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Baraminological Study of Mammalian Order Lagomorpha and Stem Lagomorphs

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Well-known for their tendency to proliferate, rabbits and hares have managed to spread to nearly every continent on Earth. They, as well as mountain-dwelling pikas, are grouped within order Lagomorpha. Rabbits and hares are considered members of family Leporidae, with rabbits represented by several genera and hares grouped in genus *Lepus,* while pikas make up the family Ochotonidae. There is only one fossil pika, represented by genus *Prolagus.* There is also a mostly extinct family of Lagomorpha called Prolagidae; it has one extant species, *Prolagus imperialis*. Overall, there are about 90 extant species of lagomorphs and over 230 species represented in the fossil record (Caravaggi 2018). The stem lagomorphs included in this study are representative species of genera *Aktashmys* and *Dawsonolagus*. Previous baraminological study was done on the Order Lagomorpha, which concluded that based on available data families Leporidae and Ochotonidae are likely monobaramins, respectively, and that Leporidae could be a holobaramin (Wood, 2008). However, the dataset used was very small, consisting of the craniomandibular characteristics of six of the eleven extant lagomorph genera. More research needed to be done before any of the initial results could be considered conclusive. With this in mind, another morphological character set was subjected to standard baraminological analysis (Wood, 2001). Published by Fostowicz-Frelik and Meng (2013), this dataset included 22 taxa representing all major groups of extinct and extant Lagomorpha as well as one outgroup, *Mimitona wana*. These were evaluated using 80 dental, cranial, and mandibular characters. After applying a character relevance cutoff of 0.95 to the dataset, 29 characters were used in the analysis. Twenty-six of these were dental characters, and 3 were for the skull. None of the mandibular characters were used, making this study less holistic. The baraminic distance correlation (BDC) showed two distinct groupings. The groups consist of both Leporidae and Ochotonidae split fairly evenly between each group, with 6 ochotonids and 6 leporids represented in one group and 2 ochotonids and 5 leporids along with 2 stem lagomorphs in the other group. Two genera, *Mimotona* and *Paleolagus*, were not positively correlated with either of those two groups. On viewing the 3D multidimensional scaling (MDS) results, the stem lagomorphs are grouped together separate from any other group, and *Mimotona wana* is distant to the other groups. There was discontinuity between the families within the two distinct groups, but the ochotonids and leporids were still much closer to each other within each group than they were to species of their respective family in the other group. This is seemingly in contrast to Wood's (2008) study which suggested that Leporidae and Ochotonidae were each monobaraminic. However, two Leporidae genera appear to be forming a "bridge" between the Leporidae species in the respective groups. It is possible that with a larger dataset and further analysis, the two groups could be shown to actually be one larger, continuous group. Although these results are unusual and unexpected, two analyses by Thompson and Wood (2018) were also both inconclusive on the baraminic status of lagomorphs. It is still possible that families Leporidae and Ochotonidae are both monobaramins, but additional research needs to be done.

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Baraminology of Pareiasauria (Amniota: Parareptilia)

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Pareiasaurs were medium- to large-sized herbivores with stocky bodies found in Middle to Upper Permian deposits. Their fossils have been found in Russia, South Africa, China, Morocco, Niger, Brazil, Germany, Scotland, Tanzania, and Zambia (Macedo Farias, et al. 2019). Pareiasaurs possessed osteoderms along their dorsal surface and many had remarkable bony bosses, protuberances, or horns on their skulls. Pareiasaurs are recovered in most phylogenies as members of Parareptilia forming the clade Pareiasauromorpha with Nycteroleteridae, which may be paraphyletic (e.g., Tsuji 2013). The distinctiveness of pareiasaurs compared to other parareptiles suggests that they might not share ancestry with other members of Parareptilia. There are no extant parareptiles, although for a time turtles were thought to be living members of this group since they shared an anapsid skull construction (e.g., Lee 1993, 1997). However, most researchers

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now favor a diapsid (e.g., Rieppel and deBraga 1996) and likely archosauromorph position for turtles (e.g., Iwabe et al. 2004).

In order to better understand the patterns of continuity and discontinuity of the pareiasaurs, a published morphological character dataset (Liu and Bever 2018) containing 139 characters (78 craniomandibular and dental; 61 postcranial) and 30 taxa (22 pareiasaurs, 8 other parareptiles) was analyzed. 25 taxa were retained for the statistical baraminological analysis (5 pareiasaurs [*Sanchuanosaurus*, *Obirkovia*, *Honania*, *Parasaurus*, and *Elginia wuyongae*] were removed for having character relevance cutoffs of less than 0.30) using BARCLAY (Wood 2020) at a 0.75 taxic relevance cutoff, which allowed for the retention of 51 characters.

