

CBS Annual Conference Abstracts 2014

A Surprising Set of Distinguishing Features Characterizing an Apobaramin, and its Larger Implications for Baraminology

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Ruminantia is an apobaramin that is thought by some Creation taxonomists to be a holobaramin (Lightner, 2012). Interestingly, Ruminantia holds a special place in scripture as being a “clean animal.” Creationist taxonomy has largely been focused on identifying what the taxonomical structure of the creation is. The overlap of an apobaramin with both a functional and ceremonial role in scripture shows an additional mode of description available to Creation taxonomists. Not only might we discover what the created order is, but what purposes the created order serves. This overlap leads us to ask similar questions of purpose about other apobaramins and holobaramins as to what God’s purpose was in creating them.

The key *internal* characteristic of Ruminantia that separates it apart from other taxonomic groups is the four-chambered stomach, which presumably relates to why God considered Ruminantia to be ceremonially clean. Because the stomach is exactly coextensive with an apobaramin, this feature appears to be unevolvable in either direction (either to gain or lose as a feature). This is, therefore, an *essential feature* of the group. Features that are exactly coextensive with a taxonomic group and serve a unique purpose seem to be especially useful for classification in creation-oriented methodologies.

What is surprising, however, is that the Bible does not use the internal characteristics of Ruminantia to identify it. Instead, the Bible uses two *external* characteristics to properly identify Ruminantia, and surprising characteristics at that. Leviticus 11:3 identifies clean animals that have a split hoof and chew the cud. There are many animals that, while not having a four-chambered stomach, perform a cud-chewing action. There are also animals that have split hoofs, but do not chew the cud. It is interesting that having a split hoof and chewing the cud uniquely identifies a branch of the Linnaean hierarchy. It is also interesting that the *number* of characters needed to make this diagnosis is so small: only two (or three, if you count being a land animal). This is made even more surprising if Ruminantia is discovered to be a holobaramin.

It is interesting to consider whether or not this pattern (apo- or holobaramins specified by a small number of specific traits) is specific to Ruminantia or is a larger feature of God’s design. Did

God intend us to be able to identify the signal of His purposes through a few diagnostic features? Many presumed apobaramins can be identified through a small number of features, such as Arachnida (8 legs), Hexapoda (3-segmented body, three sets of legs), Asteraceae (composite flowers), etc. In addition, different groupings tend to have very different identifying characteristics, perhaps because of the nature of differences within their purpose. The existence of a small number of identifying features comports well with the cognitum concept in baraminology (described in Sanders and Wise, 2003) as well as the “patterns” method of teaching taxonomy (described in Elpel, 2013).

If the pattern of Ruminantia is a global pattern instead of a local one, then this indicates the need for a shift in thinking for baraminology. While the immediate goal would continue to be the identification of baraminic groupings, the ultimate goal, as a science, would be to identify the purposes for which God made them. While the methodology for deriving purpose is still in an embryonic stage, it seems that the example of Ruminantia suggests that finding biological features that are exactly coextensive with an apobaramin or holobaramin is an important first step to discovering purpose within baraminic groupings. Another possible method of discernment would be to discover the specific directions in which a baraminic grouping is evolvable, and look at how such adaptations allow for accomplishing certain purposes. Also, baraminologists should attempt to discover whether a holobaramin or apobaramin has external, uniquely identifying combinations of features by which they can be easily identified.

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Editor: JWF

Ancestral State Reconstruction as a New Method for Identifying Baramins of Pathogens and Parasites

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Creationists have been developing various methods of identifying baramins as a way of understanding the original creation and how organisms have changed throughout history ever since the concept of baraminology was introduced. Hybridization,

baraminic distance correlation, and multidimensional scaling are some of the methods that have been widely used to infer biological boundaries of baramins (Wood 2005). However, a persistent difficulty of creationism is the presence of natural evil in the world; specifically, predators, pathogens, and parasites. Under the hypothesis that there was no death in the original creation, baramins containing “naturally evil” organisms would have looked and behaved drastically different in the pre-fall world than their modern counterparts do today. An additional tool for estimating baramins is presented here that has special significance for baramins of pathogens and parasites.

