Pine bark beetle tree damage is prevalent in the American Southwest causing millions of dollars in property damage and appears to correlate with ecological imbalance. This report is a part of an ongoing research project involving a grant funded creation-based undergraduate research project. In previous reports we report collecting pine bark beetles in traps and under the bark (Francis et al. 2015, Merril et al. 2015). We have noted that one opportunistic pine bark genus *Ips* is prevalent in wind-thrown trees in montane forests where pine bark beetle associated killing is occurring and in nearby contiguous forests where tree killing is not obvious. This suggests that beetles may play a beneficial role in a “healthy” forest. Curiously, only live trees toppled by wind appear to be infected in the healthy appearing forest. Fallen pine trees in this forest serve as a reservoir for key nutrients, including carbon and water. These trees also support a major detritivore population which serves as a significant basis for the food web in these dry climate, high desert forests. Much of the detritivore population colonizes the wood once they gain entry through the tough and dry bark. Pine bark beetles are suspected in aiding this process since they are among the first colonizers of wind-thrown trees. Creationists would expect that some creatures would be designed to promote nutrient cycling and detritivore cycles of plant material.

Since one of the goals of our research is to determine how the pine bark beetle plays a beneficial role in the forest, we have concentrated our efforts recently on the infestation of wind-thrown pine trees in the healthy appearing forest. The healthy appearing forest is at higher elevation (>8000′) and above areas of tree damage (<7000′) suggesting that a cooler more moist environment is important to beetle behavior. We have successfully collected pine bark beetles in wind-thrown trees but have not determined if these trees were pre-infected while standing. Determining time of infection will help us understand more about the life-cycle of the bark beetle and how its lifecycle might have shifted from one which promoted species richness in the forest to one which negatively impacts it. In order to establish the time of initiation of tree infection we attempted to find a recently wind-thrown pine. In early February of 2016, we detected a major wind-thrown portion of *Pinus ponderosa* within 24 to 48 hours after a winter storm. A major part of the tree was left standing and displayed a Diameter Breast Height (DBH) of 5.1′ corresponding to a tree age greater than 300 years (based on tree ring analysis of similar size trees). The portion which fell was an upper stem and measured 2.5′at its base with roughly 40-50′ of trunk on the ground and more than 30 branches over 3′ in diameter. There was no obvious tree related disease because there were no brown needles or top crown kill evident on both the standing and felled portions of the tree. Most of the wind-thrown portion of the tree showed no obvious signs of pitch tubes, boring dust, or galleries associated with pine bark beetle activity. However, there was some bark beetle activity on lower dead branches, which is fairly common in the healthy appearing standing trees of this forest.

Boring dust on small diameter branches (<1.0”), most likely from the activity of small branch specialist bark beetles *Pityophthorus* and *Pityogenes*, was detected approximately eight weeks after the tree fell. Boring dust from suspected *Ips* species was noted at 12 weeks. Beetles were captured from all dust locations. “Y”-shaped gallery morphology consistent with *Ips pini* were noted at week 12 and were observed to be constructed at a rate of 0.2”/day over a one month period. Brood chambers were noted roughly four weeks after the *Ips pini* detection. *Ips pini* consistently attacked branches which contained four to six diameter sections. By two months, one major trunk section (1-2’ DBH) showed boring dust spots, and the infection based on the observations of these spots appeared to move at roughly 10”/day. The 30’ main step portion remained uninfected one month after the initial attack. We believe that this is one of the first reports documenting the initial and ongoing infection of a wind-thrown *Pinus ponderosa*. All live standing trees within a radius of 700 meters showed no signs of bark beetle attack. However, we did find some wind-thrown branches with green needles within 600 yards which displayed boring dust. We did detect some of the small branch specialists in the needle clusters of nearby standing trees. We are currently working on theories for how *Ips* spp. are attracted to wind-thrown trees including perhaps the pheromone contribution of small branch specialist bark beetles which appear to pre-infect *Pinus*.


Cavanaugh et al. (2003) concluded that nineteen fossil equids – including *Hyracotherium* – belonged to a single monobaramin. However, baraminological studies have so far failed to establish strong evidence of discontinuity surrounding the Equidae, either because an outgroup was not included in the analysis (Cavanaugh et al. 2003) or because the datasets were not sufficiently holistic (Garner 2004). Consequently it has been impossible to determine whether the Equidae is holobaraminic.

Here I report a baraminological analysis based on Danilo et al. (2013), consisting of 26 taxa and 72 characters (six cranial and 66 dental). This dataset includes 24 characters for these taxa that are additional to those in already published datasets (Hooker 1994, Froehlich 2002, Badiola et al. 2005). Two of the ingroup taxa were equids; the rest were palaeotheres and other non-equid equoids. The outgroup taxon was the tapiromorph *Cardiolophus radinskyi*.