Baraminic distance correlation (BDC) results show two clear blocks of positive correlation (Pareiasauria and the outgroup taxa, respectively) with negative correlation or no correlation between the two blocks. Multidimensional scaling (MDS) results viewed in three dimensions show two clusters, which correspond to the two blocks of positive correlation in the BDC plot, separated by an obvious gap in morphological space. The pareiasaur *Shihtienfenia* is widely separated from the rest of the pareiasaurs but is not any closer to the outgroup than the other pareiasaurs. Similarly, the nycteroleterid *Rhipaeosaurus* is far from the other outgroup taxa but is not any closer to the pareiasaurs than the other outgroup taxa.

The clear positive correlation in the BDC plot and close clustering in MDS of pareiasaurs is strong evidence for continuity within Pareiasauria. The negative correlation surrounding the group in BDC and the large gap in multidimensional space between pareiasaurs and other parareptiles in MDS is strong evidence for discontinuity surrounding Pareiasauria. These results indicate that Pareiasauria is a holobaramin, which suggests that all pareiasaurs belong to the same created kind. This study marks the first attempt to apply statistical baraminological methods to a parareptilian group, and one of the few statistical baraminological analyses of a group found exclusively in Paleozoic rocks.

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Evidence for a Recent Transition into Parasitism within four Phyla of Marine Animals

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The flatworm *Urostoma cyprinae* lives inside the gills of the blue mussel, *Mytilus galloprovincialis* (Robledo et al. 1994, Brun et al. 1999). Although the worm is minute, when a blue mussel is heavily infested, large lesions can form on the mussel's gills. Blood cells are drawn to the damaged areas and are lost through the tissue, further harming the mussel. As a result of the infestation, the mussel's feeding and breathing is severely impaired (Robledo et al. 1994). Parasites like the flatworm *U. cyprinae* pose a particularly difficult problem for Young-Earth Creationists (YEC) who believe that the creator of *U. cyprinae* is a perfectly loving, deeply relational being (Francis 2009). Parasitism represents a corruption of harmony and unity between creatures of God's creation. It seems counterintuitive that a loving God would have created parasites to inhabit a "very good" world (Genesis 1:31). And yet, parasites currently represent over 50% of all species on earth (Weinstein and Kuris 2016). Therefore, YEC must explain the origin of the numerous and diverse parasites we see today (Blaschke 2018).

One possible explanation for parasite origins can be gleaned from their biology. Interestingly, some individuals of *U. cyprinae* exhibit a much less gruesome lifestyle. Rather than feeding on mussel tissue, they feed on microorganisms found in algae and mud on the ocean floor (Robledo et al. 1994). In this case, parasitism is facultative--the flatworm is not biologically obligated to be parasitic. In a YEC model of parasite diversification, God would have created the free-living form of *U. cyprinae* in the beginning and only after the Fall did the parasitic form adopt its currently destructive lifestyle. Are the origins of all parasites so easily explained?

In this study, we explore the diversification of parasites within four primarily marine phyla (Cnidaria, Ctenophora, Platyhelminthes, and Xenacoelomorpha) from a YEC perspective by examining the natural history of each parasite lineage, the number of parasitic lineages, and the number of species in each lineage. A parasitic lineage is an independent evolution of a parasitic clade originating from non-parasitic ancestors. The lineages researched were taken from Weinstein and Kuris (2016) and Rohde (2005) and supplemented with more recent literature when appropriate. Given the time constraints of a YEC model, the more speciose a lineage is the more difficult it becomes to explain its origins. For example, if most lineages of parasites contain >1,500 species, a recent diversification of parasites seems unlikely (Passeroidea, the most diverse baramin of vertebrates, is estimated at 1,500 species, Lightner 2013). However, if mainly lineages with <1,500 species exist, then their emergence from non-parasitic ancestors within the last 10,000 years seems more reasonable.

Collectively, the four phyla examined contain 40,272 species, 24,646 of these are parasites (61.2%). Parasitism is estimated to have arisen at least 63 times within these phyla, with an average species per lineage of 391, well below our 1,500 "reasonableness" threshold. However, the average is heavily distorted by two especially speciose lineages, the Neodermata (tapeworms and friends) with 22,000+ species, and the Myxozoa (whirling disease parasites) with 2,425 species. Remarkably, 60 out of the 63 lineages contain <12 species (95.2%).

