

# CBS Annual Conference Abstracts 2018

## Toward a Young-Earth Model of Parasite Evolution

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Parasites invade our bodies, bore through our viscera, and consume our flesh and blood. Virtually every species on earth plays host to at least one unique parasite species, meaning half of the biodiversity on earth is composed of animals that exist solely at the expense of another animal (Dobson et al. 2008). The reality of a world filled with parasites contrasts sharply with the Christian belief in an all-loving and all-powerful Creator God. Could a truly loving God intentionally create such vicious animals in their present forms? If not, how did they come to exist?

The traditional metanarrative of Christianity, Creation-Fall-Redemption, presents an ancient and powerfully compelling answer. This world is not the way it is supposed to be, it is not the way God created it. Man, the caretaker of earth, rejected his role and rejected God, and humans, along with the environment they were responsible for, were subjected to decay (Rom. 8:20). The terrible things we see in the present are corruptions of the good that once was. This solution, that creation has deteriorated from good to bad, relies on a literal Adam, a literal fall, and thus a literal reading of Genesis as historic narrative. Accompanying these beliefs is often a belief in a recent creation event approximately 6,000 years ago, and from Young Earth Creationism (YEC) arises several extraordinary scientific claims, specifically here, that all species of parasites have evolved from non-parasitic ancestors in less than 6,000 years.

To test this claim, three questions were explored: 1) how often has parasitism evolved? 2) how many species exist in each lineage? and 3) what is the ancestral state of each lineage (i.e. what were parasites before they were parasites)? The first question has been recently answered by Weinstein and Kuris (2016) who thoroughly examined every eumetazoan lineage for incidences of parasitism. They conservatively estimate that parasitism has arisen independently 223 times within Kingdom Animalia. Using their published list of parasite lineages, a subsample of 100 lineages was randomly selected and analyzed for species diversity and evolutionary history. The well-curated online species database Catalogue of Life was searched for initial species counts, which were then verified when possible through a review of recent taxonomic literature. The ancestral state of each lineage was inferred using phylogenetic trees, or, in the absence of formal phylogenetic evidence, by relying on expert testimony from peer-reviewed journals. The number of species per lineage correlates with the likelihood of that lineage having evolved in

6,000 years. The majority of parasite lineages (53%) contained <10 species total and 92% included <1,000 species. This small number of species per lineage is remarkably compatible with a YEC model that suggests a relatively recent transition of parasites from non-parasitic ancestors and provides support for the hypothesis that God did not create this world filled with parasites from the beginning.

Another component of traditional YEC is that all animals were initially created to eat plants (Sherwin, 2013). In this particular analysis, no distinctly herbivorous ancestors were found. Instead, the ancestral state of most parasites was recovered as predaceous (83%), while the rest were saprophagous (7%), fungivorous (6%), or had unknown ancestral states (4%). However, defining “predator” within a YEC framework was unexpectedly difficult. Many parasite lineages are composed of tiny marine annelids, platyhelminthes, and other animals whose ancestors relied on plankton for food. Planktivores do not consume “plants” as defined by the Hebrew word “*eseb*” of Genesis 1:30 (“to all [animals] I have given every *eseb* for food”) and therefore I scored every planktivorous ancestor as a fallen “predator”. Importantly, if plankton, or any other non-*eseb* organisms (e.g. worms, insects) were included in God’s initial dietary provisions for animals, the recovery of a significant number of “predaceous” ancestors would not be as incompatible with YEC as at first appears. This highlights the need for a deeper discussion about biological death before the fall and potential interpretations of Genesis 1:30 within the YEC community.

Dobson, A., K.D. Lafferty, A. Kuris, R. Hechinger, and W. Jetz. 2008. Homage to Linnaeus: How many parasites? How many hosts? *PNAS* 105(S1):11482–11489.

Sherwin F. 2013. Parasites—Unwelcome Guests. *Answers* (1)34–37.

Weinstein, S.B. and A.M. Kuris. 2016. Independent origins of parasitism in Animalia. *Biology letters* 12(7): 20160324.