Recent advances in phylogenetic analysis have provided the opportunity to study deep nodes within a phylogeny in an attempt to discover the morphological and molecular characterization of the ancestors of extant organisms. This technique is called ancestral state reconstruction (ASR) and is a relatively simple statistical method of tracing the evolution of traits along the branches of a phylogenetic tree (Pagel 1999). Many creationists have a very specific hypothesis about the ancestral state of organisms that are currently pathogenic/parasitic: the ancestral condition was non-pathogenic/non-parasitic. This idea can now be explicitly tested through phylogenetics and ASR analysis. The results can then be used to infer appropriate baramins of “naturally evil” organisms. This concept can be illustrated by reconstructing character states in the parasitic fly family Tachinidae.

Tachinidae are a diverse (>10,000 species) family of obligate endoparasitoid flies that attack a wide variety of arthropod hosts (Stireman et al. 2006). If these flies were non-parasitic in the original creation, specific morphological traits that are solely used for parasitism would have evolved after the fall. One such trait is the piercing ovipositor found in two of the four tachinid subfamilies, Phasiinae and Exoristinae (O’Hara 1985). Using the ASR package in Mesquite 2.74 (Maddison and Maddison 2010), ovipositor type was reconstructed at the subfamily and family nodes with maximum parsimony (MP) and maximum likelihood (ML) analyses. While the ancestral ovipositor of the Exoristinae was non-piercing (ML=98), a piercing ovipositor was recovered as the basal trait in Phasiinae (ML=91). If these subfamilies correspond to baramins, it could be inferred that there were flies with piercing ovipositors in the pre-fall world. Because this idea is incompatible with the original hypothesis of a non-parasitic creation, the ancestor of the whole family was analyzed in the same way. Interestingly, the most recent common ancestor of all tachinids was recovered as having a non-piercing ovipositor (ML=95). If the family Tachinidae is considered a baramin, this result reinforces the concept of post-flood degeneration into parasitism by tachinid flies.

Another group of destructive organisms can be found in the bark beetle genus *Dendroctonus*. These beetles have a unique symbiosis with fungal species and the ecosystem. However, they are currently destroying millions of acres of pine forest in western North America (Nikiforuk 2011). As this behavior is clearly incompatible with the idea of a mutually beneficial creation, *Dendroctonus* is a prime candidate for ASR analysis. What are the traits that cause pathogenicity? Are those traits ancestral or derived? How have they changed over time? These questions will be explored in future studies on *Dendroctonus* and its relatives.

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The Population Problem and Creationist Apologetics: From L. Euler to H.M. Morris and Back

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The “population problem” comes from the tendency of populations to increase in geometric ratio and has long been noticed by economists and biologists. The geometric growth of unchecked populations played an important role in the formulation of Darwin’s theory of natural selection. In the creation/evolution debate, Morris (1974) presented how a simple geometric model fits all known data but is incompatible with assumed “geological timescales.” From an evolutionary perspective, Milne (1984) argued that Morris’s line of argument was highly simplistic, ignoring that the population growth rate has varied greatly along history and could have been zero or negative during significant periods of time.

The well-known mathematical expression of geometric growth is based on elementary mathematics discussed in many pre-calculus textbooks. According to Klyve (2014), the great Swiss mathematician Leonhard Euler is ultimately responsible for the law of geometric growth and has influenced Darwin both indirectly (through Malthus’ famous *Essay*) as well as directly. As such Euler, “surely deserves a place in any intellectual history of Darwin’s work.”

The recognition of Euler’s contributions to the field of population dynamics usually overlooks his staunch creationist background and his apologetics motivation. Euler’s three primary works contain his principal contributions in demography: his famous calculus textbook *Introduction to the Analysis of the Infinite* (1748), his 1767 memoir entitled *A General Investigation into the Mortality and Multiplication of the Human Species* and his collaboration with the Berlineser pastor Johann Süssmilch on a work called *The Divine Order*, still considered a milestone by specialists of demographic studies (see Smith-Keyfitz, 2013 or Wachter, 2009).

One of Euler’s key results, the Euler-Lotka demographic equation, allows incorporating age-structure in population studies and has been used by the major theoreticians of Darwinism, especially since Fisher and his “actuarial approach” (Fisher 1929). Today, Euler’s equation remains a central tool in the mathematical study of Darwinian evolutionary theory (e.g., Roff 2010).

