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NEW CREATION STUDIES

ABSTRACTS

Creation Geology Society Annual Conference Abstracts 2025

Creation Biology Society Annual Conference Abstracts 2025

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Terrestrial Arthropods on the Ark? A Biostratigraphic Perspective

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When Genesis 7 says that pairs of 'everything that creeps on the ground' (ESV) were taken into the Ark, did that include terrestrial arthropods such as insects or arachnids? This question has been asked periodically by creationists; discussion has relied primarily on the Hebrew text. Jones **(1)** offered arguments from the Hebrew, contending that such species were not taken onto the Ark. Jones' arguments influenced Woodmorappe's **(2)** Ark feasibility study and Sarfati's **(3)** brief discussion. Morris **(4)** made allowance in the Ark for "approximately one million species of insects," noting many could have survived outside the Ark. Snelling **(5)** suggested that aquatic invertebrates survived outside the Ark, and that only a pair of each baramin (whether genus- or family-level) for others may have been on the Ark. Lacey **(6)** summarized several arguments from the Hebrew both for and against invertebrates being taken on the Ark.

Biostratigraphy provides an additional method to probe for an answer. Creationists can examine arthropod families which demonstrate pre-Flood lineage branching with post-Flood survival of those branches, as has been done with some vertebrate groups for Flood boundary-related questions (e.g. Arment **(7)**). If the family is a recognizable minimal boundary for most post-Flood baraminic lineages, then only one intrafamilial subgroup should be observed crossing the Flood boundary for an unclean terrestrial kind if it survived in the Ark. A Lower Cenozoic Flood Boundary is assumed—Cretaceous and lower strata are considered Flood deposition **(7)**.

The fossil record of terrestrial Pan-Arthropoda (2,862 families) was examined (PBDB; **(8-15)**), with Flood-crossing branches noted in the following families:

Acari (ticks and mites): Bdellidae, Cepheidae, Ixodidae, Neoliodidae, Trhypochthoniidae

Diplopoda (millipedes): Androgin athidae, Polyxenidae

Blattodea (cockroaches): Corydiidae

Coleoptera (beetles): Anthicidae, Anthribidae, Boganiidae, Belidae, Bostrichidae, Buprestidae, Cantharidae, Carabidae, Clambidae, Cryptophagidae, Dermestidae, Elateridae, Endomychidae, Eucnemidae, Histeridae, Hybosoridae, Hydrophilidae, Jacobsoniidae, Latridiidae, Leiodidae, Lucanidae, Melandryidae, Melridae, Ommatidae, Ptinidae, Ripiphoridae, Scarabeidae, Staphylinidae, Tenebrionidae, Tetratomidae

Diptera (flies): Atelestidae, Hybotidae, Ptychopteridae, Tanyderidae

Hemiptera (true bugs): Gelastocoridae

Hymenoptera (bees, ants, and sawflies): Embolemidae, Stephanidae, Xyelidae

Neuroptera (net-winged insects): Berothidae, Chrysopidae, Coniopterygidae, Ithonidae, Mantispidae, Osmylidae

Fifty-two out of 2,862 extant and fossil terrestrial arthropod families demonstrate multiple intrafamilial branches crossing the Flood boundary. We would expect no multi-branch crossing if terrestrial arthropods were taken into the Ark. This supports prior arguments that terrestrial arthropod survivorship took place outside the Ark. This suggests that the phrase 'in whose nostrils there was the breath of life,' is a critical modifier to the phrase 'all flesh died' in Genesis 7.

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Applying Statistical Baraminology to Invertebrates: An Exploratory Survey of Fly Kinds (Insecta: Diptera)

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Based on past statistical baraminology research, putative vertebrate holobaramins outnumber invertebrate holobaramins at a ratio of six to one (see lists in Wood **(1)**; Thompson and Wood **(2)**), yet it is unclear if any general conclusions drawn from vertebrate baraminology apply to invertebrate baraminology. To address this inequality, we attempted to infer holobaramins from 24 character matrices of dipteran taxa. The dipterans were chosen because of the extensive research on them (e.g. Marshall **(3)**) and the availability of character matrices. Diptera are also highly speciose with approximately 150,000 described species. To test whether dipteran families would be holobaramins, as observed in many vertebrate families, we collected morphological character matrices, each of which broadly sampled the taxa of one dipteran family along with outgroup taxa. Our sample represents 16% of the approximately 150 described dipteran families. According to Marshall's **(3)** classification, our sample includes 6 families of "Nematocera" and 18 families of Brachycera, and our largest group of families come from the Brachyceran Schizophora group. The number of taxa published in each matrix ranged from 8 to 186, with a mean of 70 (median 63.5). The number of published characters ranged from 20 to 220, with a mean of 102 (median 92). For each character matrix, we calculated simple matching distances from all characters (no character relevance cut off). We then performed distance correlation, medoid partitioning, and fuzzy analysis clustering using BARCLAY as in Wood **(4)**. Our results revealed that half of our matrices were inconclusive, with no clear or consistent clustering. Of the twelve matrices that produced clear, consistent clustering, seven indicated a family-level holobaramin (Empididae, Phoridae, Fanniidae, Neriidae, Diopsidae, Sepsidae, and Acroceridae), while the other five showed evidence of discontinuity dividing a family (Syrphidae, Scenopinidae, Curtonotidae, Oestridae, Culicidae). Our results indicate a higher fraction of inconclusive matrices (50%) in contrast to an analysis of mammalian character matrices with only 40% inconclusive matrices **(4)**. Most strikingly, only 29% of our matrices revealed evidence of a family-level holobaramin, whereas 57% of mammalian matrices revealed holobaramins in Wood's **(4)** analysis. Our conclusive matrices were on average smaller than our inconclusive matrices (mean 63 vs 77 taxa, 97 vs 107 characters, and 11 vs 13 outgroup taxa). Of the six "Nematocera" matrices we examined, only one of them produced conclusive results. The over-representation of so-called basal dipterans with deep fossil records (five of these families have fossil records that extend into the Mesozoic) in our inconclusive results suggests that our matrices are not adequately sampling either taxic or character diversity. We suggest that further work on the inconclusive matrices may yet reveal holobaramins via subdividing the taxic diversity to focus on individual families and a few outgroups rather than multiple whole families. Alternatively, the holobaramin of some flies may be closer to a superfamily classification that is poorly sampled in our present matrices. Our present results imply that only some dipteran holobaramins appear at roughly comparable taxonomic levels as vertebrate holobaramins.

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Observation of Plant Farming by Western Harvester Ants *(Pogonomyrmex spp.)*

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Western Harvester Ants (*Pogonomyrmex sp.*) can construct nests that house over 10,000 ants. The surface of the nest can display several square meters of denuded sandy soil arranged in a circular shape (disk), containing several nest openings (1-2 cm diameter). The worker ants cover the surface of the disk with small pebbles roughly 0.05-0.3 cm in diameter.

