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EARTH'S UPPER MANTLE VISCOSITY—
LOWER THAN ASSUMED

JOURNAL OF CREATION

An international journal devoted to the presentation and discussion of technical aspects of the sciences such as geology, biology, astronomy, etc., and also geography, archaeology, biblical history, philosophy, etc., as they relate to the study of biblical creation and Noah's Flood.

COVER: Eastern Grey Kangaroo mother and joey, Brunkerville, New South Wales, Australia

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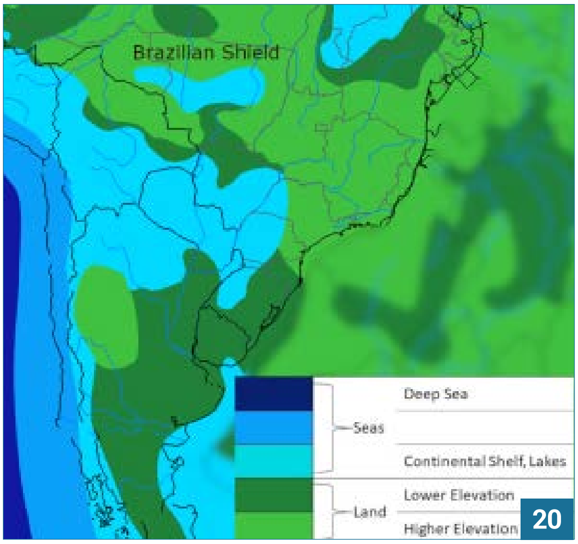

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For instructions to authors, see the last page.

Serpentinization does not build up salt formations

Stef Heerema and Gert-Jan van Heugten

The classical theory on the formation of enormous rock salt deposits (salt giants) is that of the evaporation of seawater in shallow basins over millions of years.[1] In 2018, this view was challenged by suggesting that salt giants are caused by salt magmas that solidified in between muddy Flood sediments.[2] Then, in 2019, an alternative mechanism was published by Debure *et al.*[3] in which the metamorphic serpentinization process (see below) was claimed to have formed brines that ultimately resulted in the formation of salt giants.

Debure *et al.* state:

> "… evaporation alone cannot explain salt deposits several kilometres thick (salt giants) or deposits of highly soluble evaporites (bischofite, carnallite and tachyhydrite)."

On this we agree. They give several powerful reasons why; for instance, contradictions between the amount of soluble salt, the assumed paleoclimate and the absence of fossils in the salt deposits. If salt deposits formed due to evaporation, one would expect to find the fossils of plants and animals embedded in the rock salt. Nonetheless, we object to their solution that serpentinization itself is a sufficient mechanism to explain salt giants. Furthermore, this process does not appear to fit within the framework of the biblical timescale.

From serpentinization to salt giant

Serpentinization is a process in which the sub-seafloor mantle rock peridotite transforms into serpentine. The process is expected to occur underneath the five- to ten-kilometre-thick oceanic crust (figure 1). Debure *et al.* state:

> "The associated geochemical processes involve the consumption of massive amounts of pure water, leading to the production of concentrated brines."

During the serpentinization process the volume and temperature of the rock increase. The ocean supplies the water that penetrates the rock. Assuming this is regular seawater, the unused salt becomes concentrated in a brine. For the salt to be deposited as solid structures, the brine needs to become supercritical (> 407°C and > 300 bars),[4] evaporated by solar power, or precipitated by any other process. Debure *et al.* opt for:

> "The temperature decrease that accompanies the ascent of the brine in the crust and/or the sediments lowers the salt solubility and allows salt deposition."

So, they suggest that the hot, dense brine rises up through the crust until it reaches the sea floor. The cooling down to 4°C will decrease solubility, which causes partial precipitation. Somehow this salt layer at the ocean floor will not dissolve into the ocean but form a salt giant.

Discussion

The transformation of 1 m^3 of peridotite into serpentine by seawater yields about 5 dm^3 of salt.[4] This sea salt is concentrated into a brine, whereafter the brine flows up through the earth's crust. This mechanism has to overcome several problems:

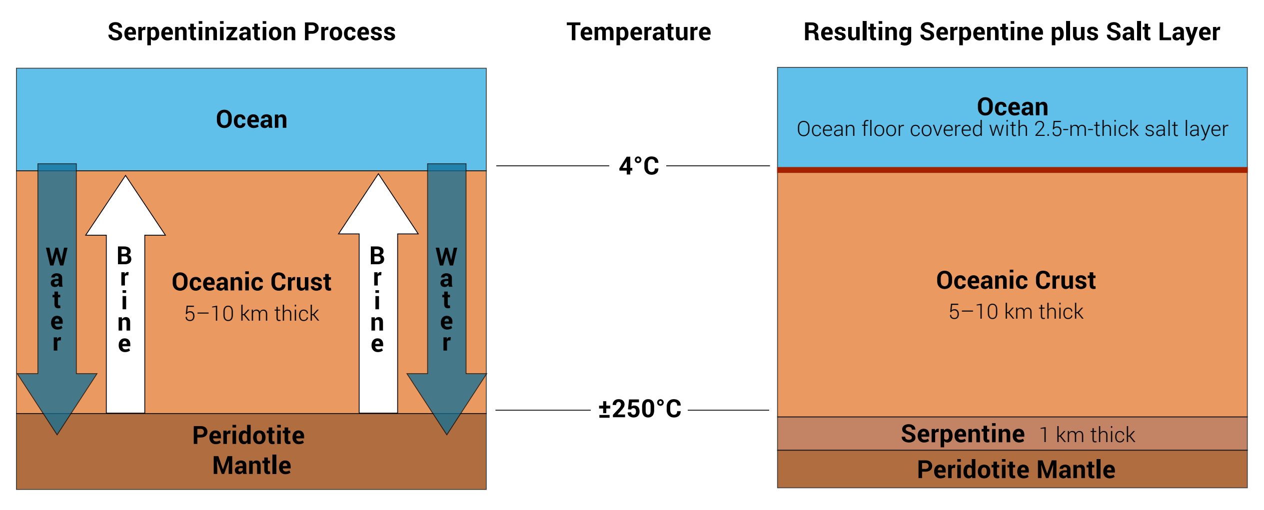

Figure 1. The serpentinization process as described by Debure *et al.*[3] Peridotite is assumed to have consumed massive amounts of water from the oceans to serpentinize. The remaining salt became concentrated in a hot brine, which rose and cooled, thus delivering the salt at the ocean floor.

- The brine is denser than the seawater that is assumed to seep down through the 5–10-km-thick crust. So, the brine will stay where it originated underneath the crust and/or will mix with the seawater that flows down. It is improbable that the downward and upward flows become separated. Debure *et al.* did not suggest a mechanism to solve this problem.
- The amount of peridotite that must be altered is beyond description. 1 km^3 of rock salt requires serpentinization of at least 200 km^3 of peridotite; that is, if *all* salt is eventually deposited in a salt giant. However, that is likely impossible, as a significant part of the salt will stay in solution (if not all, which is more likely). If a generous 50% of the formed brine will be deposited, then 400 km^3 of peridotite is required for 1 km^3 of salt. However, serpentinite (including partially serpentinized peridotite) is not abundant in the oceanic crust.[5]
- A single salt giant can contain a million km^3 of salt.[6] This requires 400 million km^3 of peridotite to be serpentinized under the favourable conditions mentioned above. Assuming a pure peridotite 1-km-thick top layer of the mantle, an area of 400 million km^2 (80% of the total global surface) had to be serpentinized for a single salt giant. That caused a 2.5-m-thick layer of pure salt spread out on the ocean floor. But how will that be accumulated into a salt giant, situated in a continental basin?
- If such large parts of the ocean floor were poisoned by such a brine, fossils should be abundantly present in the salt. But a remarkable feature of salt giants is the lack of fossils.
- In the serpentinization model, seawater seeps slowly down to the mantle, whereafter a brine plumes upward. Each 1 km^3 of salt requires 130 km^3 of seawater[7] to seep down through the solid crust. Given the salt volume required, this process will take a long time. That might not be a problem in the secular view of Debure *et al.* However, the duration of the proposed mechanism is impossible to fit in a biblical timescale.
- After the seawater slowly seeps down through the crust the actual serpentinization can start. Therefore, the water needs to diffuse into the mantle rock. Debure *et al.* state:

  > "The low water diffusion coefficient (10^{-7}–10^{-8} cm^{2}s^{-1} at 34°C) can limit the rate of serpentinization below 100°C, whereas serpentinization is more efficient at 300°C (1 km formed in 1 Ma)."[8,9]

  Again, that shows the process will not fit in a young-earth timescale.
- The seawater used in the serpentinization process likely contained the same salt concentration as today to allow for the serpentinization process to form brines. However, calculations show that year by year the seas' salt content is increasing as salts are transported to the seas via rivers but remain when water evaporates.[10] Extrapolating to the past would yield oceans of a lower salinity. This could greatly alter the time and volume for the serpentinization process.
- The formation of kilometres-high uprising salt pillars buried in sedimentary basins remains unexplained in the serpentinization model.

