

CBS Annual Conference Abstracts 2015

Epigenetics and Origins: a Kuhnian Revolution in Progress?

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A scientific revolution, as understood by Thomas Kuhn, begins when the reigning paradigm is experiencing persistent anomalies that resist attempts at resolution (Kuhn 1970). While true believers in the existing paradigm maintain their confidence that a solution to the problems will be found, a few independent thinkers may move on to the development of a competing paradigm. If these revolutionaries are successful in producing a theory with greater explanatory power, it may replace the old paradigm, as the traditional true believers pass off the scene or “convert” to the new paradigm.

During the last three decades advancements in molecular biology have generated increasing challenges to the understanding of evolution presented in the Neo-Darwinian Synthesis. These anomalies include the awesome complexity of biomolecules and biological information, orphan (ORFan) genes (Meyer 2013), the apparent demise of “junk DNA”, (Encode 2012), and epigenetics (inheritance from outside of DNA) (Carey 2012).

Epigenetics is the study of inheritable traits arising from outside of the DNA, involving processes that control the *expression* of genes without changing the DNA. An example of epigenetic, non-genetic, inheritance is a learned aversion, by mice, to a chemical odor that is inherited for several generations with no further exposure to the odor (Hughes 2014). It has also been learned that blind cave fish are not blind because of mutations. Their eye genes are all intact. The change is by epigenetic turning off of these genes. Different salamander species have external gills during all or part of their life, or just in the embryo. They all have genes for these gills, and when in their life cycle the gill genes are expressed is controlled epigenetically, with environmental stress inducing a change in the timing of gill expression if they adapt to changing environments by altering their life cycle (Cabej 2012). There are numerous and increasing known examples of epigenetic processes determining how to interpret the information in the DNA, with the non-genetic changes inherited for several or many generations. This can involve environmental induction of beneficial heritable changes.

Review of the newest editions of seven evolution textbooks and a book of evolution readings (e.g. Futuyma 2013; Serrelli and Gontier 2015) indicates that traditional Darwinists either ignore or downplay the significance of epigenetics and some other anomalies. Some more independent thinking evolutionists

point out that traditional Darwinists are ignoring three decades of molecular biology findings (Shapiro 2011; Noble 2013). In line with this criticism, four texts are representative of a novel approach, a new synthesis of evolution based on epigenetics (Pigliucci and Müller 2010). The goal of this synthesis is to provide a more effective theory of evolution, and to use epigenetic processes to explain data that are problematic for the Neo-Darwinian Synthesis. One purpose of this new synthesis is to recognize and attempt to resolve the epigenetic anomaly of apparent Lamarckian processes, or genetic foresight. If these developments represent the beginning of a Kuhnian revolution in thought, we can expect the new epigenetic theory of evolution to eventually replace the Neo-Darwinian Synthesis.

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Editor: TCW

A Note on the Firmament of Gen. 1:6-8: The Raqia and Biblical Theology

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Current debate about the raqia of Gen. 1:6-8 offers two basic options: 1) the *raqia* and its upper waters are part of an ancient Near Eastern cosmology/cosmogony, or 2) the *raqia* is the expanse of sky, and the waters above it are the clouds. This paper argues for a third option. Gen. 1:6-8 presents the *raqia* and the space it creates as a macrocosmic version of the crossing of the Red Sea. The writer is asking the original readers to take their experience at the Red Sea and understand creation as a cosmic version of that miracle. Gen. 1:6-8 thus places creation as part of a “salvific space in waters” motif. The OT canonical context would associate this “salvific space” with other OT people and passages

(the flood, Moses as infant in the reeds of Nile; Joshua, Elijah, and Elisha at the Jordan). This paper points out that numerous Hebrew words in Genesis 1 also appear in these later stories.

The *raqia* provides the preservation of salvific space. Without that preservation, the deep/abyss would consume all creation. Thus, the *raqia* and its upper waters function as a veil between the created order and God. This idea explains the vision experiences of these waters and YHWH's cosmic temple (see Ezek. 1:22-26 and 10:1 as an interpretation of Exod. 24:10).

This paper affirms wholeheartedly that Gen. 1:6-8 presents an actual, factual, historical event. It suggests that in addition to giving these historical facts, the text points beyond itself to a God-intended spiritual truth as well, much like Jesus turning the water into wine in John 2 was also a "sign" which points the reader to intended theological truths.