Although the ants remove most of the plants from the disk, we have noted that the ants also allow temporary growth of plants in the midden of the nest, which could act as a reservoir for regrowth of plants after a fire (1).

This report verifies our previous observation by noting the regrowth of plants in a midden for a second year (Spring 2025). In addition, during the late summer of 2024, we observed harvester ants shoring up several thorny seed-bearing ragweed plants (*Ambrosia psilostachya*) with a mound of pebbles at their base. We have observed thorny ragweed seeds near the active nest opening. We suggest that the harvesting of thorny seeds represents another nest design feature of harvester ants that may act as a deterrent to rodents.

Relatedly, we have also observed in four nests that, before winter, *Pogonomyrmex* close their ground-level nest entrances by filling most of them with pebbles. A lone entrance is covered with a mesh of short plant stems roughly 0 .10-0.30 cm in diameter and 0.5 to 3.0 centimeters in length, arranged in a circular-shaped area (2.0-5.5 cm diameter) surrounding the opening. The stems can be arranged in a condensed but slightly scattered pattern, often resulting in a crisscross pattern. Some seeds, including thorny ragweed seeds, are trapped under the mesh of stems.

A similar nest construction phenomenon can be observed on the nest of American Southeast harvester ants, *Pogonomyrmex badius*, which collect charcoal to construct the nest surface. A leading entomologist has tested multiple hypotheses for why the harvester ants gather charcoal but has not been able to determine the reason for this activity (2). One report, however, has shown that the charcoal, which is sequestered near the nest entrance, may absorb a chemical signal that deters other ant species (3).

We have noted that nest openings devoid of stems can easily collapse shut when under pressure. However, we have found resistance to collapse when the same amount of pressure is applied to the stem-covered openings. During the warm summer months, western harvester ants can clear a pebble-blocked nest opening often within minutes; however, during the winter, the ants appear to be much less active.

We propose that the thorn-bearing stem-covers act to protect the western harvester ant nest from aggressive seed-collecting rodents and may also support, maintain, and protect the nest opening from damage caused by water runoff from rain and melting snow in the winter months **(4)**. We also observe for the first time harvester ants supporting plants outside their disks by creating mounds of pebbles at the base of plants that produce thorny seeds. This is also consistent with the observation that plants show greater growth on the edge of the nest disk **(5)**.

These mutualistic relationships between harvester ants and plants are consistent with living creatures that possess design features that promote the preservation of both plants and ants; consistent also with the industriousness of ants noted in scripture (Proverbs 6: 6-8).

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Citation Francis J, Blaschke JD. Observation of Plant Farming by Western Harvester Ants *(Pogonomyrmex spp.)*. New Creation Studies. 2025;1(Suppl. 1):8–9.

Common Development as a Synthetic Theory of Creation Biology

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The title "Nothing in Biology Makes Sense Except in the Light of Evolution" (1) was exaggerated to fit its apologetic context. Yet, it is still true that modern evolutionary theory explains a wide variety of data from biosystematics, biogeography, comparative anatomy, embryology, molecular biology, population biology, genetics, and paleontology. Young-age creation biology has heretofore lacked a theory of similar explanatory power. Here, we offer **common development (CODE) theory** for multicellular organisms that we believe enjoys more consilience and explanatory power than even modern evolutionary theory.

Below, as we work through biological phenomena explained by CODE theory, we denote those phenomena explained by modern evolutionary theory with "$^{(+)}$", those phenomena partly explained by and partly challenging to evolutionary theory, we denote with "$^{(+/-)}$". Phenomena that evolution finds completely anomalous, we denote with "$^{(-)}$", and phenomena for which modern evolutionary theory offers neither an explanation nor an expectation we denote with "$^{(o)}$".

According to CODE theory

a. all organisms in certain large groups (*e.g.*, all plants, all animals) were created with the same **ontogenetic potentiality space** (OPS)—a tree-like branching system of potentially realizable one-way ontogenetic pathways through multidimensional character space.

b. exquisitely designed mechanisms of developmental integration yield actual morphologies that thrive in the embryological environment at every point on an OPS pathway—many of them with the potential of thriving as adult morphologies in a post-embryological environment.

c. each created organism was also created with an **ontogenetic memory**—a sequential list of each ontogenetic 'choice' made at each successive branch point on the OPS that would guide an organism's development from a single cell through the OPS pathway to the adult morphology. This ontogenetic memory is passed on to each offspring and determines that offspring's **ontogeny** (the OPS path actualized by that offspring).

At any given point in time in earth history, we suggest **CODE theory** would explain

1. the tree-like pattern of cell lineages in organismal ontogenies$^{(o)}$,
2. alternation of generations$^{(o)}$,
3. indirect development$^{(o)}$,
4. von Baer's laws$^{(o)}$,

5. the first-order nested hierarchical pattern (5a) of biological classification at all taxonomic levels(+), (5b) of adult morphologies in multidimensional character space(+), (5c) of discontinuity-bounded groups of continuity at every taxonomic level(+/-), and (5d) of consistently recognized taxa at all taxonomic levels(+/-),
6. persistence of species morphology despite changes in environment, and despite gene flow through hybrid zones(-),
7. overall cladogram similarity when constructed using adult similarity *or* duration of embryonic similarity *or* molecular similarity of any one of many biomolecules(+)—*and* homoplasious contradictions among those cladograms(-),
8. Owenian homologies, regardless of overall organismal similarity(+/-),
9. non-intermediate nature of most characters in morphologically intermediate species(+/-), and
10. similarities between humans and animals (+).

We would further suggest that CODE theory combined with rapid burial of a single, pre-Flood biota would explain Paleozoic and Mesozoic

11. stasis and abrupt appearance at every taxonomic level(+/-),
12. paucity of fossil transitional structures (-), and
13. non-intermediate nature of most characters in morphologically intermediate species(+/-).

Modern ontogenies include alternate ontogenetic pathways converging on common morphologies. This suggests that at least some OPS pathways anastomose. We believe OPS **anastomoses** would explain

14. alternate ontogenetic pathways in modern ontogenies(o),
15. Owenian analogies and cladistic homoplasies, regardless of overall organismal similarity(-).

The intraspecific heterochrony in modern ontogenies suggests that developmental integration mechanisms in ontogeny can offer options in the relative developmental rates of different parts of an organism. We believe similar **heterochrony** in the OPS would explain intraspecific heterochrony(o),

16. sexual dimorphism(o),
17. insect caste morphologies(o),
18. paedomorphic and peramorphic characters (as determined by inter-specific comparisons anywhere among organisms)(o),
19. vestigial organs (as determined by interspecific comparisons anywhere among organisms) (+/-),
20. atavisms(+/-), and
21. embryological recapitulation—both those examples that could be recapitulating earlier adult forms (+), and those that cannot (-).