Based on the historical considerations sketched above, one will discuss the importance of Morris’s and Euler’s results for

a contemporary creationist approach and more especially their relevance to help answer basic questions like

- Can evolution have universal laws from which predictions can be made despite the unusual complexity of the biological world? See e.g. Murray (2000).
- Is the geometric growth principle a good candidate as a fundamental law of nature playing a role in population biology comparable to Newton's law of inertia in physics?
- Is H.M. Morris's basic observation a valid objection to Darwinism? Does evolutionary theory fail to comply to the "uniformitarianism principle" in population biology?
- Is Morris right to say that "the burden of proof is altogether on evolutionists if they wish to promote some other model"? Is e.g. Kapitza's "phenomenological theory of world population growth", see Kapitza (1996), a credible alternative model?
- Can the more sophisticated mathematical tools, initially developed by L. Euler in the eighteenth century, be reclaimed by today's creationists?

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Editor: TCW

Research Update: Pine Bark Beetle Associated Tree Destruction in North America

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Destructive microbes and insects provide a challenge for creation biologists since their lifestyle and anatomy often appear to be designed to promote natural evil. Few insects have gained such widespread notoriety in the last few years more than the pine bark beetles since they have caused widespread deforestation and property damage which includes millions of acres. (1) Recently a grant was awarded to a team of creationists to study the pine bark beetle problem in North America. Since few creation groups have received grant funding from agencies sympathetic to a creationist approach to biological problems or the study of the natural history of organisms we offer our experiences and preliminary data here to encourage more creationists to develop scientific proposals.

Research Team Design. The Pine Bark beetle problem involves an insect with a complicated lifestyle which includes symbiosis and parasitism with plants, microbes and other insects. In light

of that we assembled a team of researchers with expertise in the area of biochemistry, genomics, entomology, microbiology, and botany. The team has held laboratory meetings in person and via skype. The group has also worked together in North American forests to obtain preliminary field data and experience firsthand the lifecycle of the pine bark beetles.

Goal and Methods. The overall goal of this project is to develop a research program which promotes scientific research and problem solving within the creation model paradigm. For instance, creationists believe that all creatures were initially created to promote beneficence within creation. Thus we can postulate that bark beetles once played an important role in the environment. To that end our preliminary literature research shows that a few studies refer to a role for bark beetles as keystone species in the forest since they increase species diversity and richness (2). Why then do bark beetles cause so much destruction in forests in the America's and Europe? To answer this question we are attempting to establish field study stations in both control (healthy) and diseased (bark beetle infested) forests of North America with the hopes of detecting changes in bark beetle lifestyle in those beetles causing widespread destruction. To that end we are developing beetle collection techniques involving both control and disease forests by extracting beetles directly from the bark or from traps containing pheromone attractants. We are also developing DNA collection techniques to analyze phylogenetic relationships among beetles as a way to also investigate how the destructive lifestyle of bark beetles arose over time.

Preliminary Data. Our initial field studies confirm that bark beetles may increase species diversity and richness by the fact that we have observed a life supporting underbark environment in trees which show bark beetle activity. For instance, we find that the underbark environment is one of the most species rich environments (preliminary observation) in the high desert ecosystems of California. In the moderately healthy pine tree forests of California we have noted small pockets of bark beetle associate tree damage involving both killing of small numbers of trees or the killing of the lower branches of some pines. This observation is also consistent with the creation of new habitat for both plant and animal species since more of the forest is exposed to sunlight. In addition we note that stressed trees attacked by fungal, insect and plant invaders such as dwarf mistletoe, are often then attacked secondarily by bark beetles. We postulate that bark beetles hasten the death of diseased and stressed trees preventing the further spread of some tree pathogens which require live trees.

In addition we have determined that beetles and DNA can be collected from trees in the forests and we are analyzing existing character sets of bark beetles in published reports to establish phylogenetic relationships.

Future Work. We also hypothesize that the lifestyle of the beetle which promotes species diversity with minimal tree destruction may be controlled primarily by pheromones and other attractant and inhibitory signals given off by species in the forests. We hypothesize that we will observe a different pattern of pheromone signal and control in diseased forests by comparison. We postulate that this work may lead to a method to control bark beetle populations in forests susceptible to widespread destruction.

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The Value of Engineering Analysis in Identifying Organisms as the Primary Cause of Adaptability

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Studying organisms by design analysis (DA) is reverse engineering. This methodical disassembly and examination of the composition and relationships of its numerous parts is powerful in identifying specific causes of function, production, and operation.