Editor: RWS

Decoupling Genetic and Species Diversity: Post-Flood DNA Substitution Rates Decrease Exponentially

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Rapid genomic changes transpired following the Flood though the exact timing is unclear. Transposable elements, chromosomal rearrangements and directional mutation have been proposed (e.g., Wood, 2003; Lightner, 2008a, 2008b, 2009; Shan 2009; Borger, 2009a, 2009b). Eocene faunal patterns suggest rapid early post-Flood diversification (Whitmore and Wise, 2008). Ancient DNA (aDNA) comparisons of three baramin provide additional evidence of rapid molecular change (Wood, 2013). A well-calibrated molecular clock would aid the determination of molecular rate changes. However, molecular clocks are disputed in both creation and evolutionary circles. One problem with molecular clocks involves difficulty in dating fossil speciation branch points. Of all the fossil record groups planktonic foraminifera provide a unique opportunity to compare molecular data to morphospecies divergences. Foraminifera morphospecies are characterized by (1) easily preserved mineralized tests, (2) enormous sample sizes, (3) global geographic dispersal, and (4) residence within marine ecosystems conducive to preservation.

Small subunit ribosomal DNA (SSU rDNA) from 70 extant individuals representing 20 species were aligned for phylogenetic analysis using PAUP*. Out of an approximate 1500 bp section, 544 were aligned for analysis. Phylogenetic analyses on planktonic foraminifera have used the Kimura 2-parameter (K2P) and Felsenstein84 (F84) models to calculate genetic distances between species (e.g., Darling et al., 1997; de Vargas et al., 1997). Here, the K2P, F84 and the more parameter-rich Hasegawa-Kishino-Yano 1985 (HKY-85) models of maximum likelihood were employed. Genetic distances of the HKY-85 results were then matched to documented species appearance data for each foraminifera group.

Results show that substitution rates of planktonic foraminifera have been slowing exponentially since the upper Oligocene (standard dating, 25 Ma). The upper Oligocene marks the first appearance of today's extant foraminiferal species. No living foraminifera species date to the currently proposed Flood/post-

Flood boundary (i.e., K-P). As a result, the rates of genetic changes in immediate post-Flood populations cannot be directly measured. However, the exponential tendency of substitution rates suggests rates were highest near the K-P boundary.

If correct for all post-Flood survivors, molecular substitution rates and species diversification is slightly decoupled. Rates of highest genetic change can be inferred to be near the boundary, diminishing over time. Yet, immediate post-Flood population diversity is low and increases in time (e.g., the Miocene for several terrestrial mammal groups). Likewise, the marine planktonic realm documents a steady increase in morphospecies diversity, measured taxonomically, toward the present.

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Editor: TCW

Handwriting on the Wall: Dual Interpretation in Creation

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Our accountability to God is based upon the clarity of his revelation to us in nature (Rom. 1). Yet in spite of God's clear revelation, humanity denies God's unmistakable message while pursuing disobedience. In response, God hides truth from the disobedient (e.g., Luke 10:21, ESV). This creates a dilemma: How can clear truths be simultaneously revealed, denied, and hidden (while seen by others)?

The dependence of old-age apologetics on naturalism make their arguments (e.g., for the anthropic principle) both unconvincing and theologically short-sighted. For young-age creationism we propose that a more Scripturally-holistic approach is needed to understand God's revelation in nature. Such a framework should include better theological assumptions regarding both (1) the contextual nature of theological/scientific argumentation

(e.g., “theory-ladenness” of observation), and (2) whether creation includes purposed complexities as a judgment for intellectual rebellion. Stated differently, evangelical apologetic approaches — rooted in positivism — simply assume a “clear revelation→objective observer” relationship. Rather, Scripture provides a more nuanced “clear revelation→truth-suppressing observers (on part of most)→(at least partially) hidden revelation→believing and non-believing observers” relationship.

Antecedent to any apologetic, therefore, we pose a more complex theological starting question: did God providentially design creation to compellingly show his existence *while also* allowing seemingly rational—yet *misleading*—interpretations of the same data? If true, a better approach to creation includes the expectation that God’s revelation in nature contains purposed, ambiguous complexities.