A review of the above (+)'s and (-)'s suggests that CODE theory has the potential of being a synthetic theory of creation biology with substantially superior explanatory power for multicellular organisms over modern evolutionary theory.

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Citation Wise KP, McLain MA. Common Development as a Synthetic Theory of Creation Biology. New Creation Studies. 2025;1(Suppl. 1):10–11.

Common Development Model for Antediluvian Biozonation and Paleontological Pattern

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The order of the fossil record has been a long-standing challenge to Flood theorists. The earliest creationist responses—beginning at least as early as Price **(1)**—focused on denying the order. This involved everything from claiming no order in the entire fossil record (Price's approach) to denying the existence or interpretation of particular stratomorphic intermediates. This approach has not stood the test of time because the fossil record really does exhibit a global pattern, and really does contain stratomorphic intermediates. A second creationist response, beginning with Clark **(2)**, is to explain fossil record order by antediluvian biozonation. This approach admits the reality of the pattern, and can be designed to generate the fossil record perfectly. However, biozonation hypotheses are typically *ad hoc*—philosophically weak because they provide no rationale for why or how God created that particular biozonation. We here offer a testable model that has the potential of explaining fossil record patterns based on a single global pattern of antediluvian biozonation.

McLain **(3)** argues for a strong morphological pattern of increasing "mammal-ness" in multiple therapsid groups through Permian and Triassic rocks in South Africa, Russia, and China. McLain suggested antediluvian biozonation to explain the up-section trend in "mammal-ness." However, McLain also recognized that the trend in characters in the "mammal-ness" trend corresponds to character trends in mammalian ontogenetic development. If the stratigraphic trend in therapsids is due to antediluvian biozonation as McLain suggests, then the geographical gradient of antediluvian therapsids followed therapsid ontogenetic development.

The ammonoids—an extinct cephalopod subclass—function as index fossils in the Mesozoic. In general, the ammonoid biostratigraphic trend is towards increased septum complexity. Because the ammonoid shell preserves septa from an ammonoid's entire life, we also know that ammonoid septum complexity increases with ontogenetic development. This would be a second example (with that of the therapsids) of a Mesozoic biostratigraphic trend corresponding to an ontogenetic trend. Rather than being a coincidence, we suggest that these two cases—one in the water realm and one in the land realm—might be providing insight into the biozonation pattern of the entire antediluvian world.

We here suggest generalizing McLain's **(3)** suggestion for therapsids into a mechanism for maintaining antediluvian biozonation for all organisms across all environments. Spectra of environmental—perhaps biomatrix—triggers, combined with common ontogenies and sensors across major groups (*e.g.*, all animals, all plants), could maintain strong biozonation across the planet. Biozones where the spectra of environmental triggers coincided with transgressing Flood waters—such as those oriented perpendicular to antediluvian shorelines—would result in a stratomorphic series of the biozone morphologies in successive Flood strata.

We would expect fossil sequences generated by this mechanism to have the following characteristics: (a) morphological trends that follow ontogenetic trends, including those with no known selective value, (b) parallel stratomorphic series in multiple groups, (c) common parallel and convergent characters, (d) stasis and abrupt appearance of taxa at all taxonomic levels, (e) seemingly unbridgeable morphological gaps between taxa, and (f) intermediates with character mosaics. These characteristics are observed in both Mesozoic synapsids and ammonoids.

We suggest that this common development model will provide explanation for many, if not most, biostratigraphic patterns in Flood sediments—*e.g.*, claimed evolutionary sequences as well as index fossil patterns used to build the global lithobiostratigraphic column.

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Common Development as a Guide for Post-Flood Intrabaraminic Diversification of Ark Organisms

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In a diagram that represents the ontogenetic cell lineages of a parent and one of its offspring, the parental ontogeny is represented as a flat-topped branching tree. The offspring ontogeny is another flat-topped branching tree atop the first, rooted in one of the terminal branches of the parent tree. This is accomplished, at the beginning of each new generation, with the 'resetting' of the first offspring cell's potency to 'totipotent.' And, although that cell generally follows the ontogenetic memory that generated it, we know that at least part of that memory can be erased (*e.g.*, the epigenetic 'choices' along its ontogenetic path). This erasure essentially allows the next generation to potentially follow a different, already extant (potential) ontogenetic pathway. From at least the time of Marsh **(1)**, such a diagram looks surprisingly similar to creationist representations of baraminic history. Antediluvian diversification looks like the parental cell lineage, the flat-top of that tree representing the extinction of most of the baramin at the time of the Flood. The post-Flood diversification looks like the offspring cell lineage tree—flat-topped with the organisms of the present.

Though Wise **(2)** did not offer an actual mechanism for post-Flood intrabaraminic diversification, he did suggest that that diversification may have been strongly analogous to cell lineage ontogenies. Although we still lack an actual mechanism, we suggest diversification and ontogeny look similar because intrabaraminic diversification involves the actualization of pre-existing ontogenetic potentiality space (OPS). As per Wise and McLain's **(3)** CODE theory, the moment before the Flood began, every individual animal possessed the same OPS (and something is probably similarly true for all plants). After the Flood decimated that population, we suggest that each ark survivor's ontogeny was 'reset,' and its ontogenetic memory was erased, back to a **baramin reset point** on the OPS. Offspring of each Flood survivor, then, had the potential to traverse any of the OPS branches downstream of the baramin reset point, just as organisms after creation had the potential to do the same downstream of the ontogenetic memory given them at creation. After the Flood, storage of the realized branch 'decisions' in ontogenetic memory then fixed subsequent post-Flood ontogenies and taxa. Diversification of this kind would explain

1. what a baramin is (all OPS morphologies downstream of a reset point),
2. why different baramins are defined at different taxonomic levels (as per the taxonomic level of their respective reset points),
3. the difficulty of distinguishing holobaraminic discontinuity among degrees of discontinuity found above and below the baramin,
4. supra-baraminic nested hierarchy,

5. (potentially) how intrabaraminic diversification was initiated across all taxa at the Flood (*e.g.*, via a common sensor activated in all organisms by a single Flood trigger),
6. how baraminic morphospace was efficiently refilled after the Flood (via already-created OPS pathways filling that space),
7. how small post-Flood populations could expand and diversify without being subject to deleterious effects of inbreeding,
8. rapid post-Flood diversification,
9. intrabaraminic stratomorphic series in post-Flood strata following lines of ontogenetic development,
10. stasis and abrupt appearance of Cenozoic taxa, and
11. intrabaraminic disparity appearing before diversity in Cenozoic sediments.