## Genomic View of *Escherichia coli* after 2,000 Generations in the Mammalian Intestine

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*Escherichia coli* is arguably the best understood of all model organisms. *E. coli* is a gram-negative facultative anaerobe that is usually citrate negative. In a famous peer reviewed study, microbiologists have tried growing one strain of *E. coli* in the laboratory for over 60,000 generations to watch it “evolve” into a citrate positive phenotype. The *in vitro* experiments to observe *E. coli* have demonstrated nothing but variation within a kind and no

new information. However, the information from growing *E. coli* to 60,000 generations has allowed us to see what the limits of natural selection are (namely, the ability to become citrate positive). But the biggest problem understanding the limits of *E. coli* evolution is that previous experiments have not occurred in a competitive environment. To address criticisms of the long-term evolution experiment and address whether natural selection operates in this experiment (i.e., survival of the fittest and reproduction), three different commensal strains of *E. coli* were inoculated into the competitive ecosystem of the streptomycin-treated mouse for over 2,000 generations. The streptomycin-treated mouse model is a competitive ecosystem because it decreases the facultative anaerobes population to below detection limits while leaving the remaining anaerobic microbiota left intact. Streptomycin-water (5 g/L) is given to the mice for at least 24 hours. Then, food and streptomycin-water are withheld from the mice to induce hunger and thirst. Overnight cultures of *E. coli* MG1655, HS, and Nissle were grown in LB supplemented with appropriate antibiotics. The overnight cultures were used to inoculate the mice to 10<sup>5</sup> colony forming units (CFUs) in 20% sucrose. Once the inoculum was consumed, food and streptomycin-water were returned to the mice *ad libitum*. Feces from the mice were collected at 5 hours, 24 hours, and every other day thereafter for fifteen days. After fifteen days, samples were collected every thirty days. The feces were resuspended in 1% tryptone and serially diluted before plating onto MacConkey Agar supplemented with streptomycin (100 µg/mL). Growth on MacConkey agar supplemented with streptomycin allows for enumeration of the specific strains of *E. coli* from the rest of the normal microbiota. Each of the strains of *E. coli* was shown to grow in the mouse intestine as evidenced by between 10<sup>5</sup> and 10<sup>6</sup> CFU/g feces. All of the colonies that grew on the MacConkey agar were subsequently picked into a 96-well plate containing LB with streptomycin, grown overnight at 37°C, and made into frozen stocks using an equal volume of 50% glycerol. The frozen stocks were stored at -80°C until they were later screened for motility (in essence, making the largest collection of *E. coli*). We observed significant changes of motility among all three strains. Motility was measured by growing the colonies in LB with streptomycin and then stabbed into motility agar. Not only did the three strains of *E. coli* become non-motile, but that they became non-motile at different rates within the intestine. The laboratory strain of *E. coli* became non-motile first, followed by the human commensal strain, and finally the probiotic strain. Interestingly, the population of *E. coli* remaining motile does not disappear entirely; the motile population returns to competitive levels for the laboratory strain of *E. coli*. As a result, the accumulation of non-motile mutations in these *E. coli* might appear to take over the population, but there are some very minor motile populations present below detection limits that reappear later on during the colonization. It thus appears that motility mutant population levels oscillate on a monthly cycle, which supports the Mueller's ratchet form of natural selection. According to Mueller's ratchet, populations do not disappear, but decrease to low levels and bounce back (ratchet) from lower levels. Non-motile populations of *E. coli* were surviving because of reproductive advantages; those advantages of being non-motile change and result in different populations being successful (i.e., returning to motile). Results from these experiments suggest

that natural selection is a real force working to preserve genetic information (i.e., motility) rather than select against it. While we observed changes to the *E. coli* genome, the *E. coli* remained *E. coli* and did not significantly change into a new species as evidenced by traditional microbiological techniques.