Scripture provides a precedent to answer our dilemma between the simultaneous clarity and hiddenness of God’s revelation. The Hebrew text frequently contains purposed linguistic ambiguity. Hebrew’s consonantal form requires the readers to supply vowels (known as “points”). Today’s Hebrew newspapers contain a consonantal text only; “pointed” newspapers exist for novice readers.

Absence of points leads, at times, to ambiguous interpretation foreign to readers of English. One ambiguity is *double meaning*. For example, based on vowel placements Jacob’s name can mean either “he *grabs the heel*” (Gen. 25:26), or “he *deceives*” (Gen. 27:36)—both an episode in Jacob’s life. Examples of intended word play exist in the hundreds within the Hebrew text. Often, *context* clarifies meaning.

Instructive here is the familiar story of the handwriting on the wall (Daniel 5:25) — an intended *double meaning*. The text—pointed above, Belshazzar’s below— reads:

מנא מנא תקל ופרסין:
מנא מנא תקל ופרסין:

The words, “mene, mene, tekem, and parsin”, have two meanings. The “obvious” meaning is an accountant’s ledger line (e.g., resembling “pounds, shillings & pence”). This explains the silence of Belshazzar’s wise men: the “obvious” monetary meaning was easily understood, yet its inapplicability to the situation generated bewilderment.

In contrast, Daniel (1) knew God, (2) saw God’s name dishonored (v. 3), (3) perceived the idolatry (v. 4), all having (4) once witnessed God’s earlier discipline of Nebuchadnezzar’s pride (v. 19-21). Only Daniel’s prophetic perspective provided the correct reading: Belshazzar was weighed in the balances, found wanting, and his kingdom was divided among his enemies. The true reading resulted only from a *God-centered context*.

Two things in our experience are directly from the mind of God: his world and his word. God’s word frequently contains double meanings. Likewise, God’s physical creation may at times function as an unpointed Hebrew text. If so, creation could be heavily context-dependent, meaning science is dependent upon God-centered interpretation (e.g., Scripture, philosophy, God’s Spirit, etc.) when ambiguity arises.

Editor: RWS

Creation as Visual Music: Repetition, Contrast, and Variation

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Sound is organized at many levels in the created order but only man has taken dominion over sound to communicate entirely new ideas and create ways of sharing new information that contains reason and emotion. God frequently commends musical worship. In later western thought the “harmony of the spheres” became the basis for the study of music “theory.” Early Greek philosophers, like Plato, wanted to understand the ratios and vibrations of the heavenly bodies. They sought to understand how a Higher Being was able to fit all of creation into such harmony.

Human beings respond to repetition and variation in music at many levels. Perhaps most do not realize how often exact repetition is used in music to drive home a key point. When one becomes aware that variation in music is balanced with repetition of a theme, they gain important insight for listening to, and singing, new pieces. Musicologists are aware of these variations in classical music. So we ask, has God also infused the plant and animal world with variation analogous to what musicians employ? And is this for the purpose of driving home “key points?”

Musical notation contains a complex system of symbols. The symbols must be decoded from one person to the next for the music to be rendered properly. Music analyzed visually or aurally, from the simplest worship styles to the most complex western classical traditions, shows that (1) literal repetition serves a building block to unify a piece, while (2) variety and contrast are keys to maintaining interest and appreciation over time.

Repetition. We are familiar with the process of repetition in simple folk music. Lullabies teach children the cadence of language through repetition. For example, “Twinkle Twinkle Little Star,” uses a repeated note pattern.

Contrast. But contrast exists in even such a small tune as twinkle. The fragment “up above the stars so high” holds contrasting, repeated notes so the listener can be convinced that the piece holds together (i.e., compare, “like a diamond in the sky.”)

Generally the music cannot be literally repeated more than twice without a slight variation (Allen Sapp, pers. comm.). Familiar patterns are mixed with new ideas, then familiar patterns within the cycle continue as long as the piece lasts. Both in improvisation and in musical notation the “creator” of music provides an analogy to the Lord who created things “after their kinds.” Likewise, baramins express similar patterns of underlying design yet contain many variations on the theme. To appreciate music we need repetition to assess the patterns before they are altered or contrasted with a new pattern. This allows us to understand their original nature at a deeper level. This type of contrast can be heard in Beethoven’s Spring Sonata. Beethoven and baramin alike may manifest the deeper Platonic tension of the “one and the many”: unity is the foundation of difference; difference is sourced in unity (Plato, *Republic*, Book 10, Section 596a-596c).