Environment-induced alternate genetic pathways in modern ontogenies suggest that at least some ontogenetic branches are 'chosen' based on sensors to physical and/or organismal environment. Such **environmental sensors** in the OPS could explain

12. environment-induced alternate genetic pathways in modern ontogenies, and
13. modern symbiosis-dependent morphologies and behaviors.
14. Similar environmental sensors during post-Flood intra-baraminic diversification could explain
15. 'adaptations',
16. parallel 'co-adaptations',
17. Cope's Rule,
18. simultaneous appearance of connected designs among related and unrelated organisms (*e.g.*, C4 photosynthesis and hypsodonty with spread of grasslands), and
19. abrupt and independent origin of entire communities.

We believe this developmental model has the potential of providing creationists their first comprehensive explanation of the post-Flood fossil record.

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Dipnoi: An Apobaramin Relative to Porolepiformes and Other Sarcopterygians

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Lungfish are a fascinating group of fish capable of breathing both water and air. They have a disjunct modern range, with each of the three living genera found on separate continents: South America, Africa, and Australia. Together with many extinct species, lungfish are placed within Dipnoi, which is often grouped with Porolepiformes in Dipnomorpha as the sister taxon to Tetrapodomorpha within Rhipidistia. Evolutionists consider this to indicate a shared common ancestry, but from a creationist perspective, lungfish should be distinct from other fishes and tetrapods. To analyze Dipnoi with statistical baraminology, three character matrices were used: Friedman (1) (26 taxa, 70 characters), Cavin et al. (2) (16 taxa, 14 characters), and Kemp et al. (3) (17 taxa, 74 characters). Each dataset was entered into BARCLAY (4) to get Pearson and Spearman baraminic distance correlation (BDC), multidimensional scaling (MDS), partitions around medoids (PAM), and fuzzy analysis (FANNY) results.

The BDC plots from Friedman (1) show two blocks of positive correlation: Dipnoi and the rest of the sarcopterygians. Similarly, MDS shows two very distinct groups, and the PAM and FANNY results also have the highest average silhouette width at the same two groups. These results strongly suggest Dipnoi is discontinuous from Porolepiformes and other sarcopterygians, indicating that Dipnoi is an apobaramin. These results agree with Cserhati (5) who concluded through mitochondrial DNA analysis that lungfishes are discontinuous from other living fish.

The BDC plots for the Cavin et al. (2) dataset show two blocks of taxa (Gnathorhizidae + non-ceratodontiforms and non-gnathorhizid Ceratodontiformes) mainly separated by negative correlation, except in the Spearman BDC, where a chain of positive correlation unites *Gnathorhiza*, *Microceratodus*, and *Ptychoceratodus*. MDS shows one large cluster separated in space from four other taxa grouped into pairs (Gnathorhizidae versus the non-ceratodontiforms). *Microceratodus* clusters with the ceratodontiforms. PAM and FANNY were both best at two groups, corresponding well with the BDC plots. However, *Microceratodus* has a negative silhouette value in the group containing Gnathorhizidae + non-ceratodontiforms.

For the Kemp et al. (3) dataset, the BDC plots separate the non-ceratodontiforms from the ceratodontiforms, although the Pearson BDC shows no correlation between the gnathorhizids and any other taxa, whereas the Spearman BDC unites them to the other ceratodontiforms with shared positive correlation. Unlike with the other two datasets we analyzed, PAM and FANNY gave different results with highest average silhouette values. The two-group model was best for FANNY (0.38) versus five groups (0.33), whereas the five-group model was best for PAM (0.39) versus two groups (0.3). The two-group PAM model places the gnathorhizids in with the non-ceratodontiforms (although with negative silhouette values), whereas in FANNY they are grouped with the ceratodontiforms. The five-group PAM model consists of Gnathorhizidae, Lepidosireniformes, non-lepidosireniform Ceratodontiformes, and two groups of non-ceratodontiform Dipnoi (*Dipterus* + *Chirodipterus* + *Ctenodus* and *Ganopristodus* + *Conchopoma* + *Sagenodus*). FANNY at five-groups, by contrast, places some of the non-lepidosireniform ceratodontiforms with the gnathorhizids and sets apart *Mioceratodus* + *Neoceratodus* + *Gosfordia* as its own group. Interestingly, the MDS results do show five clusters of taxa, which correspond to 1) *Dipterus* + *Chirodipterus*, 2) other non-ceratodontiforms, 3) Lepidosireniformes, 4) *Mioceratodus* + *Neoceratodus* + *Gosfordia*, and 5) the other ceratodontiforms (including Gnathorhizidae).

Analysis of Cavin et al. (2) and Kemp et al. (3) revealed evidence for discontinuity within Dipnoi, with good evidence for at least two holobaramins: one approximating Ceratodontoidea and the other composed of non-ceratodontoid lungfish. However, there could be as many as five holobaramins, which may be suggested by PAM and MDS. More research needs to be done to clarify the baraminic relationships within that apobaramin Dipnoi, which will be helpful for models of post-Flood lungfish biogeography.

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Progress Report on a Morphometric Analysis of Hominin Pelves