I will consider how DA may best answer the question: what is the cause of how organisms adapt to environmental niches? This begins by considering the function of adaptation in a deathless, pre-Fall world.

In Genesis 1, God commanded organisms to “fill the earth.” Earth began with a range of dynamic, non-lethal challenges, for example day-night cycles, seasons, and adjustments after creatures “filled” each other’s niches. Thus, organisms needed heritable, self-adjusting capacities from the beginning. I propose that the purpose of adaptation is to fill the earth, and not, necessarily, survival.

To show how DA could work in a creation model, we can ask this question: What if populations of organisms could be seen from a design-based perspective as traveling through diverse environments just as human-designed vehicles do? Intrinsic design controls detection of challenging exposures and specifies internally driven self-adjustments as solutions. Similarly, innate self-adjusting capacity could be true for organisms. We know that individuals (or populations over multiple generations) can actively detect environmental conditions and can express a spectrum of phenotypes from a relatively stable genotype. Enriching the phenotypic panoply is the capacity of some systems to “learn” from environmental interactions similar to IBM’s “Watson” computing system; meaning, organisms are designed with a nature devised to be nurtured. I therefore suggest that organisms undergo successful fit of traits-to-exposures, rather than of environmental sieves selecting from myriads of traits (Kirschner, 2005).

DA shows that with either human-designed or God-designed adaptable entities, function resides in systems utilizing three core components of essential, well-matched elements driving self-adjusting function: (1) input “sensors” to gather data on external conditions; (2) reference programs that define potentials of performance for specific external/internal conditions, define what conditions are “stimuli,” and utilize “logic segments” to compare input data to references; (3) output “actuators” to execute actions maintaining performance.

For instance, for genetic variability, Borger (2009) details multiple “variation inducing genetic elements” (VIGEs) while Wood (2002) described the “AGEing process.” It is plausible that these are designed systems to confer directed results including the ability for some organisms to change their own DNA with non-random output (Shapiro 2011; Lightner 2008, 2013) and in real time (Shapiro 2011).

Design analysis helps provide details for the genetics-based examples of “mediated design” adaptability proposed by Wood

(2003) wherein he hypothesized that God created “hidden” adaptations in the original. Thus, if the purpose for self-adjusting systems is to fill challenging new niches and not survival, then these papers give reason to believe that organism’s innate systems (a) already possess information to solve environmental challenges (including some that have not even appeared on earth yet,) and (b) control mechanisms to create new genetic information (Carter 2011). For instance, organisms are successfully filling the highly radioactive niche around the Chernobyl accident (Thomas 2014).

DA shows how the Fall does not necessitate any design change to adaptive capacity. Suppose that the true cause of organisms filling niches is solely their innate self-adjusting capability. Suppose further that this capability started so robust that it always possessed the potential to solve perilous, new challenges (like cooperative relationships perverted into predator-prey) in the death-filled, post-Fall world—DA’s objectivity exposes that death is just death by stripping it of imputed, mystical powers to “select” anything. Death isn’t transformed into something good, it remains an enemy and avoiding it is a problem to be solved.

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Hormonal Regulation of Human Endogenous Retroviruses

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ERVs are DNA sequences that are similar to the genomes of retroviruses. Most biologists assume that all ERVs were inserted into the genomes of cellular organisms as a consequence of retroviral infections of germ cells. The fact that humans and primate species share similar ERVs at corresponding locations is claimed to be a result of random insertions in common ancestors.

A logical creation model is that God created ERVs, at least some of them, as integral parts of cellular genomes at the beginning of life. A few ERV elements have been demonstrated to have functions that benefit the host organism. To date, most reports of such beneficial functions concern only sporadic portions of ERV elements, which many claim to be results of “cooption” or “exaptation”. A key question needs to be addressed by creationists: Why did God use these repetitive elements with their unique structural genes and regulatory sequences to perform these functions?

Based on known ERV involvement in human and animal reproduction, we hypothesized that common regulatory elements in ERVs were designed for coordinated control of interspersed ERV genes and neighboring host genes in response to host signals such as sex hormones. Coordinated regulation would argue for a general strategy in using ERV elements to organize and access genomic information. If ERVs are essential for genomic structure and function, positional homology of ERV elements between unrelated species would be out of necessity rather than as remnants of evolutionary accidents in common ancestors.