Variation. The field of music is based on variation of all sorts. Musical ideas with their contrast and variation are easily illustrated in the following examples:

- The development of musical instruments in families.
- Ever-expanding complexity of Themes with variation such as Mozart's "Ah, Vous dirai-je Maman" or Brahms "Variations on a theme by Haydn."
- "Shared meaning": using language, rhyme, or social convention to create shared musical experience.
- The rational capacity to preserve language and meaning while expanding possibilities of musical practice and notation.

Like these many examples in music where human creators vary themes to communicate their message, so too we believe God created the biotic realm with repetition, contrast, and variation inside established themes. In this sense, Creation is a type of "visual music."

"...things which are said to be made by nature are the work of divine art, and things which are made by man out of these are a work of human art. And so there are two kinds of making and production, the one human and the other divine." (Plato, *Sophist*, Sections 264^a - 267^a)

It is likewise instructive to study repetition, contrast, and variety in the field of music to compare it to God's creative effort in forming the world through his word.

Editor: TCW

Observation of *Ips* and *Dendroctonus* Pine Bark Beetle Activity in the American Southwest: *Ips pini* May Serve as a Model Organism for How Bark Beetles Can Provide Beneficial Activities in a High Desert Forest

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Western North America is currently experiencing a severe outbreak of pine beetles (*Dendroctonus* and *Ips*), the larvae of which live in the underbark environment of pine trees, eventually killing them. Entire forests have been decimated because of pine beetle outbreaks. This pathological condition contrasts with the spread of invasive species, because the pine beetles are natives. Consequently, whereas creationists might hypothesize an ecological breakdown to explain invasive species, ecological degeneration cannot be the explanation of bark beetle outbreaks. The purpose of our research is to understand bark beetles from a creationist perspective, thus providing novel insights into bark beetle control. What is the "very good" purpose of a bark beetle, and can we restore that good purpose?

Currently, large numbers of ponderosa and pinyon pines are dying in the Mount Pinos district of the Los Padres National Forest. A major five-year drought is believed to contribute to an increase in bark beetle associated tree killing. It is difficult to determine which beetle species directly kills trees because multiple species can infect trees. We have abundant preliminary evidence from analysis of galleries and collection of live beetles that *Ips pini* and other *Ips* species may directly kill pinyon pines. We find that *Ips* is not indisputably implicated in the killing of White fir and Jeffrey pines, morality of which varies with elevation. Numerous

White fir and Jeffrey pines (in groups of 10-50) are dying or expressing top kill at 6000-7000 feet, but essentially no trees are being killed by bark beetles at 8000 feet or higher in the areas we have examined.

Curiously, we do find *Ips pini* active at higher elevations where no bark beetle associated tree damage or death is obvious. They are associated in high number (hundreds to thousands per tree) with freshly toppled wind-thrown trees but no dead standing or dead toppled trees. We even find *Ips pini* specifically infecting branches from live trees which have been removed by the scraping action of falling dead trees while the dead fallen tree shows no *Ips pini* infection. In addition, all standing trees within a 500 yard radius of the infected wind-thrown trees show no signs of infection as determined by the lack of entry bore holes. *Ips pini* leave characteristic and very obvious entry bore holes (1-3 cm diameter) which contain very distinct red boring dust on the outside layers of bark. Some of these trees, which are estimated to be over 300 years old (as determined by tree ring analysis of fallen trees) were noted to have fallen recently because of the green needles still associated with the tree. It is interesting to note that the infection of the wind-thrown trees with *Ips pini* is rapid and begins at the crown of the tree primarily in branches of 10 cm diameter or greater.

We used moisture probes to measure the percent water retention of the under-bark environment of large (4-5 ft DBH) dead trees and nascent forest floor. We find that the under-bark environment holds water at a near constant level throughout the dry summer months while surrounding soil areas desiccate rapidly. Furthermore it appears that this moist under-bark environment provides a rich habitat for development of fungus and insect communities and provides an important link to the food web of the high desert environment.

We suggest that the initial infecting *Ips* beetles are pioneering species that help form a rich under-bark habitat. This environment is then cultivated by many wood-boring insects and microbes which provide a substrate for the successive colonization by other invertebrate species. The number of species supported over time by the establishment of this water oasis in the desert suggest that *Ips pini* is acting as a keystone species and may be demonstrating how bark beetles were designed to promote life in pre-Fall and post-Fall ecosystems.