Conclusion

Even from a secular point of view, it seems a stretch to try and use serpentinization to explain salt giants. Given the higher density of the resulting brine, it is highly unlikely that it ever was able to pass through the crust to reach the ocean floor above. In the unlikely event that salt layers were formed in the depths of the oceans, they should have contained fossils, which the salt giants do not. Moreover, the serpentinization process only addresses the existence of salt layers, whereas salt tectonics needs to be explained as well.

From a biblical perspective it is even more improbable to form salt giants solely through the serpentinization process. The oceans likely could not provide the necessary salt, and the process takes too long to fit a biblical timescale.

Biblical creationists would be better served by exploring other models, such as a primary igneous origin for salt,[11] which provide better fits for the geological evidence and the biblical timescale.

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Did the earth ever wobble twelve degrees?

D. Russell Humphreys

A recent non-technical science article[1] cited magnetic field data from rocks suggesting that the earth wobbled away from its spin axis by 12°, and then back to normal, when Cretaceous (dinosaur-bearing) strata were being laid down. The article was based on a technical article[2] that actually contains good evidence for the young-earth timescale, it turns out.

The authors took over a thousand inch-diameter samples from a limestone cliff in Italy and measured the orientation of the earth's magnetic field recorded in each of them, as illustrated in figure 1.

They measured the *declination* (horizontal difference between magnetic north and today's geographic north) and *inclination* (dip angle from today's vertical) in each sample. The inclination tells the magnetic latitude. The large number of samples tell a detailed story of the earth's magnetic field at the moments the limestone slurry hardened, like cement, in a sequence going upward in the formation.

At first, I was puzzled why the authors were so sure their data pointed to a mechanical tilting of the earth's crust and mantle relative to its spin axis (which would stay pointed at the North Star), rather than tilting of its magnetic axis relative to its spin axis. The latter would be a simple change in the orientation of the electric currents in the core, something much less ponderous than a movement of the whole earth. I now realize their choice of interpretation was required by their belief in the Axial Field Hypothesis. That is a model that secular paleomagnetics specialists have to assume in order to derive latitudes and orientations for the tectonic plates from their magnetic data. Here's a quote from the textbook for the course I took on that subject:

> "The *time-averaged* geomagnetic field should, therefore, correspond with that of an *axial* [lined up with the spin axis] geocentric dipole and all other features should be effectively *averaged* out if the geomagnetic field is sampled over periods of a few thousand to a million years or so [emphases added]."[3]

Historical compass readings show that the magnetic north pole has stayed within 25° of the geographic North Pole (which is on the spin axis) for more than 400 years.[4] But the magnetic pole has wandered almost completely around the geographic pole during that time. So if that behaviour remained the same over thousands of years, the *average* magnetic pole position would be roughly the same as the spin axis pole.

Figure 2 of the article shows their results; i.e. magnetic directions plotted versus *assigned* geologic time. Each of the points in the figure is the average of many dozen samples, each figure point supposedly representing a one-million-year period. From 86 to 78 Ma, the recorded magnetic directions show clearly an upward and westward bump, by about 12°, followed by a return to normal just as rapidly.

Standard plate tectonics says the time interval of 8 Ma is too short for the tectonic plate Italy is on to have changed its geographic latitude and orientation very much, certainly not 10° or so. So Mitchell *et al.* have to assume that the magnetic field is what moved, not the tectonic plate. But since they think that each of the points indicates an average over one million years, they also have to assume that the magnetic pole and the geographic pole were essentially the same, for each of their points.

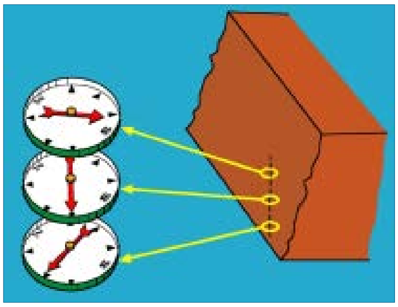

Figure 1. Samples of sedimentary rock record the direction of the earth's magnetic field when the rock hardened.

Those assumptions require a mechanical wobble of the earth's mantle relative to its spin axis. In other words, instead of allowing a fast electric-current variation in the earth's core, they have to insist that the whole mantle and crust of the earth moved, a much more ponderous operation.

But if we allow a much shorter timescale, then we can have a much more plausible explanation. If each graph point was separated from its neighbours by, say, hours, then each point would be recording a true deviation of the magnetic field from the spin axis. It is much more reasonable to suppose that the (lightweight) electric currents in the core changed their orientation that fast (at a time when creationist models say the magnetic field was reversing its polarity every few days), rather than to suppose that the whole earth changed its orientation. Thus, the data in this article support a young earth.

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A more likely origin of massive dolomite deposits

Michael J. Oard

Dolomite is the common name for a carbonate rock mostly composed of the mineral dolomite ($CaMg(CO_3)_2$).[1] It is sometimes called dolostone. To qualify as dolomite, more than 50% of the carbonate must be the mineral dolomite. Intermediates between limestone, calcite ($CaCO_3$), and dolomite are high magnesium calcite or 'protodolomite'. Sedimentary rocks usually have a high percentage of limestone and dolomite, but rarely possess much of the intermediates,[2] although a perfectly stoichiometric dolomite with 50% calcium and 50% magnesium is rare. There is usually a small percentage more calcium.

Dolomite occurrence

Although estimates vary, carbonate rocks make up from 20 to 25% of all sedimentary rocks.[3] Dolomite is most extensive in the Precambrian and early Paleozoic. It is also poorly fossiliferous. The abundance of dolomite in the Proterozoic suggests that these rocks were deposited in a different environment from today: "The extraordinary abundance of dolomite in the Proterozoic challenges our understanding of Precambrian marine environments."[4] The amount of dolomite varies vertically through the Phanerozoic rock record, being more than 50% of all carbonates in the Ordovician to Lower Carboniferous and the Triassic to Mid Cretaceous of the geological column.[5] Limestone dominates the late Paleozoic, the late Mesozoic, and the Cenozoic.[4] Some scientists dispute this trend, claiming the amount of dolomite increases with older age.[6] If dolomite is half the carbonate rocks, then dolomite makes up a little more than 10% of all sedimentary rocks.

Dolomite can be thick and widespread, such as massive Cambrian dolomite in the Yangtze Gorges (China) area that "has a thickness ranging from several hundreds to more than one thousand meters across an area of ~500,000 square kilometers."[7]

The dolomite problem

In contrast with such thick widespread dolomites in the sedimentary rocks today, dolomite formation is rare and isolated. Moreover, sedimentary rock dolomite is mostly stoichiometric and ordered, while dolomite formed today is not. Ordered dolomite is the condition in which all calcium ions and all magnesium ions alternate in layers with the CO_3 ion in between. There is no mixture of calcium and magnesium ions in any one layer. When dolomite does form today it does so only in very warm saline water. Therefore, the origin of dolomite presents a conundrum for uniformitarianism. This has been dubbed the 'Dolomite Problem'. Scientists have attempted to solve this problem for over 200 years and have published hundreds of research papers attempting to account for its formation. Ning *et al.* summarize:

> "The origin of ancient massive dolostone, i.e. continuous dolostone sequence with a thickness >100 m and a platform-wide distribution, is the key issue of the 'Dolomite Problem' that cannot be clearly demonstrated by any existing dolomitization model individually or sequentially. … Dolomite, one of the most enigmatic minerals, is abundant in pre-Cenozoic strata but rare in Cenozoic and modern sediments. … [This dolomite problem] has puzzled geologists for more than 200 years (Warren, 2000). … How ancient 'massive dolostone', referring to continuous dolostone deposition with hundreds to thousands [sic] meters in thickness and hundreds of thousands [sic] square kilometers in area (or platform-wide distribution), could be formed, given modern dolomite is restricted in specific geographic environments and normally presents as thin layers."[8]

Dott earlier stated that the origin of dolomite is one of several major geological puzzles:

> "When I was a student half a century ago, the origin of pure quartz sheet sandstones, then called orthoquartzites [now called quartz arenites], was considered a major puzzle. Together with the origin of dolomite, red beds, black shale, and banded iron formation, they made up a group of seemingly intractable geological problems. Even now, 50 odd years later, their origins are still being debated."[9]

Clearly, uniformitarian scientists still cannot explain why ~10% of sedimentary rocks are dolomite.

Primary or replacement dolomite?

