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Executive Editor

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Contributed Abstracts

C1. Estimating Active Information in Adaptive Mutagenesis

J. Bartlett
Blyth Institute

One of the key tasks of creation biology is to understand the logic of creation itself—to comprehend the design of the Creator. Functional adaptation and biological imperfection are two aspects of the created order of life for which any theory of creation must address (Wood and Murray, 2003). One key issue in addressing these topics is differentiating between genetic changes which are functional adaptations and those which are a result of the curse. Bartlett (2009) introduced a second-order mutational classification scheme to aid in such differentiation, noting that fitness measurements alone are insufficient to determine if a mutational mechanism is consistent or inconsistent with the overall design of the organism. While many criteria in the classification scheme are measurable, mutational mechanism was not given a quantitative measurement. Here we will use the Active Information metric introduced by Dembski and Marks (2009) to try to measure the mutational mechanism criteria quantitatively.

Active Information is a metric originally developed for computer search procedures that measures the amount of information that a search procedure contributes to finding an appropriate target. A random search with uniform probability has no Active Information, a search which consistently leads away from its target has negative Active Information, and a search which consistently leads towards its target has positive Active Information. Active Information is measured by comparing the probabilities of a search hitting its target with the probability of a random search hitting the same targets. The difference in probability is expressed in bits, computed by $\log_2(1/p)$.

Historically, Active Information has only been applied to computer-based evolutionary algorithms. However, it can also be applied to biological systems. Applying Active Information to the Somatic Hypermutation (SMH) process for refining binding sites during an immune response makes an excellent test case for using this concept biologically. Because SMH primarily works by restricting the physical range of base pairs that it mutates (Papavasiliou & Schatz 2002), it simplifies the Active

Information calculations. One can simply subtract $\log_2(\text{SMH mutation space})$ from $\log_2(\text{whole genome size})$ and estimate that the SMH process contributes approximately 22 bits of Active Information to the search. Additional factors can complicate this estimate, such as taking into account the number of mutations required for hitting the target.

This is a surprise to some, because the SMH process uses a sort of “shotgun” approach to generating novelty. But the point of active information is that, even though it is a shotgun approach, the changes are limited only to one gene, rather than spread out across the whole genome. The active information is the amount of restriction that the process applies which contributes to the likelihood of finding a target. Searches that are more highly focused than SMH would have more active information, and those that are less focused would have less.

The same idea can be applied to other mutational processes, such as the SOS response system in bacteria. However, because in many of these systems the mutations are spaced throughout the genome, it is more difficult to calculate the Active Information involved.

Mutational processes that have zero or negative Active Information are probably not part of an organism’s design, while processes having large positive amounts of Active Information probably are. In addition, comparing the amounts of Active Information in different types of mutational processes may help lead to a general theory of functional adaptation in creation biology.

Editor: RWS

- Bartlett, J.L. 2009. Towards a creationary classification of mutations. *Answers Research Journal* 2:169-174.
- Dembski, W.A. and R.J. Marks. 2009. Conservation of information in search: measuring the cost of success. *IEEE Transactions on Systems, Man and Cybernetics A, Systems & Humans* 5(5):1051-1061.
- Papavasiliou, F.N. and D.G. Schatz. 2002. Somatic hypermutation of immunoglobulin genes: merging mechanisms for genetic diversity. *Cell* 109(2, Supplement 1) 1:S35-S44.
- Wood, T. C. and M. J. Murray. 2003. *Understanding the Pattern of Life: Origins and Organization of the Species*. Broadman and Holman, Nashville.

C2. Developing an Approach to Non-Physical Cognitive Causation in a Creation Perspective

J. Bartlett
Blyth Institute

The creation biology view of the human is not restricted to the categories present in physicalist worldviews, yet little has been done to expand on the what creation biology means for anthropology. The causative categories in the physicalist paradigm are limited to chance and law (Murphy 1999). Creation biology, on the other hand, is not so limited (Herrmann 2006).