## Continuous Environmental Tracking: A Creationist Explanation for Biological Convergences

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Continuous Environmental Tracking (CET) is an engineering-based, organism-focused framework of biological adaptation (Guliuzza 2016). CET uses the following assumptions: 1. The same engineering principles that underly human-engineered tracking systems like cruise control apply equally to biological systems. 2. Organisms purposefully track environmental changes to deploy appropriate adaptable responses. These assumptions are supported by identifying within biological adaptable systems certain elements that define and mark design engineering, which are: analysis, synthesis, design, assembly, performance, sustainability, and termination/recycling.

The specific engineering elements of *design* and *performance* would give a deterministic nature to CET's operation that could differentiate it from stochastic models. Here, I analyze four studies since 2016 to identify engineering design and performance elements to distinguish between deterministic and stochastic mechanisms. Each study describes the repetitive expression of highly similar traits by unrelated or geographically separated organisms after they migrate to similar habitats. Evolutionists invoked convergent evolution to explain them. But the engineering performance element of CET suggests that if two organisms are actively tracking similar environmental changes, then the similar features can be explained by engineering principles. Although I do not have solid data that this theory refutes evolutionary mechanisms, I present it as a viable alternative model. For instance, the engineering design element of CET expects outcomes indicative of innate logic purposefully programmed to track changes and, thus, should be characterized as targeted, repeatable, predictable, widespread, and relatively rapid—outcome descriptors differing sharply to expectations of chance-based models.

The first study reports that after hurricanes decimated *Anolis* lizard populations on seven small islands with scrawny stems and twigs, researchers repopulated them with lizards from a nearby large, forested island (Losos 2017). Losos's discussion gives indicators that trait expression was a consequence of engineering performance since he described that average limb length steadily declined "in lockstep" on "all seven islands" over the course of only four years. Prior experience with *Anolis* enabled Losos to "predict" that legs would become better suited to twigs—which happened. These repetitive and predictable outcomes point to internal programming designed to consistently track vegetative changes.

In Brazil, geckos were rapidly isolated from mainland counterparts, and each other, when flooding for a reservoir created five new islands (de Amorim, E. et al. 2017). Large geckos shortly went extinct. That within 15 years each island's smaller gecko population ate larger prey and had independently adjusted with

equivalent responses (notably bigger mouths and heads relative to body length) suggests a necessary performance derived from internal logic. Designed programming is implied since the mechanisms were described as “predictable” and “precise.”

Descendants of short-tailed, prairie-dwelling mice (*Peromyscus maniculatus*) pioneered isolated forests. The researcher’s descriptions of findings intimate both engineering performance and design since each sub-population “repeatedly” increased the number and the length of tail vertebrae “implicating similar mechanisms of tail elongation” and not by “stochastic processes” (Kingsley et al. 2017).

Finally, Borowsky reports on a collection of studies about diverse arthropods, amphibians, and fishes that pioneer caves. The findings strongly indicate designed programming prescribing targeted solutions to cave-specific challenges since each kind “repeatedly” express similar traits converging on loss of eyes, depigmentation, circadian rhythmicity, and augmentation of other senses (Borowsky 2018). At least 200 cavefish species have adapted independently from surface ancestors.

The widespread repeatability and predictability of similar trait expressions which are targeted solutions to changing external challenges—which are the descriptors of deterministic mechanisms—in these studies match the characteristics of how human-engineered environmental tracking systems work. CET offers a plausible way to reinterpret the data for observable biological convergences from traditional stochastic explanations to one postulating that designed programming directs multiple organisms to track similar environmental changes, which functions to deploy similar and suitable responses.

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- de Amorim, E. et al. 2017. Lizards on newly created islands independently and rapidly adapt in morphology and diet. *PNAS* 114(33):8812–8816.
- Guliuza, R.J. 2016. Environmental Tracking: Theoretical Considerations of Engineered Mechanisms Within Populations to Continually Fill the Earth Across Generations. *Journal of Creation Theology and Science Series B: Life Sciences* 6:61-62.
- Kingsley, E. P. et al. 2017. The ultimate and proximate mechanisms driving the evolution of long tails in forest deer mice. *Evolution* 71(2):261–273.
- Losos, J. B. 2017. *Improbable Destinies: Fate, Chance, and the Future of Evolution*. New York: Riverhead Books.