Primary dolomite is dolomite that precipitates directly from solution, while replacement dolomite is believed to have replaced limestone by high magnesium fluid flow. For this to be true both the amount of fluid flow[10] and the amount of available magnesium[11] must have been huge. It is estimated that 1,000 units of fluid flow is needed to dolomitize one unit volume,[5] and 350 kg of Mg is needed to dolomitize 1 m^3 of limestone with a porosity of 7%.[11] Of course the fluid flow of magnesium ions decreases away from a potential source—one of the many problems with dolomitizing a huge limestone formation. This is one reason why it supposedly takes millions of years for dolomite to form. The problem with primary precipitation is that a tremendous kinetic barrier exists.[12] Presently seawater is 10–100 times supersaturated with magnesium,[10] yet dolomite is not precipitating today. Land discovered that dolomite would not precipitate even at 1,000-fold supersaturation at temperatures of 25°C after 32 years.[13] This kinetic barrier can be overcome by increasing the temperature of the fluid (see below).

In hot saline pools today, dolomite, other carbonates, and evaporites[14] are being locally deposited with the help of microbes that overcome the kinetic barrier.[12] Most of the dolomite is precipitated in the pores of other sediments.[10] This has given rise to the microbial theory for sedimentary rock dolomite,[15] but this theory is still under debate.[16]

Because of the difficulties involved in the formation of large-scale massive dolomite at present-day temperatures, replacement has become the consensus for the origin of dolomite: "It is typically a consensus that ancient massive dolostone was generated by the replacement of Ca-carbonate precursors."[7] The replacement process is also called dolomitization. But most researchers at least believe some dolomite is primary.[17] Still, replacement has its own problems:

> "Massive dolostone formation not only needs to overcome the kinetic barrier imposed by Mg^{2+} hydration, but also requires sufficient Mg-bearing fluids and a long-term pumping mechanism."[7]

The amount of fluid that must flow through the limestone is impressive (see above). What would be the origin of these fluids? Then what kind of pump could have lasted unchanged for a million years?

Secular explanations

Numerous models have been invented to try and explain the Dolomite Problem. All of them have severe limitations:

> "However, the application of these models individually or sequentially to interpret ancient massive dolostone is difficult … . For example, it remains unclear whether massive dolostone formation involves with [sic] a single or multiple dolomitization events [sic] or how to recognize/sequence dolomitization events in the stratigraphic record. Neither is [sic] known about the Mg source or the mechanism that effectively pumps Mg into thick carbonate deposits in [sic] the platform scale."[7]

Multiple injections of dolomitization fluid?

Ning *et al*. add another hypothesis, which is that there may have been multiple numerous dolomitization events on a layer thickness of 1 m over millions of years. They point out that dolomitization is not by hydrothermal flow, since there is an absence of hydrothermal veins. With multiple events, the huge volume of limestone need not be

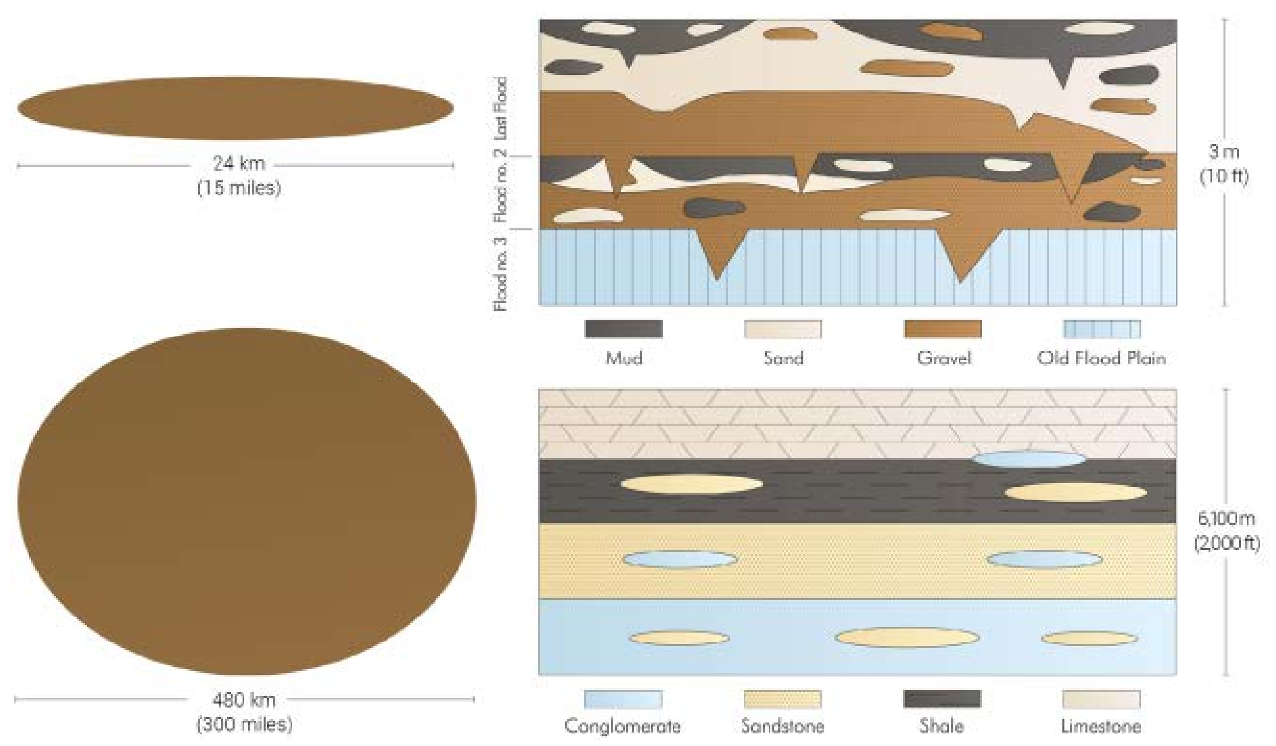

Figure 1. A schematic comparing the dimensions of sediments laid down today over small areas (top left) with rapid vertical and horizontal sediment changes (top right) to sedimentary rock lithologies commonly laid down over much larger areas (bottom, left) and much thicker (bottom, right). Note the different scales. The top right panel, representing today, indicates erosion of previously laid down sediments with changing small-scale horizontal and vertical facies changes. This is unlike what is *actually* observed today in the rocks with one layer laid on top of another with little or no erosion (bottom right). (Drawn by Melanie Richard.)

dolomitized all at once. So this solves a major problem.[18] The researchers suggest possible multiple sea level changes as a cause for these many events, believing slight changes in the Mg isotope (δ^{26}Mg) ratio can explain the cycles. The Mg isotope cycles only vary between –1.5‰ and –1.9‰ (per mil or one one-thousandths). These differences are quite small, making it likely other processes could mask small changes in this ratio. The idea is considered only 'a possible solution'.[18]

Possible Flood explanations

The Dolomite Problem may hinge on the widespread commitment to uniformitarianism. Secular scientists assume that dolomite formed under near present-day Earth surface temperatures.[19] This is the major reason why the Dolomite Problem has been such a strong challenge for over 200 years.

It is also unlikely that dolomitization of limestone could produce massive dolomite deposits hundreds of metres thick over hundreds of thousands of square kilometres in the short timescale of biblical Earth history. Therefore, I believe that the massive dolomite deposits were primary deposits with only some later minor secondary dolomitization. The massive scale of dolomite deposition matches the scale of deposition during the global Flood, laying down these carbonates over vast areas with one deposit forming on top of the other in quick succession. This is exactly what we see today in the layers of sedimentary rocks.[20] These huge formations defy uniformitarianism, which should produce only small-scale local horizontal and vertical sedimentation patterns (figure 1).

It is known that dolomite much more easily precipitates at higher temperatures and higher Mg/Ca ratios.[19] Stoichiometry ordering increases under these conditions, similar to many dolomites found in the rock record. So, high water temperatures seem able to account for the origin of dolomite:

> "Only at temperatures over about 100°C, well beyond those expected for synsedimentary dolomite formation, can dolomite be readily precipitated in experiments."[21]

The temperature should be over 150°C, and the higher the temperature the faster dolomite precipitates and the more ordered the atomic structure.[22,23]

During the Flood, high temperatures would most likely exist early due to the onslaught of the waters from the fountains of the great deep and associated volcanism. This is possibly why most of the thickest dolomite is found in the Precambrian and in the Paleozoic, tailing off in the Mesozoic and virtually ending by the time of Cenozoic deposition. Temperatures would likely have remained hotter in the early basins and cooled as thick sediments were deposited on the continents during the Mesozoic and Cenozoic, forming predominantly limestone in the upper layers.