Here we report our laboratory investigations of HERV expression and its relationship with female sex hormones *in vivo* and *in vitro*. The *in vivo* studies quantified HERV transcripts in white blood cells of reproductive-age women. Using quantitative PCR, we demonstrated that expression of syncytin-1 and HERV-K genes in white blood cells is negatively correlated with plasma levels of progesterone and estradiol during the menstrual cycle, with correlation coefficients varying between -0.53 and -0.94 for progesterone, and between -0.77 and -0.83 for estradiol. The *in vitro* studies used cultures of peripheral blood mononuclear (PBMN) cells grown in the absence or presence of progesterone and estradiol in the medium. We found that expression of HERV genes is stimulated by a combination of estradiol and progesterone at physiological concentrations. The average increase in expression was between 2 to 5 fold. In contrast, expression of HERV elements in male PBMN cells is slightly repressed by female sex hormones.

The significance of HERV activities in PBMN cells (mostly lymphocytes) is unclear. The Env protein of some HERV elements is known to be immunosuppressive, and has been speculated to play a role in maternal tolerance of the semiallogeneic fetus. Further analyses of HERV expression in cell cultures and their response to hormonal regulation are under way.

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Editor: TCW

Ontogeny as a Diversification Analog

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Ontogeny is here proposed to offer powerful analogies to post-Flood diversification.

1. The Flood's population bottleneck, the increase in post-Flood fossil species diversity, high intra-baraminic species diversity, and derived species in the days of Job and Abraham collectively suggest that the species diversity in many baramins increased two or three orders of magnitude in only a couple centuries after the Flood. The analog of cellular differentiation rapidly increases cell type diversity (by greater than two orders of magnitude in humans).

2. The high diversity of revealed (not human-created) breeds, cultivars, and varieties, the abrupt appearance of post-Flood sub-baraminic taxa, and the short post-Flood geological timescale

collectively suggest that new sub-baraminic taxa were generated in single generations. The modern analog of cellular differentiation increases cell-type diversity via intermediate-lacking transitions.

3. The correlation of paleontological first appearance of sub-baraminic taxa with both the order of branching in cladistic analyses and the order of successively smaller nested groups in clustering analyses suggest diversification produced morphologies that converged on the nested hierarchal pattern of similarity of modern species. The modern analog of cellular differentiation generates a branching cell lineage that morphologically converges on the nested hierarchy of cell types in the adult organism.

4. The progressively later appearance of progressively lower intra-baraminic taxa in post-Flood sediments (i.e. disparity before diversity), the short durations of sub-baraminic fossil taxa immediately following the Flood, and the large morphological jumps in the lower Tertiary equid stratomorphic series collectively suggest that the pattern of diversification appeared more analogous to the growth of a clonal colony of trees than the growth of a single tree. The modern analog of cellular differentiation utilizes short-duration ontogeny-specific cell lines to develop cell type disparity before cell type diversity.

5. The stasis of species in recorded human history, the stasis of post-Flood species through multiple lithologies, the persistence of modern species despite hybrid zones and inter-specific hybrids, and true-breeding wild populations that can generate a diversity of breeds, cultivars, and varieties collectively suggest that diversification terminates with internally-constrained species morphologies. The modern analog of cellular differentiation generates permanent adult cell morphologies.

6. The abundance of life at the original creation, the uniqueness of the population bottleneck at the Flood, and the fact that diversification is at best very limited in the present collectively suggest that the post-Flood diversification was a unique event designed to restore lost biodiversity. The modern analog of vegetative reproduction initiates a deterministic process of cellular differentiation to regenerate an entire plant from a portion of the parent organism.

7. The correspondence of specialized designs in fossil species with inferred climate suggests diversification generated morphologies that fit the environment. The modern analog of polyphenism generates alternate environment-fitting adult morphologies depending upon which ontogeny is stimulated by environmental triggers.