BDISTMDS version 2.0 was used to carry out a baraminic distance correlation analysis on this dataset (Wood 2008). All characters with less than 75% relevance were eliminated, leaving 57 characters; all the cranial characters were excluded. Three clusters of taxa can be discerned: (1) Five palaeotheres: *Anchilophus dumasi* + *Paranchilophus remyi* + *Lophiotherium cervulum* + *Palaeotherium magnum* + *Plagiolophus minor*; (2) Most other taxa, including the equids and the outgroup taxon; (3) Four species of the genus *Pachynolophus*: *Pachy. bretensis* + *Pachy. garimondi* + *Pachy. lavocati* + *Pachy. zambranensis*. The first group shows significant negative correlations with the second group; the third group shows no positive correlations with members of the first group but some positive and some negative correlations with members of the second group. *Eurohippus parvulus* is neither positively nor negatively correlated with any other taxon.

The analysis was re-run, with the first discontinuity-bounded group of five taxa excluded from the dataset. The aim was to see whether this would help to resolve any discontinuities among the remaining taxa. All characters with less than 75% relevance were excluded, leaving 21 taxa and 54 characters. Again, all six cranial characters were excluded. The outgroup taxon is neither positively nor negatively correlated with any other taxon. *Eurohippus parvulus* is negatively correlated with *Xenicohippus osborni*, but otherwise not positively or negatively correlated with any other taxon. Excluding these taxa, two clusters are evident: (1) Four species of the genus *Pachynolophus*: *Pachy. bretensis* + *Pachy. garimondi* + *Pachy. lavocati* + *Pachy. zambranensis*. (2) All remaining taxa, including the equids. Where statistically significant correlations are evident between the two groups, most are negative; however species of *Pachynolophus* occur in both groups and some are positively correlated with one another. Perhaps notably, the equid, *Plioliophus vulpiceps*, is negatively correlated with all four members of the *Pachynolophus* cluster.

Danilo et al. (2013, p. 205) point out that many of the species in this dataset are defined with only one tooth row or some isolated teeth. Thus, despite the inclusion of additional characters, the available datasets are still very non-holistic and it would be inappropriate to draw strong conclusions. However, from the second analysis a weak conclusion can be drawn of morphological discontinuity between the group that includes the equids and the group comprising *Pachy. bretensis* + *Pachy. garimondi* + *Pachy. lavocati* + *Pachy. zambranensis*.
with antibiotic profile, toxin genes and place of acquisition. There is a variation of S. aureus strains – but most change is found in tightly knit groups: households, dorms, and other close living quarters. The bacteria are “ping-ponging” around among students, changing as they go.

Liberty students carry both CA-MRSA over HA-MRSA strains. Many Liberty students were found to be hosts for multiple MRSA strains. In most cases, the right and left nares fielded separate strains. In one case, a student hosted similar HA-MRSA in each nostril, and a different intermediate MRSA strain in the left armpit. This further suggests that some individuals may host multiple strains of a species.

From preliminary growth curve tests, it was found that CA-MRSA isolates grow faster at 37°C (body temperature) than the HA-MRSA isolates. More CA-MRSA colonies were found than HA-MRSA after 12, 24, and 48 hours. CA-MRSA on average had larger colonies that grew faster than HA-MRSA. This may indicate that CA-MRSA isolates may have greater “fitness” than HA-MRSA. They may have the ability to colonize and outcompete competitors than their HA-MRSA counterparts. Further growth curves using Trypticase Soy (TSA) and Brain Heart Infusion (BHI) agars add support to this finding.

Recently, we have studied the comparative fitness between CA-MRSA and HA-MRSA to determine whether antibiotic resistance provides an enhanced fitness. Thus, repetitive antibiogram testing (Kirby-Bauer disk diffusion) aims to further confirm the antibiotic sensitivities of collected MRSA isolates. After determining the MRSA isolates antibiotic resistance profile, broth culture growth curves were used to determine a more precise growth rate profiles using the strains previously studied. In addition, investigation into the virulence factor profile of CA-MRSA and HA-MRSA will begin with hemolytic testing. We are examining correlations among virulence factors (ex. alpha, beta, and delta hemolysins), antibiotic resistance, and “genetic loads” (plasmid and phage genes) on isolates from Liberty University students. In addition, this will allow a better understanding of each type’s fitness and determine whether antibiotic resistant “superbugs” with a wide array of antibiotic resistance are truly fitter than other bacteria with less antibiotic resistance. The study has implications for the clinic and whether this is “evolution in action.”

Our current research focuses on 1) examining comparative fitness between CA-MRSA and HA-MRSA isolates and 2) studying correlations between virulence factors (esp. hemolysins and pigments), antibiotic resistance capacity, and growth rates to determine which factor(s) are a true indicator of biological “fitness.”


