



A REVIEW OF THE LAST DECADE OF CREATION BIOLOGY RESEARCH ON NATURAL HISTORY, 2003-2012

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ABSTRACT

Creationists and evolutionists radically differ in their proposed natural history, with creationists looking to sudden origins at creation and the Fall and to catastrophes at the Flood and Babel to explain features of the living world. Over the past decade creationists have made important advances in understanding this unique, biological natural history. The emerging model proposes the existence of created kinds, phylogenetically – and possibly morphologically – discontinuous from other created kinds. Within these created kinds, species developed very rapidly after the Flood, possibly by a mechanism of directed mutations involving transposable elements. The development of natural evil, while partially explicable by degeneration, is now understood to be a designed part of God’s curse on creation. Though a full understanding of design has not been achieved, creationists have expanded our understanding of God’s original plan for the organisms that occupy His creation.

INTRODUCTION

Young earth creationists have approached the discipline of biology in a variety of ways. Some follow the tradition of Paley in attempting to identify evidence of the Creator in the intricacies of living things. This tradition can be seen in the work of creationists interested in intelligent design (e.g., Manning, 2003; Brand, 2008; Armitage, 2011). Others focus specifically on identifying evidence in favor of uniquely creationist claims, such as the recent genetic history of humanity (e.g., Carter *et al.*, 2008). Others have followed the tradition of offering criticism of evolution (e.g., Armitage and Howe, 2007a). Genetic calculations and simulations have been especially popular in recent years (e.g., ReMine, 2006; Sanford *et al.*, 2008). Still others have attempted to provide uniquely creationist theories to account for the origin of species, the dispersal of land animals after the Flood, and other biological phenomena related to natural history from a creationist perspective.

Here, the term “creation biology” will be limited to research work related to developing a model of biological natural history that is explicitly – and in some cases inextricably – young-earth creationist. Though the term “creation biology” could legitimately describe any of the areas mentioned above, the restricted usage herein is strictly intended to provide a convenient shorthand for the more cumbersome “creationist biological research on natural history,” and

should not be understood to imply that other forms of creationist biology research are unimportant or insignificant. Modern creation biology research (in the sense of natural history) follows in the tradition of such creationists as Harold Clark (1940), Frank Marsh (1947), and Will Tinkle (1967), and conforms to the important goal of the International Conference on Creationism: “developing and systematizing the creation model of origins.” Even creationists who question whether natural history is the proper domain of scientific investigation recognize that science can contribute to our tentative understanding of past events (Reed, 2003).

Creation biology research can be placed in five broad categories: identification of created kinds (biosystematics), understanding the development of phenotypic and genetic diversity within created kinds (speciation), the growth and dispersal of populations after the Flood (biogeography), the origin of pathology and natural evil, and the explanation of broad patterns of biological similarity, which are rooted in God’s original design. As mentioned above, these categories are not intended to exhaustively catalogue all creationists’ research on biological subjects. Indeed, other important biology research outside of these five themes has been conducted by creationists over the past decade (e.g., Armitage and Mullisen, 2003; Carter *et al.*, 2008; Woodmorappe, 2003a). These five areas, however, provide a convenient, overarching structure to think about the natural history of organisms in God’s creation.

CREATED KINDS

Identification of created kinds (or baramins to use Marsh’s term) has by far experienced the most development of any area of creation biology during the last decade. Marsh’s approach of tabulating interspecific hybridization has been applied in Camelidae (Wolfrom, 2003), Ursidae (Tyler, 2006; Hennigan, 2010), Canidae (Pendragon, 2011), Felidae (Crompton and Winkler, 2006; Pendragon and Winkler, 2011), Bovidae (Lightner, 2006a, 2007), Cervidae (Lightner, 2006b), Passeriformes (Lightner, 2010a), Psittaciformes (Landgren *et al.*, 2011), Galliformes (McConnachie and Brophy, 2008), Accipitridae (Wood, 2005a, p. 150), various snake genera and families (Hennigan, 2005; Fankhauser and Cumming, 2008), Testudines (Brophy *et al.*, 2006), Ambystomatidae (Brophy and Kramer, 2007), Solanaceae (Wise, 2005), Sarraceniaceae and Nepenthaceae (Sanders and Wood, 2007), and Aizoaceae (Kutzelnigg, 2009). The results indicate that interspecific and intergeneric hybridization is surprisingly common, implying that the baramin for certain groups must lie at a level above the genus.

Using molecular sequence data has been comparatively sparse in the identification of created kinds. Diehl (2003), Wood (2005a), and Lightner (2012) have used it specifically to supplement hybridization summaries or other indirect methods of estimating created kinds. The rationale is that species within the genetic range of two species known to hybridize are probably in the same baramin. This allows additional species to be included in a created kind even when evidence of hybridization is absent.