This pattern suggests that the pre-Flood/Flood boundary may be below at least some of the Precambrian sedimentary rocks.[20] This deduction is supported by raindrop imprints, black shale, impacts, etc. in the Precambrian that continue up into the Paleozoic.[24,25]

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Ooids grew rapidly in the Flood

Michael J. Oard

Ooids are small, nearly spherical, layered grains, usually of calcium carbonate, that are less than 1–2 mm in diameter (figure 1). Pisoids, or giant ooids, are similar to ooids but are larger than 2 mm, often much larger. Ooids form today in shallow, warm littoral zones (shallow marine environments), the kind found in the Bahamas or Persian Gulf. After further sedimentation, the ooids can be cemented together to form a sedimentary rock called oolite.

How do ooids form today?

The ooid forms as a series of concentric shells around a nucleus, which can be a shell fragment, quartz grain, or other small fragment. The concentric shells, called the cortex, are added and then rounded by abrasion. The elongated calcium carbonate crystals can be arranged radially, tangentially, or randomly. Most present-day ooids are of aragonite, a polymorph of calcite. They have abrasion bands that increase in number away from the centre.

They mostly form today in the water column during suspension in a Ca-rich environment but undergo abrasion from grain-to-grain and grain-to-bed contact that rounds and erodes them, forming the thin, dark abrasion surfaces (figure 2). Modern ooids are small because abrasion is more efficient than the precipitation of carbonates.

Ancient ooids different from modern ones

Ooids are common in sedimentary rocks of all ages from the Mesoarchean to the present (figure 2).[1,2] Ancient ooids, those in sedimentary rocks, differ from modern ooids. They are predominantly calcite, having either formed as calcite or as a replacement of metastable aragonite. Ancient ooids are larger than modern ones, especially in the Proterozoic, and can reach 1 cm in diameter. Ancient ooids also have a predominantly radial crystal arrangement within the cortex with fringing carbonate cement that has a rough, angular surface. Modern ooids have predominantly tangential crystals. As a result of these differences from modern ones, ooids are not well understood: “A comprehensive explanation for the formation of these remarkable carbonate grains still eludes geologists after over a century of study.”[3]

Uniformitarian scientists believe ooids can tell us something about the geochemistry and paleoenvironments of the oceans in the past. However, modern environments make poor analogues for ancient ooids. So, if the origin of ooids is not understood, ooids cannot be used to infer past conditions.

One would think that ooids that continue to grow in the sediments and in contact with 6–8 other ooids would grow into one mass. However, ooids retain their sphericity because the force of crystallization pushes the spheres apart, keeping the individual spheres separate.[1] Thin abrasion bands that increase toward the outer layers are believed to be from greater abrasion with increasing grain mass.

Some believe ooids can form within the sediments

Some researchers believe ancient ooids are larger than present-day ooids because they mostly formed within sediments that had a high supersaturation of calcium carbonate or carbon dioxide.[1] Anderson *et al*. state that there are “exquisitely preserved oolites through time that suggests that some ancient ooids may have grown within the sediment pile”.[3] However, the porewater in modern carbonates has *low* dissolved carbonate and carbon dioxide. As a result, ooid growth does not occur within carbonate sediments today. The researchers believe conditions could have been different in the past, with high levels of carbonate dissolved in the porewater. If this were true, ooids could have grown larger in the past because they were not restricted by the dynamic balance of calcium carbonate precipitation and abrasion in the water column. However, such a mechanism depends upon non-uniformitarian conditions.

Anderson *et al*. suggest that the properties of ancient ooids can be explained by their ‘bedform model’ in which ooids cycle in and out of underwater dunes. While in the dune, the ooid grows because high porewater carbonate or carbon dioxide precipitates carbonate cement. Then the ooids pass through the dune as the dune migrates. They then pass out of the dune and into the water column where abrasion forms

Figure 1. Modern ooids from a beach on Joulter Cays, the Bahamas

the rounded abrasion bands. The abrasion bands would thus be a measure of the number of cycles through and out of the dunes. Thus, the cortical part is just carbonate cements, which are the same as the fringing cement. With a longer time in the sediments, assuming deep time, and a short abrasion period, some researchers believe they can explain the growth of larger ooids in the past.

Figure 2. A thin slice of calcitic ooids from the Carmel Formation, Middle Jurassic, southern Utah, USA

Questions on the dune cycling hypothesis

However, the researchers have to abandon the uniformitarian principle in order to claim that ancient sediments, usually deposited at a rate of a few cm per thousand years, had much more porewater carbon dioxide or dissolved carbonate than observed today. Although theoretically possible that ooids could pass through a dune during dune migration, it is unknown whether they actually have. Based on the number of abrasion bands, the ooids would have had to cycle through the dunes multiple times. Wouldn't ooids be eroded by abrasion in a dune? The scenario seems unlikely.

The classic model

A better model has been suggested by Trower *et al*.[2,4] They support the classic model in which ooids grow fully suspended above the bottom of a Ca supersaturated water column. The ooids grow proportional to the amount of Ca supersaturation that causes faster precipitation. Increasing agitation for a longer time of suspension allows for greater growth until the ooid is finally buried. They examined ooids in a high-energy shoal environment, but the ooids were small. Microorganisms did not aid growth, as some mechanisms postulate, but in fact were destructive. Trower *et al*. also applied the conditions of the natural environment in a lab and discovered that ooids grow much faster to equilibrium than postulated for carbon-14 measurements on natural ooids:

> "Ooid abrasion and precipitation rates in the experiments were four orders of magnitude faster than radiocarbon net growth rates of natural ooids, implying that ooids approach a stable size representing a dynamic equilibrium between precipitation and abrasion."[5]

The problem with this mechanism is uniformitarianism demands too little agitation. Also, when the ooid is buried, the undersaturation of Ca can cause dissolution of the ooid.

The Flood would provide a better mechanism

It is unlikely that during the Flood rapid sedimentation would have allowed ooids to pass out of the sediment and back into the water column. The water column as well as the porewater during the Flood would have had some areas that were supersaturated with calcium. Greater turbulence would be expected, allowing for a longer time in suspension. This would have allowed enough time for greater growth and less abrasion, as Trower *et al*. discovered in the shoal area with the most agitation.[4] Therefore, the ooids could have grown rapidly in Flood conditions without needing the amount of time that radiocarbon measurements indicate. The abrasion marks likely occurred within the water column during fast growth, but abrasion likely was less because it would have been from grain-to-grain friction and not grain-to-bed friction. The latter would have caused greater erosion.

If the Proterozoic sedimentary rocks are from the very early Flood as indicated by impacts and other features,[6] greater Ca supersaturation and turbulence would have occurred when the biblical mechanisms would have been the most powerful. This may have allowed for especially large Proterozoic ooids. Ooids could even be a proxy for floodwater chemistry.

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The warrah—shrinking dates for the Falkland Islands wolf

Andrew Sibley

The warrah, or Falkland Islands wolf (*Dusicyon australis,* originally *Canis antarcticus*), aka the Falkland fox, was present on the Falkland Islands when the first European settlers arrived in the 18th and 19th centuries. At the time, they believed they were the earliest to arrive on the uninhabited group of islands. These isolated islands are located at the bottom of the South Atlantic Ocean, several hundred kilometres east of South America. The first recorded landing was by Captain John Strong in 1690, and the early settlers were mainly British, French, and Spanish. Some gaucho farmers from the South American mainland were also hired because of their ranching and horse-riding expertise.

The common name warrah (figures 1, 2) is an anglicized form of *aguará*, which means 'fox' in the Guaraní language. It was so named because the gauchos saw similarities to the mainland maned wolf *Chrysocyon brachyurus*—called *aguará guazú*, meaning large fox.

With the *Beagle* voyage, Captain Robert FitzRoy brought back several specimens of the warrah to the UK. A number of others followed in subsequent years, one presented to the London Zoo in 1868.

Regrettably, the warrah became extinct by 1876. This was a fate Darwin had warned about because of the activity of the settlers. The animal was hunted for its desirable fur, and to protect the imported sheep. And it was not afraid of humans, which made it easy prey. Its diet mainly consisted of penguins, geese, flightless ducks, and small seals.

Where did the warrah come from?

From the time Darwin and FitzRoy arrived on the *Beagle*, attempts have been made to explain how and when the warrah first came to the islands. Darwin commented on the unusual presence of such an animal on the isolated islands. "As far as I am aware, there is no other instance in any part of the world, of so small a mass of broken land, distant from a continent, possessing so large a quadruped peculiar to itself."[1] Somehow the warrah had managed to cross the ocean from South America, the nearest part of which is some 500 km (300 miles) away.

There are various proposals as to how this occurred. One suggestion is that an ice bridge from Patagonia had developed at the peak of the Ice Age when sea levels were significantly lower.

