necessary to determine if the kind was always symbiotic and gave rise to parasitic and free-living forms.

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Editor: RWS

Baraminology of Non-Cynodont Therapsids I: “Basal” Therapsids, Biarmosuchians, and Dinocephalians

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Non-mammalian therapsids are a diverse group of Permian – Cretaceous synapsids thought to be the evolutionary link between “pelycosaurs” (Carboniferous and Permian) and mammals (Triassic and younger). Except for the Cynodontia, all six major non-mammalian therapsid taxa – Biarmosuchia (B), Dinocephalia (D), Anomodontia (A), Gorgonopsia (G), Therocephalia (T), and Cynodontia (C) – appear in the Middle Permian. The sudden, simultaneous appearance of 5 of the 6 therapsid subtaxa in the fossil record combined with the large disparities between them (Kemp, 2009), suggests that they are most likely apobaramins. This study is split between two abstracts, the first here covering “basal” therapsids, biarmosuchians, and dinocephalians. BDISTMDS (Wood, 2008) was applied to four separate datasets. At a 0.75 character relevance cutoff, the number of characters (exclusively craniodental) and the number of taxa utilized from the datasets are as follows:

- “Basal” therapsids: Amson and Laurin (2011) dataset; 48 characters; 23 taxa (2 ‘pelycosaurs’, *Tetraceratops*, *Raranimus*, 7B, 6D, 3A, 3G). BDC/3D MDS continuity and discontinuity among the taxa suggest B+A+G and Dinocephalia are both apobaramins. *Tetraceratops* and *Raranimus* do not share continuity with any other therapsids.
- Biarmosuchia: Sidor and Rubidge (2006) dataset; 44 characters, 15 taxa (2 ‘pelycosaurs’, 7B, 4D, 2A) & Day et al. (2016) dataset; 21 characters, 16 taxa (all B). BDC/3D MDS discontinuity exists between Biarmosuchia and D and A, but with G is unknown, so Biarmosuchia is a tentative apobaramin. BDC/3D MDS continuity and discontinuity suggests two tentative biarmosuchian holobaramins (Burnetiamorpha (less *Bullacephalus* and *Pachydictes*, both of which share no continuity with any other taxa); the remaining biarmosuchians).
- Dinocephalia: Cisneros et al. (2012) dataset; 41 characters; 13 taxa (1B, 12D). Anteosaurids are the only well-represented dinocephalians in this dataset. BDC/3D MDS continuity among Anteosauridae (less *Archaeosyodon*), and discontinuity with

other dinocephalians in the analysis, suggests it is a holobaramin. Discontinuity within a likely apobaraminic Dinocephalia (based on the Amson and Laurin (2011) analysis above) suggests there are other dinocephalian holobaramins than just Anteosauridae.

These four analyses show discontinuity among some of the therapsid subtaxa, and they fail to show continuity between “pelycosaurs”, “basal” therapsids (*Tetraceratops* and *Raranimus*), and the major therapsid subtaxa. Future work on non-anteosaurid dinocephalians, including Tapinocephalia and Estemmenosuchidae will allow for a better understanding of the baraminological relationships of these animals.

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Editor: KPW

Baraminology of Non-Cynodont Therapsids II: Anomodonts, Gorgonopsians, and Therocephalians

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In this study, I continue the task of discerning the baraminological relationships of non-mammalian therapsids (Permian – Cretaceous), which are divided into six major taxa: Biarmosuchia (B), Dinocephalia (D), Anomodontia (A), Gorgonopsia (G), Therocephalia (T), and Cynodontia (C). BDISTMDS (Wood, 2008) was applied to four separate datasets: “basal” anomodonts (Liu et al., 2010), anomodonts (Fröbisch, 2007), gorgonopsians (Gebauer, 2009), and therocephalians (Huttenlocker, 2009). All four datasets were analyzed at a 0.75 character relevance cutoff with the number of characters (exclusively craniodental) and the number of taxa utilized from the datasets listed as follows:

- “Basal” anomodonts: Liu et al. (2010) dataset; 64 characters; 15 taxa (1 “pelycosaur”, 2B, 3D, 1G, 8A). BDC/3D MDS discontinuity exists between “basal” anomodonts and *Biseridens* + the outgroup (B, D, G, and the “pelycosaur” *Dimetrodon*). This analysis, which included over half of the known “basal” anomodonts, suggests “basal” anomodontia (less *Biseridens*) is a holobaramin.
- Anomodontia: Fröbisch (2007) dataset; 58 characters; 42 taxa (1D, 1G, 1T, 39A). BDC/3D MDS discontinuity exists between Dicynodontia and the basal anomodonts + the outgroup (T, D, and G), but less than half the known dicynodont genera are represented, so Dicynodontia is a tentative holobaramin.
- Gorgonopsia: Gebauer (2009) dataset; 43 characters; 15 taxa (all G). BDC/3D MDS discontinuity is lacking, but less than half of the known gorgonopsian genera are represented

and there is no outgroup. Thus Gorgonopsia is a tentative monobaramin. Other analyses have shown discontinuity between Dinocephalia, Anomodontia, and Therocephalia and the one or more gorgonopsian taxa used as outgroups. This, combined with the disparities between gorgonopsians and other therapsids noted in the conventional literature (Kemp, 2009), make me suspect that Gorgonopsia will turn out to be a holobaramin or apobaramin pending further research.

- Therocephalia: Huttenlocker (2009) dataset; 94 characters; 30 taxa (1B, 1D, 1A, 1G, 3C, 23T). BDC/3D MDS discontinuity between B+D+A+G and T+C (Eutheriodonta) and between T and C suggest three apobaramins (B+D+A+G, Eutheriodonta, and Therocephalia). BDC/3D MDS continuity and discontinuity suggest three or four therocephalian holobaramins: Scylacosauridae + *Lycosuchus*, Akidnognathidae, Whaitsiidae + Hofmeyriidae, and Baurioidea. Whaitsiidae + Hofmeyriidae and Baurioidea may be united by continuity, which would suggest they are a single holobaramin.

These four analyses—combined with the four analyses from my first abstract on “basal” therapsids, biarmosuchians, and dinocephalians—demonstrate that there is not a continuous chain of forms from sphenacodontian pelycosaurs to cynodonts. Rather, there is evidence for discontinuity surrounding most of the six major therapsid subtaxa, and there is evidence for discontinuity within these subtaxa (e.g., Therocephalia and Anomodontia).

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Editor: KPW

Bounded Forms Most Beautiful: A Creationist Analysis of McGhee’s Periodic Table of Life

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The precise definition, scope and number of biological categories found in Genesis one is still hotly debated. Despite the popularity of baraminology (Wood, 2005), lack of consensus has hampered efforts towards a parsimonious alternative model of discontinuity, which might replace universal common descent. Here, one alternative approach to discontinuity found in the evolutionary literature (i.e. convergent morphologies for major type of locomotion, as discussed by McGhee, (2007, 2008, 2011)) is co-opted to function instead as a creationist reinterpretation of the Genesis ‘kinds’.

Given its prime place in Scripture, Genesis one is given priority in theoretical biosystematics over other Scriptural passages

discussing biological ‘kinds’.

Regarding biological scope, Genesis one includes all possible forms of earth life because a) unlike ancient cosmogonies with a purely man-centred interest in classification, this chapter has a scientific and objective interest (Westermann, 1984) and b) according to the principle of sufficient reason, a perfect creation should reflect the full diversity of the Trinity.

Methodologically, I identify the single major shared characteristic between all of the biological categories created on the same creation day: 3, 5 or 6 as being ‘locomotory type’. This major shared characteristic is then taken as the main component of a redefinition of ‘kind’ (Hebrew: *min*). Subsequently, a pattern appears to emerge among seven biological categories named in the text of Genesis one (delineated below), and comparisons with the periodic table of elements become tentatively possible:

Let’s examine Day 3. All morphologies of Day 3 comprise two ‘categories’ named in verse 11 as ‘esebh (small vegetation) and ‘es (large vegetation). It may be inferred that all morphologies in both these two categories are sessile (and dissipative, as neither have nephesh). Sessile is here defined as any organism which spends the majority of its adult life attached to or rooted in substrate and unable to move around, or is moved solely by external wind/ocean currents. Dissipative is defined as any organism originally designed with a temporary life-cycle involving complete decomposition, rather than with immortality. ‘Grass’ (*dese*) (v 12a) refers to vegetation as a whole and so is not a ‘kind’. Three other reasons why ‘grass’ is not counted here are: it is not qualified as self-propagating, nor directly accompanied by the phrase ‘according to its kind’, nor mentioned in vv 29-30 (cf. Kelly, 2004; Wenham, 1987).