This overwhelming pattern of parasite evolution fits well with a YEC model of life's history and the abundance of lineages with <12 species indicates that parasitism may not persist very long and only rarely leads to explosive diversification. As evidence of transition from non-parasite to parasite, many species were found to use similar consumer strategies as their free-living sister taxa, simply switching from consuming unicellular organisms, diatoms, or other small animals, to consuming the tissue of the host (e.g. *Micropharynx parasitica*, a flatworm that lives and feeds on thorny skates and differs from its non-parasitic sister taxa only in its source of nutrients). Additionally, the transition into parasitism often does not require novel adaptations, (e.g. *Avagina vivipara*, a xenacoelomorph without any morphological adaptations to parasitism who lives in the esophagus of its host). We conclude that the collective evidence observed in flatworm and cnidarian parasites (i.e. numerous independent transitions into parasitism, each with low diversity) is compatible with a YEC model of post-Fall parasite diversification.

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Plants as Instruments of Blessing and Curse in the Primeval History

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Plants appear at key junctures in the Bible and serve as indicators of God's blessing and curse. Attention to the Bible's treatment of plants in literary context of Genesis 1-11 reveals that its priority is not to provide comprehensive taxonomies but to distinguish life before and after the fall. The creation narrative presents plants as a blessing, while the fall and flood narratives mingle blessing and curse.

In Genesis 1:1-2:3, God creates plants on day three to benefit creatures made on days five and six. God calls earth to sprout *deshe, eseb,* and *etz* (Gen 1:11-12). *Deshe* is not part of a trichotomy of grasses, herbs, and trees, but plants generally. The single cognate verb and the lack of repetition of *deshe* in 1:29-30 favor dichotomy. Origin, sequence, distinctions in seed production, created kinds, and ultimately provision of food take priority over comprehensive taxonomy as concerns of the text. The types of plants presented serve as food and are instruments of blessing in a "very good" creation (Gen 1:29-31).

The fall account adds curse to blessing. The background statements in Genesis 2:5-6 and the narrative of 2:15 are key components for understanding the role of plants in the world after human disobedience. Genesis 2:5-17 interweaves background descriptions (2:5-6, 10-14) with historical narrative (2:7-9, 15-17).

Genesis 2:5-6 describes a time before any bush of the field (*siah hassade*), herb of the field (*eseb hassade*), or man to work the soil (*adam l'avod et-haadamah*) existed, foreshadowing the man eating not merely the creation *eseb* but a more specific subset, *eseb hassade* (3:18), and working the soil (3:23). While setting up the fall narrative, plants still indicate only blessing, with difficulties attending food acquisition coming later. God plants the garden, places (*sim*) the man there (2:7-8), and causes beautiful and edible trees to emerge, as well as the tree of life and the tree of the knowledge of good and evil (2:9).

After describing Eden's river-divisions and geography (2:10-14), the narrative resumes in 2:15, which contains a verb (*nuh*) and two infinitives of purpose (*l'ovdah ul'shomrah*) key to one's understanding of pre-fall plants. Translating 2:15b as God "placed him in the garden to work and keep it" suggests work responsibilities relating to the garden's fruit trees and seeing *avad* and *shamar* with meanings similar to their uses in 3:23-24 (work, guard). An alternative, God "caused him to rest…to worship and obey" points to other uses of the *nuh*, *avad*, and *shamar* roots in the Pentateuch as well the morphology and grammar of the verbs. In the next verb, God commands him (2:16). The soil-service of 2:5 comes in 3:23, indicating food's pre-fall abundance. The first translation sees some kind of pre-fall agriculture; the latter sees no kind of soil-work until human disobedience.

Curse follows eating from the forbidden tree (2:16-17; 3:1-6). The man and woman produce fig-leaf coverings and hide among the trees. God interrogates and sentences, reprimanding the man for listening to her voice regarding the tree, and announcing major changes (3:7-19). Food will come from a cursed ground (*adamah*) and be eaten after painful toil (3:17). Frustrating thorns (*qotz*) and thistles (*dardar*) will spring forth. Man must eat *eseb hasadde* (cf. 2:5) by the sweat of his face (3:18-19). Man will eat food but return to dust (3:19). God denies access to the tree of life (3:22) and banishes him "to cultivate the soil" (3:23, echoing 2:5). Cain is similarly described (4:2), whom God sentences and curses "from the soil," restricting his farming endeavors (4:11-12).