Thanks to the internet-accessible BDISTMDS software (Wood, 2008a), statistical baraminology, though controversial, grew rapidly over the past decade. Using methods summarized by Wood and Murray (2003) and the “refined baramin concept” of Wood *et al.* (2003), Cavanaugh *et al.*’s (2003) analysis of equid fossils reportedly confirmed that all equids from *Hyracotherium* to *Equus* were members of a single baramin. Wood’s (2005a) review of the animals and plants of

the Galápagos and a later compendium of animal and plant baramins (Wood, 2008b) expanded the application of these methods to 63 additional character sets. At the time, that brought the total to 74 character sets analyzed using statistical baraminology methods and published as papers or monographs. Since 2008, only one significant statistical baraminology study has appeared, that of the hominids (Wood, 2010a). Additional applications have been described in abstracts but as yet have not been published as papers (Cavanaugh, 2003, 2006, 2011; Cavanaugh and Sternberg, 2005; Garner, 2003a; Mace and Wood, 2005; McConnachie and Brophy, 2008; McLain, 2011, 2012; Sanders, 2010a, 2012; Wood, 2006a, 2007a, 2009a, 2010b, 2012a; Wood *et al.*, 2011a; Wood *et al.* 2011b).

Though statistical baraminology appears popular, the methods and results have been criticized (Bolnick, 2006; Williams, 2004). Molén (2009, 2010) rejected Cavanaugh *et al.*'s (2003) study of equids, instead arguing that the three equid subfamilies constituted three created kinds. Several critics (Menton *et al.*, 2010) rejected Wood's (2010a) controversial inclusion of *Homo habilis*, *H. rudolfensis*, and *Australopithecus sediba* in the human baramin. A common theme in these criticisms is the issue of character selection, which can easily alter the results of a statistical analysis and has been acknowledged as a drawback to statistical baraminology (Wood, 2006b, 2010a, 2011a). A more challenging critique came from Senter (2010), who used statistical baraminology techniques to argue that birds evolved from dinosaurs. Wood (2011b) disputed Senter's results, arguing that Senter's own data supports separating birds from dinosaurs. In a more detailed response, Senter (2011) argued that most dinosaurs should be included in a single created kind.

These criticisms highlight technical and theoretical drawbacks of statistical baraminology. Nevertheless, the methods can still be useful within certain acknowledged limits. Techniques such as multidimensional scaling (Wood, 2005b) and bootstrapping (Wood, 2008a) have been introduced to address some of the shortcomings. When these techniques are used in conjunction with multiple character sets covering the same set of species and with other baramin identification methods (such as hybridization), statistical baraminology can be of help to identifying baramins, although it is clear that these statistical methods cannot be relied upon solely to identify created kinds.

Finally, there have been recent attempts to delineate large numbers of created kinds at once. One such method uses Wise's (2009) post-Flood continuity criterion, which states that the lowest taxonomic level with a continuous fossil record back to the Flood/post-Flood boundary can be considered a baramin. Using this method, Wise estimated that there are 97-203 terrestrial mammal baramins, depending on a number of factors including where the Flood/post-Flood boundary is placed. Since then, Sanders (2011) applied the criterion to angiosperms and concluded that there might be as few as 50 baramins.

More recently, Lightner (2012) and Hennigan (2013) published descriptions of terrestrial mammal and amphibian baramins, respectively, based on a suite of criteria but primarily relying on identification of mammal cognita (Lightner *et al.*, 2011). Since cognita studies were not specifically devised to identify baramins but instead to explore how human cognition relates to classification (Sanders and Wise, 2003), it is unclear whether these studies will withstand rigorous analysis by other creationists. Whatever its methodological merits or deficiencies, these

studies will certainly serve as a reference point for future research on mammalian baramins.

Despite the occasional controversy, the results of hybridization studies, statistical baraminology, and utilization of the post-Flood continuity criterion tend to agree in the broadest terms.

Creationists, as they have for centuries (Garner, 2009; Wood, 2008c), still affirm that species were not uniquely created. Instead, created kinds contain multiple species as well as genera. In a review of created kinds, Wood (2006b) reaffirmed Price's (1938) original speculation that the created kind might be approximated by the family in modern taxonomic nomenclature.