Both the Day 3 categories (small and large vegetation) fall under McGhee’s single periodic group entitled “no locomotion” in his Table 7.1 (cf. McGhee, 2011, p.261), which summarises all known periodic (or convergent) morphologies for earth based life by how or whether they move. Apart from immobility, sessile creatures appear further distinguished in Genesis 1:11 by whether their reproductive particles (seed, spores, spermatozoa in corals etc.) are naked or enclosed in energy-rich packing.

Let’s examine Day 5. All morphologies of Day 5 comprise two ‘categories’ transliterated *šereš* (swarming things) and ‘*ōp* (flying things), since logically and ethologically, *tannin* (i.e. sea monsters of v 21a) form part of the *šereš* (of v 20a), which move in waters (rather than air). We may infer that all morphologies in both these categories locomote through yielding fluids (of varying compressibility). These fall under McGhee’s two convergent morphology group-columns “swimming and flying” (ibid.), both of which share 3-dimensional locomotion.

Finally, let’s consider Day 6. All morphologies created on this day comprise three ‘categories’ (undisputed in number) transliterated *hayyat hā’āreš* (those living on the earth), *behema* (beasts) and *remeš* (creatures that keep close to the ground). Since all three had no fear of humans until later (Genesis 9:2), demarcations are again not anthropocentric but rather objective. Critically, one may infer that all morphologies in these categories locomote across a solid, unyielding fulcrum via points of attachment or contact. These may fall under McGhee’s two convergent morphology groups “walking and crawling” (ibid.), both of which share 2-dimensional locomotion. Uncertainties surround the question

of why there is a third category of Day 6 locomotors employed in Genesis one. One could infer from the text that physical scale vs. gravitation or other physico-mathematical demarcations not yet fully identified might elucidate this.

‘Kind’ boundaries in Genesis one have traditionally been interpreted via baraminology through the hybridization criterion, yet other possibilities certainly exist. Notably, Genesis chapter one presents seven named ‘kinds’ which group all organisms (except humans) in periodic/convergent morphology boundaries by their scale, much like the periodic table of elements groups all elements in seven reactive groups (possessing identical quantum orbital states and similar properties) by their atomic mass. Hence, biological convergence may somehow be equivalent to inherent energy states, and type of locomotion and physical scale may be the two main criteria by which God arranged living forms on earth.

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Editor: KPW

MHC Diversity: Evidence for Humans Evolving as a Population?

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In *Adam and The Genome*, Dennis Venema argues high diversity at particular genetic loci among humans is evidence we did not begin from two individuals (nor ever experience a substantial bottleneck event) but instead evolved as a population (Venema & McKnight, 2017). A bottleneck event, he reasons, would result in low genetic diversity for hundreds of thousands of years if it did not first lead to demise through susceptibility to disease. Venema presents the plight of the Tasmanian devil as an example of what to expect as a consequence of a bottleneck event in the distant past.

An unusual form of cancer is decimating Tasmanian devil populations: cancerous cells are passed from one devil to another through biting (Morris et al., 2012). Originating in another individual, these cells should display foreign MHC type I molecules and trigger an immune response in the new host. (MHC type I molecules are found on the surface of vertebrate cells and present peptides derived from intracellular proteins for immune surveillance (Janeway et al., 2001).) Tasmanian devils, however, do not recognize the cancerous cells as foreign. While genes coding for MHC are typically extremely polymorphic among vertebrate species, devils possess low MHC diversity (Morris et al., 2012). This lack of diversity—presumably caused by a bottleneck event—provides a possible explanation for devils’ susceptibility to the cancer. Venema concludes: “[A]ll devils are so genetically similar to one another that the cancer

cells do not trigger an immune response” (Venema & McKnight, 2017). Subsequent research unreported in *Adam and the Genome*, however, demonstrates low MHC diversity is *not* the cause of devils’ susceptibility to cancer (Siddle et al., 2013). Instead, cancerous cells down-regulate genes essential to the antigen-processing pathway so MHC molecules never make it to the cell surface, leaving nothing for the host to recognize as foreign.