Other causative categories appear to be present within the world, at the very least within humans, including perception, creative problem-solving, and choice. Deuteronomy 30:19, Joshua 24:15, and Genesis 4:6-7 all record places where God calls his people to choose, and Exodus 35:30-36:2 indicates that at least certain types of creativity go beyond the physical. This treatment will focus on developing a rational framework for investigating creative problem-solving without reducing it to physicalist causal categories. These causative categories should not be viewed as being necessarily restricted to only humans, though the methods described here would prevent their investigation on animals.

Alan Turing, one of the founders of modern computational theory, suggested an approach for formally dealing with non-physically-computable operations. Turing introduced the concept of an oracle. An oracle is a theoretical construct which computes the result of a computation that is known to be uncomputable by algorithmic means, and therefore unimplementable physically (Turing 1965).

For instance, the halting problem in computer science states that every program with fixed inputs will either halt or it won't. However, there is no computable way to determine whether or not a program will halt. So, a halting problem oracle is a theoretical operator which would tell whether or not a given program can halt. Such an operator cannot be implemented physically, but its powers are roughly describable and can be used to reason about computations that cannot be performed. Turing, for instance, used oracles to show that there are problems that are harder than the halting problem. Robertson (1999) showed that similar problems, despite being unsolvable physically, are solvable by humans, though he failed to develop this concept further.

Therefore, a constructive approach to human cognition for creation biology would be to use the oracle concept to model human problem-solving. It would evaluate a variety of oracle concepts, and then measure their applicability to humans, including how universal the ability to solve them is, and what contributions training and intuition play in them. These could then be used to generate a broader model of cognitive causation in creation biology than is available in physicalist systems.

Each oracle concept would be measured by coming up with problem sets related to the oracle, and measuring how long it takes people to solve the problem with training and without training. In addition, to judge intuitional responses, a person would be given only two seconds to make a judgment on a problem after they have comprehended it.

Oracles which have high intuitional responses for everyone

should be considered basic parts of human cognition. Those that have high intuitional responses for some and not for others should be further examined to see what the differences are between the two groups. Oracles which have low intuitional responses, but high responses non-intuitionally should be further investigated to see what the thinking process was to generate the solution in order to detect what underlying oracles may potentially exist there.

Some potential oracle concepts might include the original Turing halting-problem oracle, a “framing” oracle which restricts attention to relevant information, or a “tool” oracle which selects appropriate mental tools for a task.

Editor: RWS

- Herrmann, R. A. 2006. The rationality of hypothesized immaterial mental processes. *Creation Research Society Quarterly* 43(2):127-129.
- Murphy, N. 1999. Physicalism without reductionism: towards a scientifically, philosophically, and theologically sound portrait of human nature. *Zygon* 34(4):551-570.
- Robertson, D. S. 1999. Algorithmic information theory, free will, and the Turing test. *Complexity* 4(3):25-34.
- Turing, A. M. 1965. Systems of logic based on ordinals. *Proceedings of the London Mathematical Society* S2-45(1):161-228.

C3. Grasses and Shrubs or Grain and Thorn-bushes? The Vegetation of Genesis 2.5

I. Demme
Independent Scholar

There is a tendency among creation accounts to describe the primeval world by the absence of things known in the present. Genesis 2.5-6 introduces the account of what came from the original creation (2.4 - 4.26) by describing a world that differs from ours in the absence of two categories of vegetation, but interpretations of what these categories are vary widely, as do interpretations of the relationship of these verses to the rest of Genesis 2-4. This paper argues that the absence of “*siach* of the field” (שִׁיחַ הַשָּׂדֶה) and “*eseb* of the field” (עֵשֶׂב הַשָּׂדֶה) in Genesis 2.5 contrasts a prelapsarian relationship of humanity to the vegetable world with subsequent changes.

“*Eseb*” (עֵשֶׂב), generally translated as “plant,” is used in the Hebrew Bible to denote grasses and low-lying plants that are eaten by animals or humans. It occurs in construct with “field” (שָׂדֶה) seven times, and I contend that the compound “plants of the field” (עֵשֶׂב הַשָּׂדֶה) refers specifically to cultivated crops. “*Siach*” (שִׁיחַ) is a more difficult term, which occurs only here, in Genesis 21.15, Job 30.4, and 30.7. In 21.15, it is the plant in the Negev under which Hagar places an adolescent Ishmael. Job, describing the living conditions of outcasts from society, says in 30.4 that “they gather orache among the *siach* and feed on the roots of brooms” and later in verse 7 that “they brayed like donkeys among the *sichim*, and came together under the nettles.” Although *siach* appears related to modern Arabic and Syriac names for *Artemisia judaica*, the Akkadian cognates are much more general (“sprout” and “shoot”), and based on the usage in Job I suggest that it may describe thorny plants.