SPECIATION AND DIVERSIFICATION

If created kinds contain so many species, where did those species come from? How did they become so well adapted to their biotic and abiotic environments? Some creationists have insisted that all biological changes are degenerative (Kunkle, 2003), but others have looked to more creative mechanisms to explain speciation. Wood and Murray (2003, pp. 170-173) argued biblically and scientifically for rapid, post-Flood speciation, based on an earlier argument by Wood (2002a). Wood (2008b) later explored the relationship between population growth and speciation rate, concluding that the speciation rate reached its peak shortly after the Flood and declined exponentially to the present day.

All of these arguments were based on the assumption that most baramins are speciose, which was only recently tested by Wood (2011c). By surveying the number of species in terrestrial mammal families (assuming each family descended from an ancestral pair aboard the Ark), Wood found that the vast majority had relatively few species. Nevertheless, most families had extinct species known only as fossils, and the largest mammal families still had hundreds of species. Thus, while rapid speciation is not applicable to every (or even most) baramins, it remains an important question for those extremely speciose baramins.

One common creationist explanation of speciation, which goes by a variety of names, attributes speciation to created allelic diversity. Originally inspired by the work of creationist Byron Nelson (1927) and called the "theory of heterozygous creation" by Tinkle (1967), this model posits that God created organisms with allelic diversity which was sorted out into different lineages that became modern species. Though this seemingly easily resolves the origin of intrabaraminic diversity, creationists over the last ten years have begun to propose far more creative ideas about the origin of species, thanks in part to a greater appreciation of comparative genomics.

In a series of papers, Lightner (2006c, 2008a, 2009a, 2010b) documented significant karyotypic changes within several well-established baramins. The canid baramin was particularly variable, with the red fox (*Vulpes vulpes*) having just 34 chromosomes and the domestic dog (*Canis lupus familiaris*) having 78. The Arctic fox (*Alopex lagopus*) has a polymorphic karyotype, with some individuals having 48 chromosomes and others having 50. These examples and others like them imply that diversification and speciation is not merely the phenotypic outworking of a relatively stable genotype. Instead, chromosomes are also as variable as organismal morphology.

To account for these types of changes, creationists have proposed models of genome

modification called “genomic modularity” (Wood, 2003a), “variation-inducing genetic elements” (Borger, 2009a, 2009b), or “transposon amplification” (Shan, 2009). According to these models, rapid emergence of phenotypic and chromosomal variation within a baramin is attributed to the action of transposable elements (Surtees, 2007). Alternatively, Lightner (2011a) argued that PRDM9, a protein involved in aligning chromosomes during meiosis, might be a mechanism to generate chromosomal variability, given the highly variable nature of the PRDM9’s DNA-binding domain. There is little doubt that transposable elements have induced genomic variation in some baramins; however, the sufficiency of any chromosomal-modification models to account for *all* post-Flood biological change is questionable.

One problem is a lack of correlation between benign phenotypic change and chromosomal rearrangement. For example, camels and llamas have been successfully hybridized and are thus members of the same baramin (Wolfrom, 2003). Despite their significant phenotypic differences, their chromosome count is the same: $2n = 74$ (Bunch *et al.*, 1985). Conversely, in the example of the polymorphic Arctic fox chromosomes cited by Lightner (2009a), there was no documented phenotypic change despite a significant chromosomal alteration.

Even more important is the evidence of single nucleotide and other mutations presumably unrelated to transposition. According to Lightner’s research (2008b, 2009a, 2009b, 2009c), there is a great deal more allelic diversity than can be explained by either the theory of heterozygous creation or by any of the chromosomal rearrangement models. Purdom and Anderson (2008) argued for adaptive mutations in the bacterium *Escherichia coli*. Furthermore, Wood’s (2012b) recent analysis of human mitochondrial DNA supports the inference of a highly accelerated mutation rate around the time of the Flood. An additional mechanism of increased genetic change around the time of the Flood is therefore necessary and might be linked more directly to phenotypic change.

To account for all types of genetic changes observed within baramins, Lightner (2009b) argued that “genomes ... were designed to be able to undergo adaptive genetic changes,” which echoes earlier claims by Williams (2005, 2008a, 2008b), Borger (2008), Ashcraft (2004), and Wood (2003b). According to Lightner (2011b), at least some genetic changes are directed and adaptive due in part to pleiotropic responses to environmental cues. In contrast, Wood’s (2003b) “mediated design” model attributes complex phenotypes to an original creation of inactive genetic material that was later activated by some random mutation. Williams (2008c) argued for a similar model to explain diversification of grasses, emphasizing that diversification is a “designed, built-in potential for variation.” In any of these cases, rapid, adaptive changes within baramins could be explained. We presently lack a clear understanding of how these pre-designed changes could happen and why they happened so specifically around the time of the Flood.