Editor: NAD

A Microbe Interface System: Design Analysis Confers Better Understanding of our "Immune" System

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Using design analysis helps explain the enigma of creature's immune systems (Francis 2013) by revealing system elements functioning with matching characteristics distinctive of all interface systems.

I propose design analysis (DA) as a useful investigative approach to biological systems. Biological research is reverse engineering which methodically disassembles systems. DA, however, begins with researchers forward engineering systems by thinking through major elements and assembly sequences to

achieve outcomes (e.g., vision). Reference to similar human-made systems is valuable. This endeavor aids predicting findings before reverse engineering, assists correlating functions of discoveries, and helps rank their significance (i.e., indispensable to aesthetic). DA's distinguishing assumption, when applied to biology, draws from the reality that for human-designed entities 100% of functional causality originates from within—notably environment-related activities. DA methodology describes all, but only measurable, innate elements scrutinizing to neither omit nor concoct anything confusing clarity of a trait's true cause for success/failure at solving environmental challenges. DA rules, therefore, confine undetectable expressions of environmental agency to supposition. To illustrate DA, consider the design premise underlying the innovative understanding of the essential microbial "organosubstrate of life" by Francis (2009). Changing views by microbiologists like Gordon's (2012) who, "saw our relationship with microbes portrayed in warlike, rather than in mutually beneficial, terms" reinforce Francis' concept. Would our understanding of immune systems be different with a fresh look by DA coupled with Francis' enhanced conception of our microbiota?

How could engineers overcome human-microbe dissimilarities and distinct boundaries to produce beneficial interactions? Some bridging mechanism is a design absolute. A logical solution connects them via an interface. Per Clark and Petrini (2012), interfaces are regulatory-communication systems facilitating harmonious information/product exchanges. Designers use in-depth knowledge of both unrelated entities to integrate their functions into three indispensable interface elements:

- 1) **Authentication** mechanisms differentiating self and non-self entities;
- 2) **Protocols** standardizing rules/processes governing exchange; functioning through
- 3) **Medium** conditions mutually accessible to both entities.

DA-based investigations anticipate that an innate, actual interface system (not a social interface) fully controls human-to-microbe associations—with human elements displaying three distinguishing characteristics.

"Warlike" functions usually portray immune systems in humans. Yet, DA correlated findings suggest a vital linking system harmonizing individuals—a microbe interface system (MIS)—better analogized as a "business" relationship of reciprocating "requester-provider" transactions. 1) Authentication of "self"- "non-self" occurs via pattern recognition receptors identifying molecular arrangements on microbes. Detectors bind specific microbial features, largely the toll-like receptor subgroup exemplifying entity-to-entity bridging characteristics (Roach et al. 2005). 2) Protocols standardize reciprocal processes like nutrient-product transactions or host control of microbiota composition and microbiota control of lymphoid development and epithelial function via MyD88-dependent, RegIII γ signaling pathways (Hooper et al. 2012). 3) Medium biochemical conditions accessed by host and microbe such as defensin-bacterial interactions through covalent charge modification of anionic molecules on bacterial envelopes or altering membrane fluidity (Peschel 2002).

Interpretations of "immune" systems constrained in death-survival paradigms are liable to mislead. For creationists, pre-Fall "defensive" systems may be enigmatic; interface systems

as a design absolute to harmonize autonomous entities are not. Therefore, rules used in DA may assist clarity of explanation and recognizing causality when drawing from findings in literature possibly biased by naturalistic assumptions. Since humans have associated with trillions of microbes from Creation, then the presence of some interface was a certainty from a design standpoint. The human MIS has likely *not* changed significantly from its original, and continuing, primary *regulatory* purpose. Cell-destructive capacity for regulatory purposes was MIS design feature. Even post-Fall destruction for subsequent defensive purposes is still a subtype of regulation.