Even if low MHC diversity had been the cause of Tasmanian devil susceptibility to the cancer, it would not establish Venema’s principle of reduced genetic variability persisting for hundreds of millennia after a bottleneck event. Devils likely experienced a bottleneck only hundreds of years ago and thus the lack of MHC diversity has not been demonstrated to persist for millennia (Morris et al., 2012). Interestingly, island fox populations have experienced severe population bottlenecks in recent decades but balancing selection has maintained a high level of heterozygosity at MHC loci in these populations (Aguilar et al., 2004). Mechanisms may thus exist that preserve MHC diversity in the event of a bottleneck, the current plight of Tasmanian devils notwithstanding.

Finally, higher MHC diversity could have been found among the 8 humans leaving the ark than that observed for present-day devils. Humans have 3 MHC type I loci, so each individual could have expressed 6 alleles (assuming heterozygosity at each locus) for a total of 30 in the gene pool. This diversity could have been maintained by balancing selection. Furthermore, human MHC genes have high CpG dinucleotide content, making them especially amenable to gene conversion events that could generate new diversity (Klitz et al., 2012); this may have been especially important for the post-diluvian population. The propensity of MHC genes for gene conversion events has led researchers to remark about their “level of evolutionary design” (Klitz et al., 2012); we agree design is evident even as we disagree regarding its agency.

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Editor: JWF

Preliminary Baraminological Analysis of Lycopods, Zosterophylls, and Rhyniophytes

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This study attempts the statistical baraminology of Lower and

Middle Paleozoic lycopsids and plants that are conventionally thought to be the ancestral complex of land plants—the zosterophylls and rhyniophytes, which were important members of the hypothesized creationist pre-Flood floating-forest biome (Wise 2003). Two published data sets covering these groups were analyzed to obtain baraminic correlations (BDC) and multidimensional scaling (MDS) plots using the BDISTMDS program (Wood 2008). Data for 25 taxa of rhyniophytes, zosterophylls, and representative lycopsids/“protolycopsids,” and ferns came from Gensel (1992). This set contained only 12 characters focused on sporangia, leaf types, and xylem features. Data for 17 taxa of woody Carboniferous coal forest lycopsids came from Bateman et al. (1992). This data set contained 115 characters that are holistic for the woody lycopsids, but includes variations on many structures lacking from the rhyniophytes, zosterophylls, and even herbaceous lycopsids. Four basic analyses were made: 1) The Gensel data set, 2) the Bateman data set, 3) combined set 1 of 42 taxa and 127 characters in which the Bateman taxa were scored for the 12 characters in the Gensel set and the Gensel taxa were scored for the 115 characters in the Bateman data with inapplicable traits scored as separate character states (The lycopsid *Selaginella*, often considered its own order, was added and scored for all 127 characters.), and 4) combined set 2 was reduced from combined set 1 to contain only 53 characters by excluding characters that are relevant only to the woody lycopsid taxa. The BDC graph of Gensel’s data separates the ferns but the remaining taxa compose four overlapping groups. The MDS plot shows the ferns well separated from two fairly tight, separated groups (lycopsids; the spiny zosterophylls but excluding *Zosterophyllum*) and a more diffuse cloud composed of the remaining taxa arching between the two. The Bateman data of woody lycopsids yielded in both BDC and MDS four distinct groups (shrubs, trees branched terminally, trees with side branches, unbranched trees) that were strongly to weakly discontinuous. Combined set 1 produced two discontinuous groups in BDC: 1) woody lycopsids + *Selaginella*; 2) herbaceous lycopsids + all remaining taxa. The MDS of this matrix shows two well-separated arches (one of woody lycopsids and one with tighter clusterings of lycopsids/“protolycopsids,” ferns, and zosterophylls/rhyniophytes) with *Selaginella* positioned between them. However combined set 2 is more complex: BDC has the woody lycopsid group mostly discontinuous from zosterophylls, rhyniophytes, and “protolycopsids.” However, three genera of the woody lycopsid group (the shrubs) were continuous with herbaceous lycopsids, which were continuous with “protolycopsids,” which were continuous with the ferns. MDS showed ferns clearly separated from all remaining taxa, which formed a single arc connected in the middle by *Selaginella* and the shrub lycopsids. These results show that the choice of characters strongly influence the groupings. Combined set 1 unduly weights characters that unite woody lycopsids, lumping everything else as a cluster. Likewise, Gensel’s data set appears to lack sufficient characters and holism to adequately distinguish zosterophylls from rhyniophytes. Taken together, these analyses can be used to suggest the following: 1) Ferns are distinct from other seedless plants. 2) At minimum there are two baramins of lycopsids (the *Lycopodium*-like lycopsids and the woody lycopsids + *Selaginella*). 3) There may be a maximum of six to