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Among young-age creationists, disagreement over the habitual bipedality of *Australopithecus* persists **(1)**. The shape of the pelvic girdle is a key feature for understanding a fossil hominin's locomotory ability. Among extant quadrupedal apes, hemipelves or innominates are relatively flat, superoinferiorly extended, with broad, laterally directed ilia. Their sacra are superoinferiorly elongated and mediolaterally narrow. In contrast, modern human innominates are much shorter and rounder, with ilia that curve to approach the sagittal plane. Modern human sacra are mediolaterally wider than they are superoinferiorly long. These differences reflect specializations for habitual bipedality in *Homo sapiens* and specializations needed for the unique, quadrupedal knucklewalking practiced by extant apes. If *Australopithecus* were habitually bipedal, we might expect their pelvic shape to resemble that of *Homo sapiens* more than that of extant apes. Alternatively, if *Australopithecus* were not habitual bipeds, we might expect their pelvic girdles to resemble extant apes or present a shape distinct from both *Homo sapiens* and extant apes. Here, we evaluate pelvic shape using casts of 19 innominates of fossil hominins, most of which are fragmentary and could provide only partial data. We also examined casts of one right and one left innominate from each of the extant species *Homo sapiens*, *Gorilla gorilla*, *Pan troglodytes*, and *Pongo pygmaeus*. Our fossil sample included five specimens attributed to Neandertal or *Homo heidelbergensis* (Kabwe E720, Krapina 207, Feldhofer 1, Tabun, and Arago 44), four specimens attributed to *Homo erectus s.l.* (UA 173+405, OH 28, KNM-ER 3228, and KNM-WT 15000 L), eight specimens attributed to *Australopithecus* (MH1, MH2, AL-288-1, Sts 65, Sts 14 L, Sts 14 R, MLD 25, and MLD 7/8), and two putative *Paranthropus* specimens (SK 3155b and SK 50). We measured 33 linear and angular variables for these specimens. Due to incompleteness of fossil specimens, measurements per fossil range from 9 (Sts 65) to 29 (Sts 14 R). Using these measurements, we performed a preliminary morphometric analysis using standard Euclidean distances, principal coordinates analysis (PCoA), and medoid partitioning in R (r-project.org). Two-dimensional PCoA neatly separates the great apes from the hominins along the first coordinate. Along the second coordinate, members of *Australopithecus* and *Homo* partially separate with overlap. The Nariokotome innominate KNM-WT 15000 L appears in the range of the *Australopithecus* region, and the two *Paranthopus* specimens SK 50 and SK 3155b appear within the *Homo* and *Australopithecus* region respectively. To determine if any of these trends could be recognized as clusters, we applied medoid partitioning to our Euclidean distances for 2-5 clusters. We found that partitioning at two clusters gave the highest average silhouette width (0.61), with 5-cluster partitioning the next best with an average silhouette width of 0.5. Two-cluster medoid partitioning separated great apes from hominins. Beginning at 3-cluster partitioning (average silhouette width 0.45), the hominins separate into two clusters roughly corresponding to *Homo* and *Australopithecus,* with *Paranthropus* SK 50 in the *Homo* cluster and Neandertal Tabun, and *Homo erectus* KNM-WT 15000 L in the *Australopithecus* cluster. At four clusters, medoid partition separates gorillas from the other extant great apes, and five clusters separates the chimps and orangutans. These preliminary results appear to indicate that the typical australopith innominate exhibits a different shape than the typical *Homo* innominate, but the difference between habitually quadrupedal animals and hominins overshadows these differences. This suggests that the major difference in the pelves examined is between quadrupeds like chimpanzees and bipeds like *Australopithecus*. To extend these preliminary findings, we intend to increase the sample of extant innominate measurements using hundreds of 3D scans from Morphosource (morphosource.org) and with these new measurements to perform a more rigorous morphometric and cluster analysis.

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A Survey of Contemporary Evolution and Its Implications for Post-flood Speciation Models

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Current creation models depend on rapid speciation to explain the biodiversity of life today. Darwinian mechanisms such as natural selection cannot account for so much speciation in the time between the worldwide flood and the present. Creationists need new mechanisms to account for dramatic genetic evolution. While this paper will not propose novel mechanisms to explain all speciation, it will survey known research on contemporary evolution to identify what natural conditions can cause rapid speciation to occur. Contemporary evolution refers to the evolution of traits in short time scales (years to decades). Genetic speciation is defined as a population becoming a new species over time.

One example of contemporary evolution is the European blackcaps, a songbird species that changed morphologically in response to new migration routes **(1)**. This theory fits nicely in a post-flood model in which avian kinds rapidly speciate as they develop migration patterns. In cichlid fish, phenotypic differences emerged in reproductively isolated fish populations that both lived in Lake Victoria **(2)**. This research also suggests that sensory drive is another factor that induces contemporary evolution. Allopatric adaptation can also drive contemporary evolution, as demonstrated by the Galapagos tortoises. As a tortoise population colonizes new land, it rapidly adapts to new environments. New traits arise quickly through allopatric speciation **(3)**.

Contemporary evolution occurs in a wide range of species. Several other examples could be listed here. While only a comparative few have been directly documented, these cases are diverse in nature, encompassing species in major vertebrate classes.

One form of contemporary evolution is adaptive radiation, or the rapid diversification of one species into many forms. Current research suggests that four driving forces can drive rapid adaptive radiation **(4-5)**. These forces are new land to colonize, major extinction events, development of new resources, and novel innovations. So, even if mechanisms for rapid evolution are not totally understood, contemporary evolution in the form of adaptive radiation is predictable. Today's ecologists and evolutionary biologists would therefore consider the post-flood world to be a hotbed for adaptive radiation and, by extension, rapid speciation.

None of these examples or driving forces establish true mechanisms for genetic speciation. But they do inform speciation models in certain key aspects. First, this research reveals that adaptations and diversification often occur much faster than originally thought. Second, it describes the circumstances that can lead to rapid diversification. For example, the founder effect is thought to be an important factor in post-flood diversification **(6)**. Contemporary evolution suggests that other similar influences are also at play. Organism-focused creation models, involving factors like developmental plasticity and environmental tracking, are relevant and may even be enhanced under the conditions described. It is likely a combination of all these factors that will help uncover the mechanism for rapid speciation.

While these mechanisms remain ambiguous, certain factors have been identified as directly leading to diversification in short time spans. Creationists should consider sensory drive, new migration routes, and allopatric colonization as important factors for speciation models.

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Towards A Baraminology of Mesozoic Mammaliaforms

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Most modern mammal orders, and many families, can be traced back through the Cenozoic to near the K-Pg boundary. However, few of those groups can be found in the Mesozoic. Instead, the Mesozoic often has unique mammal groups. Previous baraminological work has focused on non-mammaliaform cynodonts (e.g. Talavera and McLain **(1)**) and a few Mesozoic mammaliaforms (eutriconodonts and docodonts **(2)**). However, several Mesozoic mammaliaform groups have not been investigated with baraminology at all.

I analyzed a large dataset including both cynodonts and mammals with statistical baraminological methods. The Huttenlocker et al. **(3)** dataset includes 538 morphological characters and 125 taxa—seven non-mammaliaform cynodonts, nine non-mammalian mammaliaforms, and 110 mammals (including haramiyids, australosphenidans, multituberculates, eutriconodonts, and therians). I used BARCLAY **(4)** to analyze the dataset with Pearson and Spearman baraminic distance correlation (BDC), 3D multidimensional scaling (MDS), partitions around medoids (PAM), and fuzzy analysis (FANNY). Since this dataset contains a wide range of taxa representing multiple created kinds, analysis of the entire dataset results in the masking of discontinuity. As a result, I divided up the dataset into taxonomic subsets.

Initial results for non-therians show four groups (multituberculates + haramiyids, australosphenidans, non-mammals, and other non-therians); as a result, I analyzed each of these groups separately. For Haramiyida + Multituberculata, BDC shows evidence for three groups—Multituberculata, Euharamiyida, and non-euharamiyid Haramiyida—, whereas the MDS results show two and PAM and FANNY have nearly equal values at 2-5 groups. In the australosphenidan subset, BDC, MDS, PAM, and FANNY all recognize four groups: Shuotheriidae, Henosferidae, Ausktribosphenidae, and Monotremata.