Environmental Tracking: Theoretical Considerations of Engineered Mechanisms Within Populations to Continuously Fill the Earth Across Generations
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I propose that God designed organisms to change with the environment in a manner analogous to human-designed tracking drones. Previous concepts have suggested that organisms track environmental change as per Van Valen’s Red Queen hypothesis or are nudged by natural selection to the peaks of changing fitness landscapes. These differ from my proposition in that they see organisms as passively driven by the vicissitudes of environmental changes over time. Organism’s changing forms are imposed on them from without. In contrast, I suggest active organisms detect and track the changes of essentially passive conditions external to them.

How might engineers design an autonomous organism to routinely match specific traits to environmental changes? That question brings design analysis (DA) into biological research. DA begins with thinking through major elements and assembly sequences necessary to achieve an outcome (e.g., tracking). Reference to similar human-made systems is valuable. This endeavor helps predict findings before reverse engineering and assists correlating discovered biological components to a function within systems.

The purpose of most tracking systems is to produce information that can be used to interpret an uncertain environment. Human tracking systems contain the following core elements: (C1) sensors (that detect conditions to which the system responds); (C2) logical algorithms (that specify responses of the system for each environmental condition); (C3) chronometer (that ticks out the timing specified in each algorithm); and (C4) output responses (that permit the system to act as specified).

Sensors are key elements at entity-environment interfaces. They are the principle trigger of innate, self-adjusting systems which facilitate an organism’s environmental tracking in at least four ways: 1) detect and utilize specific properties of nature; 2) detect external interface elements enabling mutual relationships; 3) detect conditions specified by the organism’ algorithm to be a “stimulus”; and 4) detect stimuli from parents in developing offspring.

Sensors may be coupled to internal oscillators in tracking systems. A Monarch Butterfly’s internal clock and eyes make up a time-compensated sun compass to accurately navigate to precise locations. Organisms also use these same sensors and condition-consequence logical algorithms to track environmental changes over time. Small livebearing fish, Poecilia mexicana, repeatedly colonize H2S-rich freshwater springs after detecting the pollutant. Their algorithms direct responses regulating the expression of hundreds of genes (Kelly 2016). Podarcis sicula lizards can detect dietary changes, and offspring rapidly developed gut cecal valves (Herrel 2008).

Organisms seem to possess each of these elements. The wide variety of environmentally-sensitive sensors in organisms and the epigenetic changes occurring in direct response to environmental stimuli, suggest organisms possess the necessary sensors (C1).
The one-to-one correspondence between particular environmental stimuli and particular epigenetic changes, suggest epigenetic mechanisms include (C2) logical algorithms. The circadian rhythms, seasonal and annual behaviors, and longevity programs so widespread in organisms, and the consistent timing of epigenetic changes, suggest organisms possess the necessary chronometer (C3). The consistent epigenetic responses for each environmental stimulus suggests organisms have been programmed with the necessary output responses (C4).

Populations of organisms could be seen from a design-based perspective as traveling through diverse environments and self-adjusting to even subtle changes very similarly to human-designed vehicles. Engineers know that with tracking vehicles all responses are produced internally. There is no direct link between external condition and response. Then perhaps with organisms, the environment cannot directly induce any internal changes either. The tight organism-environment relationship may be explained by populations of active organisms continuously tracking environmental changes. Innate mechanisms express inheritable phenotypes that bear problem solving potential which precedes environmental challenges.

Continuous environmental tracking may be how God displays His creatures’ extraordinary self-adjusting ability. What emerges is not a static picture. Rather, this is a spectacular kaleidoscope of innovative solutions to environmental challenges—demonstrating the depth and breadth of God’s engineering genius.


**Using Petaloid *Trillium erectum* to Study *Trillium* Genetics and Baraminology**

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Independent Scholar

The *Trillium* genus (Melanthiaceae) provides an opportunity to study species diversification because there are both strong similarity (such as an easily recognized form) and great diversity (so many species) in a single group. In terms of similarity, current baraminology suggests that the genus *Trillium* forms a monobaramin, with other genera of the Melanthiaceae, such as *Paris* and *Daiswa*, forming a separate monobaramin (Wood 2008). In terms of diversity, early research suggested that additional species of *Trillium* are being produced through interspecific crosses and chromosome duplication (Haga 1956), and *Trillium* has long been known for producing mutations which cause dramatic morphological changes (Weston 1916).

One opportunity to study the *Trillium* baramin comes from a colony of *Trillium erectum* designated *T. erectum* ‘plenum,’ which demonstrated petaloidy (the transformation of floral organs into petals). This colony was examined in order to develop a hypothesis about the genetic cause of the petaloidy. Five morphological traits were identified: petaloidy, additional whorls, irregular numbers of petals per whorl, variegated petals, and petaloid stamens which bore an anther. Many of these petaloid anthers contained pollen, which demonstrated an average of 65% viability.