eight baramins of lycopsids (especially if the “protolycopsids” are included). 4) Additional characters that more fully characterize the various zosterophylls, rhyniophytes, protolycopsids, and herbaceous lycopsids must be obtained by further study of the primary paleobotanical literature before definitive conclusion can be drawn.

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Editor: MI

Applying Baraminological Methods to Understand Mammal-like Cynodonts

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Non-mammalian cynodonts are the most mammal-like of the various non-mammalian therapsid subtaxa, and their fossil record extends from the Upper Permian to the middle Cretaceous. Basal cynodonts are thought to have produced Epicynodontia and then Eucynodontia, which in turn produced two groups: Cynognathia and Probainognathia. There is controversy as to which probainognathian group is the sister taxon to mammals. Non-mammalian cynodonts are conventionally considered to show transition between “reptiles” and mammals through changes in their palate, jaw to ear evolution, decrease of lumbar ribs, and change in stance from sprawling to erect. We suspect that there are different created kinds of cynodonts and that true mammals did not evolve from cynodonts. In order to determine if there is discontinuity within Cynodontia, we used BDISTMDS v. 2.0 (Wood, 2008) to analyze a dataset from Ruta et al. (2013), which contained 54 taxa (representing all major non-mammalian cynodont groups and two morganucodont mammaliaforms) and 150 craniodental and postcranial characters. After a character relevance cutoff of 0.75 and a 0.35 taxic relevance cutoff (to ensure that at least 50% of the characters were represented), 41 genera, still representing all major non-mammalian cynodont groups and two mammaliaforms, and 88 craniodental characters remained.

Our BDC result showed four blocks of significant positive correlation. The smallest block, corresponding to the family Tritylodontidae, showed no positive correlation with any other taxa in the analysis and significant negative correlation with many. A second block of taxa sharing positive correlation, corresponding to tritheledontids, brasilodontids, *Therioherpeton*, and morganucodonts, showed either a lack of correlation or significant negative correlation with all other taxa except in the case of *Therioherpeton*, which positively correlated with four taxa from another block (*Chiniquodon*, *Ectenion*, *Lumkuia*, and *Probainognathus*). The rest of the cynodonts fall into two larger

blocks of positive correlation that share some positive correlation between them. The 3D MDS results agree with the BDC in showing four clusters of taxa, two of which (Tritylodontidae and Tritheledontidae + Brasilodontidae + *Therioherpeton* + Morganucodonta (TBTM)) appear to be very distant from every other cluster, whereas the other two clusters of cynodont taxa are more closely spaced.

We determined to perform a second analysis of the dataset, this time removing the tritylodontids in order to resolve any discontinuities among remaining taxa. The new BDC graph has three blocks of positive correlation: one block contains the tritheledontids, brasilodontids, *Therioherpeton*, and morganucodonts, while the other two contain the rest of the cynodonts. Although the groups were more defined, *Therioherpeton* still showed positive correlation with *Chiniquodon*, but with a low bootstrap value (60%). We suspect that this positive correlation is not representative of true continuity, a suspicion that is reinforced by the 3D MDS results of the non-tritylodontid study, which shows a clear gap in character space between the TBTM cluster and the rest of the cynodonts, although with a stress of 0.162 in three dimensions.