The flood account shows plants as reminders of blessing and curse. A tree-wood construction (6:14) preserves humanity through judgment. The olive leaf signals hope for land's reappearance (8:11). Perpetual seedtime and harvest guarantee reproduction (8:22). Man's dietary expansion suggests food scarcity (9:3). Like Adam and Cain, Noah becomes "a man of the soil." He plants a vineyard and becomes drunk from its wine, an event paralleling Genesis 3, including human nakedness, covering, and curse (9:20-27).

Plants were originally instruments of blessing, but curse was added to the blessing in the wake of human disobedience. Creation, perpetual reproduction, and cultivation possibilities witness to blessing while agricultural frustrations and the subsequent returning to dust witness to curse.

Community, Autonomy, and the Emergence of Parasitism

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The existence of parasitic animals presents a challenge to Young-Earth Creationism (YEC) not only due to their destructive lifestyle but also because there are *so many of them*. Parasitism has arisen independently in at least 223 animal lineages (Weinstein and Kuris 2016) and parasites collectively represent half of all described species, making parasitism the most common consumer strategy on the planet (Price 1980; Dobson et al. 2008). A world created writhing with so many harmful animals contrasts acutely with the image of a loving Creator and a very good creation (Gen. 1:31; Mace et al. 2003; Ingle 2015). Many creationists therefore hypothesize that parasitism arose from mutualistic or commensal organisms after the fall as relationships deteriorated over time (Francis 2009; Sherwin 2013; Ingle and Aaron 2015; Blaschke 2018). If all animals were created non-parasitic only 6,000 years ago, it seems reasonable to expect that parasitism would be relatively rare today. Why then, is parasitism so common and what can the emergence of parasitism reveal about God through nature?

Here, we work towards answering these questions by analyzing patterns of parasite diversification within four primarily marine phyla (Cnidaria, Ctenophora, Platyhelminthes, and Xenacoelomorpha). We conducted analyses using both a “broad” and “strict” definition of parasitism. Our “broad” definition includes any organism listed as a parasite from Weinstein and Kuris (2016) (parasite = any individual that obtains nutrients from a single host) or Boero and Bouillon (2005) (parasite = any individual that lives inside another). However, many species are ambiguously parasitic for one or more of the following reasons: 1) their parasitic behavior can only be inferred based on association with a host, no documented fitness costs on their hosts yet exist (e.g. *Meara* spp.), 2) they are opportunistic rather than obligate parasites (e.g. *Sarsia bella*), 3) one life stage is parasitic while another is free-living (e.g. *Larsonia pterophylla*), or 4) they only harm the host when present in unusual abundance (e.g. *Waminoa brickneri*). Therefore, our “strict” definition of parasite included only obligate parasites that inflict documented fitness costs on their hosts under normal circumstances and in all life stages (e.g. *Taenia saginata*, the beef tapeworm).

The biology and natural history of each parasitic lineage was examined through a systematic literature review and species numbers were calculated using Roskov et al. (2019). Within these four phyla and according to a broad definition, parasitism has emerged independently at least 63 times. In contrast, using a strict definition of parasitism reduces the number of parasitic lineages from 63 to only 10 (84.2% decrease), primarily due to the ambiguously harmful symbiotic relationship between many sea anemones and their oftentimes living substrates. This result highlights how the definition of “parasite” drastically affects how much of the world we see as writhing with parasites or not.

Our goal here is not to redefine parasitism in order to artificially deflate the number of parasites for a YEC model to explain. Rather, our results simply illustrate the inadequacy of discrete classifications, like “parasite” or “predator”, to accurately depict the complex continuum of animal interactions. Parasitism is common because ecosystems are dynamic places where nutrients are obtained whenever and however possible. An animal may be “parasitic” at a certain stage of life, at a certain point in time, or on a certain kind of host, and completely harmless or even beneficial at a different life stage, time, or place.

This observation reveals two significant things about how nature reflects the character of the Creator. First, animals exist in perpetual and intimate *community* and these intricate relationships are meant to reflect the harmony and unity of the Trinity. Second, animals behave *autonomously* and thus reflect the perfectly free nature of God. As a result of this freedom, animals are allowed by God to behave in contrast to his desire for harmonious relationships. Arising then from community and autonomy, parasitism can emerge quickly in nature as ecosystems and the relationships within them change through time. The dual concepts of community and creaturely autonomy grounded within a YEC framework offer one potential explanation for how parasitism rapidly became ubiquitous after the fall.