Many commentators see a direct allusion in 2.5 to the curse pronounced on the ground in 3.18, where it is said that the ground will produce “thorns and thistles” and Adam will eat “plants of the field” (עֵשֶׂב הַשָּׂדֶה) through toil, described further in 3.23 when

humankind is expelled from Eden “to till the ground” (אֶת־הָאָדָמָה לְעֹבֵד וְלְצִבְרָה). If the use of these phrases is not coincidental, this suggests that the absence of crops and plows in 2.5 is a good state of affairs that lasts until the curse and expulsion. If so, the “*siach*” probably refers to something like the “thorns and thistles.”

On the other hand, several commentators see a parallel problem-cause-solution structure in Genesis 2.5-7. There are no wild or cultivated plants (problem), because there is no rain or cultivator (cause), so God sends rain and creates a cultivator (solution). This presumes that the absence of *siach* and *eseb* is a negative situation that requires a remedy, yet as noted above, it seems that 3.18 connects them with the negative results of the curse on the ground and banishment from Eden. Secondly, the semantic and literary structure of the surrounding text seems to suggest a rhetorical function for 2.7 that is unrelated to 2.5-6. The account from 2.4 to 3.24 follows a chiasmic structure and the first segment (2.4-17) is built around five *wayyiqtol* verbs describing Yahweh’s primary actions. Adam’s creation belongs rhetorically and structurally to this primary story, while 2.5-6, which uses a very different (almost poetic) sentence structure and verbal forms, serves as an independent unit that introduces the primary account.

Consequently, I argue that the absence of field-thorns and field-crops functions as a positive and anticipatory description of the prelapsarian world, much like the the absences of death, strife, and carnivory that introduce other ancient accounts of creation. “*Eseb* of the field” describes those plant species which have originated as a result of human agriculture—our struggle to wrest food from the ground, while “*siach* of the field” describes one or more categories of inedible plant that stubbornly resist our agricultural efforts with previously unnecessary defenses.

Editor: RWS

C4. Use of Halobacteria as a Model Research Organism in the Undergraduate Research Laboratory

J.W. Francis

The Master’s College

One of the major challenges to creation biology is to understand mechanisms of population control allowing for sustained long term growth, as might be expected in the pre-Fall world. Population control in macroorganisms is difficult to imagine without organismal death. Since the Bible implies that only animals and humans did not die before the Fall, populations of microbes could be controlled in the same ways they are today. In particular, the existence of antibiotics might be explained as a pre-Fall mechanism of microbe population control.

Because a majority of biologists with a creation perspective are in undergraduate Christian colleges, implementing research to address such questions while involving undergraduates is a second major challenge because of time and funding constraints. Yet, providing undergraduate research experiences is invaluable in that it promotes student understanding of biological concepts, from both creation and conventional perspectives, and also helps prepare students for graduate school and professional programs.

Therefore, model organisms which are affordable yet allow students to obtain data rapidly and easily are preferable in the undergraduate research setting.

After trial and error, I have found that research projects based on invertebrate and microbial model organisms are highly adaptable to the undergraduate research laboratory, primarily, because these organisms are easily maintained in this setting. Recently, I established a halobacterium research project in an undergraduate research lab. *Halobacterium* sp. NRC-1 is an extremophile—an organism that thrives in extreme conditions. NRC-1 are salt-loving archaeobacteria found in solar salterns and other high salt environments. They grow readily on salt agar plates (25% salt). Cultures of halobacteria are rarely contaminated because the eubacteria and fungal organisms which normally inhabit the human body and surrounding environment cannot grow in the high salt growing media; thus, the time and funds spent on preventing contamination is minimal. Furthermore, halobacteria are not known to be pathogenic in animal systems.