Recent research

Recent analysis of mutational changes in mitochondrial DNA (mtDNA), using DNA from four museum exhibits, enabled comparison with living canids in South America. The closest living relative was identified to be the maned wolf.[2] The study estimated the date of divergence between it and the warrah to be between 4.2–8.9 Ma, giving a median of 6.7 Ma. The problem with this estimate is that the evolutionary narrative proposes that canids did not enter South America until after the Panamanian land bridge had been formed, around 3 Ma. This would locate the common ancestor of both in North America, which appears wholly unrealistic.

The most recent common ancestor of the warrah specimens was estimated to have lived 330 ka ago, with a 95% probability range of 70–640 ka. The study's authors suggest the animal arrived in the Falkland Islands on glacial ice, whether as a bridge or rafting.[2]

However, another comparison of mtDNA, taken from remains of an extinct continental relative species *Dusicyon avus*, leads to an estimate for isolation from the South American common ancestor at 16 ka, with a range 8–31 ka. This correlates with the evolutionary dates for the Ice Age of the late Pleistocene, when transit across an ice bridge may have been feasible.[3] *Dusicyon avus* was once believed to have become extinct several thousand years ago, but another study using calibrated carbon dating has suggested it survived until

Figure 1. Drawing of the warrah (from Darwin[10])

Figure 2. Warrah specimen located in the Otago museum, Dunedin, New Zealand

Image: Kane Fleury, Otago Museum/Wikimedia, CC BY 4.0

324–496 years BP. A combination of hunting and climate change may have been the reason for its demise.[4] There is however good reason to believe that mtDNA analyses are unreliable, and that the presence of the animal in such a remote spot can be readily fitted within the biblical timeframe. Morphological and 'microevolutionary' changes, and mutational changes in recent generations, are found to vary with time, and found to be far greater than those inferred from the fossil record. This supports the view that the long ages imputed into the fossil record by secular science are greatly exaggerated.[5,6]

Recent discoveries raise new possibility

More recently, archaeological evidence has come to light that Fuegian Indians (figure 3) may have arrived in the Falkland Islands several centuries earlier than the Europeans, and brought with them their hunting dogs.[7,8] Unlike European domesticated dogs, these were thought likely to be "domesticated *Dusicyon* stock" that could thus readily have been ancestral to *D. australis*.[7]

Figure 3. Fuegian of Tierra del Fuego, painted in watercolour by Conrad Martens as part of the Beagle voyage (1832–1834)

Evidence of settlement by Fuegians has been found on several islands, including a spear point and carbon-dated charcoal on the western New Island. Evidence of fire activity has been found, together with mixed marine vertebrate bones, dated to a time prior to European settlement. The fires, bones and artefacts are consistent with the culture of the Yaghan (Yámana) people from Tierra del Fuego.

The New Island bone remains give dates between 675 and 530 BP (AD 1275 to 1420), and are consistent with the age of the charcoal. Darwin also reported that tree trunks and canoes had washed ashore from Tierra del Fuego in previous times. Instead, the evidence tentatively supports the idea that those dug-out vessels had transported the Fuegians to the oceanic islands.[9]

Summary

The presence of the warrah in the Falkland Islands can be explained better within the biblical timeframe, whether the animals arrived over an ice bridge, or were brought as hunting dogs by the Fuegians. As new evidence has arisen, dating methods applied to the warrah that once yielded ages of millions of years, are brought down to several thousand years, or even a few hundred.

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Globally extensive Cenozoic coals indicate high post-Flood boundary

Timothy L. Clarey, Davis J. Werner, and Jeffrey P. Tomkins

Thick Cenozoic (with respect to the secular understanding of the geologic column) coal beds have been discovered on nearly every continent (figure 1). North America has its most extensive and thickest coal beds in the Lower Cenozoic section of the Powder River Basin, Wyoming.[1,2] Powder River Basin coal beds, which are all within Paleogene system rock layers, contain the largest reserves of low-sulfur subbituminous coal in the world.[1] At least six individual coal beds in the Powder River Basin exceed 30 m in thickness and extend outwards in excess of 120 km.[2] The Big George coal seam alone exceeds 70 m in thickness.[1] Unlike Carboniferous coal beds, most of the Powder River Basin coal beds are composed of angiosperms and gymnosperms like the metasequoia.[3]

Cenozoic coal beds in South America are also the thickest and most extensive compared to other coal layers.[4] Cenozoic coal beds alone make up about one half of all coal in South America and the tonnage is estimated to be greater than that found in any other geologic system or combination of systems.[4]

Germany, one of the largest coal producers in Europe, has approximately 65% of its coal reserves in Cenozoic rocks.[5]

Australia has vast coal beds in the Cenozoic basins along the country's southern boundary, especially in the onshore and offshore portions of the Gippsland Basin.[6] Here, the Miocene brown coals of the onshore Latrobe Valley are up to 200 m thick.[6]

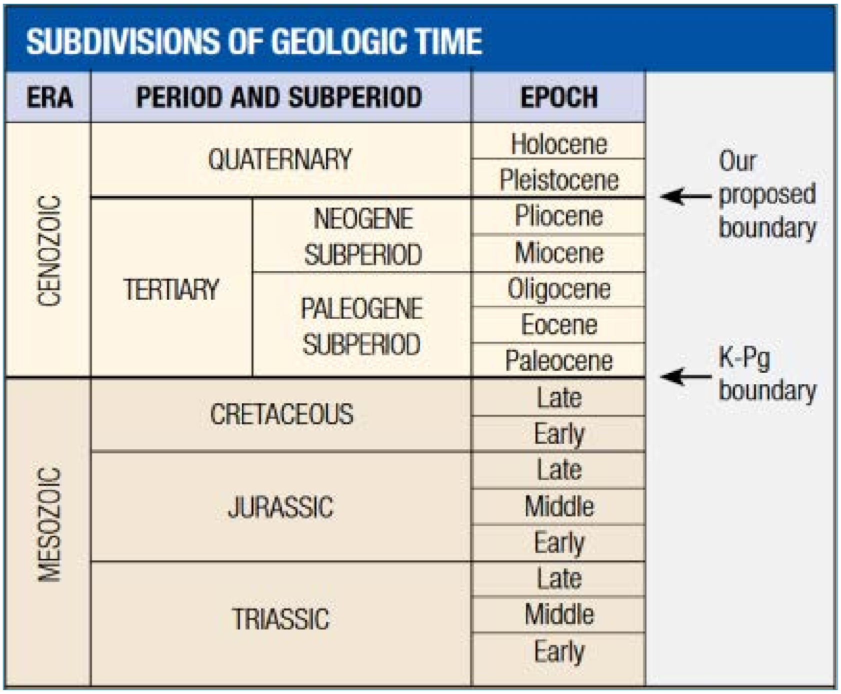
China has significant volumes of Cenozoic coal both onshore and offshore. The onshore coals are mostly in eastern China, found in Cenozoic-age basins. Early Cenozoic, Paleogene coals are found onshore in northeastern China, whereas the younger Neogene coals dominate the onshore in southeastern China (figure 1).[7] A single Paleogene coal seam in the Fushun Basin was found to be 70 m thick.[7] The Xianfeng, Xiaolongtan, and Zhaotong Basins of southeastern China contain Neogene coal beds that attain thicknesses of 237 m, 223 m and 140 m, respectively.[7] These Chinese Cenozoic coals are composed of predominantly angiosperm plants, as noted for the Powder River Basin coals in the US.[7]

Cenozoic coals of offshore Asia

An extensive Cenozoic coal deposit is also found in offshore China, offshore southeast Asia, and north and east of Russia under the Sea of Okhotsk and the Arctic Ocean (Laptev Sea and East Siberian Sea).[8–13] The South China Sea has some of the deepest Cenozoic coals discovered to date and in the deepest water. Oil wells in an area of the southern South China Sea known as North Luconia (about 280 km west of Borneo) encountered Oligocene coal beds within a 1,500 m section of sediment that today resides 3,000 m below sea level.[14]

Uniformitarian scientists believe all coals accumulate *in situ* and not by transport. So how do they justify these thick coal beds that accumulated so far offshore and in such deep water? Evolutionary geologist Peter Lunt tried to explain:

> "Coal-bearing Late Oligocene beds are known in several wells in North Luconia, but now in water depths of more than 1,000 m, with these coals typically 3 km or more below modern sea level. These wells therefore indicate 3 km or more of basement



SUBDIVISIONS OF GEOLOGIC TIME

ERA	PERIOD AND SUBPERIOD		EPOCH
CENOZOIC	QUATERNARY		Holocene
			Pleistocene
	TERTIARY	NEOGENE SUBPERIOD	Pliocene
			Miocene
		PALEOGENE SUBPERIOD	Oligocene
			Eocene
			Paleocene
MESOZOIC	CRETACEOUS		Late
			Early
	JURASSIC		Late
			Middle
			Early
	TRIASSIC		Late
			Middle
			Early

Figure 1. Partial geologic timescale showing the subdivisions of the Mesozoic and Cenozoic. Image credit: Susan Windsor, ICR

> [crustal] subsidence since the Late Oligocene."[14]

Lunt added that the depth of these coal beds complicates the necessary subsidence history of the area:

> "Geohistory analysis of the G10-1 well shows that the Oligocene section [containing coal beds] drilled there is both thick and rapidly deposited. The facies [perceived environment] is remarkably consistent over the 2,100 m of section, with facies … suggesting coastal to very shallow marine throughout."[14]

Lunt explained that the lack of variation within the vast coal-rich Oligocene section (greater than 10,000 km^2) was simply due to these thick coal beds having sunk at exactly the same rate as the coal was accumulating, keeping the coal swamps constantly at about sea level.[14] Maintaining such a perfect balance of subsidence and deposition while a 1,500-m-thick section was accumulating across such a wide area seems highly improbable; such explanations are based on supposition and bring belief to the issue, not fact.