Literature research indicated that four of the traits identified could be caused by a mutation in a C class gene. C class genes are MADS box genes which function in determining floral organ identity, promoting fertility, and controlling floral meristem growth. Mutations in C class genes generally cause petaloidy, infertility, and formation of additional whorls replacing the fourth whorl of the flower (Bowman et al. 1989; Coen and Meyerowitz 1991). On occasion, C class mutations have also been observed to cause variegated petals and irregular numbers and positions of petals (Bowman et al. 1989).

Further research on monocot order Liliales, which includes *Trillium*, indicated that C class gene underexpression is linked to petaloidy in genus *Lilium* (Akita et al. 2011). Similarly, it is causes both petaloidy and additional whorls in genus *Tulipa* (Kanno et al. 2007). Since C class genes are strongly conserved, a C class gene mutation in *Trillium* might similarly cause petaloidy and additional whorls, suggesting that *T. erectum* ‘plenum’ has a C class mutation.

However, the formation of anthers with fertile pollen is stimulated by C class genes. Thus, a C class mutant should not bear pollen. This apparent contradiction between the type of petaloidy and the fertility raises questions about the connection between different roles of C class genes in *Trillium*.

*Trillium erectum* ‘plenum’ therefore provides an opportunity to study C class genes in the *Trillium* baramin. Further research should include an attempt to identify and sequence C class genes in both *T. erectum* ‘plenum’ and wild type *T. erectum*. This would allow study of the roles of C class genes in *Trillium*, and might assist in understanding of diversification mechanisms in the *Trillium* baramin by demonstrating how a genetic mutation in *Trillium* can cause a morphological change. An attempt should also be made to sequence and compare C class genes in a variety of *Trillium* species. Identification of homology in C class genes would be expected within the *Trillium* holobaramin, and this should be done in conjunction with delimiting the holobaramin. Thus, research on C class genes in *Trillium* would enable study of both the clear morphological similarities and the rapid diversification in the *Trillium* baramin.


Editor: RWS
Hybridization and speciation have been hot topics in evolutionary biology, with recent studies highlighting the role of sexual selection and recombination in driving adaptive radiation. The Grants’ work on Galápagos finches emphasized that hybridization can lead to the formation of new species, sometimes becoming reproductively isolated from both parent species (Grant and Grant, 2014). Hybridization clearly affected average beak size in the finches they studied, and restored much of the lost variability after strong natural selection removed it during a drought.

Hybridization has been a hot topic in the literature as it relates to speciation, with the Journal of Evolutionary Biology devoting the February 2013 issue to the topic. Hybridization can have a variety of effects depending on the circumstances, from the coalescence of two or more species to formation of a new species (Abbott et al. 2013). Further, it has increasingly been implicated in adaptive radiations, where there is rapid diversification of organisms to fill a variety of new niches (Ford et al. 2015; Palmer and Kronforst 2015; Stankowski and Streisfeld 2015).

There appears to be several mechanisms by which hybridization can contribute to adaptation and speciation. When a population acquires adaptive alleles though hybridization, this is known as adaptive introgression, which can allow the population to persist and thrive as it faces future environmental challenges. This was noted in the medium ground finch population on Daphne Major island in the Galápagos (Grant and Grant, 2014). Other times hybrids may end up forming their own population that becomes reproductively isolated from both parent species.

However, the results can be far more dramatic than this. Hybridization can potentially provide alleles that aid in further adaptation and diversification, sometimes enabling the offspring to exploit new niches. Recombination can link or unlink genes in ways that may further promote adaptation and/or speciation (Seehausen 2013). Hybridization tends to increase heterozygosity, and heterozygosity has been shown to be positively correlated with mutation rate, thus increasing diversity even more (Amos 2016; Jin et al., 2016; Yang et al., 2015).

From a creationist standpoint, speciation within created kinds can be seen as part of the process of God’s creatures diversifying as they fill the earth according to God’s directive. This diversification not only allows creatures to adapt to their current environment, but, by maintaining the diversity in different populations, important alleles can be brought back into a population through hybridization. In addition to allowing for recovery from strong natural selection, hybridization can play a key role in further adaptation and radiation. Thus speciation is not only part of God’s providential care for his creatures, it also provides us with an amazing array of beauty to inspire appreciation for our creative Maker.


Hormone Regulation of Human Endogenous Retroviruses in Jurkat Cells

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Human endogenous retroviruses (HERVs) are repetitive genetic elements constituting ~8% of the human genome (Cooper and Hausman 2007, pp. 162-163). Most biologists believe they are remnants of ancient retroviruses randomly inserted into the host’s germline genome. Because human and ape endogenous retroviruses are orthologous in positions and in sequences, evolutionists use them as proof of common ancestry. However, there are cumulative evidences that some HERV elements perform essential physiological functions such as formation of the placenta (Mallet et al. 2004). In order for creationists to argue that HERVs were created in situ, we need to find the purposes of the unique design of retroviral elements and of their widespread distribution in the genome. Since the long terminal repeats (LTRs) of HERVs contain enhancers and promoters, it is reasonable to hypothesize their functions in coordinating the transcription of interspersed genes.