Despite the lack of postcranial characters, we conclude that Tritylodontidae is likely a holobaramin because the tritylodontids are discontinuous from all the other cynodonts included in this analysis and continuous with each other. We also suspect that TBTM may represent a holobaramin because this group is discontinuous from all other cynodonts and its members share continuity. Interestingly, this study shows that some mammaliaforms (*Morganucodon* and *Sinoconodon*) share continuity with some cynodonts. The morphological evidence does not support the evolution of cynodonts from a common ancestor, but rather the creationist claim of multiple created kinds. Specifically, we do not see evidence of tritylodontids or a TBTM group arising out of more “basal” cynodonts, although we currently cannot detect discontinuity among the more “basal” cynodonts. Because we only had two mammaliaform taxa in this analysis, we were unable to test whether morganucodonts are discontinuous with other mammaliaforms.

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Editor: TH

Step-Down Saltational Intrabaraminic Diversification

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The mechanism of post-Flood intrabaraminic diversification is unknown. However, the peculiar course that organisms followed in the process of diversification places constraints upon—and may even provide clues as to—the nature of that diversification mechanism. This paper offers further characterization of post-Flood diversification, with the hope that it may help identify that mechanism.

1) Intrabaraminic diversification was extremely rapid for the

first few centuries following the Flood. This is collectively evidenced by the Flood’s diversity bottleneck, the high species diversity of many modern baramins, the appearance of crown species very quickly after the Flood, and the short time scale of the creation model.

2) If the Flood/post-Flood boundary is somewhere near the base of the Paleogene, the catastrophic nature and large sediment volume of both Paleogene and Neogene rocks, combined with the creation model’s short time scale, suggest centuries of extremely high preservation rates for terrestrial and marine organisms following the Flood. This, in turn, suggests a remarkably complete post-Flood fossil record, with most biostratigraphic gaps probably no more than decades in length. Consequently, the paucity of inter-specific stratomorphic intermediates in Paleogene and Neogene rocks suggests that the intrabaraminic diversification mechanism was actually saltational—i.e. intrabaraminic taxa arose *without* morphological intermediates.

3) The magnitude of morphological change during intrabaraminic diversification decreased with time following the Flood. This is collectively evidenced by the ‘bushy’ nature claimed for (intrabaraminic) evolutionary trees, the appearance of disparity before diversity in the Cenozoic record of baramins, the appearance of higher taxa before lower taxa as evidenced by both Cenozoic mammal baramins and Jeanson’s (2015) mtDNA data, and the decreasing size of morphological transitions in the fossil equid ANOPA diagram with stratigraphic level.

These observations, in turn, suggest that the intrabaraminic diversification mechanism was designed to initially generate large morphological changes, then, with time, progressively step down the size of the morphological jump. I describe this diversification as ‘step-down saltational’ intrabaraminic diversification (SDSID).

Theoretical applications for SDSID include: (1) SDSID combined with environmental triggers would permit organisms to track the exponentially higher rates of environmental change immediately following the Flood, and step down that change rate with the decrease in rate of environmental change; and (2) if God selected Flood survivor(s) near the center of a baramin’s morphology space and designed SDSID with a random direction of morphological change at each origination event, baraminic disparity would be generated very efficiently.

SDSID might well provide an elegant explanation for: (1) the nested hierarchy of sub-baraminic taxa within baramins; (2) the regular geometric patterns observed in ANOPA and MDS (e.g. the tetrahedral pattern of Anserinae [Wood 2008:57-60] and Sulidae [Wood 2005:133-146]); and (3) the arcuate pattern so common in ANOPA and MDS (e.g. Spheniscidae in Wood 2005; Galagonidae, Viverridae, Talpidae, Hippopotamidae, Spheniscidae, Salamandridae, Pholcidae, Theridiidae, Sironidae, Coelopidae, Lophopidae, Saururaceae, Aristolochiaceae, Nymphaeaceae, and Moringaceae in Wood 2008).

As a more specific application, SDSID is consistent with what we know about the diversification of the equids—a holobaraminic group which seems to track post-Flood climate. Hypothetical diversification trees can be generated from the stratigraphic ranges and ANOPA positions of the 19 equid genera (of 32 known equid genera) in Cavanaugh et al. (2003). The diversification trees involving the least number of transitions over the shortest morphological distance show decreasing morphological change

both in real time and with the number of transitions since the hypothetical ark ancestor.