## A New Method of Teaching the Origins of Biological Similarity

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Traditionally, people have sought to explain the patterns visible among living things with only a single explanation. Creationists often want every feature in every organism to be directly related to God’s special, supernatural creative act. However, attributing the origin of every feature of every organism only to God’s initial creative act leads to issues in natural evil (e.g., venom, parasitism). Additionally, such an explanation is unable to account for the fascinating patterns present in biogeography. Darwin countered with a different, all-encompassing theory: all similarities between organisms are because of shared ancestry. However, since Darwin it has been recognized that many traits, assumed to be homologous, have independently arisen in various lineages through convergence or as a result of horizontal gene transfer

(HGT). Neither explanation is exhaustive, and modern creationist models take into account aspects from both explanations. Unfortunately, many Christians, have misconceptions or only vague ideas of how to understand biological similarity, which can lead to an unfortunate lack of desire to engage in origins sciences and a wariness of any discussion related to biological change.

As a result, I have created a new teaching device that I have used in courses at The Master’s University (TMU) to explain the origins of biological similarity. I explain to students that all organisms are united by *Common Design*. Whether things were created *ex nihilo* in the Creation Week or changed and developed in real time in our world according to the way God built them and sustains them, all of the patterns of life are due to God’s creative genius. Even though all things are related by *Common Design*, the similarity we see in nature is a result of one or more of the four expressions of *Common Design: Common Blueprint, Common Descent, Common Event, and Common Function*.

By *Common Blueprint*, I mean that organisms exist in nested hierarchies because of a shared blueprint used by the Creator. An example of *Common Blueprint* is that all horses are mammals, all mammals are amniotes, and all amniotes are tetrapods.

By *Common Descent*, I mean that some organisms share similarities because they share a common ancestor. An example of *Common Descent* would be the shared body plans of horses, zebras, and donkeys, since they all descended from the same pair of organisms that disembarked from Noah’s ark.

By *Common Event*, I mean that some organisms share similarities they developed in real time because of similar events that happened to them or their ancestors. This category includes convergence (regardless of the source) and horizontal gene transfer. An example of *Common Event* would be the surprisingly similar appearance of horses and the proterotheriid litoptern *Thoatherium*, an extinct South American endemic hoofed mammal. Both animals possess a single hoof on each foot despite being descended from multiple-toed ancestors. They independently developed their similar features on separate continents.

By *Common Function*, I mean that some organisms share similarities because of their created function, but unrelated to a nested hierarchy. An example would be how horses and crabs both have legs because God designed both of them to be able to walk.

The four expressions of *Common Design* can be broken down into some interesting comparisons. Two of the four are traits that would conventionally be considered homologies (*Common Blueprint* and *Common Descent*), whereas the other two are traits that are conventionally considered analogies (*Common Event* and *Common Function*). In a different pairing of the expressions, two of the four happen in real time (*Common Descent* and *Common Event*), whereas the other two were made *ex nihilo* (*Common Blueprint* and *Common Function*).

After using this scheme in multiple classes at TMU, students have had positive reactions. In vertebrate paleontology class, we used this framework on multiple occasions when students would ask about the origins of particular similarities they noticed between creatures, whether it was hominids or cynodonts. It is my hope that further implementation of this framework will be helpful for Christian students attempting to think through the complexities of biological origins and similarity and will assist

them in seeing God's glory in every aspect of His creation.

## Applying Baraminological Methods to Understand "Basal" Mammaliaforms

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"Basal" mammaliaforms (Upper Triassic – Lower Jurassic) are a group of Mesozoic animals considered by the conventional evolutionary paradigm to be transitional between non-mammalian cynodonts and true mammals. In general, morganucodonts are seen as the most basal mammaliaforms, followed by docodonts, and then true mammals, which contains many Mesozoic groups such as "symmetrodonts" and eutriconodonts. Mesozoic mammaliaforms have been largely overlooked in creationist studies, but discerning their baraminological relationships is important to understanding the relationship of non-mammalian cynodonts to mammals.