In our laboratory, we have identified a novel bacteriostatic antibiotic of *Halobacterium* sp. NRC-1. Surprisingly, this antibiotic was isolated from commercial paper disks used to test the antibiotic sensitivity of eubacteria. We have discovered that the inhibitor alone inhibits halobacterium growth and is commonly used in the pharmaceutical industry; it is non-toxic to mammals and eubacteria. This antiobiotic inhibits the growth of a variety of species of halobacteria in a dose dependent manner on both solid and liquid media but has no effect on eubacteria under similar conditions. Because halophiles contaminate several commercial processes, the inhibitor has potential commercial application (patent pending).

In preliminary studies, we have noted that the growth of halobacteria on salt-agar plates follows a remarkable cyclical pattern of death and growth. This pattern of growth suggests that a halophage (virus) or halocin (toxin) is modulating the growth of these bacteria on solid surfaces. Consequently, these data suggest that viruses and toxins, which we often perceive as agents of natural evil because they cause illness, may be acting as agents of population control allowing for sustained long term growth on substrates with limiting growth factors. Thus, as a model organism in an undergraduate research setting, halobacteria offer promise as we investigate the origin of natural evil and its relation to population dynamics.

Editor: GP

C5. Baraminic Status of the Verbenaceae (Verbena Family)

R.W. Sanders

Bryan College

Recent studies of natural evil of chemical defenses and prickles in *Lantana* (Verbenaceae s. str., Lamiales) have been hampered because the baramin to which *Lantana* belongs remains unidentified. Thus, the extent to which these defenses represent original design versus historical modifications has not yet been determined. The present study was undertaken to correct this hiatus.

A holistic comparative data set was developed from the literature

for the Verbenaceae (25 of the 34 genera, all tribes represented) and genera representing other Lamiales and the Boraginaceae in the Boraginales/Solanales as near and far outgroups, respectively (Cronquist 1981; Sanders 2001; Atkins 2004; and numerous smaller articles and published figures). The data matrix (44 taxa × 84 characters, all with relevance >0.95) was analyzed using the BDISTMDS program (Wood 2008) to obtain baraminological distances, distance correlations, correlation bootstrap values, and multidimensional scaling coordinates for all pairs of taxa. The baraminic distance correlations resulted in three distinct clusters, the Verbenaceae, the remaining Lamiales (“Lamiales-1”), and the Boraginaceae. The Boraginaceae were partially negatively correlated (none with bootstrap values >90%) with the Verbenaceae and neither positively nor negatively correlated with the Lamiales-1. The latter consisted of two subclusters, the Lamiaceae and the remaining families (“Lamiales-1A”), which were united by positive correlations (none with bootstrap values >90%) among seven pairs of genera. The Lamiaceae were sparsely negatively correlated (none with bootstrap values >90%) with the Verbenaceae, and the Lamiales-1A (except the Phymaceae and Avicenniaceae) were consistently negatively correlated (2% with bootstrap values >90%) with the Verbenaceae. All genera of the Verbenaceae were positively correlated (80% with bootstrap values >90%) with each other except for *Petrea* and *Xolocotzia* with *Glandularia*, *Junellia*, *Pitraea*, *Priva*, and *Verbena*, which represent the ends of a variation spectrum in the family. 3D stress of the MDS analysis was 0.288 with minimum stress of 0.049 in dimension 11. In the 3D projection of the MDS results, the Verbenaceae were separated in a planar array on one side. On the opposite side of the origin, the outgroups formed a bent planar or almost triangular array with the Boraginaceae well separated at one extremity and the Lamiales-1A at the other. The Verbenaceae were separated from the outgroups by a distance of 0.298. The nearest outgroup, Phymaceae, was not correlated with any Verbenaceae or Lamiaceae and was positively correlated with only six members of Lamiales-1A. Adjacent members of the Verbenaceae were separated by a maximum distance of 0.238 (*Lantana-Xolocotzia*).