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Editor: RWS

Language in DNA? Analysis of Statistical Linguistic Features in Human Chromosome 1

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Since the discovery of DNA structure, linguistic terms (e.g., code, transcription, translation) have been used to describe many DNA functions. Recent studies, however, have shown that the linguistic features of DNA encompass the entire genome, rather than just coding sequences. Frequencies of DNA oligonucleotides in genome samples follow a Zipfian distribution (Mantegna et al. 1994), which is the same distribution followed by words in language (Ferrer-i-Cancho, et al. 2010). These studies are occasionally cited by creationists as possible evidence of design in noncoding DNA (Standish 2002, Bergman 2001); however, language is not the only explanation for Zipfian distributions. Many phenomena display a Zipfian distribution as a result of growth by preferential attachment (Newman 2005). How can we tell if the Zipfian distribution of oligonucleotides in genomes is the result of language or some other preferential attachment model? Previous research focused on different oligomer lengths and is therefore non-systematic in approach. For example, Mantegna et al. (1994) examined trimers through octamers, Yonezawa (1999) examined hexamers, and Csürös et al. (2007) examined 12-mers and 13-mers. We sought to provide a more comprehensive analysis by systematically examining dimers through 40-mers to determine whether patterns of oligonucleotides are best explained by preferential attachment or linguistic properties.

We examined human chromosome 1 by counting frequencies of oligonucleotides of length 2-20, 25, 30, 35, and 40 nucleotides. For 3-mers through 14-mers, we found no evidence of a Zipfian

distribution. Instead, we found that these shorter oligonucleotides were adequately described by a multimodal lognormal distribution where each mode correlated with the presence of CpG dinucleotides, which occur at a low frequency in the human genome. This multimodal distribution was also noted by Csűrös et al. (2007). The Zipfian distribution appears at 15-mers, corresponding to the point at which >87% of all possible oligonucleotides of length 15 were not found on chromosome 1, and persists through 40-mers.

As a control, oligonucleotide counts were repeated for 9-mers, 15-mers, and 40-mers on a chromosome possessing the same length and nucleotide frequencies as human chromosome 1 but a random sequence. We found that the random chromosome did not display any Zipfian distributions, indicating that those observed on the real chromosome 1 should not be expected from random oligonucleotides.

In order to determine which model best explains oligonucleotide frequency distributions in chromosome 1, high frequency 40-mers (those occurring >10 times on the chromosome) were compared to known repetitive elements in RepBase v. 20.03 (Jurka et al. 2005) using FASTA (Pearson 2000). More than 90% of the 178,750 high frequency 40-mers matched known repetitive elements in RepBase.

Based on these results, we conclude that the “linguistic pattern” in DNA arises from repeat sequences that have already been biologically characterized. This suggests that the Zipfian distribution present in oligonucleotide frequencies is indicative of preferential attachment rather than linguistic properties. Therefore, based on oligonucleotide frequencies alone, we cannot conclude that linguistic characteristics of DNA are the results of a language. Further, since repetitive elements are known to accumulate by a preferential growth model, we cannot claim that the Zipfian distribution is exclusively explained by an intentional design mechanism.

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Editor: NAD

Testing for Bias in an Original Baraminic Distance Dataset

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Besides striving for holistic datasets, researchers still face uncertainty in the method of selecting characters to optimize accuracy in baraminic distance analysis. In other words, to what extent does character selection bias the results toward accepting a certain group versus a more or a less inclusive group as the holobaramin? Most analyses to date have relied on published cladistic datasets, which may be biased toward differentiating ingroups from outgroups or differentiating among ingroup taxa. This study uses an original dataset (Sanders in press) that was developed for baraminic distance analysis of the verbena family (Verbenaceae). It is holistic, containing at least one character to differentiate any given taxon and using all known characters that differentiate tribes of the Verbenaceae, as well as the Verbenaceae from near and far outgroup families.

To test for bias, the dataset was manipulated in two main ways: using all characters with subsets of taxa and using all taxa with subsets of characters. The Verbenaceae and its tribes were analyzed individually and in combination with each other and various outgroups. Five datasets were composed using 20 randomly selected characters of the original 80. Other character subsets were obtained by 1) sequentially adding taxa and a differentiating character until all taxa were included, and 2) choosing one character that would bifurcate taxa and repeating with all subsequent subsets of taxa. If a previously selected character served to differentiate taxa, it was used instead of adding another character. A subdataset of excluded structurally or developmentally dependent characters was not conducted because the original dataset consisted of essentially all independent characters. The matrices were analyzed using the BDISTMDS program package available on the Core Academy of Science website (www.coresci.org/bdist.html; Wood 2008) to obtain baraminic distances (BDIST), baraminic distance correlations (BDC), correlation bootstrap values, and multidimensional scaling coordinates (MDS) for all pairs of taxa. Character relevance was set to a minimum of 95%. The coordinates were displayed using the MAGE software package (Richardson & Presley 2006).