In order to understand these relationships, we used BDISTMDS v. 2.0 (Wood, 2008) to carry out BDC (baraminic distance correlation) analysis on two datasets (Gaetano and Rougier, 2011; Meng et al., 2015) containing "basal" mammaliaforms, which we also visualized with MDS (multidimensional scaling). The dataset from Gaetano and Rougier (2011) contained 36 taxa (eutriconodonts, amphiletherians, and "basal" mammaliaforms) and 92 characters (71 dental, 21 mandibular). After a character relevance cutoff of 0.75 (which we used in all of our analyses), 53 characters remained. We excluded the eutriconodonts and ran the dataset a second time (23 taxa and 63 characters). We also analyzed the dataset from Meng et. al. (2015) focused on docodonts (23 taxa and 36 of 47 characters (42 dental, 5 mandibular)).

Our BDC results for Gaetano and Rougier (2011) showed three blocks of positive correlation. The block corresponding to Eutriconodonta showed only one instance of positive correlation outside the block (*Victoriaconodon* and *Comodon* with a low bootstrap value of 66%) and showed negative correlation with many other taxa. The smaller block ("basal" mammaliaforms) and the larger block (amphiletherians) showed some instances of positive correlation with each other. The MDS results for this analysis show three distinct clusters of taxa separated by gaps in morphological space, corresponding to the three blocks from the BDC. In the subset analysis lacking the eutriconodonts, there were two distinct blocks ("basal" mammaliaforms and amphiletherians) sharing no positive correlation and often sharing negative correlation, and the MDS results also showed two distinct clusters. Our BDC results from Meng et. al. (2015) showed two blocks of positive correlation that were mostly separated by negative correlation. The MDS results for Meng et al. (2015) are less clear than the BDC results. The "basal" mammaliaforms are closely clustered and far from any other taxa, but the docodonts are split up into three major clusters: a cluster containing most of the taxa, a cluster of three (*Haldanodon*, *Docodon*, and *Docofossor*), and a cluster of two (*Tikitherium* and *Gondtherium*).

We interpret Eutriconodonta to be a holobaramin because of their evidence for internal continuity (positive correlation and close clustering) and discontinuity with other taxa (negative correlation and gaps in morphological space) in the Gaetano

and Rougier (2011) analysis. The subset analysis also reveals that the "basal" amphiletherian taxa (ASA: Amphilestidae + "Symmetrodonta" + *Amphitherium*) are discontinuous from the "basal" mammaliaform taxa and may constitute a holobaramin. In the Meng et.al. (2015) analysis, we concluded that Docodonta is discontinuous from the other "basal" mammaliaform taxa, and that it may be a holobaramin, although the MDS results suggest there may be some discontinuities within Docodonta.

Because of this study, and our earlier work on non-mammalian cynodonts (Talavera and McLain, 2017), we conclude that there is evidence for discontinuity between groups considered transitional between non-mammalian cynodonts and true mammals. Rather than seeing a continuous grade from cynodont to mammal, these studies are showing that the spectrum is punctuated by discontinuities, as is expected from a creationist perspective.

- Gaetano L.C. and G.W. Rougier. 2011. New materials of *Argentoconodon furiatorum* (Mammaliaformes, Triconodontidae) from the Jurassic of Argentina and its bearing on triconodont phylogeny. *Journal of Vertebrate Paleontology* 31:829-843.
- Meng, Q.J., Q. Ji, Y.G. Zhang, D. Liu, D.M. Grossnickle, and Z.X. Luo. 2015. An arboreal docodont from the Jurassic and mammaliaform ecological diversification. *Science* 347:764-768.
- Talavera, A. and M. McLain. 2017. Applying baraminological methods to understand mammal-like cynodonts. *Journal of Creation Theology and Science Series B: Life Sciences* 7:7.
- Wood, T.C. 2008. Baraminic distance, bootstraps, and BDISTMDS. *Occasional Papers of the Baraminology Study Group* 12:1-17.