These results support the holobaraminic status of the Verbenaceae *s. str.* and previous baraminological studies frequently placing the holobaramin boundary at the conventional taxonomic rank of family. It is of interest that these results detected the discontinuity between the Verbenaceae *s. str.* and genera previously placed in the Verbenaceae *s. l.* (represented by *Clerodendrum*, *Holmskioldia*, *Petitia* in this study), a distinction which has been recognized widely only since 1992 on the basis of several morphological and molecular cladistic analyses. BDISTMDS also clearly separates the Verbenaceae from the Lamiaceae (once thought to be derived from or share a most recent common ancestor with Verbenaceae), as well as the segregate families Avicenniaceae and Phymaceae, sometimes included in the Verbenaceae. Thus, there is now evidence to posit that ancestral Verbenaceae were created on Day 3. However, these data do not resolve whether any modern genus or even tribe was part of the Verbenaceae archaebaramin. Thus, it cannot yet be determined if *Lantana* existed prior to Noah’s Flood or originated as part of the post-Flood (Cenozoic) diversification of the Verbenaceae.

- Atkins, S. 2004. Verbenaceae. In: Kubitzki, K. and J.W. Kadereit, eds. *The Families and Genera of Vascular Plants, Volume VII: Lamiales (excluding the Acanthaceae including Avicenniaceae)*. Springer Verlag, Berlin, pp. 449-468.
- Cronquist, A. 1981. *An Integrated System of Classification of Flowering Plants*. Columbia University Press, New York, NY.
- Sanders, R.W. 2001. The genera of Verbenaceae in the Southeastern United States. *Harvard Papers in Botany* 5: 303-358.
- Wood, T.C. 2008. BDISTMDS software, v. 1.0. Center for Origins Research, Bryan College. Distributed by the author.

C6. Revisiting the “Clear Synapomorphy” Criterion

G. Wilson

New St. Andrews College

Ascertaining holobaramins is worthy of study if for no other reason than to think God’s thoughts after Him. With the advent of statistical baraminology, the synapomorphy criterion, one of Wise’s (1992) 15 practical membership criteria, has received little attention. This paper argues that more careful analysis of synapomorphies is needed in ascertaining holobaramins before conclusions are drawn.

Wise states, “It is suggested that a holobaramin should be definable in terms of characteristics which are shared among *all members of the group* (by common ancestry) but which also *distinguish that group* from others (emphasis mine).” In a creationist context synapomorphy can be defined as any uniquely designed trait (internal or external) that is indicative of and shared by all members of the same holobaramin. The trait can be expressed or unexpressed. It is not just a variation of a trait due to different alleles (straight vs. kinky hair) nor is it a trait shared by more than one holobaramin, e.g. vertebrae.

In subdividing apobaramins using statistical methods, such as baraminic distance correlation, lack of synapomorphies often is not adequately considered as evidence of discontinuity. For example, based primarily on results of statistical baraminology, Wood (2006) has provisionally suggested that family appears to be an approximation for the “created kind,” although he makes clear that “bias and character selection prevents firm conclusions” and concedes that it “may have biased the search for baramins.” Likewise Wood (2008) lists 49 taxa that have been classified as holobaramins; most are families but some are larger though not greater than suborder. However the following apomorphies are not shared by all members of the holobaramins recognized by Wood (2008): 1) plastral hinges in box turtles (*Terrapene*) but not in all Testudinoidea (holobaramin = multiple families of Cryptodires including Testudinoidea); 2) flippers in Carettochelyidae but not in Trionychidae (holobaramin = Trionychidoidea); 3) synapomorphic differences in vegetative and reproductive morphology between many grass genera (holobaramin = Poaceae). Thus, application of the synapomorphy criterion suggests instead that the holobaramin boundary would be at a lower taxonomic level.

Clearly, holobaramin delimitation is robust when boundaries deduced from statistical methods coincide with monobaramins established through the additive criterion of hybridization. In the absence of clear hybridization data that corroborate statistical data,

holobaraminic status should be clearly acknowledged as being a tentative hypothesis unless it unequivocally passes the “Clear Synapomorphies” criterion. When clear synapomorphies are not phenotypically shared by all members of a putative holobaramin, more research is needed before drawing conclusions from the statistical methods. Since created kinds were discernable to Adam by gestalt, I maintain that the presence of clearly visible synapomorphies would have been essential for Adam to delineate the differences between kinds. If we take this criterion seriously, future research in baraminology should ask this question: When testing for holobaraminic status, if an apomorphy is not shared by all its members, is there at least genetic evidence to suggest the apomorphy has the potential to develop in those presumed extant members lacking it? If it is phenotypically and genotypically absent, holobaraminic status should be tentatively denied. A greater understanding and identification of gene modules or gene regulatory networks responsible for a particular apomorphy is necessary to arrive at meaningful conclusions. In the absence of genomic analytic tools, phenotypic plasticity, ecomorphological, and karyological studies could also help detect unexpressed synapomorphies in a particular group.