The strong analogy between ontogeny and diversification is helpful in the creation model. First, the analogy increases the plausibility of diversification. Not observed in the present, rapid post-Flood diversification is only a theoretical inference in the creation model. That God employed such a process is more plausible when a strong analogy exists among other biological processes designed by the same Creator. Second, the analogy helps map out the potential explanatory power of diversification. If diversification is analogous to ontogeny, diversification is very likely to explain a wide range of observed neontological and paleontological data. Third, the analogy may aid in discovering the mechanism of diversification. If the processes of ontogeny and diversification are similar, the location and nature of their respective mechanisms may also be similar. Fourth, developmental biology may be a fruitful search area for theories

to explain other known biological phenomena. For example, ontogeny may provide insight into how a host of biological designs appeared after Fall (e.g. carnivory, defense mechanisms, camouflage). Fifth, known processes of ontogeny may provide further insight into biology. For example, epigenetic processes of ontogeny may provide insight into the origin of less deterministic biological phenomena such as communities, or (as suggested by an anonymous reviewer), adult stem cells with repair functions may suggest organisms exist in the present designed to restore compromised ecosystems or biodiversity.

Editor: TH

Spectra of Perfection: A Case for Biological Imperfection before the Fall

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Although the pre-Fall world was ‘very good’ (Gen. 1:31), it was not ‘perfect’ (i.e. it did not exhibit every meaning of ‘perfect’). For example, if God created a diversity of form, then for many characters some forms would be judged less perfect than other forms – and thus not ‘perfect’. Claims of pre-Fall perfection also increase the contrast of the pre- and post-Fall worlds, thus exacerbating the theodicy challenge of reconciling God’s character in these worlds. Furthermore, if even part of God’s rationale for permitting sin into the world was to increase His glory by highlighting otherwise invisible attributes, then He might use non-sin-related ‘imperfection’ in a similar manner. This paper proposes that God purposely introduced non-sin-related biological ‘imperfection’ into the pre-Fall world to illustrate His infinite nature.

According to Romans 1:18-20, God illustrated His invisible attributes in the visible creation – including the infinite nature of those attributes. This paper proposes that to illustrate the infinite nature of His attributes God created spectra of perfection – each spectrum designed to illustrate the infinite nature of one divine attribute. First, God specially designed the creation to properly illustrate the attribute, and second, God specially designed humans to recognize the illustration. For each attribute, God chose a physical trait to illustrate the attribute and designed different components of His creation to exist with different degrees (or perfections) of that trait. Some things lack the trait; other things contain a miniscule measure of the trait; other things possess small or intermediate measures; and others still exhibit the trait in large measure. Simultaneously, God endowed humans with the innate 1) tendency to recognize the different perfections of the trait in the creation; 2) compulsion to order the different perfections into a spectrum of perfection of that trait; and 3) a tendency to extrapolate the spectrum beyond what is observed towards an infinite manifestation of that trait. Although spectra of perfection do not lead to full comprehension of the infinite, they lift the human heart towards the perfection of God’s attributes.

The host of less-than-perfect forms in the pre-Fall world was not the result of any rebellion against God, thus they are neither moral evil, nor the result of moral evil. It is further proposed that they are not examples of biological evil because (a) all of them were local organism/environment optima; (b) none of them resulted in death or suffering of animals or humans; and (c) any harm with

regards to one trait (e.g. herbivory’s harm to plants), is balanced by God’s other purposes (e.g. animal food, oxygen, shelter). As creationists develop a biological imperfection model, some of that imperfection should be considered a part of the pre-Fall world and not the result of the Fall. Furthermore, since many of these less-than-perfect forms are marshaled as evidence of evolutionary theory, creationists can develop superior explanations of such imperfection. A few examples of the spectrum of perfection principle might include, but would not have to be limited to the following:

- to illustrate His infinite beauty, God not only created awesomely beautiful organisms, but even in the ‘very good’ creation He endowed different organisms with different degrees of what we might judge to be ugliness;
- to illustrate His infinite unity, God not only created species so mutually beneficial to one another as to appear to be one organism (e.g. lichens), but even in the ‘very good’ creation He created a spectrum of perfection of mutualism – including relationships we might judge to be deleterious to one of the organisms (e.g. to a plants eaten by an animal);
- to illustrate His infinite vitality, God not only endowed humans with biological life, soul life, spiritual life, and even abundant life, He created things without life and organisms with a spectrum of perfection of life;
- to illustrate His infinite personhood, God not only endowed humans with a large measure of personhood, He measured out various amounts of will, emotion, humor, and self-awareness to various animals;
- to illustrate His infinite uniqueness, God not only divided organisms by discontinuities, He separated organisms by a spectrum of different similarities and discontinuities.