## Plato and Divine Revelation

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Similarities between Plato (c426-c348 B.C.) and scriptural claims are so significant, that some—from Aristobulus of Alexandria (fl. 181-124 B.C.) to Gmirkin (2016)—have suggested some sort of connection. Yet, since almost certainly Plato knew nothing about Scripture and his writings had no impact upon Scripture, the Scripture/Plato similarities may be interpreted to indicate Scripture is unnecessary for salvation, thus challenging the doctrine of scriptural sufficiency.

What claims of Plato converge on Scripture? Plato believes his chief purpose is understanding that which was eternal\*, unchanging\*, invisible\*, and perfect\* (e.g. *Timaeus* 51e-52a). This includes 'ideas' such as truth\* (e.g. *Laches* 100b), beauty\* and righteousness\* and justice\* and goodness\* (e.g. *Parmenides* 130b-131a), 'templates' for physical things (e.g. *Parmenides* 130c; *Republic* 6.484d), and 'concepts', such as rest and motion, likeness and unlikeness, largeness and smallness (e.g. *Parmenides* 129d-131a). Plato believes these things were all in a unified\* (*Parmenides* 129c-130a), beautiful\* (*Symposium* 211d-212a), harmonic\* order\* (*Republic* 6.500b-c), all summarized by 'the good\*' (*Republic* 6.508d). Because Plato also believes every physical event has to have cause (e.g. *Euthyphro* 10c) and purpose, he concludes that mind and manipulative ability are also needed. He then concludes (*Timaeus* 28a-e) that the universe came to be according to the purpose\*, will\*, and power\* of one creator god.

Among the Plato/Scripture similarities, asterisked items are attributes of God. God could have taught Plato these invisible aspects of Himself through illustrations in the creation (Romans

1:18-20). The constructs in God's mind used to create the illustrations and the constructs in the human mind God created to understand the illustrations, would correspond to Plato's 'templates' and 'concepts', respectively. Thus all Plato/Scripture similarities may be examples of truths God teaches *all* people through general revelation.

Although Plato accepts some truths about God, he by no means weaves them into a proper view of God. Plato applies personal attributes (the last three asterisked attributes) to his creator god. But Plato locates the remaining attributes in an impersonal, ideal 'world' distinct from the creator god. Plato also envisions the creator god submissive to the ideal world by striving to fashion the physical into as faithful a picture of the ideal world as possible. Furthermore, physical world evil suggests to Plato that evil was there from the physical world's beginning, and that the creator god does not have ultimate power over it. Plato, then, posits at least three separate eternal entities, evil, the ideal world, and a creator God, with the creator god lacking power over the other two. Thus, Plato's thought can be seen as an example of a person getting *some* truth about God from general revelation, but (without special revelation) being unable to come to a full knowledge of God—certainly not to saving faith in God. Rather than challenge Scripture's sufficiency, a comparison of Scripture and Plato reinforces the doctrine of the sufficiency of Scripture.

Gmirkin, RE. 2016. *Plato and the Creation of the Hebrew Bible*. Routledge, London.

## George McCready Price's Strange Theodicy and its Impact on Creationism

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From its inception in the fifth century A.D., the dominant Christian theodicy in church history has been Augustin's free-will defense (see, e.g., Whitney 1993). In fact, regarding the origin of *natural* evil, no other theodicy provides adequate explanation aside from Augustin's suggestion that natural evil is the result of a divine curse in response to man's sin. Yet, since Augustin's theodicy provides adequate explanation *only* with a young earth (Wise 2017), young-age creationism provides the only adequate explanation for natural evil (something claimed by Price 1913:263-266; 1916:91-119; 1942b:85).