For non-mammals, cynodonts share no positive correlation with mammaliaforms in BDC except *Adelobasileus* and *Sinoconodon* (and *Megazostrodon* in Spearman). Both BDC plots show shared positive correlation between docodonts and morganucodonts. In MDS, the cynodonts + *Adelobasileus* + *Sinoconodon* form one cluster, the docodonts + *Hadrocodium* another, and the morganudcodonts fall into the gap between the two. PAM and FANNY are best at two, four, and five groups.

For the remaining non-therians, three groups are visible in BDC and MDS: Eutriconodonta, Symmetrodonta, and other theriimorphs. PAM and FANNY are best at four groups (separating out Aegialodontidae).

The therian subset BDC shows three groups, and MDS shows two parallel trajectories (metatherians and eutherians). However, PAM and FANNY had the best values at higher group numbers. For better understanding, I separated the therians into three subsets: 1) Eutheria, 2) Metatheria, and 3) "basal" Theria (includes "basal" eutherians and metatherians from the previous two subsets).

For Eutheria, BDC, PAM, and FANNY show two groups: extant Eutheria and fossil Eutheria + *Erinaceus*. The MDS plot shows three groups (separating out Glires). The metatherian subset BDC shows three groups (Deltatheroidea, Diprotodontia, and other metatheres). PAM and FANNY were best at two or three groups. The "basal" therian subset BDC and MDS show two groups: Eutheria and Metatheria. PAM is best at five groups, although two- and three-group models were close. The five-group model split into Deltatheroidea, non-deltatheroid Metatheria, Protungulatidae, and two groups of eutherians. FANNY is best at two groups.

In conclusion, I find evidence for discontinuity within the Mesozoic mammaliamorphs. The following groups have evidence for internal continuity and appear bounded by discontinuity, making them good candidates for holobaramins: Euharamiyida, Shuotheriidae, Ausktribosphenidae, Henosferidae, Docodonta, Eutriconodonta, Symmetrodonta (Zhangheotheriidae + Spalacotheriidae), non-symmetrodont "basal" therians, and Deltatheroidea. Multituberculata, Monotremata, "basal" Metatheria, "basal" Eutheria, Marsupialia, and Placentalia appear holobaraminic, but are likely apobaramins as the dataset is missing many taxa in these groups. This analysis of a large Mesozoic mammal dataset should be refined with datasets on particular mammal groups in the future.

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Evidence in Sepkoski's Marine Genera Data for Two Distinct Antediluvian Marine Biotas

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Sepkoski's (1) compendium of stratigraphic ranges of marine genera is the most complete global dataset available of any kind for the fossil record. As such, it is an appropriate dataset for observing paleontological patterns of a global flood event. Sepkoski (1) includes the biostratigraphic zone for the first and last appearance of 36,332 distinct taxa. If stratigraphic termini with question marks are assumed to be known at the next highest biostratigraphic level, 24,957 distinct taxa have biostratigraphic ranges with both endpoints known at the stage level or equivalent. 14,707 distinct taxa have biostratigraphic ranges a bit less than twice as finely defined.

In our analysis, Sepkoski's (1) biostratigraphic ranges were quantified in three ways—in radiometric years (from Gradstein et al. (2)), in 'stage' numbers (from 1 as the oldest, to 97 as the youngest), and in 'substage' numbers (from 1 as the oldest, to 171 as the youngest). For community structure analysis, Sepkoski's classification of genera was utilized to roughly the level of class.

We performed K-means clustering analysis on both Sepkoski's 'stage'-level and 'substage'-level data, using both radiometric and 'stage'/'substage' scales. Silhouette score analysis for up to twenty clusters (K=2-20) revealed the same strong pattern for two clusters (K=2) over the next best patterns (K=3, and K=4 just below K=3) for both 'stage' and 'substage' levels. Class-level cluster composition was also very similar for both the 'stage' and 'substage' levels. The same number and similar composition of Cluster 1 and Cluster 2 (the biostratigraphically lower and higher clusters, respectively) suggests the biotic assemblages are robust.

If the major groups with the highest genus-level diversity are placed in broad marine faunal trophic categories, (with the notable exception of large nektonic forms) Clusters 1 and 2 are rather similar in trophic structure (16% and 16% infaunal, 19% and 15% mobile benthic, 10% and 7% sessile benthic, 9% and 10% small nektonic, and 10% and 26% large nektonic). This similarity, combined with what looks like a typical marine trophic structure, as well as different dominant higher taxa in each category (brachiopod vs. bivalve infauna, trilobite vs. gastropod mobile benthics, rugosan coral vs. bryozoan sessile benthics, ostracod vs. foraminifera small nektonics, and nautiloid vs. ammonoid large nektonics) suggests these two clusters represent two very distinct marine biomes.

Visual comparison of the two clusters with the distribution of the five major 'mass extinctions', as well as the transgressive, highstand, and regressive portions of the five megasequences, displays no obvious correlative pattern. However, the largest 'mass extinction' (at the Permo-Triassic boundary) corresponds to a nearly complete boundary between the two clusters. Its location in Flood deposits strongly suggests that the Permo-

Triassic ‘mass extinction’ event is a transition in the burial of two distinct antediluvian marine biomes. The large difference in large nektonic forms between the two clusters can then be explained as due to differential mobility.

Since most, if not all, of these taxa are shallow (photic zone) marine animals, each complete biome is best understood as associated with a distinct continent. This suggests the two biomes come from two separate antediluvian continents. The Cluster 2 biome is the same biome that lives in the shallow marine realm surrounding all modern continents. The Permo-Triassic faunal turnover event then represents the extinction of the Cluster 1 biome at the end of Paleozoic Flood deposition. The modern marine fauna is included in Cluster 2 because the modern fauna is descendent from the only marine biome that survived the Flood. Since all the modern continents were part of a single antediluvian super-continent, it is likely that the Cluster 2 fauna inhabited the marine margins of that super-continent.

Where, then, did the Cluster 1 fauna live? We provisionally suggest that the terrestrial fauna missing from Flood sediments (angiosperm plants, [modern] mammals, and humans) lived on (and provided a complete trophic structure for) a continent that did not survive the Flood. We suggest that the Cluster 1 marine fauna lived on the margins of that continent.

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Fossils Tell Time: Machine Learning Test of Paleogeographic and Ecological Ordering

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The fossil record displays consistent temporal ordering traditionally interpreted through evolutionary frameworks spanning deep time. Young-age creation models propose alternatives where fossil sequences reflect systematic burial of organisms from distinct ecological zones during the global Flood, coupled with catastrophic plate tectonics (1-4). However, these ecological burial models have lacked rigorous quantitative testing. This study employs machine learning to test whether biological complexity, ecological zonation, and paleogeographic position can predict stratigraphic age, offering empirical validation to long-held intuitive creation frameworks.