In general, the most distant taxa in less inclusive taxon datasets showed either no correlation or significant negative correlation with some remaining taxa. However bootstrap values of the negative correlations was mostly less than 60%, while the positive correlations were mostly greater than 60%. In addition, the MDS generally showed no clear gaps, suggesting that taxa within the subdatasets were not separated by a discontinuity. Randomized characters generally produced results similar to the full data set, while the minimum differentiating datasets showed negatively correlated taxon groups that were connected by intermediates resulting in no discontinuity among any groups.

These results suggest that the original dataset was not biased toward the family level over that of the tribe or genus as holobaramin. It also suggests that multiple correlated but independent characters possessed by a group should be included to truly capture the distinctiveness of the group. It is possible that BDC overestimates discontinuity while MDS may underestimate

it, such that each compliments the other in analyses. Sanders (2013) surveyed plant families with a Genesis Flood fossil record and suggested that the Verbenaceae could either be a baramin or subbaraminic group in a larger baramin composed of the whole order Lamiales. The present data are insufficient to analyze whether the baramin may be at the order level, but future work will strive to resolve that issue.

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Editor: JWF

Paleontological Notes on the Baraminology of Frogs

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The Post-Flood Continuity Criterion (PFCC; Wise 2009) was applied to the Superorder Salientia using Sanchiz (1998). As per Wise (2009), Paleocene sediments were assumed to separate Flood and post-Flood sediments, and modern Salientia taxa were assumed to reflect the actual discontinuity structure of Salientia morphospace.

Although salientians are diverse (>4800 species), <1% of that diversity is known from pre-Paleocene sediments. Those species, however, represent the full disparity of living salientians (all three suborders and all four superfamilies in the Order Anura), plus the only other order and five of the seven species not classified in higher taxa. Consequently, fossil Salientia exhibit disparity-before-diversity (Gould 1989) – a fossil pattern unexplainable in evolutionary theory, but expected of a Flood that successively buried high-disparity, sub-global-diversity environments. Furthermore, since Proanura is known only from one Triassic species, and none of the five unclassified species are known from post-Cretaceous sediments, salientians exhibit disparity decimation explainable by a global Flood.

Of the eight non-anuran species, only one has been classified into higher taxa, so the number of non-anuran baramins known is at least two and no more than eight.

Among anurans, all super-familial taxa, but only 1/3 of the familial taxa are known from both Flood and post-Flood sediments, and <42% (10 of 24) of the living families have a fossil record back to the Eocene. Thus, if anurans were on the ark, the PFCC suggests anuran baramins are defined at the family to superfamily level.

Of the three Suborder Archaeobatrachia families: Leiopelmatidae (South American Jurassic and New Zealand Pleistocene through Recent); Discoglossidae (continuous Eocene to Recent record: from European Eocene *Latonia*-like species, expanding successively into Africa and North America); and Ascaphidae (North American Recent). As per the PFCC, archaeobatrachians include 2 baramins.

Of the three Superfamily Pipoidea families: Pipidae

(discontinuous Paleocene to Recent record: from South American Paleocene *Xenopus*-like forms, expanding into Africa); Palaeobatrachidae (continuous Paleocene to Recent record: from European Paleocene *Palaeobatrachus*, expanding into North America); and Rhinophrynidae (North American Oligocene, Pleistocene, and Present). As per the PFCC, pipoideans include 2 baramins.

Of the three Superfamily Pelabatoidea families: Pelobatidae (continuous Eocene to Recent record: from North American and European *Eopelobates*-like species, expanding into South America then Africa); Pelodytidae (continuous Eocene to Recent record: from European Eocene *Pelodytes*, expanding into North America); and Megophryidae (Recent, Asia). As per the PFCC, pelabatoideans include 2 baramins.

Of the eight Superfamily Hyloidea families: Leptodactylidae (nearly continuous Paleocene to Recent record: from South American Paleocene *Caudiverbera*, expanding into Central America); Bufonidae (continuous Eocene to Recent record: from European Eocene *Bufo*, spreading into Africa, Asia, North and South America); Myobatrachidae (nearly continuous Oligocene to Recent Record: from Australian Oligocene *Limnodynastes*-like forms, spreading into India); Hylidae (continuous Oligocene to Recent record: from Canadian Oligocene *Hyla*, expanding into Central and South America, then Europe); plus five families known only from the Recent. As per the PFCC, hyloideans include at most 4 baramins, and probably 2.