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Chromosome 2 Fusion in Human History

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Chromosome banding patterns illustrated in Yunis and Pakash (1982:Figure 2) suggested **(A)** the short arms of two chromosomes with similar structure to chimp Chromosomes 2A and 2B fused end-to-end to produce human Chromosome 2, **(B)** the fusion event involved the complete loss of both telomeres and occurred at the 2q14 end of 2q13, and **(C)** the deactivated centromere of 2B is located in 2q21.2. Since 1982, consilience of inductions of considerable data have confirmed all three claims:

1. Juxtaposed on either side of Chr2: 113,602,929 on human genome assembly GRCh38.p13 (at the 2q14 end of 2q13; here referred to as 2fus), are multiple homologous sequences in reverse orientation.
2. Juxtaposed on either side of Chr2: 132,247,344-132,247,569 on human genome assembly GRCh38.p13 (in 2q21.2; here referred to as 2cen’) are homologous alphoid

sequences in reverse orientation—just as are found on opposite sides of centromeres.

3. In dozens of ways, DNA sequencing and FISH hybridization indicate the 2fus region is telomeric. In fact, from 2fus towards 2cen, 83% of >193,000 base pairs show ≥97% identity with 22qtel from telomere towards centromere. Similarly, from 2fus towards 2qtel, 93% of >250,000 base pairs show ~98% identity with 9ptel from telomere towards centromere.
4. DNA sequencing and FISH hybridization indicate the region about 2cen' is centromeric.
5. DNA sequencing and FISH hybridization indicate synteny between the region across 2cen' and across the centromere of chimp Chromosome 2B, as well as between the region across 2fus and across the short-arm subtelomeres of chimp Chromosomes 2A and 2B if they were oriented end-to-end.

Evidence for end-to-end fusion of chimp-*like* chromosomes to generate human Chromosome 2 is profound, but evidence that the original chromosomes were ape (rather than human) is, at best, very weak. Contrary to a chimp origin, 32-bp subtelomere satellite DNA found in nearly half of the chimp telomeres—including 2Aptel and 2Bptel—is found nowhere in the 2fus region (nor anywhere else in the human genome). Yet, consistent with a human origin, both the 2fus and 2cen' regions host sequences found elsewhere in the human genome, but nowhere in the chimp genome.

Of all the critiques of fusion theory published by Tomkins (see Tomkins 2018 for a complete bibliography), the most substantial is that both 2fus and 2cen' are located in the first intron of an active gene. However, in each case, the first intron is huge, and though the first exon of the gene is located at multiple sites across the human genome, it is *not* an exon in any of the genes sharing sequence identity with the gene. This suggests that both genes could have functioned on Chromosomes 2A and 2B before fusion without the first exon, and then added the first exon beyond 2fus and 2cen' subsequent to the fusion event.

The fusion evidenced on human Chromosome 2 has no parallel anywhere else in either the human genome, nor at any point in development. Being neither a mark of maturity nor necessary, I know of no reason for God to create evidence of a fusion event that never actually occurred. Therefore, I suggest there was a point in human history when two human chromosomes similar to modern chimp Chromosomes 2A and 2B actually fused end-to-end, short arm to short arm. Since, as far as we know, all humans have the single Chromosome 2 condition, the fusion event must have occurred before the Babel dispersion prevented spread of the fused chromosome condition to all humanity. That it occurred deep in human history is confirmed by evidence of fusion in both Neandertal and Denisovan DNA. In fact, for complete fixation of the condition, the fusion event most likely occurred when human population was very small—*i.e.* either soon after the creation event or soon after the Flood's population bottleneck.

Chromosome 2 fusion evidence could contribute to interesting discussion on topics as diverse as creation with appearance of history, non-pathological chromosome rearrangement, and human population genetics.

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Schwartz's Fish Hybrids in Baraminology

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Following Frank Marsh, modern creationists—especially those of the European school—have adopted hybridization as a criterion for identifying created kinds. And, it is largely because true hybridization (utilization of DNA from both parents) has yielded no inter-family hybridization among mammals and birds, that many creationists believe the created kind is at the level of the taxonomic family.

Creationists have done little in fish baraminology. Out of >500 fish families, Wood (2008) applied statistical baraminology to only four fish families, and fish hybridization data has not been utilized. Frank Schwartz's fish hybrid bibliographies (1972, 1981) collectively report ~12,000 inter-specific hybridizations from ~2,900 references. Schwartz's data is nearly ready for Hybridatabase submission.

As demonstration of the potential value of Schwartz's data, Schwartz reports 40 inter-generic hybrid crosses from 22 references in the family Gasterosteidae. The gasterosteid hybridogram unites all the family's genera except *Culaea*. Statistical baraminology, however (Wood 2008), unites *Culaea* with *Pungitius*, so hybridization plus sufficient similarity unite all gasterosteids into a single monobaramin.