Involvement of HERV elements in reproduction and in embryonic development lead us to hypothesize that HERVs are controlled by female sex hormones. Hormonal regulation would support the argument that HERVs are integral parts of the human genome and therefore were probably created in the beginning. We have previously discovered that HERV transcription in peripheral leukocytes followed a monthly pattern during the menstrual cycle of reproductive-age women (Loggans et al. 2009). Expression of HERV genes were negatively correlated with plasma concentrations of progesterone and estradiol in cycling females.

Editor: PG
Pennsylvanian and Lower Permian coals are the marattialean tree—especially Eggert 1961; Bateman 1994). Dominating Upper the paleobotany of the two most prominent plant contributors to coastal swamp, delta plain and river levee environments. To forming environment from plants grown in place) deposits in authigenic and autochthonous (manufactured through a soil—sedimentary, non-local transportation) nature of Pennsylvanian plants and explain the detrital and allochthonous (water-borne consistent with the biblical Genesis Flood, to incorporate living after four hours of treatment, consistent with the findings in male PBMN cells.

If the results are confirmed, the next step is to analyze the mechanisms of hormonal regulation of HERVs in Jurkat cells, and on the potential function of HERVs in modulating immunity. Cooper, G. M. and R. E. Hausman. 2007. The Cell, a Molecular Approach, 4th ed. ASM Press, Washington, DC.


Editor: JWF

Biology of Rhizomorphic Lycopsids and Psaronius Tree-ferns in Relation to the Floating Mat Model for the Origin of Coal
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We extend the Floating Mat Model of Austin (1979), which is consistent with the biblical Genesis Flood, to incorporate living plants and explain the detrital and allochthonous (water-borne sedimentary, non-local transportation) nature of Pennsylvanian and similar coal beds. This is in contradistinction to the prevailing old-age model of coal formation, which treats coal beds as authigenic and autochthonous (manufactured through a soil—forming environment from plants grown in place) deposits in coastal swamp, delta plain and river levee environments. To help discriminate between the two models, we evaluate here the paleobotany of the two most prominent plant contributors to Carboniferous and Lower Pennsian coal beds. Dominating Middle Pennsylvanian coals are rhizomorphic tree lycopsids (see especially Eggert 1961; Bateman 1994). Dominating Upper Pennsylvanian and Lower Pennsian coals are the marattialean tree-


The anatomy of the tree lycopsids strongly suggests they were floating aquatic plants, not soil-rooted swamp plants. We conclude that lycopsid trunks and rhizomorphs contained truly hollow cavities filled with air (as opposed to aerenchymous tissue), an interpretation favored by many creationist writers. Mega sporangia of the dominant trees were attached to the subtending leaves and appear to have been dispersed as “boats with sails” to allow fertilization and germination to occur while the megagametophytes floated on water. Rhizomorphs developed to nearly full size while the trunk meristem was still gradually broadening but not elongating. Thus, sporophyte saplings were free-floating “star-fish” with aquatic, probably photosynthetic “bottle-brush arms,” radiating at a low negative angle from horizontal, which could not become embedded in soil and retain right-angle attachment of their appendages. After the branched rhizomorph became more or less full sized and intertwined to form a stable mat, then the main trunk elongated vertically more or less at full diameter, becoming a hollow cylinder supported by cortex tissue (“bark”), not the xylem (“wood”) tissue of familiar trees. The reproductive phase of tree lycopsids, when the plants produced terminal or lateral branches that bore spores, was short lived. Thus, most of the life of the lycopsid tree was spent as a “hairy pole,” which would be stable on its floating mat.

The stem of Psaronius was a narrow, upwardly thickening cane that was supported entirely by a buttressing jacket of adventitious roots. The inner roots were fused to the stem with spongy tissue, while the outer roots were free and abruptly flared into a skirt spreading across the substrate. Both root types were filled with extensive air-chambers. Conventional paleoecology places Psaronius rooted on swamp levees. However, trunk bases rooted in soil have never been found. Weiss (2011) suggests the flared roots formed a skirting raft allowing the tree to float on water or thin mud, with the stem base rotting and the increasing weight of growing trees forcing an increasingly thick skirt and lower “trunk” deeper into the water to counterbalance the upright weight. The gametophytes are unknown, though likely were photosynthetic and thalloid as in living relatives. Spores were small and airborne, and, even if lacking aquatic specializations, germination to form gametophytes could easily have been realized on floating debris.

Therefore, given the evidence against soil rooting of the tree lycopsids and Psaronius, these data support these plants as constituents of extensive living floating mats to provide detrital sediments as a source for coal. We believe these data coordinate well with five sedimentary characteristics favoring the Floating Mat Model for the origin of coal: (1) composition, (2) texture, (3) structure, (4) form, and (5) association.