Phanerozoic fossil occurrences were analyzed across a range of complexity, geography, and ecology from the PaleoBiology Database (N=29,334). Each fossil was characterized by: 1) complexity scores based on taxonomic hierarchy; 2) ecological zone scores indicating paleoenvironmental habitat; and 3) paleogeographic coordinates (paleolat/paleolng). Direct temporal indicators were excluded to ensure genuine predictive testing. Machine learning models—Random Forest (ensemble decision trees) and Neural Networks (interconnected computational nodes)—predicted geological periods using 75/25 train-test splits. Performance was assessed via accuracy and F1-scores, with SHAP analysis determining feature importance.

Machine learning models demonstrated exceptional predictive performance. Random Forest achieved remarkable accuracies: complexity model (99.80%), ecological model (99.90%), and combined model (99.93%). Neural Network models also performed strongly (93.22%-96.21% accuracy). SHAP analysis additionally revealed paleogeographic coordinates as overwhelmingly dominant predictors, followed by ecological zonation, with complexity showing least influence. Confusion matrices confirmed near-perfect classification with distinct, non-overlapping spatial clustering for each geological period.

Results validate general aspects of ecological burial models while revealing critical insights. The exceptional predictive accuracies confirm that biological complexity, ecological zonation, and geographic positioning contain profound temporal signals, strongly supporting creation model approaches. However, paleogeographic dominance presents an intriguing challenge: distinct spatial “fingerprints” for each period suggest stable, structured geographic configurations rather than chaotic or episodic change expected in a brief Flood event.

These findings indicate Flood models must incorporate more sophisticated mechanisms: either highly structured catastrophic plate tectonic scenarios producing distinct geographic states during Flood phases, or complex pre-Flood spatial zonations aligning with observed patterns. Machine learning provides powerful quantitative tools for creation research, enabling rigorous hypothesis testing that advances theoretical frameworks. The strong paleogeographic signal represents an exciting research frontier requiring innovative explanatory mechanisms that accompany tectonic catastrophe.

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NEW CREATION STUDIES

Volume 1 | Supplemental 1 | 2025

Creation Geology Society Annual Conference Abstracts 2025

These abstracts were presented at the Creation Geology Society portion of the annual Origins conference on July 20-23, 2025 at Bryan College, Dayton, TN.

Mapping an Ordovician Hyper-Concentrated Density Flow Complex in Southeastern Missouri

Z. Klein

Ammonite Mass Kill Event, Lower Jurassic Limestone, Southeastern France

S.A. Austin

Initial Response to Helble's Critique of Creationist research on the Coconino Sandstone

P.A. Garner, J.H. Whitmore

Contextualizing Genesis 1:31's "very good"

K. P. Coulson

Mapping an Ordovician Hyper-Concentrated Density Flow Complex in Southeastern Missouri

Z. Klein
Independent Scholar

The Kimmswick Formation, of Late Ordovician age, crops out along the western edge of the Mississippi River Valley in southeastern Missouri. It is conventionally interpreted as a shallow carbonate platform, with some areas reflecting wave-dominated, high-energy deposition (1). A series of repeating, massive, inverse-graded to normal-graded limestone beds occurs in the lower Kimmswick Formation at several localities. One distinctive basal bed, containing large fossils, has been formally named the Kimmswick Nautiloid Bed (KNB). Previous work defined the KNB as a persistent bed of orthocone nautiloid fossils showing preferential orientation and a characteristic inverse-to-normal grading from base to top (2).

This study presents updated mapping and descriptions of the KNB and associated units across more than 60 square miles in Jefferson County, south of St. Louis. The KNB consistently overlies the House Springs K-Bentonite, a key marker used for correlating outcrops. The KNB averages 3–5 feet in thickness but thickens northwestward to as much as 15 feet. While nautiloid fossils are concentrated within the KNB, the overlying beds share similar thickness, composition, and fossil assemblages (excluding nautiloids) and are interpreted as rhythmites. Overlying these rhythmite beds is an unnamed member of the Kimmswick Formation, composed of alternating bands of chert, chert nodules, and dark limestone beds.

Previous research in the Grand Canyon proposed that a hyper-concentrated density flow caused a mass-kill of orthocone nautiloids in the Redwall Limestone (Mississippian age; (3-4)). Comparable sedimentary features in different regions and stratigraphic settings may support a similar flow origin for these carbonate beds. The KNB shares several features with the Whitmore Nautiloid Bed of the Redwall Limestone, including fossil orientation, inverse-to-normal grading, bed thickening in the direction of flow, and overlying rhythmic limestone and chert layers. Further study of the KNB and its stratigraphic context may yield added insights into high-energy depositional processes in Earth history.

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Ammonite Mass Kill Event, Lower Jurassic Limestone, Southeastern France

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North of the city of Digne-les-Bains in southeastern France is an extraordinary Lower Jurassic limestone outcrop known as the "Ammonite Slab" (French: "Dalles aux Ammonites"). The slab (lat/long: 44.1194 N, 06.2340 E) is a bedding surface with area of about 320 square meters, dipping 60 degrees eastward, and exposing more than 1,550 cephalopod fossils (greater than 90% ammonites of genus Coroniceras with some nautilus). The "slab" was discovered during road construction in 1941. Japan, recognizing the uniqueness of the deposit, offered to quarry the limestone and put it on display in Japan. French authorities refused but made the Japanese a plaster cast. The outcrop at Digne-les-Bains is now preserved and designated a geopark.

Benthic bivalves, belemnites and crinoids also occur in the very coarse limestone bed that is up to 0.5 meter thick. Ammonites occur as the uppermost surface of that coarse limestone bed. The largest ammonite on the slab is 70 centimeters diameter. Northward the ammonite limestone bed is concealed within a strata sequence, but drill core allows extension of the ammonite bed underground to an area of at least several thousand square meters.

Detailed photography of the limestone outcrop reveals an assemblage of features which are critical to interpretation of depositional environment. Three lines of evidence indicate mass kill of ammonites. First, ammonites are the benthic community that would be last-deposited within the fining-upward sequence during the wake of a submarine debris flow. The vertical sequence of limestone does indicate the wake of a carbonate debris flow. Second, diameters of ammonites appear to be log-normally distributed indicating complete killing of the entire population of benthic organisms. Third, ammonite coil-orientation pattern fails simple randomness constraints indicating that bodies occupied shells during current orientation. These evidences argue for current deposition of the coarse lime sediment and fossils by a single underwater debris flow. The data are best interpreted as an ammonite mass kill and burial event.