Curiously, Schwartz (1972) contains 541 inter-family hybridization claims for 55 (of 448) fish families from 115 sources. These claims include inter-order crosses for 23 (of ~40) fish orders and inter-infraclass crosses for 5 (of 9) teleost sub-taxa. There are even claims of Chondrostei-Teleostei crosses. Of the taxa involved in hybridizations, indirect hybridization unites 50 families, 21 orders, 5 teleost subclades, and the Chondrostei and Teleostei—*i.e.*, ~25,000 fish species (all but about 1,200)—into a single group. This group not only includes fish with and without scales (thus apparently uniting multiple biblical kinds), but also includes many very easily recognizable fish morphologies (*i.e.*, probable cognita)—*e.g.*, catfish, flatfish, sturgeons, angelfish. With regards to defining biblical kinds among fish, hybridization is either to be abandoned, or a baraminically useful hybridization criterion needs to be defined for fish (as it was for mammals).

Closed libraries and language barriers prevented examination of all inter-family and gasterosteid-genera hybridization sources (34 [30%]) and 10 [45%] respectively). However, what was examined was informative. Of the gasterosteid sources examined, two merely cited the claims of others, six turned out to be intra-genus crosses, and one was an unsuccessful hybridization. We deduce that Schwartz's sources must be examined before being used in baraminology studies. Thus, though the remaining 12 gasterosteid sources unite all the genera except *Culaea*, we cannot conclude that Gasterosteidae is a monobaramin until this conclusion is derived directly from original sources.

Among the inter-family sources examined, various degrees of hybrid success are reported between fish families. In a typical fish life cycle, in the hours following the male's application of sperm to the eggs, fertilization, cleavage, gastrulation, embryonic differentiation, and hatching occurs. In the following days the larva absorbs its yolk sac to become a fry, and over the following months to years the fry becomes a juvenile, then an adult. According to the Schwartz inter-family hybrid sources examined, high mortality rates are common in every developmental stage—even for intraspecific crosses. Fish sperm tends to stimulate fish eggs to progress to various developmental stages, even if the sperm are from very different higher taxa. Although some crosses develop parthogenetically, some sources document hybrids with fully incorporated inter-family sperm DNA surviving well into late embryonic development. Although none of the sources examined report inter-family hybrids surviving to adulthood, multiple sources report successful hatchings—even of hybrids bearing paternal characteristics. This observation seems equally true among the different gasterosteid genera, between different families from the same superfamily, different superfamilies in the same order, different orders in the same teleost subclade, and even between different teleost subclades.

Since hybrid claims unite what are probably multiple cognita, a baraminologically useful hybribization criterion must require more than gastrula development and the acceptance of DNA from both parents—as in mammals. If useful at all, development to at least juvenile (and perhaps adult) stage will be required among fish.

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Function in Genetic Redundancy

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Roughly 40% of the human genome is repetitive DNA. In purposeless processes like evolution, repetition is likely non-functional—an artifact of on-going purposeless processes like sequence duplication. In contrast, creationism expects such common features to be designed. Insight into God's intention for repetitive DNA may be seen in His design for repetition in Scripture.

As God authored Scripture, He included redundancy at all passage lengths. He repeated words within passages (*e.g.*, '*bâra*' thrice and 'âs*ah*' ten times in Genesis One), between nearby accounts (*e.g.*, 'image' in Genesis 1 and 5), and even across distant passages (*e.g.*, 'seed', 'blood', 'promise'). He repeated phrases similarly (*e.g.*, 'according to kind' ten times in Genesis One, 'and he died' eight times in Genesis 5 and a ninth time in Gen. 9:29, 'blood sacrifice' and 'high priest' across both testaments). Scripture repeats genealogies (*e.g.*, I Chronicles with multiple locations, Matthew 1 with Luke 3 and Genesis 5 and 11), psalms (*e.g.*, Psalms 14 and 53, Psalm 18 with II Sam. 22), and even major parts of entire books (*e.g.*, between Kings and Chronicles, among the synoptic gospels). One of the scriptural genres (Hebrew poetry) is even characterized by repetition (juxtaposition of parallel couplets).