As much as we want to provide creationist organizations and the lay public with good answers, it is of paramount importance that our conclusions are not premature, that we have considered all relevant data, and that we have interpreted it circumspectly using sound biblical and scientific principles. If we are too inclusive with our holobaramins (family and above) without considering synapomorphic evidence, it could lead the lay public to make unwarranted generalizations among untested taxa. This would be unfortunate especially when families among many invertebrates exhibit much more disparity than do vertebrates.

Editor: RWS

Wise, K.P. 1992. Practical baraminology. *Creation Ex Nihilo Technical Journal* 6:122-137.

Wood, T. C. 2006. The current status of baraminology. *Creation Research Society Quarterly* 43(3) 149-158.

Wood, T. C. 2008. Animal and plant baramins. *CORE Issues in Creation* 3: 1-258.

C7. Dominion: Human *raison d'être*, Foundation of Bioethics, Foundation of Environmentalism

K.P. Wise

Truett-McConnell College

The divine plan for humans—even before their creation - was that they were to be rulers over all created life and the earth (Gen. 1:26). By authority's extension and Psa. 8:6, human authority is over all things created—ultimately even angels. Assigned by God independent of either human ability or response, this responsibility lies upon all humans, even after the Fall. And, given the active verbs used in Gen. 1:28, it is command. This work is what humans were created for—what they have always done, what they will always do, and the only thing that will fulfill them.

The creation passage also provides principles for that rule: 1) The royal imagery in Gen. 1:26-28 and the shepherd king theme throughout Scripture indicates that humans are to *serve*—serve subjects and God. 2) The priestly imagery in Gen. 1-2 and the

priest theme throughout Scripture indicates humans are to bring subjects into their worship of God by assisting their subjects in reaching their intended roles of bringing glory to God. 3) The image/likeness status of humans as per Gen. 1:26-28 and the use of the Hebrew and Greek words throughout Scripture indicate that humans are God's representatives to, and stewards of, those things created. Rather than taking away our responsibility of rulership, the Fall in Genesis 3 *increases* our responsibility, for since the Fall, subjects must be redeemed towards the shalom of the original creation.

To fulfill their function as rulers, humans are to continue God's creation by revealing the potential God placed within their subjects. God is glorified as that realized potential is acknowledged to be from God and as the realized potential displays the attributes of God. Humans bring glory to God as they maximize in their subjects a) aesthetics, by such things as arranging, ordering, trimming, shaping, cleaning, adorning, grooming, coloring, and flavoring; b) productivity, fruitfulness, and resourcefulness, by such things as training, pruning, cultivating, providing light, water, and nutrients; c) health, by such things as comforting, healing, curing, counseling, and tending; d) unity and diversity, by such things as placing, mixing, introducing, and breeding; and e) freedom, maturity, and autonomy, by such things as educating, encouraging, and nourishing.

The dominion role of humans not only defines the function and purpose of humanity, it lays a foundation for ethics. We are responsible for, and must give account for how well we cared for everything under our authority - from our souls, bodies, and spirits, to our children, students, and employees, to our pets, all animals, and the entire planet Earth. We must serve (meet the needs of) our subjects and maximize the aesthetics, productivity, health, unity, diversity, and freedom of our subjects - all to the glory of God. This provides care and protection for the entire creation without invoking 'tree-hugging', 'animal rights', or earth as organism (gaia) justifications. The optimum conditions of the pre-Fall world can also provide the additional ethical constraint of a creation normative—namely that the creation is not to be modified to a form never intended by the Creator.