Along a related but completely different line of thought, Francis (2009) suggested that symbiosis could be involved in the process of speciation. Perhaps the most obvious example is the case of lichens, symbioses between algae and fungi, but Francis pointed out that symbioses between microbes and macroorganisms can lead to both reproductive isolation and morphological changes. Though symbiosis would be unlikely to explain genomic changes associated with speciation, it is likely that symbiosis could be an important factor in initial stages of species

formation.

BIOGEOGRAPHY

Compared to identifying baramins and studying speciation, creationists have studied biogeography much less. Early work was done by Howe (1979), Howe and Lammerts (1980), and Woodmorappe (1990). Wood and Murray (2003, chap. 12) reviewed the subject, especially highlighting the post-Flood debris rafting model of Wise and Croxton (2003). Statham (2010) also endorsed rafting as a possible mechanism for post-Flood dispersal. According to the model, floating mats of debris from the pre-Flood forests served as platforms for dispersal immediately after the Flood. Though speculative, the model can explain a great deal of data (Wise and Croxton, 2003).

There has been limited work testing the predictions of the rafting model. Wood's (2005a) study of the Galápagos Islands utilized the debris raft theory and also implied that the dispersal rate of animals in the past must have been higher than it is today since there is little evidence of recent inter-island dispersal within the archipelago. Sanders (2009) also examined endemic plant species on oceanic islands as a test case for creationist models of speciation, and he also endorsed the debris rafting model as an aid to island dispersal. Whitmore and Wise's (2008) study of the fossils of the Eocene Green River Formation of Wyoming suggested that numerous terrestrial animals had already dispersed to North America within just a few years of the Flood, thus necessitating a rapid means of transoceanic dispersal, which rafting could provide.

In addition to the rafting model, Froede (2003) emphasized the potential role of storms, especially African dust storms, in dispersal of plants, insects, and birds. He cited numerous studies of African dust blown to the Americas, and he emphasized the chaotic weather immediately after the Flood as an important factor that would magnify the ability of storms to disperse wind-born organisms.

Challenges to creationist biogeography remain. Wise and Croxton's (2003) rafting model is not universally accepted. In a recent paper, Johnson (2012) argued for vicariant dispersal based on continental division in the lifetime of Peleg. Weaknesses of this model include the exegetical (Fouts, 1998) and geophysical problems (Snelling, 1995) associated with rapid continental movement in the lifetime of Peleg, which render the premise unlikely. Likewise, since it is a model of continental dispersal, it still requires some mechanism of dispersal to oceanic islands such as Galápagos, which were never part of any continent.

Other questions remain for all potential creationist biogeography models. In particular, how does the debris rafting model relate to the geography and climate of the world immediately following the Flood? How do the continental interchanges inferred from the fossil record relate to post-Flood dispersal? How do we explain the unique species of Australia? These questions likely have answers, but there will need to be a more concentrated creationist research effort to answer them.

NATURAL EVIL

Creationists have devoted far greater research efforts to pathology and natural evil than to biogeography. Creationists traditionally assert that the original creation was free from animal and human death, following Stambaugh's (1992; 2008) arguments that biblical "life" and "death" include only humans and animals. Smith (2007) similarly argued that the language of Romans 8:19-23 indicated that the corruption of creation was "cosmic and universal." This has been a frequent point of contention between young-earth and progressive creationists (Sarfati, 2005; Henry, 2006).

Recently, some creationists have argued for a more complex understanding of death before the Fall. Berndt (2003) argued that allowing for fish death before the Fall was permissible, and Kennard (2008) emphasized a continuum from alive to dead, noting that Hebrew terms for *life* can apply even to the recently living. Aside from these minor points, no young-earth creationist has publicly endorsed terrestrial animal death prior to the Fall.

If there was no animal or human death in the pre-Fall world, it follows that organisms or features that cause or benefit from animal death must have existed in a much different form in that pre-Fall creation. Such features might include predators (Gurney, 2004), parasites, microbial pathogens (Gillen, 2008; Kim, 2006), and toxins and poisons. Wilson (2007) argued that defense features of potential prey organisms would also be a likely consequence of the Fall. Immune systems are clearly designed, used today for defense against pathogens but also to interact with beneficial microbes (Francis, 2003; Gillen and Sherwin, 2005).

As in the case of speciation, getting a sense of the larger scope of the problem is essential to understand the nature and origin of natural evil. In that light, Francis (2003) noted that "less than one percent of all microbes and viruses" are pathogenic. Loucks (2009) cited a similar figure for pathogenic fungi. The ubiquity of microbes and viruses suggests that they serve an important, designed function (Francis, 2003; Francis and Purdom, 2009). Francis (2003) argued that microbes primarily serve to facilitate the interaction of macroorganisms with the inert physical environment, thus forming an organosubstrate or biomatrix (Francis, 2008). Indeed, Gillen (2007) documented many beneficial and essential functions of microbes in creation, and Hennigan's (2009a) discussion of arbuscular mycorrhizal fungi directly supports the organosubstrate model.