Of the five Superfamily Ranoidea families: Ranidae (continuous Eocene to Recent record: from European Eocene *Rana*, expanding successively into North America, Asia, and Africa); Microhylidae and Rhacophoridae (discontinuous Eocene to Recent record: from European Eocene taxa); plus two families known only from the Recent. As per the PFCC, ranoideans include at most 3 baramins.

If salientians were on the ark, the PFCC suggests that only about 13-15 salientian baramins were created. On the other hand, if salientians were to survive the Flood outside the ark during a prolonged larval stage, limited trans-latitudinal transport (Wise 1992) may explain how northern and Gondwana lineages within superfamilies re-established themselves in the same hemisphere after the Flood. If so, the salientian baramins could be as few as seven in number (the 5 anuran superfamilies and 2 non-anuran baramins).

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Editor: JWF

AIM Teleology and a Creationist Philosophy of Science

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Christian believers are to accept (Hosea 6:6), pursue (Proverbs 2:3-5) and grow in (II Peter 3:18) the knowledge of God and accept (Ephesians 2:8-9), live in (Romans 1:17), and abound in faith (II Cor. 8:7). The physical world also reveals knowledge

(Psalm 19:2) of the nature of God (Romans 1:18-20). From these truths we suggest that God created so that humans would forever grow in the knowledge of and dependence upon God. We believe this AIM (Asymptotic IMaging) teleology – where humans asymptotically converge on perfect imaging of God – provides a foundation for a distinctly Christian epistemology. Here we pursue the implications of AIM teleology for a Christian philosophy of science.

If God created the physical world so that humans could forever grow in the knowledge of God, then several things are true about humans (*e.g.* human senses, memory, and reason are generally reliable) and several things are true about the physical world: *e.g.* it exists; it has an order simple enough to be discerned by individual humans; its regularities are unifiable and continuous in space and time; it contains truth; truths about its visible things yield truths about unseen things; there is value in understanding its truth; and its truths are cumulative. All these claims are presuppositions of science – assumptions which must be assumed to do science and must be true for science to work. AIM teleology provides a philosophical foundation for the presuppositions of science – a foundation unknown outside of Christian doctrine. Since it argues for the truth of the presuppositions of science, AIM teleology also explains why science has been so successful at acquiring truth about the physical world.

If God created the physical world so that humans could forever grow in the knowledge of God, then both the structure of the physical world and the nature of human reason somehow converge on the nature of God. This would explain a) how space and time are both *a priori* modes of human perception (Kant, *Critique of Pure Reason*) and actual physical entities; b) how logic is both the *a priori* mode of human reason (Kant, *ibid.*) and, historically, a very successful means of understanding both the physical world and God; and c) how mathematics is both a human-constructed

world of perfection and a near-approximation of the imperfect and finite physical world.

Because God also created the physical world so that humans would forever grow in *dependence* upon God, God placed critical truths only in His Word and created the physical world with sufficient ambiguity that faith in His Word is necessary to accurately choose the correct physical world interpretations in a number of key areas of thought. This explains a number of the limitations and failures of science: *e.g.* why the physical world is philosophically under-determined; why multiple competing hypotheses are common; why theories of science can never be more than tentative truths; why science alone cannot identify absolute truth; how science can be so very wrong for so long about so many things; why proof (*e.g.* Aristotle's demonstrative syllogism) is not part of science; why proofs of God fail; why natural theology without scriptural data fails; and why Augustine's concern is unjustified that science may discover truths requiring Scripture's reinterpretation. If AIM teleology is true, God's Word should not only be a part of the methodology of science, but should have higher authority than human observation and reason.

At least since the founding of the Royal Society of London in the seventeenth century, input from the Word of God has been excluded from the standard methodology of modern science ('Wordless science'). AIM teleology would explain why this Wordless science has converged on many false inferences about God and interpretations of the physical world – especially in studies of pre-Abraham history. We believe that the inclusion of biblical truth should prevent some of these mistakes and increase the efficiency and accuracy of scientific studies. To justify the use of Scripture, we recommend that creationists adopt an epistemology of science (such as is suggested by AIM teleology) that embraces the use of God's Word in studying the world.

Editor: RWS