The divine image possessed by humans permits humans to use animals for human benefit (*e.g.* food, medical research, labor), but the dominion mandate condemns the ill-treatment of those animals. The dominion mandate provides both justification and constraints on cosmetic enhancement, gene therapy, and drug use and development. It condemns such things as torture, killing for sport, and pollution, and it provides justification for both human and veterinary medicine, pain management, breeding, gene transplantation, plant and animal cloning, animal population management, adult stem cell research, resource management, biodiversity and environmental preservation.

Editor: RWS

C8. Species and Genus Counts for Terrestrial Mammal Families Reveals Evidence for and against Widespread Intrabaraminic Diversification

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Limited evolution has been a feature of creationist or otherwise Christian reactions to evolution since the earliest twentieth century (Wood 2008). Agreement on the mechanism by which species originate has not been forthcoming, however. Some argue for acceptance of neodarwinian mechanisms (Marsh 1947), while others appeal to Mendelian genetics (Tinkle 1967; Sarfati 1999) or genomic or chromosomal rearrangements (Wood 2003). Lacking in all of these discussions is a general recognition of the magnitude of the problem, which can be provided by a complete list of all created kinds. Such a list would provide an account of the number of species within each created kind, which in turn can tell us the maximum number of species that have been produced since creation. Since such a list is not forthcoming in the near future (due to the technical challenges of identifying created kinds), we can proceed only by estimating the membership of created kinds. Surveys of baramins (Wood 2006) and basic types (Scherer 1993) suggest that the subfamily or family might approximate the created kind among mammals. To estimate the magnitude of speciation among terrestrial mammals, I surveyed the number of species and/or genera in mammal families (exclusive of Hominidae) in three comprehensive treatments of mammal classification: Nowak (1999), McKenna and Bell (1997), and Wilson and Reeder (2005). Nowak lists only Recent taxa and organizes the terrestrial members into 127 families. These families have a median three genera and eight species. Only 37 families (29%) have 20 species or more. The five most speciose families are Pteropodidae (169), Sciuridae (272), Soricidae (322), Vespertilionidae (342), and Muridae (1336). Wilson and Reeder also list only Recent taxa and recognize 136 families, with a median of three genera and eight species. Only 43 families (31.6%) have 20 species or more. The five most speciose families are Sciuridae (278 spp.), Soricidae (376 spp.), Vespertilionidae (407 spp.), Cricetidae (681 spp.), and Muridae (730 spp.). McKenna and Bell list extant and fossil mammals and recognize 347 terrestrial families with a median of five genera (species are not listed). Only 108 families have Recent members, of which 22 have no fossil members. Nearly 69% of the terrestrial mammal families are therefore known only as fossils. The five families with the most genera are Soricidae (79), Sciuridae (86), Mustelidae (120), Bovidae (191), and Muridae (471). In all three sources, the number of genera are distributed according to a power law. Since the approximation of created kind as family is based on very few examples, these inferences must be considered extremely preliminary. Nevertheless, the large number of families with very few species or genera implies that speciation has not been widespread. Likewise, the very few families with many species or genera implies that speciation can be extravagant in some instances. Any theories of speciation will have to account for both trends: lack of speciation in most families, spectacular speciation in a few.

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- Marsh, F.L. 1947. *Evolution, Creation, and Science*, 2nd ed. Review and Herald Publishing Association, Washington, D.C.
- McKenna, M.C. and S.K. Bell. *Classification of Mammals above the Species Level*. Columbia University Press, New York.
- Nowak, R.M. 1999. *Walker's Mammals of the World*, 6th ed. Johns Hopkins University Press, Baltimore.
- Sarfati, J. 1999. *Refuting Evolution*. Master Books, Green Forest, Arkansas.
- Scherer, S. 1993. Basic types of life. In: Scherer, S. (ed). *Typen des Lebens*. Pascal-Verlag, Berlin.
- Tinkle, W.J. 1967. *Heredity: A Study in Science and the Bible*. St. Thomas Press, Houston, TX.
- Wilson, D.E. and D.M. Reeder, eds. 2005. *Mammal Species of the World*. 3rd ed. Johns Hopkins University Press, Baltimore.
- Wood, T.C. 2003. Perspectives on AGEing, a young-earth creation diversification model. In: Ivey, R.L., ed. *Proceedings of the Fifth International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, pp. 479-489.
- Wood, T.C. 2006. The current status of baraminology. *Creation Research Society Quarterly* 43(3):149-158.
- Wood, T.C. 2008. Species variability and creationism. *Origins (GRI)* 62:6-25.