Aristotle’s Intuition – Derivable from Theism While Contrary to Naturalism

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Truett-McConnel College

Modern science owes much to Aristotle, even though his scientific methodology (primary use of deductive syllogism) is no longer followed and many of his claims about the universe have been rejected (e.g. eternal universe, perfect heavens, up-and-down-moving elements). Most of Aristotle’s enduring contributions are among his intuitions, not his deductions.

In what follows, Aristotle’s claim is considered an intuition if it is neither obviously justifiable in Aristotle’s materialistic worldview, nor justified in Aristotle’s writings. Aristotle’s intuitive claims include presuppositions of modern science:

1. the universe exists (Physics 193a.3-5);
2. the universe is ordered (‘nature is everywhere the cause of order’: Physics 252a.12-13);
3. the universe’s order is simple (Physics 259a.7-13; Heavens 302b.28-30);
4. the universe’s order is understandable (‘being [is] knowable’: Physics 189a.12-13);
5. human senses are reliable (‘perception is never in error’: Soul 428b.18-19);
6. mathematics simulates the universe (Heavens 299a.14-15; Metaphysics 995a.15-18);
7. natural law is invariant (‘the same cause always produces the same effect’: Generation & Corruption 336a.27-28);
8. the universe’s structure includes symmetry (e.g. Generation & Corruption 330b.7).

Aristotle’s claims also include:

9. the universe is beautiful (‘the... end of nature is a form of the beautiful’: Animal Parts 645a.7-26);
10. everything has purpose (e.g. ‘nature never makes anything without a purpose’: Soul 432b.21-23);
11. the universe is designed (‘nature acts like an intelligent workman’: Animal Generation 731a.24);
12. the universe is awesome (‘every realm of nature is marvelous’: Animal Parts 644b.32-35 & 645a.7-18);
13. natural classification is nested hierarchy (Animal Parts 643a.14-16);
14. humans intuit natural classification (‘recognize natural groups by instincts of mankind’: Animal Parts 643b.10-15);
15. humans conceptualize only in time (‘we think only in connection with time’: Memory 450a.8-10);
16. humans conceptualize only in space (‘nothing not in a place is perceptible’: Heavens 276b.11-12); and
17. the universe strives for the divine (‘living things try to partake in the divine’: Soul 415a.28-415b.2).

All these intuitive claims are consistent with a Christian worldview. God creating the physical world with illustrations of His nature (Rom. 1:18-21) justifies Aristotle’s intuitive claims 1-12. The universe exists with an understandable order and humans have been given senses, minds, and language capable of detecting and understanding that order (claims 1-6) SO THAT we can see God’s attributes in the creation. God’s unchanging nature is pictured in the invariance of natural law (claim 7), God’s beauty is pictured in the universe’s symmetry and beauty (claim 8-9), God’s omniscience and sovereignty is pictured in the universe’s purpose and design (claims 10-11), and God’s awesomeness is pictured in the universe’s awesomeness (claim 12).

According to Wise’s ‘AIM Teleology’, God created the physical world so humanity could converge on a full knowledge of God. Since this explains why God created the physical world with illustrations of His nature, it also justifies Aristotle’s intuitive claims 1-12. This claim also justifies the remaining intuitive claims of Aristotle: God designed the creation classifiable into a nested hierarchy (claim 13) to illustrate His own hierarchal nature; God created the human brain/soul capable of intuitively recognizing nested hierarchy (claim 14); God created things in space and time as physical illustrations of His invisible nature (claim 15); God created the human brain/soul only capable of perceiving in space and time (claim 16); God created the universe so that it would draw humanity towards the perfection of God (claim 17).

The above observations stimulate interesting considerations, including: (1) Aristotle’s intuitive claims refute naturalism (e.g. claims 10 & 11 suggest an intelligence independent of the universe); (2) God included such a compelling testimony to Himself in the creation that even those with strong naturalistic bias intuitively accept truths unjustifiable in their own worldview; (3) Without justification from a theistic worldview, Aristotle’s intuitive claims are fatal to a stable philosophy of science (e.g. Hume argues from claims 15 & 16 that there is no way of knowing whether the physical world exists); and (4) the major failures in Aristotle’s deductions arise from a rejection of the other major claim of AIM Teleology (since God requires faith, He made it impossible to deduce truth from human reason alone).

Simple Math, Language, and Mind: An Alternative Megahistory Outline of Science

K.P. Wise
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When God seeks to awe Job with His nature, He provides a couple examples from the ‘ordinances of the heavens’ (Job 38:31-33), several examples from earth’s origin and processes (Job 38:4-30), and considerable discussion and numerous examples from the biological world (38:40-41:34). This, combined with Job’s response to examples in the same categories (in chapters 9, 12, and 25) suggest first that humans are innately impressed with items in these categories (i.e. they are designed to awe us), and second, God may have designed progressively greater complexity in celestial, terrestrial and biological creations.