In Augustinian fashion, Ellen Gould White (1828-1915) (White 1858, 1864, 1870, 1890, 1911) suggested that both Lucifer and humans were created as 'free moral agents'—even with Satan having limited authority to tempt them—and that moral evil began with Lucifer's choice (White, all five editions). Divergent from Augustin, White claimed (1) Lucifer's fall occurred sometime after a divine deliberation to create man and the actual creation of man (White 1858 & 1864; not specified in 1870, 1890, 1911), (2) God allowed the spread of natural evil to demonstrate to angels how horrible sin really was—and, ultimately, to justify His

judgment on moral evil (White, all five editions), and (3) Father and Son first discussed the matter of Jesus' sacrifice *after* man fell (White, all five editions) [NOTE: Claim 3 makes it seem to White's readers that God created humans without foreknowledge of their Fall.].

George McCready Price (1870-1963) expanded (altered?) White's point 1 by claiming (1') Satan fell at some unknown time *long before* Gen. 1:1 (Price 1916:89). Price altered White's point 2 by claiming (2') God specially designed (and created) the Earth and its attendant Solar System as a place where (in demonstration to the angels) natural evil could spread, without threatening the purity of heaven (Price 1916:89; 1934:156-157; 1942:41-45, 83-89). I call this theodicy Price's 'evil showcase' theory (PEST).

PEST explains (1) how Price (1902:112; 1941:10-14) could exclude from the creation of Genesis 1 all the universe outside the Solar System; (2) how Price could limit the Genesis 3 curse to the earth (Price 1942a:31-32), (3) why Price argues so strongly for the physical degeneration after the Fall of everything created in Genesis One (e.g. earth's matter [e.g. Price 1917:23-30], climate [e.g. Price 1930:130], plants and animals [e.g. Price 1906:70-71], humans [e.g. Price 1942a:83-84], and culture [e.g. Price 1916:150]), and (4) how Price could condemn eternal punishment of unbelievers (Price 1942a:163-164).

However, PEST also seems to question human free will—given Earth's design to spread natural evil, Earth's creation *after* Satan introduced evil, and Price's claim that the fall of a morally free being was nearly inevitable (e.g. Price 1942:104). This in turn raises disturbing questions about man's culpability for sin—which, in turn, seems to question the necessity of Jesus's sacrifice.

Via those who were influenced by Price, PEST might also have led to tendencies among some modern creationists to insist on human giants in Flood sediments, degeneration of human culture, modern organisms growing larger in antediluvian times, and diversification of organisms arising from degeneration and splitting of originally-created genetic information (the latter argued by Price 1924:34-36).

Price, G.M. 1902. *Outlines of Modern Christianity and Modern Science*.

Price, G.M. 1906. *Illogical Geology*.

Price, G.M. 1913. *Fundamentals of Geology*.

Price, G.M. 1916. *Back to the Bible*.

Price, G.M. 1917. *Q.E.D.*

Price, G.M. 1924. *The Phantom of Organic Evolution*.

Price, G.M. 1930. *A History of Some Scientific Blunders*.

Price, G.M. 1934. *Modern Discoveries Which Help Us to Believe*.

Price, G.M. 1941. *Genesis Vindicated*.

Price, G.M. 1942a. *If You were the Creator*.

Price, G.M. 1942b. *How the World Began*.

White, E.G. 1858. *Spiritual Gifts 1:17-28*, which passage was revised to create

White, E.G. 1864. *Spiritual Gifts 3:33-47*, and revised again to create

White, E.G. 1870. *The Spirit of Prophecy 1:17-54, Volume 1*, and revised again to

create White, E.G. 1890. *Conflict of the Ages 1:17-70*, and revised again to

create White, E.G. 1911. *Conflict of the Ages 1:33-62*, Second Edition.

Whitney, B.L. 1993. *Theodicy: Annotated Bibliography on the Problem of Evil*.

Wise, K.P. 2017. Paleoevil, Theodicy, and Models of Earth History. *Journal of Biblical and Theological Studies* 2(2):299-320.