Creationists frequently appeal to degeneration to explain natural evil (e.g., Schragin, 2004). According to this model, pathology appears when a previously benign feature becomes harmful due to an intrinsic change or to movement into a new environment. For example, Wood (2002b) argued that anthrax was an otherwise harmless soil bacterium unless inhaled. Mace *et al.* (2003) argued that a highly interconnected ecosystem (such as a bio-matrix) can become pathological when even minor problems arise, and Hennigan (2009b) emphasized increasingly dysfunctional relationships at the heart of modern ecological problems. Purdom (2009) argued that there were no examples of "intentional pathogenic mechanisms" in microbes, but instead that most pathogens were closely related to free-living nonpathogens. Gillen and Sherwin (2006) argued that the origin of the plague pathogen *Yersinia pestis* occurred by "genomic decay and corruption" in the form of chromosomal DNA deletion. Sherwin (2009) also noted that

nonpathogenic amoebas related to the pathogenic *Entamoeba histolytica* reside in the human gut, thus indicating that the pathogenic form must be a minor variation from the nonpathogenic.

Recently, creationists have begun to question the sufficiency of the degeneration model. Armitage's (2007) microscopy work supports the inference of exquisite design in a variety of parasites. Gillen and Sherwin (2006) noted that *Y. pestis* became a pathogen only upon acquisition of "corrupted" plasmid genes. In a survey of bacterial genomes, Wood (2007b) found that the genomes of pathogenic bacteria were not significantly smaller than congeneric free-living bacteria. If degeneration manifests as a loss of something (like genes), pathogenic bacteria gain as much as they lose when compared to their nonpathogenic relatives. Likewise, Purdom (2009) emphasized the importance of horizontal gene transfer in bacterial pathogenesis.

In the area of macroorganisms, Wilson (2004) argued that predatory features of animals are too obviously designed to be explained as degenerations. As noted above, Wilson (2007) later argued that defense structures that protect against predation also bear the marks of intentional design rather than degeneration. Oliver (2009) made a similar argument specifically about snakes and the designs they possess for detecting, dispatching, and consuming prey. In an essay on natural evil, Wood (2007c) argued that degeneration was a poor explanation for the complexities of anthrax toxins or schistosome life cycles.

Thus, creationists have begun turning to design to explain aspects of natural evil. How this design is accomplished is still open to discussion. Wood (2007c) suggested direct creation as a mechanism, although he did not elaborate. Wilson (2004) proposed that organisms were created with a contingent genome, with a set of genes designed for life in the pre-Fall world and a set designed for the fallen world. Armitage and Howe (2007b) suggested a similar model for the origin of pathogenic fungi, and Oliver (2009) suggested a similar explanation for the origin of venomous snakes. At the Fall, God merely activated genes designed for the fallen world.

In a twist on the origin of viruses, Liu and Soper (2009) proposed that some viruses might have been designed as features of macroorganismal genomes, which have now escaped into the environment. They cited retroviruses in support of their hypothesis, but recent reports of filovirus and bornavirus genes in the genomes of some mammals would support their hypothesis for other viruses as well (Horie *et al.*, 2010; Taylor *et al.*, 2010). This hypothesis might fit with theories of genomic change discussed above, in that viruses might have been originally designed to generate genomic diversity in macroorganisms but escaped and became pathogenic.

In the area of toxins and poisons, work by Bergman (1995, 1997) revealed that there is no easy division between "toxic" and "nontoxic." Instead, the toxicity of substances is related to dosage. Recent discussions of specific toxin proteins have been limited. In his discussion of anthrax, Wood (2002b) noted that the origin of anthrax toxin proteins "remains enigmatic," but in a followup essay (2007c), he implicated design as the source of these proteins. In a detailed study of cholera toxin (CT), Francis and Wood (2008) proposed that CT might have a beneficial function in certain arthropods, which would make its pathogenicity in humans an example of ecological displacement. Lightner's (2010c) review of shrew toxins highlighted the possibility of directed mutation in their origin, thus also implicating design. Sanders (2008) noted that the toxic compounds of *Lantana* were chemically related to compounds that had therapeutic

applications in humans.

Regarding pathogenic bacteria, Kim (2008) made the intriguing proposal that modern pathogens were originally created to target and destroy cancerous cells of macroorganisms. Thus, their ability to destroy cells using sophisticated toxins would be part of the initial design to keep macroorganisms healthy. After the Fall, the specificity of these bacteria broke down, and toxins were targeted to healthy tissues as well as abnormal tumors.