The wells drilled in North Luconia also show a thick deep-water Miocene section deposited directly on top of the coal-rich beds. This requires the land surface to have instantly dropped about 1,500 m from one deposit to the next. Lunt discovered that the Mulu-1 well "is quite exceptional in the extremity of events it shows", adding more coincidences to his uniformitarian story.[14]

In total, over 3,000 m of subsidence had to take place in the southern South China Sea (1,500 m for the Oligocene coal beds and then a second 1,500 m to accommodate the deep-water Miocene rocks deposited on top). Subsidence is defined as the sudden sinking or gradual downward settling of the surface of the earth in a certain region with little or no horizontal motion. However, this particular act of subsidence had to be nearly instantaneous to change from a perceived 'coastal' environment to a 'deep-water' environment across the Oligocene-Miocene boundary. This explanation truly exceeds credible science.

Cenozoic coals are from Flood runoff

Evolutionary scientists insist coal originated from plants that grew in place. They interpret even offshore coals as the remnants of vast swamps that must have once existed where the coal is located. But Cenozoic coals are globally too extensive, currently located far offshore, and are sometimes buried over 3 km deep. There is no known land area in the South China Sea area for these coals to have grown upon, nor are there known instances of drastic sea level change to accommodate the findings. Instead, uniformitarian doctrine requires outlandish stories of thousands of metres of near instant sea level change.

Advocates of a post-Flood boundary at the K-Pg (Cretaceous-Paleogene) in the creation science community are in an equal quandary. Onshore and offshore Cenozoic coal deposits found globally, and in such thicknesses and extent, cannot be dismissed as the results of local post-flood catastrophes, especially the massive volumes of Cenozoic coals observed in deep water.

Placing the post-Flood boundary at the Neogene–Quaternary, near the top of the Cenozoic, better explains the rock and paleontological data (figure 1).[15–17] Our conclusion is that all the onshore and the offshore Cenozoic coal beds were produced by the runoff processes late in the Flood. Vast forests of trees living on the pre-Flood uplands were ripped from the land as the floodwaters crested on Day 150. These huge mats of vegetation were trapped in subsiding Cenozoic basins buttressed by adjacent mountains that were simultaneously rising as the water began to recede. Other vast mats of vegetation may have been transported *en masse* off the various continents and buried in the ocean as the Flood continued to recede, creating vast Cenozoic coal beds offshore. This scenario best explains the Cenozoic coals found both onshore and offshore.

This interpretation also helps explain the dominance of angiosperm plants in the Cenozoic strata and in the Cenozoic coals.[7] The pre-Flood world was apparently stratified by ecological zones.[18] Paleozoic coals, like those found in Lower Carboniferous and Permian rocks, are dominated by wetland and coastal plants living at near sea level such as lycopods and pteridosperms.[7] Mesozoic coals are dominated by gymnosperms, ginkgos, and cycads, plants living at slightly higher elevation.[7] Finally, Cenozoic coals are composed of mostly angiosperms and some gymnosperms that were living at the pre-Flood highest elevations.[7] As the Flood sequentially progressed from Day 1 to Day 150, it inundated higher and higher ecological zones, resulting in the stratified fossils and coals we observe globally.[18]

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Evolution of the neuron

Jerry Bergman

The chasm that exists between nerve cells and their proposed evolutionary precursor cells has never been bridged by evidence, nor even by theoretical just-so stories. The problem of the evolutionary origin of the neuron is widely acknowledged by many evolutionists. The reasons why this gap exists, and will never be filled, are documented here. The first neuron must have had all of its basic parts assembled and integrated properly in order to function as a neuron.

A neuron is another name for a nerve cell. It transmits information within an organism (for example sensory information), to the brain. It communicates with other such cells by specialized connections, which are actually switches called 'synapses' (see figure 1). Nerve cells are employed in all animals except placozoa and sponges. Placozoa, the simplest existing non-parasitic metazoan, are small, marine, free-living multicellular organisms. Sponges (phylum Porifera) are multicellular metazoan filter feeders, the bodies of which are saturated with pores and channels, allowing water to circulate through them so they can absorb nutrients. As will be discussed, structures used by both of these animals have been proposed as supporting evolutionary ancestors of neurons.

In order to send messages, nerve cells employ a combination of electrical and chemical signals, which can be excitatory or inhibitory. The three neuron types are sensory neurons, motor neurons, and interneurons. Sensory neurons receive signals generated in the sensory organs, (such as the eyes, ears, skin, olfactory organs, and taste buds) in response to light, sound, touch, pain, smell, and taste. They then transmit the information to the spinal cord or brain for processing and responding. Motor neurons receive signals from the brain and/or the spinal cord, to regulate muscle contractions and glandular output. Interneurons connect neurons to other neurons.

Anatomy and physiology of neurons

Every neuron consists of a compact cell body called a soma, which,

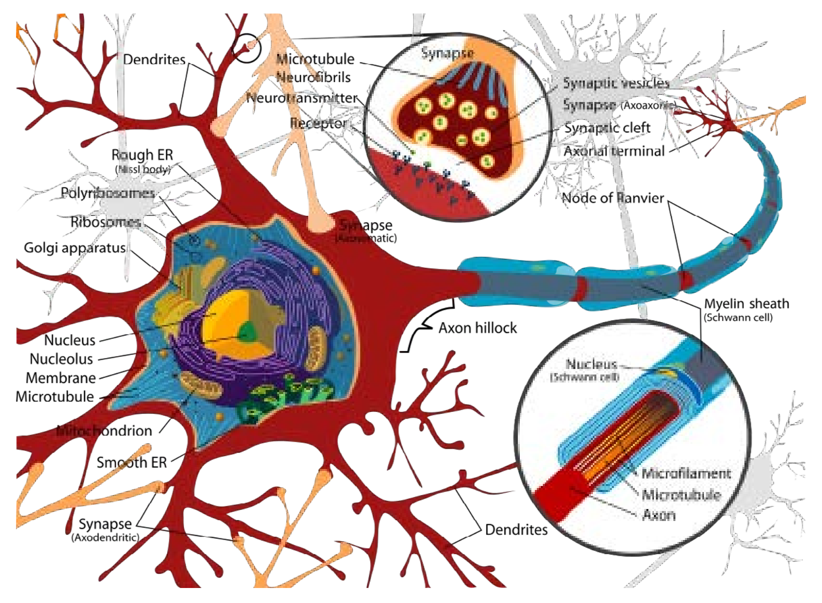

Figure 1. A diagram of a neuron showing its components and the synapse in some detail

as is true of most cell types other than a few enucleated types (e.g. human red blood cells), has a nucleus. The nucleus contains DNA and part of the cellular machinery required to produce protein to repair and maintain the nerve cell. Most neurons have many dendrites, plus a long single axon (figure 1). Dendrites extend out a few hundred micrometres from the soma or cell body. The axon is the thin ‘cable’ along which the signal travels, and nerve fibres consist of bundles of axons. It leaves the soma at a swelling called the axon hillock. In humans, axons can be metres in length. At the farthest tip of the axons are terminals called synapses, where the neuron can transmit the signal across the synapse gap to another cell. The synapse regulates, by a system of chemical neurotransmitters, if the signal should cross to the next step in its journey (figure 1).

Evolution of the neuron

The first proposed evolutionary precursors to neurons are the cell types known as choanocytes or ‘collar cells’. Choanocytes are flagellated cells connected to a protoplasm collar located at the base of a flagellum (figure 2). They line the internal chambers of sponges. Their function is to move water into the sponge, where nutrients are then absorbed from the water. Choanocytes have a very different design to nerve cells but are proposed as the precursors of neurons because they have a flagellum, and because no better proposal exists. Nerve cells do not have a flagellum, but their axons look superficially like flagella. Note the contrast between the neuron in figure 1 and the choanocyte in figure 2.