Not all Scriptural repetition is textual. Some is oral (from syllabic sounds to the sounds of words to the meter of entire passages). Some is in actions required of His people (*e.g.*, from daily worship to weakly Sabbaths, to annual feasts). Scriptural repetition also displays a spectrum of similarity. Textual repetition ranges from letter-by-letter identity to conceptual identity lacking common words or phrases. Vocal repetition ranges from partial identity (alliteration, rhyme) to homonyms, to identical words. Some repetition is continuous; other repetition is discontinuous (*e.g.* Kings versus Chronicles).

Scriptural redundancy is abundant, ubiquitous, and fulfills many purposes. Minimally, redundancy beautifies and unifies the text, reminds forgetful people of important facts, marks locations containing deep meaning, links distant passages for expanded meaning and proper context, and provides multiple perspectives for key events. Since the same God Who authored Scripture also created life, it is entirely possible that God intentionally placed redundancy into DNA. This would not only explain the abundance and ubiquity of DNA redundancy, but it would suggest there are multiple, interwoven functions of DNA redundancy. Different degrees of similarity in DNA sequences would also be in line with the sort of redundancy found in Scripture.

Three examples suggest that functions for DNA redundancy may have analogues among the functions of scriptural redundancy. For example, scriptural repetition can indicate where further study is warranted. Analogously, because DNA splicing is facilitated with sequence overlap, some redundant sequences might have been placed as strategic sites for chromosome repair, as well as for insertions and deletions. Second, since some Scriptural repetition seems to be there for beauty, perhaps some DNA repetition (such as the HORs of alpha satellite) is designed to pay tribute to the beauty of the Designer. Third, scriptural repetition connects distant passages for the reader. Perhaps, analogously, DNA redundancy coordinates genetic activity across the human genome. High identity DNA sequences are drawn together (*e.g.*, DNA clones are drawn to sequence-similar sections of the human genome while DNA is condensed). So perhaps similar sequences at different locations on the DNA are drawn together during the normal function of DNA. This would draw different chromosomes or different portions of the same chromosome into proximity for inter-gene regulation and gene-gene interaction. Such long-distance interactions could facilitate coordination of genetic activity across an organism's entire body. Genetic sequences with this kind of function could explain such things as long blocks of genetic identity between and among different chromosomes and multiple copies of genes located on different chromosomes. This may also provide a functional role for 'pseudogenes'—non-coding homologs of coding genes situated where they are to bring distant portions of the genome into proximity. This might even explain why the same pseudogenes are located in the same position in the genomes of multiple organisms—*e.g.*, between humans and chimps.

I suggest that the study of scriptural redundancy by biblical scholars can provide insight into the purpose of DNA redundancy found in the human genome.

Expanding the Toolkit of Statistical Baraminology with BARCLAY: Baraminology and Cluster Analysis

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A statistical approach to baraminology using discrete character data was introduced by Robinson and Cavanaugh (1998a, 1998b) with two papers on catarrhine primates and felids. Subsequently the methods were implemented in a web application BDISTMDS that allowed the user to perform baraminic distance correlation (BDC) with bootstrapping and classical multidimensional scaling (MDS) (Wood 2008). These methods have been applied to numerous character sets to develop a baraminological perspective on horse evolution (Cavanaugh et al. 2003), the relationships of birds and dinosaurs (Garner et al. 2013), Devonian tetrapods (Garner and Asher 2018), and hominins (Wood 2016). Throughout these studies, the core methods of BDC and MDS have remained largely unchanged, but these methods can be revised and new methods can be added. In particular, Reeves (in press) recommended using a Jaccard coefficient in addition to the simple matching baraminic distance, avoiding the parametric Pearson coefficient, and most importantly using existing clustering analysis techniques.

To expand the methodology, the BDISTMDS application has been retired, and a new web application BARCLAY (Baraminology and Cluster Analysis) is undergoing development. The initial release includes the original methodology of BDISTMDS but also provides the following new features:

- The distance metric can be set to either the simple matching distance (classical "baraminic distance") or a Jaccard coefficient. The Jaccard distance is for use on character sets where zero encodes the absence of a character state. The Jaccard distance does not count matches where both taxa lack a character state.
- The character relevance cutoff can now be set to zero, which effectively forces BARCLAY to use all characters in calculating distances.
- BDC can now be calculated with either Pearson or Spearman correlations. In BDISTMDS, Pearson correlations are used by default, but the assumptions of the correlation are not met. Hence, the nonparametric Spearman correlation is to be preferred and is the default option in BARCLAY, and the Pearson correlation should be deprecated. Pearson is retained as an option for analysis of previous studies that use this correlation.
- Medoid partitioning and fuzzy analysis are added in response to recommendations by Reeves (in press). Both are implemented via the PAM and FANNY algorithms in R (Kaufman and Rousseeuw 1990). BARCLAY can generate a text-based report for each algorithm or create a color-coded silhouette plot.