DESIGN

Traditionally, creationists have considered design in a Paleyan sense, as a conclusion to be inferred from evidence. In the past decade, creation biologists have worked to develop a much deeper understanding of design, looking beyond just the inference of design to its meaning, interpretation, and practical application. Echoing Doyle's (2008) claim that "design for the biblical God is hardly limited to what is needed for survival," Henriksen (2010) argued that focusing exclusively on inferring design from function can lead to a sterile view of design that misses "beautiful meaningful form and the will of the Creator."

Discussions of design in the Fall (Wilson, 2004; Oliver, 2009; Wood, 2007c) exemplify an approach to design beyond mere inference. Whereas design of certain features of natural evil is an inevitable conclusion, the Fall provides the context whereby the unpleasant implications can be understood and reconciled with an otherwise benevolent creator. Likewise, according to Schragin (2004, 2005), initial design parameters can offer guidance in ministering to the fallen creation and achieving optimal health. Other new design-related theories also attempt to provide a larger context for understanding design, and some have fascinating implications for otherwise challenging creationist research problems.

According to Francis's (2003, 2008) organosubstrate and bio-matrix models, microbes should be considered as a kind of living environment that provides direct and indirect benefits to macroorganisms. One intriguing corollary of this idea is that bacteria might be thought of as "extracellular organelles that help living things interact with their environment" (Purdum and Francis, 2008). This idea might help us explain the longstanding mystery of why mitochondria and chloroplasts have attributes similar to bacteria (Buratovich, 2005). Rather than evidence of the evolutionary origin of eukaryotes, we might view bacteria and organelles as parts of one vast, created bio-matrix, some members of which are mostly free-living while others form extremely close symbioses with other cells.

Another important area of design research concerns understanding the created similarities between different organisms. In the past, creationists resisted explaining similarity (Marsh, 1947, pp. 225-226) or appealed to a common creator (ReMine, 1993, p. 22), but recently creationists have recognized the need to distinguish between created similarities and those that result from post-Creation changes (Liu, 2008, 2009). The need for an adequate explanation of similarity has been magnified in recent years, with Christians such as Collins (2006) and Venema (2010) emphasizing the similarity of human and chimpanzee genomes as evidence of human evolution. If humans are created separately from chimpanzees, then the similarity of the human and chimp genomes must be the result of an intentional design (Wood, 2006c). A good

understanding of biological similarity in general would tremendously aid in formulating explanations of genome similarity.

Creationists have only recently begun exploring broad patterns of biological similarity. The research has followed two basic lines, attempts to study the patterns directly and attempts to explain what the patterns might mean. Sanders and Wise (2003) introduced a completely novel systematics concept, the cognitum, “a group of organisms recognized through the human cognitive senses as belonging together and sharing an underlying, unifying gestalt.” One objective of cognitum studies is to provide a means of evaluating higher classification above the level of baramin. Thus, one could speak of mammals or birds as real cognita, even though both groups contain multiple baramins. Cognita also encapsulate our own human experience with similarity, which hopefully will aid us in better understanding God’s design as a form of revelation or communication. According to Sanders and Wise (2003), “God purposely created organisms in a pattern specifically recognizable to man and created man capable of recognizing that pattern.”

Since the introduction of the cognitum, two additional cognita studies have appeared. Brophy (2005) showed 57 photographs of tetrapods to 67 college students and asked them to sort the photographs into groups. The results revealed that the “bird cognitum” (corresponding to the traditional class Aves) was generally more recognizable than the mammal cognitum. Amphibia and Reptilia were less recognized by the students. In a survey of angiosperm cognita, Sanders (2010b) utilized five expert angiosperm classifications to identify core groups of taxa that were recognized by all five. He found 63 different cognita at the family/order level, which is comparable to his estimate of the number of angiosperm baramins (Sanders, 2011).

In both studies, Brophy (2005) and Sanders (2010b) found that “fuzzy boundary” taxa could be identified between different groups. For example, Brophy noted that approximately 75% of respondents identified the pangolin as a reptile or otherwise excluded it from the mammal cognitum. Sanders’s survey found 264 different groups of species that were “boundary groups” between the cognita (where different experts classified the boundary groups in different cognita). These results reveal that our perceptions of biological similarity very often transcend the rigorous scientific desire for a single, “correct” classification and according to Sanders (2010b), “highlight the mosaic nature” of living things.