Comparing and contrasting Aristotle’s 6th century B.C. thought with that of common Greek culture, previous Greek philosophers, and his mentor Plato, it appears that Aristotle strove to be a materialistic/naturalistic purist. In spite of this, he suggested...
a god-like first mover to explain celestial motions, assigned elements semi-mystical qualities to explain vertical terrestrial motions, proposed a non-materialistic ‘soul’ to explain the growth and development of organisms, and a possibly distinct rational ‘soul’ to explain human reason. Aristotle’s naturalism seems to fail him with regards to those very things God placed in the creation to awe us.

According to conventional versions of the history of science, ‘modern science’ is something analogous to a distinct ‘being’ that did not exist before its ‘birth’ in the second half of the 17th century. As per the conventional story,

- ‘birth pains’ included the publication of Copernicus’ heliocentric theory (1543) and Galileo’s challenges to Aristotelian physics (from 1609 to 1616);
- the ‘birth’ was founding of the Royal Society of London in 1660;
- the ‘new life’ included a new methodology (inducing the nature of reality using empiricism a la Baconian experimentation, instead of deducing the nature of reality using reason a la Aristotelian logic) and a new perspective (the universe operates according to a finite set of ‘natural laws,’ each characterized by a simple mathematical equation);
- the ‘first cry’ was the publication of Newton’s Principia (1687);
- the ‘maturation’ is seen over the next three centuries in the discovery of a host of natural laws, an explosion of understanding in astronomy, physics, and chemistry, the birth of subdisciplines such as thermodynamics, fluid dynamics, quantum mechanics, and relativistic physics, as well as innumerable applications in industry, transportation, energy, home conveniences, etc.

Unfortunately for the conventional version of the history of science, the 16th and 17th centuries see no substantial modification of methodology or perspective in the biological sciences. Though atoms of organisms ‘obey’ natural laws, natural laws do not exist in biology. The simple mathematics of the physical sciences do not seem to work on organisms.

I suggest that (1) what is conventionally described as ‘the origin of modern science’ is actually only ‘the origin of modern physical science’; (2) the success of the physical sciences is because physical bodies operate according to simpler mathematical principles than does everything else in the creation; and (3) the primary pattern of biology (e.g. development, physiology) is based on language, and language is not characterizable by simple mathematics.

If these claims are true (a) the history of science needs a complete revision, with ‘modern physical science’ representing merely an advance in understanding of the simplest patterns of God’s creation, and the whole history of science addressing more and more complex issues in a step-wise fashion; (b) human perception of creation’s complexity needs a complete revision to one that accepts a hierarchy of complexities (e.g. simple mathematics of physical bodies, language of organisms, structure of mind); (c) the status of scientific disciplines needs a complete revision, for physics is neither the greatest, nor the most difficult, nor the most foundational of the sciences, but rather merely the simplest of sciences; (d) the definition of science needs a complete revision, for mathematics, natural law, and ‘scientific method’ apply to only the study of creation’s simplest patterns; and (e) the 1961 discovery of the genetic code may have been the first birth pang (recognition of language in biology) leading to the birth of ‘modern biology’, and may portend a tremendous explosion in biological discoveries of the future (assuming we look for language).