Editor: TH

Species as Brushstrokes: The Revelatory Species Concept in Creationism

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Previously defined species concepts can be broadly classified into three categories: antirealist, typological and evolutionary. The correspondence of folk and scientific classifications, the distinctiveness of kinds implied in Genesis One, the hierarchal classifications of Scripture, and the stability of kinds implied in Adam’s naming of the animals collectively suggest that creationists should reject antirealist species concepts. The partial success of developmental biology in establishing a physical basis of development, combined with the likely absence of the ancient Greek logos, suggest that creationists should also reject typological species concepts. Evolutionary species concepts should also be rejected. Though the most popular species concept and definition in biology – and creationism – Ernst Mayr introduced the biological species concept and definition in 1942 as part of a systematic effort to reinterpret the biological world in the light of neodarwinism. Creationists should replace existing species concepts and definitions with those of a distinctly creationist nature. Romans 1:18-20 suggests that God created the universe with physical illustrations of His invisible attributes and God created humans with the ability to recognize those illustrations.

As a distinctly creationist species concept, it is here proposed that species were created as basic characters or brushstrokes of many of these illustrations (here named the revelatory species concept). To properly recognize these illustrations, it is also here proposed that humans were created to recognize the species taxon by being endowed with the ability to characterize entities with the simplest possible approximations (what is here called the abstractification process). According to the revelatory species concept, organisms were created in taxa (recognizable groups of similar, stable morphologies distinct from all other taxa). The least inclusive taxa (the finest brushstrokes) are species. As a consequence of the abstractification process, humans not only innately recognize species, but also innately classify organisms into nested hierarchies that, in fact, reflect creation's true hierarchal design. The revelatory species concept is not only distinctly creationist, but it also has considerable explanatory power. First, since it is a realist species concept, the revelatory species concept is superior to antirealist concepts at explaining the evidence that species are real (mentioned above). Second, the revelatory species concept suggests that God endowed organisms with reproductive and ontogenetic processes so that species could function as revelatory brushstrokes. The extraordinary design of these processes would explain the inspiration for the typological species concepts of Plato, Neo-Platonists, and even the otherwise strongly materialistic Aristotle. Third, the morphological species definition is consistent with the revelatory species concept. The revelatory species concept would explain why the morphological species definition is the definition of choice for the vast majority of taxonomists of modern science – including by those who believe in species concepts contrary to the morphological species definition. The revelatory species concept would also explain: 1) the biological observations of Cenozoic species stasis, even through changing lithology and climate; 2) uniform species morphology across wide geographic ranges, through geographical heterogeneity, across genetically distinct populations, and into reproductively isolated areas; and 3) stability of morphology in spite of natural hybrid zones; and 4) the commonness and ease of inter-specific hybridization.

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Further Investigations of the Baraminology of Weevils (Curculionidae): Is Platypodinae a Holobaramin?

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Even though insect species vastly outnumber any other animal group on the planet, analyses of insect baramins are few and therefore warrant further investigation. The first insect baraminology study was a statistical evaluation of the largest known animal family, Curculionidae (Wood 2005), an economically important group of more than 40,000 herbivorous beetle species, which includes many crop pests as well as bark beetles in the subfamilies Scolytinae and Platypodinae. Until recently, both bark beetle subfamilies were considered separate families Scolytidae and Platypodidae, but phylogenetic studies of morphological (Kuschel et al. 2000) and molecular (Farrell et al. 2001) characters place them within the Curculionidae. Further, the Platypodinae appear to be nested