Still other studies of biological similarity have attempted to test the possibility that discontinuity is a significant part of the pattern of similarity. Even in his earliest writings, Frank Marsh stressed the “discontinuity between kinds now so widely evident in nature” (Marsh, 1947, p. 133). This idea has been revived in what Wood (2009b, 2011a) called the discontinuity hypothesis that “organisms were created in discrete, discontinuous groups that are recognizably different from all other organisms.” These groups can correspond to baramins or groups of baramins; thus, the search for discontinuity transcends simply identifying created kinds.

In an early survey, Wood (2009b) combined the discontinuity hypothesis with Price’s (1938) speculation that the taxonomic rank of family corresponds to the created kind to test whether statistical baraminology could detect discontinuity around families. Based on 73 statistical baraminology studies, Wood found that the discontinuity hypothesis was correct in only 60% of

the cases, although he remained optimistic that a larger sample of studies would reveal evidence of widespread discontinuity. A more recent analysis of 512 discrete character sets using the baraminic distance correlation method did not reveal any more evidence of discontinuity around families than would be expected by chance (Wood, 2012c). The failure to detect discontinuity in this study could be caused by a failure of the methods or the lack of discontinuity around families.

One could make a more qualitative argument for discontinuity based on the number of mammal families with few species (see Wood, 2011c). Since these species are different enough from others to warrant a separate family designation, those differences could be considered indirect evidence of the presence of discontinuity. Likewise at higher levels of classification: separation into different orders, classes, or phyla could indicate greater and greater recognition of discontinuity. Even the creation account of Genesis seems to imply a discontinuity between dwellers of the land, air, and sea, though we must be careful not to read too much into the scripture (Lightner, 2010d).

An obvious problem with all such discontinuity arguments is the existence of intermediate or “transitional” forms that possess characteristics of two otherwise discontinuous groups. Intermediate forms are considered by most evolutionary biologists as important evidence in favor of common ancestry (e.g., Angielczyk, 2009; Chiappe, 2009; Prothero, 2009). In the past decade, there have been many fossil discoveries purported to be intermediate forms, including baleen whales with teeth (Fitzgerald, 2006), dinosaurs with feather-like integumentary structures (Hu *et al.*, 2009), human-like australopiths (Berger *et al.*, 2010), and a toothed turtle with a partial shell (Li *et al.*, 2008). Recently, evolutionary biologists have urged a re-thinking of the entire concept of “transitional form,” especially as represented by the popular idea of the “missing link” (Mead, 2009), which ironically has a rich history prior to the publication of *Origin of Species* (Kjærgaard, 2011). Rhetorically, the phrase “missing link” gives the false impression that there are no known intermediates, and conceptually, it emphasizes a linear rather than tree-like view of evolution.

Creationists always have a great deal to say on the subject of intermediate forms, much of it aimed at discrediting the intermediate status of the proposed transitional organism (e.g., Silvestru, 2006; Coppedge, 2010; Line, 2010). Others have attempted to offer interpretations of intermediate fossils. For example, based on their baraminological analysis of fossil equids, Cavanaugh *et al.* (2003) argued that intermediate fossil equids represent the real descendants of the horses that survived the Flood aboard Noah’s Ark.

Intermediate taxa that appear to unite different baramins may themselves represent unique baramins that occupy a designed position between different forms. Wood (2011b) found evidence of discontinuity between deinonychosaurian dinosaurs and Mesozoic Avialae and between archaeocetes and extant cetaceans (Mace and Wood, 2005). The interpretation of inter-baraminic intermediates would therefore be rooted in God’s original design plan for biological similarities.

An emerging theme in creationist thought on transitional forms is the “mosaic” or “chimeric” nature of intermediates. The concept of organisms designed in a modular fashion, with similar

parts used in different created kinds, has been present in creationist thinking for thirty years (e.g., Jones, 1982; Morris and Parker, 1982; Wise, 1995). As noted above, Sanders (2010b) emphasized mosaics in his interpretation of angiosperm cognita, and mosaics appear frequently in discussions of Devonian tetrapods (Garner, 2003; Jaroncyk and Doyle, 2007; Sarfati, 2007). Woodmorappe (2002, 2003b) emphasized the occurrence of homoplasy and “reversals” – characteristics of mosaics – in his studies of theropods and archaeocetes. Though not all proposed mosaics are accepted by all creationists (Wood, 2011d), mosaics are increasingly recognized as important features of God’s original design (Garner, 2006).

In all discussions of mosaics, creationists agree that these are not evolutionary transitions, but creationist interpretations of mosaics vary. Wise (2008) suggested that mosaics are simply good design. Sarfati (2007) and Garner (2008) proposed that *Tiktaalik* might represent a resident of Wise’s (2003a) hypothesized pre-Flood floating forest. Thus, *Tiktaalik*’s mosaic of characters found in fish and terrestrial tetrapods represents a unique adaptation to an intermediate, semi-aquatic environment.