One reason given for difficulty in documenting the evolution of neurons is the belief that soft tissue is not preserved in the fossil record. On the other hand, there is no shortage of living fossils, such as Cnidaria (including jellyfish), which, on the evolutionary timescale, “showed relatively little morphological change in the last 500 million years” since they first appeared in the fossil record.[1] Darwinists argue without direct evidence that neurons must have evolved much farther back in time. In this case, time is used to explain away the lack of fossil evidence.

Another proposed precursor to neurons is the mesenchymal cell. These have cellular protrusions that resemble modern interneuron and motor neuron morphologies.[2] Mesenchymal cells are undifferentiated stem cells that are able to develop into connective tissue, blood vessels, and lymphatic tissue cells, respectively. How they could have evolved into actual nerve cells is unknown. Stem cells are programmed to develop into certain cell types and will not develop into neurons unless the appropriate program exists and is triggered, and the environment is supportive of a neuron.

Neurons are irreducibly complex,so Stetka admits:

> “We know neurons didn’t arrive in an instant. Instead, they evolved from relatively simple elaborations on earlier cell types and traits, *maybe* from epithelial cells, the cells that make up our skin; or from choanocytes, the early assemblers of animal life [emphasis added].”[3]

Assuming that a functional nerve cell could have evolved, the next step is for these nerve cells to evolve into nerve nets composed of neurons with neurites (a collective name for both axons and dendrites) in a mesh-like arrangement covering large parts of the animal body. This design is employed in modern ctenophores and cnidarians.[4] The nerve net requires directions to assemble the net to function, involving a sensory system to receive information, and a muscle or other system to respond to the information. Until these systems are in place, the nerve net will be worse than useless and, at best, will just sit there and waste space and nutrients.

Nonetheless, the nerve net is considered one ‘hypothesis’ (among many) for the evolution of the central nervous system.[4] The problem is that at this level evolutionists assume nerves have already evolved. Consequently, the focus of this review is the supposed evolution of the neurons themselves from some non-nerve cell. As Arendt writes: “Major questions in the evolution of neurons and nervous systems

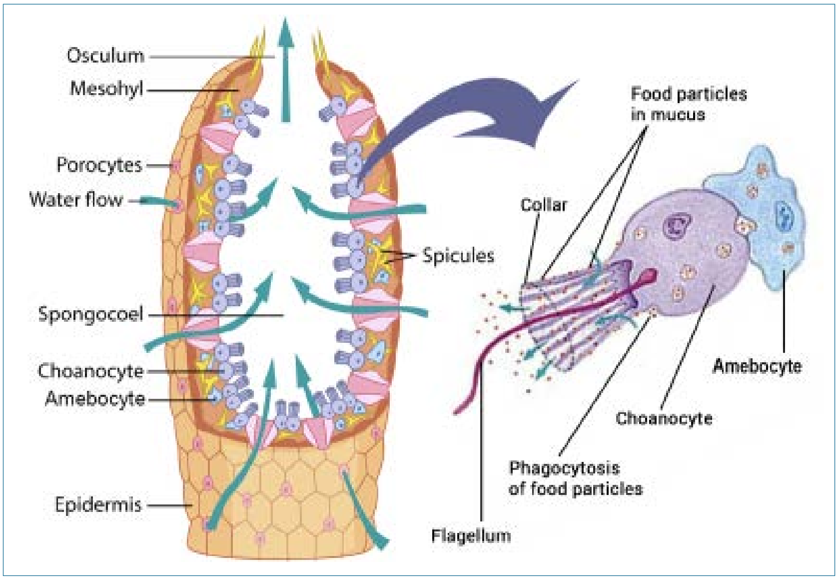

Image: Choanocyte (right)—The Wonderful World of Kingdom Animalia/CC BY 4.0 [modified]

Figure 2. The placement of the choanocyte in the sponge arms. Choanocytes line the gastrovascular cavity of the sponge, and their function is to bring food to the amebocyte cells for digestion.

remain unsolved, such as the origin of the first neuron … ."[4]

Major problems for evolution

The major problem for evolution is that the neuron is one of the most complex cells in the body, and the gap between a neuron and all other cells is enormous (see figures 1 and 2).[5] The human brain, containing some 100 billion neurons, which together form a complex network, has been called "the most complex object in the known universe".[6]

Another problem for evolution is that, although all neurons have the same basic parts, many differences exist. Some axons are covered by a myelin sheath (see figure 1), composed of protein and lipids, in a manner similar to the insulation that surrounds electrical wires. The myelin sheath's function is to speed up nerve transmission. Its deterioration, such as by an autoimmune disorder, causes debilitating diseases such as multiple sclerosis. These and other differences, such as the tissue types that develop into neurons in various animals, have forced some researchers to conclude: "Did neurons evolve more than once? Almost certainly."[1]

Consider the following:

> "Even if ctenophores and cnidarians are sister groups, with a neuron-carrying ancestor, some cnidarian neurons derive from endodermal cells rather than from epidermal cells, as is the norm, and the same epitheliomuscular cells in Hydra, a cnidarian, can be transformed into neurons by perturbing neurogenesis … . The multiple origins of neurons may, if fact, be why defining 'neuron' is so difficult, and why defining the origin of neurons is so complex."[1]

Genetic comparisons, which were expected to solve the phylogeny of neuron evolution, have only made the problem worse:

> "Does the feature's absence in clade 2 mean that the feature was never present in the ancestors of clade 2, or was it present in clade 2's ancestors but subsequently lost? A second phylogenomic problem is posed by convergent evolution (or 'homoplasy' in genetic terminology): a feature or a molecule that is present in two clades might have evolved independently in each clade. Both of these problems, secondary loss and homoplasy, confound the interpretation of evolutionary relationships."[7]

Further complicating the evolutionary story is the conjecture that the "Three kinds of gated channels probably evolved independently."[7] For a nerve impulse to be carried forward, it must cross a gated channel between the axon and the next cell structure. Gated channels are molecules that form synaptic structures which control the messages' travel from the sensory receptor across the neuron to the message receptor (the brain, for example).

The three kinds of gated channels are 1) the voltage-gated channel, 2) the stretch-gated channel, and 3) the ligand-gated channel.

The voltage-gated channel is a membrane that opens and closes in response to changes in membrane potential (voltage). In neurons, the sodium and potassium channels are examples of this type. The stretch-gated channels respond to membrane stress and are common in sensory cells. Lastly, ligand-gated channels are a group of trans-membrane ion-channel proteins which open to allow ions (including Na+, K+, Ca++, and/or Cl−) to pass through the membrane in response to a chemical messenger (i.e. a ligand), such as a neurotransmitter (figure 1).

This is another example of the issue:

> "… whether neurons evolved only once or have different evolutionary origins—as suggested for example by the major differences in transmitter usage, synapse architecture and neuronal morphology observed in ctenophore, cnidarian and bilaterian nervous systems."[4]

A non-evolutionary explanation accounts for this situation quite well. Each type and its claimed ancestors were separately designed; thus, the very implausible multiple evolution origin of the neuron and evolutionary-loss hypothesis are unnecessary.

Conclusion

"How did a structure as complex as our own brain ever evolve? ... biologists have pondered this question since Charles Darwin."[7] And the fact is that, more than 150 years later, "The evolution of neurons and the nervous system is one of the remaining great mysteries of animal evolution."[4] A great chasm exists between the postulated precursor cells, the choanocytes, and the neurons that exist in every animal except placozoa and sponges. Nevertheless, much research has been expended to answer this question because in the study of the nervous system, "One of the most exciting questions [in evolution] is when and in what form *the first neuron* emerged … [emphasis in original]."[4]

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South American paleontology supports a Neogene-Quaternary (N-Q) Flood boundary

Jeffrey P. Tomkins and Timothy L. Clarey

Determining where the global Flood of Genesis terminated in the sedimentary rock record is of great importance in developing a credible overall model of the Flood. If the Flood is terminated too low, as is the case with proposing a Cretaceous-Paleogene (K-Pg, formerly K-T) boundary, then it becomes necessary to introduce rather wild speculative ideas to explain Cenozoic fossils. For example, one K-Pg boundary proponent has claimed that legged proto-whale creatures walked off Noah's Ark and then somehow morphed into the diversity of marine mammals we know as extant whales within 200 years post-Flood.[1] Then, these hyper-evolved whales somehow became buried and fossilized in local post-Flood catastrophes. However, a global map of Cetacean fossil locations (all Cenozoic) demonstrates that whale fossils cover nearly all continental margins and the breadth of Europe—fully negating this contention of localized post-Flood burials (figure 1).[2]

Another problem with an early K-Pg flood boundary is that it must explain all the global Cenozoic strata with local-to-regional post-Flood catastrophes. However, the recent mapping of global megaseqeunces has shown how utterly untenable this assertion is. The latest stratigraphic data from North America, South America, Africa, and Europe indicates that approximately 30% of all Flood sediments are Cenozoic, specifically the Tejas Megasequence.[3–7] And in many places in the world, the bulk of the Tejas section is dominated by marine deposits,[6,7] contrary to the claims made by Whitmore.[8] Local catastrophes cannot explain these extensive marine post–K-Pg deposits found globally, especially in the Middle East and Turkey.[7] Nor can they explain the 105,000 km^2, 400 m-thick, Whopper Sand found 300+ km offshore, in the deep Gulf of Mexico, in water 2,100 m to 3,000 m deep.[6] This basal Tejas sand deposit is best explained as a product of the initial massive runoff of the Flood.[6] How could such a massive offshore sandstone and 30% of the sedimentary rock record be realistically attributed to local post-Flood catastrophes?