Future development will focus on creating a batch mode for rapid calculations using a large number of character sets and a new bootstrapping implementation. Further details on the methods described herein are forthcoming (Wood, in preparation). Stable releases of BARCLAY will be available at coresci.org/barclay.

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A Baraminological Analysis of Fossil Mysticetes

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Cetaceans are a diverse group of highly-specialized mammals with many purported transitional forms. These fossils are often used as exemplary evidence of macroevolutionary change, yet previous creationist work has revealed the potential presence of discontinuity within the Cetacea, indicating the presence of multiple baramins (Mace and Wood 2005, Wood 2007). To further evaluate cetacean baraminology, we obtained a supermatrix compiled by Fordyce and Marx (2018). The matrix consisted of 106 cetacean taxa and 275 characters (274 morphological and one chromosome count). The taxa represented five Odontoceti, three Llanocetidae, three Mammalodontidae, seven Aetiocetidae, seven Eomysticetidae, seven stem taxa of the crown mysticetes, 71 crown mysticetes, and *Coronodon havensteini* (a toothed mysticete), *Morawanocetus yabukii* (a putative aetiocetid), and *Zygorhiza kochii* (a basilosaurid). To examine relationships between these major clades, five submatrices of paired, adjacent clades were formed from the supermatrix. These matrices consisted of the following adjacent clades: Odontoceti/Llanocetidae, Llanocetidae/Mammalodontidae, Mammalodontidae/Aetiocetidae, Aetiocetidae/Eomysticetidae, and Eomysticetidae/stem taxa of the crown mysticetes. Crown mysticetes were also examined separately. Baraminic distance correlation (BDC) was calculated for each submatrix using BARCLAY (Wood 2020). All characters and taxa for each submatrix were used to calculate distances. In three of the submatrices (Mammalodontidae/Aetiocetidae, Aetiocetidae/Eomysticetidae, and Eomysticetidae/stem taxa of the crown mysticetes), the clades could be readily identified by the presence of significant, positive BDC between the members. Similarly, significant, negative BDC was observed between Mammalodontidae and Aetiocetidae, between Aetiocetidae and

Eomysticetidae, and between Eomysticetidae and the stem taxa of the crown mysticetes. In the analysis of the crown mysticetes, three clusters could be discerned by the presence of significant, positive BDC within each group: Balaenidae, Balaenopteridae, and a cluster consisting of stem Balaenopteroidea and Cetotheriidae (excluding *Caperea* and *Miocaperea*). Significant, negative BDC was observed between the Balaenidae and the remaining crown taxa. Significant, negative BDC was also observed between Balaenopteridae and Cetotheriidae, but not between Balaenopteridae and the stem Balaenopteroidea. Instead, members of Balaenopteridae and the stem Balaenopteroidea shared significant, positive BDC, making one larger cluster consisting of Cetotheriidae and Balaenopteroidea and excluding *Caperea* and *Miocaperea*. *Caperea* and *Miocaperea* share significant, positive BDC with only three taxa: *Eubalaena shinshuensis*, *Herpetocetus morrowi*, and *Herpetocetus bramblei*. The remaining submatrices did not show clear evidence of clustering. In the Odontoceti/Llanocetidae submatrix, *Physeter macrocephalus* exhibited significant, negative BDC with the Llanocetidae, but no other significant, negative BDC was observed. Significant, positive BDC was observed within the Llanocetidae and within a group consisting of *Olympicetus*, *Archaeodelphis*, and *Albertocetus*. In the Llanocetidae/Mammalodontidae submatrix, significant, positive BDC was observed between *Mammalodon hakataramea* and *Mammalodon colliveri* and between *M. hakataramea* and *Janjucetus*. Significant, negative BDC was observed between *Llanocetus denticrenatus* and *Mammalodon colliveri*. Based on these results, we suggest that three mysticete families probably correspond to holobaramins: Eomysticetidae, Aetiocetidae, and Balaenidae. Mammalodontidae could also be a holobaramin, but clear evidence discontinuity between mammalodontids and llanocetids is lacking. A group consisting of Cetotheriidae and Balaenopteroidea (excluding *Caperea* and *Miocaperea*) could also be a holobaramin, but further study is warranted given the presence of significant, negative BDC within the group. The lack of significant, negative BDC between the odontocetes and mysticetes could be an artifact of the small sample size. These results significantly expand the previous work that looked at a far smaller sample of mysticetes.

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