within the Scolytinae, making “Scolytinae” paraphyletic. Wood's (2005) baraminological study of curculionids evaluated a single set of mostly larval characters and failed to distinguish any discontinuity between curculionids and other members of the superfamily Curculionoidea. The lack of observed discontinuity was interpreted as evidence that the baramin to which the weevils belong is larger than family Curculionidae. Because one statistical analysis of a single set of characters is insufficient to reliably establish a baramin, I evaluated two additional morphological character sets using standard statistical baraminology techniques (for a review, see Wood 2008). The first, published by Jordal et al. (2011) included 128 mostly adult characters scored for 112 curculionoid weevils. After filtering for 0.95 character relevance, 89 characters were used to calculate baraminic distances. The baraminic distance correlation (BDC) results revealed two very well-defined groups marked by significant, positive BDC within each group. All correlations between the groups showed significant, negative BDC. The groups correspond to weevil subfamily Platypodinae (the ambrosia beetles) and all other taxa. The 3D MDS results (stress = 0.22) support the inference of the same two separate clusters of taxa. The second character set came from Kuschel et al. (2000) and consisted of 80 characters scored for 35 taxa. After filtering for 0.95 character relevance, 62 characters were used to calculate baraminic distances. BDC results also revealed two well-defined groups, one of which consisted of the ten Platypodinae taxa and *Schedlarius* (subfamily Coptonotinae). The other group contained all other taxa. Even though correlations between the two groups were statistically significant and negative, there was one important exception, the taxa *Schedlarius* and *Mecopelmus* (subfamily Coptonotinae), which shared significant, positive BDC. *Mecopelmus* also shared significant, positive BDC with six scolytine bark beetle taxa and *Coptonotus* (subfamily Coptonotinae). The 3D MDS confirmed the presence of two groups (stress = 0.068), but *Schedlarius* and *Mecopelmus* are separated from the Platypodinae group (average baraminic distance 0.39, compared to 0.077 average baraminic distance between platypodine taxa), suggesting that they are not actually part of that group. In contrast to Wood's (2005) study, these two analyses suggest there is at least one discontinuity within the curculionids, between the Platypodinae and all other weevil taxa. Additional studies would be desirable to more firmly establish the presence of this discontinuity. Based on this present study, we may hypothesize that Platypodinae is a holobaramin, which suggests that the entire curculionid family consists of multiple created kinds. In addition, these results call for a closer scrutiny of “Scolytinae,” within which Platypodinae is supposed to be nested.

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Psychological Considerations on the Recognition of the Human Holobaramin

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The 2010 publication of the first statistical baraminology study of hominins sparked intense controversy due to the inclusion in the human baramin of *Homo habilis*, *Homo rudolfensis*, and *Australopithecus sediba* (Wood 2010). Aside from the scientific merits of human baraminology, there appears to be a deeply intuitive rejection of these taxa being included in the human family tree. It is possible that the intensity of these reactions could be related to the psychological concepts of dehumanization and infra-humanization. Dehumanization is the tendency to deny full humanness to an individual or group (Haslam 2006). The closely related notion of infra-humanization is the tendency to view members of an out-group as less human than in-group members (Leyens et al. 2007). Historically, these concepts are associated with racism and genocide, but recent research has focused on subtler and more common forms of dehumanization. Leyens et al. (2001) found that infra-humanization cannot be reduced to simple in-group favoritism, since both positive and negative human emotions tend to be denied to out-group members. In an especially relevant study, Capozza et al. (2009) artificially generated eighteen images of faces using computer morphing software to blend a human and chimpanzee face. The images represented a continuum from full chimpanzee to full human with precisely controlled increments of ape-ness. Study subjects were shown the faces and asked to classify them as ape or human. Faces less than 42.1% human were readily classified as ape, and faces more than 78.9% human were readily classified as human. The most intermediate faces (around 50% human) elicited the most differences in classification between different study subjects, as expected. More importantly, study subjects were significantly more likely to classify ambiguous faces as human when they were informed that the human faces came from their own ethnic group. Thus, a subject's judgment of "human" was influenced by their perception of personal similarity or kinship: different ethnic groups were more likely to be classified as "apes."

This research has direct relevance to the question of human baraminology, where fossil forms are categorized as ape or human, and intermediate categories are disqualified. I propose that innate tendencies to "protect the in-group" by excluding individuals of different or ambiguous appearance from the group "humanity" are complicating factors in the quest to identify the human holobaramin. These innate tendencies are amplified by the perceived theological importance of human creation, thereby leading to especially intense resistance to including fossil forms like *Australopithecus sediba* in the human holobaramin. Even within the field of human evolution studies, the phenomenon of dehumanization has been noted in both the exclusion of "early" hominids from the "family of Man" and in post-World War II tendencies to overcompensate for the dehumanization of the Holocaust by including very different taxa in the ancestry of humanity (Proctor 2003). Because of dehumanization research, creationist disagreements over the categorization of fragmentary hominid fossils should not be interpreted as evidence against the creationist assertion of separate creation of humans and apes.

Instead, these disagreements are normal consequences of human bias. Consequently, creationists ought to be especially careful in evaluating human baraminology, lest unconscious biases become more important than the data of paleontology, genetics, and scripture in determining what is or is not human.

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