Baraminological Analysis of Cranial Characters Implies that Homo floresiensis was Human
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In 2003, skeletal remains of a hominin were recovered from the Liang Bua cave on the island of Flores, Indonesia. Researchers initially assigned it to a new species Homo floresiensis (Brown et al. 2004), but others have argued that the remains were those of an individual with a developmental pathology, typically a form of microcephaly (see Line 2006). Previously, Wise (2004) argued that Homo floresiensis was a human based on cultural and paleontological considerations, but Wood’s (2010) hominin baraminology study failed to support this claim. Here, two additional character matrices that include H. floresiensis are examined using baraminic distance correlation (BDC) and multidimensional scaling (MDS). The first character matrix is a supermatrix compiled by Dembo et al. (2015) and includes 24 taxa and 380 craniomandibular characters. To calculate baraminic distances, fourteen taxa were included (H. floresiensis and the thirteen taxa with taxon relevance >0.4). After filtering for character relevance >0.75, 107 characters were used to calculate baraminic distances. BDC results reveal three groups and two lone taxa. One large group contains all taxa in Homo, and two smaller groups include Paranthropus and extant apes respectively. Within each group, taxa are joined by significant positive BDC. A. africans and A. afarensis are not correlated with any other taxa. Significant, negative BDC is limited to two correlations (P. robustus vs chimpanzee and P. boisei vs. H. floresiensis). H. floresiensis is positively correlated with H. sapiens, H. erectus, and H. habilis, but the bootstrap values are all <90%, indicating that the correlations are highly dependent on a specific subset of characters. MDS reveals a tight cluster of Homo taxa, with H. floresiensis as a substantial outlier, but the stress of the 3D MDS is unusually high (0.2), indicating that the exact positions in the 3D projection may be unrepresentative of the baraminic distances. The second character matrix was compiled by Zeitoun et al. (2016) exclusively from hominin calvaria. Thirty-one individual fossils are treated as OTUs, with four outgroups: extant chimps and gorillas, Sts 5 (A. africans) and KNM-ER 406 (Paranthropus). After filtering for 0.75 character relevance, 185 of the 468 characters were used to calculate baraminic distances for all OTUs. The BDC results reveal three well-defined clusters. The outgroup chimpanzee, gorilla, and KNM-ER 406 form one cluster, all of which are negatively correlated with members of Homo. KNM-ER 3733, 3883, and 1813 form a second cluster, but all BDC with these taxa have bootstrap values <90%. The third cluster consists of the remaining Homo OTUs, including LB1 (Homo floresiensis). Sts 5 is not positively correlated with any OTUs, but shares significant, negative BDC with nine
members of the *Homo* cluster (bootstrap values <90%). LB1 shares significant, positive BDC with thirteen other members of the *Homo* cluster, but all bootstrap values are <90%. MDS reveals a loose cluster of *Homo* OTUs with a gap separating the outgroup OTUs, but the cluster of KNM-ER 3733, 3883, and 1813 is not evident. Trinil 2 (*H. erectus*) is an outlier from the main cluster in the MDS results, and shares significant, positive BDC with only two other *Homo* OTUs. The stress for the 3D MDS is 0.42. Together, these results imply that LB1, *Homo floresiensis*, is part of a group of taxa that includes modern humans and is separate from australopiths and extant apes. From this, we may tentatively conclude that *H. floresiensis* is indeed human, confirming Wise’s (2004) initial assessment.


**There is Probably More Than One Ratite Holobaramin**

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The flightless ratite birds include living ostriches, emus, rheas, cassowaries, and kiwis and the extinct elephant birds and moas. Ratites are a common example of vicariant evolution, since modern ratites are found exclusively in the southern hemisphere and were presumed to be monophyletic. Wood and Murray (2003, p. 196) even suggested that ratites could be a single holobaramin, thus accounting for their anatomical similarity and biogeography. Recent molecular studies have revealed that the ratites are not monophyletic, thus necessitating a revision of the standard evolutionary account of their origin and biogeography (Harshman et al. 2008, Mitchell et al. 2014). To evaluate the baraminology of ratites, two character matrices were obtained from the published literature and analyzed using baraminic distance correlation (BDC) and multidimensional scaling analyses (MDS). The first matrix consists of 58 skeletal characters and eight taxa, compiled by Lee et al. (1997). Forty-six characters had character relevance >95% and were used to calculate baraminic distances. BDC results reveal three ratite clusters of two taxa each: (1) *Struthio/Rhea*, (2) *Dromaius/Casuarius*, and (3) *Apteryx/Dinornithids*. Both *Struthio* and *Rhea* shared significant, negative BDC with the two outgroup taxa Tinamidae and a composite Anseriformes/Galliformes taxon. MDS revealed three well-defined ratite clusters that correspond to the clusters found in BDC (3D stress = 0.034). The second matrix consists of 179 skeletal characters and 28 taxa, compiled by Worthy and Scofield (2012) and Worthy et al. (2014). After filtering for 0.95 character relevance, 129 characters were used to calculate baraminic distances. BDC results reveal three ratite clusters: (1) Struthionidae, Rheidae, Dromaiidae, and Casuariidae, (2) Apterygidae, and (3) Dinornithiformes and Aepyorniidae. The Tinamids share significant, positive BDC with all outgroup taxa. Significant, negative BDC occurs between every ratite cluster but especially between the Struthionid and Dinornithiform clusters. MDS confirms the presence of these three well-separated ratite clusters, although the 3D stress is moderately high (0.16). Taken together, these two character sets suggest discontinuities are present within the ratite groups. Both character matrices support including *Struthio* and *Rhea* in a single baramin and *Dromaius* and *Casuarias* in a single baramin, but the earlier character matrix of Lee et al. separate these two pairs of genera while Worthy et al. put them together in a single cluster. Likewise, *Apteryx* is separated from Dinornithids using Worthy et al.’s characters but included in the same cluster in Lee et al.’s characters. Since Worthy et al. (2014) included a much greater taxon and character sample in their matrix, we may tentatively conclude that there are three ratite holobaramins, corresponding to the clusters described from the BDC and MDS analysis of Worthy et al.’s characters. Since ratites likely form more than one baramin, Wood and Murray’s (2003) description of their biogeography needs to be revised. We may also note that analyses of both character sets separated the tinamous from all ratite clusters, implying that the ancestral ratite baramins were terrestrial creatures at creation.


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