C9. A Re-evaluation of the Baraminic Status of *Australopithecus sediba* Using Cranial and Postcranial Characters

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In a recent study, Wood (2010) hypothesized that *Australopithecus sediba* was a member of the human holobaramin (i.e., descended from Adam and Eve). His initial study was based solely on cranial characters, but baraminology studies should be based on holistic characters. Since the original description of *A. sediba* by Berger et al. (2010) also listed 78 postcranial characteristics (Table S2), I re-evaluated the baraminic status of *A. sediba* using postcranial characters, the original 69 cranial characters and a combined cranial/postcranial character set. The postcranial characters listed by Berger et al. (2010) included descriptions of only six taxa: *A. afarensis*, *A. africanus*, *A. sediba*, *Homo habilis*, *Homo* sp. indeterminate, and *Homo erectus*. Consequently, I used a character relevance cutoff of 0.75 for all analyses to ensure the maximum number of characters for baraminic distance correlation (BDC) and multidimensional scaling (MDS). Fifty-two postcranial characters were used to calculate baraminic distances. BDC results revealed only two taxon pairs with positive BDC: *Homo* sp./*H. erectus* and *A. afarensis*/*A. africanus*. Negative BDC was observed between three taxon pairs: *Homo* sp./*A. africanus*, *Homo* sp./*A. afarensis*, and *H. erectus*/*A. afarensis*. All correlations had bootstrap values <90%, and *A. sediba* was not positively or negatively correlated with any other taxa. MDS reveals an irregular tetrahedron with *Homo* sp./*H. erectus*, *A. afarensis*/*A. africanus*, *A. sediba*, and *H. habilis* at the vertices (3D stress 0.093). Adding the 69 cranial characters to the postcranial characters necessitated removing the *Homo* sp. indeterminate taxon that was not included in the cranial character set, and 140 of the 147 postcranial and cranial characters were used to calculate baraminic distances. Only *H. erectus* and *A. afarensis* showed significant, negative BDC (bootstrap value <90%). No taxa were positively correlated. The MDS results revealed a crude arc, with taxa arranged in the following order: *A. afarensis*, *A. africanus*, *A. sediba*, *H. habilis*, and *H. erectus* (3D stress 0.094). *A. sediba* is nearly equidistant between *A. africanus* and *H. habilis* (0.382 and 0.366 baraminic

distances respectively). Using just the cranial characters for these five taxa (no characters eliminated), the BDC results showed negative correlation between *A. sediba* and *A. afarensis* and between *H. erectus* and *A. afarensis* (bootstrap values <90%). No positive BDC was observed. The MDS results (3D stress 0.083) were consistent with Wood's (2010) original analysis. *A. sediba* clustered with both *Homo* species (mean baraminic distance 0.386), and *A. africanus* and *A. afarensis* were separated from the *Homo/A. sediba* cluster (mean baraminic distance 0.555). These results indicate that the postcranial characteristics of *A. sediba* do not favor a classification as *Homo* or *Australopithecus*. Since the full cranial character set with 12 taxa reveals positive BDC between *A. sediba* and *Homo* taxa, the failure to observe significant BDC in the present study with just five taxa is likely the result of too few taxa. Considering the MDS results of the cranial characters alone, *A. sediba* still clusters with *Homo* species. Given the uninformative BDC results, the present analyses do not falsify Wood's (2010) original hypothesis that *A. sediba* is a member of the human holobaramin. Future studies should focus on expanding the number of taxa to include additional *Homo*, *Australopithecus*, and extant ape taxa.

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- Berger, L.R., D. J. de Ruiter, S. E. Churchill, P. Schmid, K. J. Carlson, P. H. G. M. Dirks, and J. M. Kibii. 2010. *Australopithecus sediba*: a new species of Homo-like australopith from South Africa. *Science* 328:195–204.
- Wood, T.C. 2010. Baraminological analysis places *Homo habilis*, *Homo rudolfensis*, and *Australopithecus sediba* in the human holobaramin. *Answers Research Journal* 3:71-90.