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Initial Response to Helble's Critique of Creationist research on the Coconino Sandstone

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Hydrologist Tim Helble has published two critiques of creationist research concerning the Coconino Sandstone (Leonardian, Arizona). His 2011 paper **(1)** argued that ordinary sediment transport processes could not have deposited this rock unit within the Flood timeframe, and in 2024 **(2)** he responded to a range of data collected by creationists that challenges the conventional eolian interpretation. Helble (**(2)** p. 102) concedes that the creationist findings "may have the positive effect of spurring future researchers to collect more data and develop an improved hypothesis." However, he asserts that creationists "missed opportunities to increase scientific understanding of the Coconino" by limiting themselves to "the older research tradition" (i.e. descriptive) instead of adopting a more process-oriented approach. Of course, this approach is acceptable if older descriptions are absent or incorrect, which was often the case for the Coconino Sandstone. Moreover, there is a certain irony in these criticisms, given 1) that Helble offers almost no new data of his own but simply reasserts conventional arguments, many of which we have already addressed, and 2) that the process-oriented approach (e.g. applying criteria to distinguish grainflow and grainfall stratification at outcrop scale) is a major focus of continuing research. Here we present an initial response to Helble's criticisms of our research.

In his 2011 paper **(1)**, Helble argues that the sediment transport rates associated with modern sand wave deposition are inadequate to explain how the Coconino Sandstone could have deposited in a matter of days. He calls this problem "the Achilles' heel of Flood geology" (p. 38). However, he presents what is essentially a "strawman" argument. While we think the Coconino Sandstone was most likely deposited by non-eolian (subaqueous) processes, based on the new data we have presented, and while we have suggested that the closest modern analogue for the cross-bedding and other features found in the sandstone are marine sand waves, we recognize that sand waves are an imperfect model. The Flood was a unique, unrepeatable event, and the Flood model requires extrapolations beyond conditions that prevail in the present-day. This means we will never be able to observe the exact depositional processes that made the Coconino Sandstone in laboratory flumes or in nature. Stansbury's study of the Whitmore Nautiloid Bed **(3)** suggested that rapidly moving underwater debris flows were the primary mechanism for transporting large quantities of sediment continent-wide during the Flood. He concluded that the flow that deposited the Nautiloid Bed underwent transformation as it travelled from east to west, becoming dilute and turbulent and depositing a thick set of cross-bedded dunes. This may be a model to explore for the Coconino Sandstone and other similar deposits. We think there is potential for computer-based simulations to supplement outcrop and flume studies in the development of a realistic depositional model and we urge further work in this area. Helble's most recent paper **(2)** reasserts many of the same arguments for an eolian origin of the Coconino Sandstone that have been made for more than 90 years. Some of the same arguments were presented in The Grand Canyon, Monument to an Ancient Earth, a book for which Helble was a co-editor **(4)**. Helble presents almost no new data, whereas Whitmore, Garner, Strom, Brand, and others have presented an array of new data based on original field and laboratory work that forcefully challenges the traditional eolian interpretation. We have previously explained why Helble's arguments are flawed (e.g. Whitmore and Garner **(5)**), but Helble either glosses over the importance of our new findings (concerning, e.g. cross-bed angles, ripples, rounding and sorting, timing of the sand injectites, vertebrate trackways, "raindrop" imprints, micas, dolomite, angular feldspars, grain frosting, and unit thickness) or fails to appreciate their significance in his defense of an eolian origin. To give one example, Helble points out that marine carbonate grains can be blown considerable distances inland and suggests that this explains the dolomite ooids found in the Coconino Sandstone. However, a high proportion of wind-transported carbonate grains typically show signs of damage (e.g. Murray **(6)**), unlike the Coconino Sandstone ooids, which show few, if any, signs of abrasion and no signs of breakage (**(7)** p.526).

One area where Helble is to be commended is his attempt to give an alternative explanation for what we claim are parabolic recumbent folds in the Coconino Sandstone near Sedona, Arizona. Gerald Bryant, who also studied folds in the Navajo Sandstone, analysed our Lizard Head fold (**(2)** see note 62; also personal communication with JHW in 2021). Only one of our Sedona locations was apparently examined. Although Helble and Bryant present some new details, they fail to grapple with or even mention an important piece of data: the Lizard Head structure is clearly a recumbent fold that can be traced on both the north and south sides of the ridge for at least 50 meters within a bounded cross-bed set. They fail to explain how a slumped desert dune, or groundwater migration, can form a continuous parabolic fold covering this distance. We continue to maintain that the best interpretation of the Coconino Sandstone is one involving subaqueous deposition as proposed in our 2018 summary paper.

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4 Davidson G, Ranney W, Helble TK. The Grand Canyon, Monument to an Ancient Earth: Can Noah's Flood Explain the Grand Canyon? Hill C, editor. Grand Rapids, MI: Kregel Publications; 2016. 240 p.

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Citation Garner PA, Whitmore JH. Initial Response to Helble's Critique of Creationist research on the Coconino Sandstone. New Creation Studies. 2025;1(Suppl. 1):33–34.

Contextualizing Gensis 1:31's "very good"

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In Genesis 1:31, God calls His completed creation "very good,"—a phrase that has traditionally been set in contrast to the effects of the curse in Genesis 3. In light of modern science and the belief in deep time, however, a growing number of evangelicals have sought to uncouple "very good" from its creational context in early Genesis, and move it into the eschatological future. Proponents of this recontextualization, no longer "look back" to Genesis to explain the presence of animal suffering and natural disasters, but instead envision a gradual perfecting of the natural order from an original, prelapsarian "state of chaos." Nature will achieve perfection only in the eschaton when, "death shall be no more, neither shall there be mourning, nor crying, nor pain anymore, for the former things have passed away" (Rev. 21:4b ESV). "Good" is thus reinterpreted in terms of Christian growth, maturity, sanctification, salvation, and future glory.

In contrast to this narrative, I will argue that "very good" must find its interpretive corollary in the closest contextual passage of Scripture—Genesis 3—and can in no way be linked to spiritual growth, salvation, forgiveness, perseverance, or a future eschatological hope. This is not to say that God does not use suffering to procure "greater goods." The suffering of Christ on the cross definitely serves to justify several types of "greater good" theodicies. Genesis 1:31's "very good," however, has nothing to do with "greater good" theodicies and must be understood as a contrast to Genesis 3 and all that is "very bad."

I will lastly challenge the claim that natural evil is intrinsically good, by using instances of natural evil that go beyond the innocuous, cherry-picked examples common to most "chaos to order," eschatological defenses.

Citation Coulson KP. Contextualizing Gensis 1:31's "very good." New Creation Studies. 2025;1(Suppl. 1):35.