Statistical baraminology, through the technique of multidimensional scaling, provides a novel means of evaluating mosaics that are purported to be intermediate forms. By estimating organismal positions in character space, we can define an intermediate as a taxon or cluster of taxa that lie between two other taxa or clusters of taxa. Given that definition, Wood and Cavanaugh (2003) argued that fossil equids and living *Flaveria* species form trajectories in character space, with real intermediate taxa between the ends of the trajectories. In the case of the turtles, however, Wood (2005a) argued that there was a persistent discontinuity between turtles and other taxa, and even the discovery of the toothed Triassic turtle *Odontochelys* did not bridge that gap (Wood, 2009a). Similarly, evaluation of numerous archaeocete fossils does not fully support their classification as intermediates between land animals and extant whales (Mace and Wood, 2005; Wood, 2006a; Wood, 2007a).

A vulnerability in all discontinuity studies is the potential for future discoveries that bridge gaps. Senter’s (2010) recent analysis of coelurosaurian dinosaurs and birds revealed that apparent discontinuities have been steadily filled by new discoveries over the past ninety years. Even without new discoveries, Sober (2009) recently argued that the discovery of even a few transitional forms provides more confirmatory evidence for common ancestry than any persistent discontinuities favor separate ancestry. Although a complete response to Sober’s argument exceeds the scope of this paper, a few comments are in order. As noted above, creationists can think of intermediates in two different ways, within or between baramins. Intermediate taxa within baramins may serve to unite disparate branches or morphological forms of the same created kind. These intermediates offer no threat to creationist claims, insofar as the collapsing of certain apparent discontinuities does not necessarily invalidate the claim of widespread discontinuity, in the same way that the occasional albino tiger does not invalidate the claim that tigers are orange and black. Newly discovered intermediates that do seem to unite two well-supported baramins would have to be evaluated as information becomes available.

THE EMERGING MODEL

Overall, the developing creation biology model proposes the existence of created kinds,

phylogenetically – and possibly morphologically – discontinuous from other created kinds. Within these created kinds, species have developed very rapidly after the Flood, potentially by a mechanism of directed mutations involving transposable elements. The development of natural evil after the Fall, while partially explicable by degeneration, is now understood to be a designed part of God’s curse on creation.

This creation biology model is surprisingly dynamic. Instead of the stereotypical view of special creation as “the doctrine that each species, living and extinct, was created independently by God, essentially in its present form” (Futuyma, 2009, p. 610), creationists increasingly embrace sometimes radical changes within created kinds. The reality of speciation can be supported from multiple lines of evidence, and the malleability of chromosomes and genomes are also acknowledged. Long gone are the days of species fixity (Wood, 2008c; Garner, 2009).

As befits a creationist model of biology, one striking feature is the extent to which design has become a defining feature of the model. From Lightner’s hypothesis of designed mutations to Wilson’s dual gene hypothesis, design is a crucial feature for understanding how organisms could survive so much change, both in the environment and their own physical forms. Certainly, the model of random mutations and natural selection has been discarded by many creationists (e.g., Sanford *et al.*, 2008). The centrality of design to understanding broader issues in creationism, and especially the question of intermediate forms, remains an area of needed research.

Beyond just the value to biologists, the development of a creation biology model also undergirds the development of creationist paleontology. A complete model of creationist paleontology requires creationist understandings of biology and geology. Creationists have made some important strides in paleontology over the last decade, including theoretical modeling (e.g., Wise, 2003a, 2003b), taphonomy research (e.g., Brand *et al.*, 2003; Brand *et al.*, 2004), and field studies and excavations (e.g., Austin, 2003; Wise and Snelling, 2005; Chadwick *et al.*, 2006; Turner *et al.*, 2010). However, some important aspects of creationist geology that are essential to interpreting fossils remain controversial, especially the pre-Flood/Flood and Flood/post-Flood boundaries (Wise and Snelling, 2005; Whitmore and Garner, 2008; Oard and Froede, 2008; Oard, 2010a, 2010b).

The past decade has seen important growth in creation biology beyond just the research progress discussed in this review. The Creation Biology Society, established in 1996, began holding annual conferences in 2004, and the members continue to make important progress in creation biology research. A decade ago, most creation biology research was limited to publications in creationist books and journals. Today, creation biology research has reached mainstream journals, though largely in a negative, critical way (Wood, 2011b). If creation biologists continue their dedication to their work and their Creator, creation biology should experience similar growth over the next decade and beyond.

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