Just as SDSID can generate intrabaraminic nested hierarchical patterns, SDSID can also generate a sub-baraminic group showing within-group continuity at substantial morphological distance from all other taxa of the same baramin. BDC and MDS applied to such a sub-baraminic group could easily misidentify it as a holobaramin. This may explain how Wood (2008) could identify taxa as holobaraminic that Wise (2009) would suggest are actually sub-baraminic (e.g. Galagonidae, Leporidae, Phocidae, Erinaceinae, Mormoopidae, Hippopotamidae + *Merycopotamus/Libycosaurus*).

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Editor: MAM

Baraminological Analysis of Sphenisciformes Supports their Holobaraminic Status and Reveals a Biological Trajectory

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Previous baraminology analyses of penguins focused on the extant family Spheniscidae, concluding tentatively that the penguins are a holobaramin (Wood 2005, pp. 125-131; Wood 2008, pp. 81-84). Evidence for discontinuity from other birds seemed firm, but evidence of continuity within modern penguins was less clear. Omitted from these earlier studies were all fossil penguins. A recent phylogenetic analysis of extant and fossil penguins (Aves: Sphenisciformes) by Ksepka et al. (2012) provides an opportunity to re-evaluate penguin baraminology using an updated version of the character set used by Wood (2008, pp. 81-84). The morphological character set of Ksepka et al. (2012) consists of 245 skeletal characters scored for 71 taxa as given in the Nexus file from the online supplementary data. The taxon set consists of 15 outgroup taxa, 19 extant penguin species, and 37 fossil sphenisciforms from nearly the entire Cenozoic stratigraphic record. Ksepka's (2012) morphological character set was used to calculate baraminic distance correlation (BDC) and multidimensional scaling (MDS). In order to retain as many fossil sphenisciform taxa as possible, only taxa with less than 20% of character states known were excluded from the

analysis, leaving 57 taxa for calculating baraminic distances. The character set was also filtered with a character relevance cutoff of 0.75, leaving 82 characters. BDC and MDS were calculated using BDISTMDS (<http://www.coresci.org/bdist.html>), and bootstrap values were calculated from 100 pseudoreplicates for the BDC results. BDC revealed two clear clusters of taxa roughly corresponding to Sphenisciformes and the outgroup taxa. The exception are the Paleocene sphenisciforms of genus *Waimanu*. *Waimanu manneringi* exhibited positive BDC only with other sphenisciforms, but *W. tuatahi* had significant, positive BDC with all members of the outgroup, *W. manneringi*, and three other sphenisciforms. Bootstrap values for positive BDC involving *W. tuatahi* is fairly low, except for correlations with four outgroup taxa and *W. manneringi*, all of which had bootstraps >90%. Outgroup taxa share significant, positive BDC with no sphenisciforms other than *W. tuatahi*. Significant, negative BDC was observed between most outgroup taxa and sphenisciforms, with the exception of comparisons involving *W. tuatahi*. Within Sphenisciformes, significant, negative BDC was observed for comparisons involving *W. tuatahi*, *W. manneringi*, *Perudyptes devriesi*, *Paleeudyptes klekowskii*, and *Paleeudyptes gunnari*. All negative BDC involving *Perudyptes* or *Paleeudyptes* and other sphenisciforms have bootstrap values less than 90%, but 45 instances of negative BDC involving a sphenisciform and one of the two *Waimanu* species had bootstrap values exceeding 90%. MDS results reveal two main clusters of taxa corresponding to Sphenisciformes and the outgroups (3D stress 0.09, minimal stress 0.08 at five dimensions). Outliers include both *Waimanu* species and *Pygoscelis grandis*. The sphenisciform cluster is highly diffuse and forms a crude biological trajectory (Wood and Cavanaugh 2003) with Paleocene and Eocene forms on one end and a tight cluster of extant sphenisciforms on the other. Taken together, the BDC and MDS results imply that Sphenisciformes is a holobaramin. Significant, negative BDC between sphenisciforms and the outgroup supports the inference of discontinuity, and the MDS and positive BDC support the continuity of most sphenisciforms. The biological trajectory also supports the monobaraminic status of the sphenisciforms. Based on the present results the position of the *Waimanu* taxa is uncertain. *W. tuatahi* is more similar to outgroup taxa than to sphenisciforms, but neither *Waimanu* taxa are closely clustered with any other taxa in the present sample. Resolution of their baraminic status will await further research.

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