Not only does stratigraphy and sedimentary geology strongly support a late Flood boundary at the top of the Cenozoic, near the Neogene-Quaternary (N-Q), but so does the extensive paleontology of the Cenozoic.[9] An analysis of plant and animal fossils from South America also fully supports an upper Cenozoic N-Q Flood boundary.

Central Andean Plateau

In 2020, paleontologists reported that fossil pollen, leaf and fruit

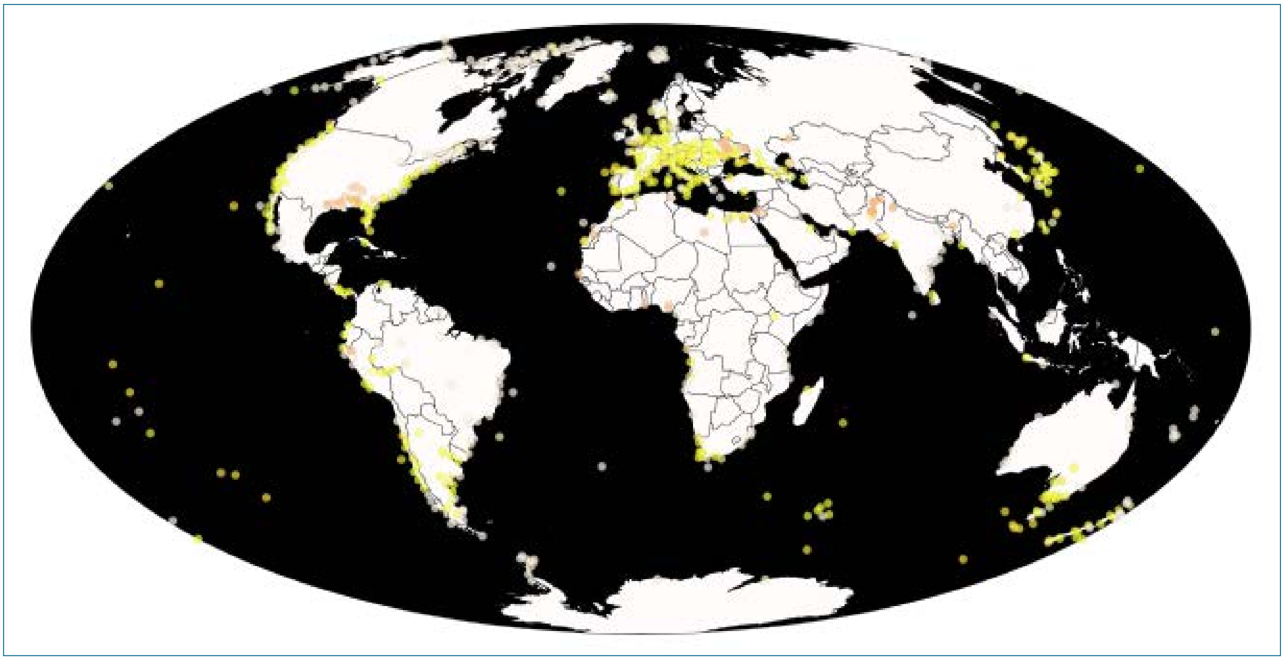

Figure 1. Global map of all known Cetacea fossil locations using the Paleobiology Database (paleobiodb.org). All occurrences are listed as Cenozoic.

impressions, and petrified wood were found in multiple locations in Cenozoic strata across the massive Central Andean Plateau in South America.[10] The fossils were collected from both Pliocene and Miocene layers in the Descanso Formation of the Descanso-Yauri Basin in southern Peru. This extensive sedimentary basin covers an approximate area of 1,242 km^2. These thick Cenozoic basin deposits developed during the late Flood as mountain ranges were being uplifted, shedding massive amounts of sediment as the floodwaters drained off the continents. Plants and animals living at higher pre-Flood elevations became trapped and buried in these sediments. In addition, these late-Flood deposits had an obvious propensity to collect in large basins that would have formed at the base of the newly uplifted mountain ranges. A striking example of this sort of scenario in North America would be the Cenozoic basins within the interior region of the Rocky Mountains. Likewise, the Descanso-Yauri Basin in South America and its fossil assemblage developed as the Andes Mountains were uplifted.

Uniformitarian researchers who documented the Central Andean Plateau paleontology claimed that an ancient lush and rainy ecosystem existed ‘in-place’ in the basin during the Miocene and Pliocene because the plants were semi-tropical. The problem is that these reconstructed hypothetical ecosystems stand in direct contrast to the present harsh environment in which the fossils now exist and have existed since the Paleocene and Eocene, when the Andes were formed. At present, the Central Andean Plateau has an average annual temperature of 8°C and an average annual precipitation of only 500–760 mm. The region is also inundated by cold and strong winds throughout the year along with extreme temperature fluctuations on both a daily and seasonal basis. As a result, the only type of vegetation that currently grows there consists of high-altitude hardy grasses and shrubs. Of course, this whole ecological discrepancy is easily explained by the model of the global Flood, which predicts that a generally lush environment existed globally in the pre-Flood world. These Miocene and Pliocene plant fossils were merely transported from their previous pre-Flood verdant locations and buried in the newly developed basins late in the receding phase of the Flood. Claims that local catastrophes in a warmer post-Flood world can explain these semi-tropical plant fossils are precluded by the high elevation of the Andes in place since the Eocene (prior to the Miocene and Pliocene).

An Amazon inland sea or global Flood deposition

Over the past 15 years, evolutionists have claimed that a massive marine wetland twice the size of Texas was trapped east of the Andes Mountains and westernmost Brazil, spilling over into Peru and Colombia and covering the western Amazon drainage basin.[11] However, paleontological studies of Miocene fossils in the region reveal a very different and conflicting story. Fossils have been discovered representing both freshwater and saltwater environments in the same sedimentary layers. Thus, evolutionists are confused as to how these fossils got mixed together.

In a 2019 *Journal of Biogeography* paper, the authors reported finding fossil mangroves and associated coastal plants in the middle of the Amazon which they thought conclusively showed various marine incursions in South America.[12] In an earlier 2017 study, scientists discovered fossilized shark teeth along with marine mantis shrimp in the same Miocene strata.[13] In 2006, a study reported the presence of anchovies, sharks, herring, marine invertebrates, and stingrays, also suggesting a saltwater origin for the rocks.[14] However, the same rocks also contained a large number of diverse freshwater mollusks.[14] In fact, for the past 40 years scientists have been finding over 50 different species of freshwater mollusks in these sediments.[14] Taken as a whole, the rich diversity of plant and animal (land and marine) fossils appears to represent a combination of mixed environments revealing a diversity of life not normally found together.

Evolutionists explain the mixing of these marine and non-marine fossils using multiple marine incursions during the Miocene, when the ocean allegedly surged into the western Amazon, creating a continuous inland sea. Then, it is claimed that saltwater currents from the north would have mixed with fresh water from torrential rains. It is also believed that the marine flooding periods would have been relatively brief and that for most of the epoch the ocean receded, leaving a huge inland freshwater wetland of interconnected lakes and channels connecting to the Caribbean to the north.

However, the evolutionary explanation does not account for the necessary rise and fall of the land surface during the Miocene, nor do they offer a mechanism for these ocean incursions. Physical evidence for this ‘yo-yoing’ of the land as a possible mechanism is currently lacking. A better explanation that settles the debate involves the Miocene strata forming as part of the receding phase of the global Flood. As the Flood reached its highest level on Day 150, it washed away all sorts of upland plants and animals from interior regions, including some from freshwater environments.[6] The Guiana and Brazilian Shields east of the ‘Amazon sea’ study area were the closest pre-Flood uplands and likely sources for these Miocene fossils (figure 2).[15] Massive tsunami-like wave pulses generated by plate movement continued through the Tejas Megasequence (which includes Miocene strata), transporting these

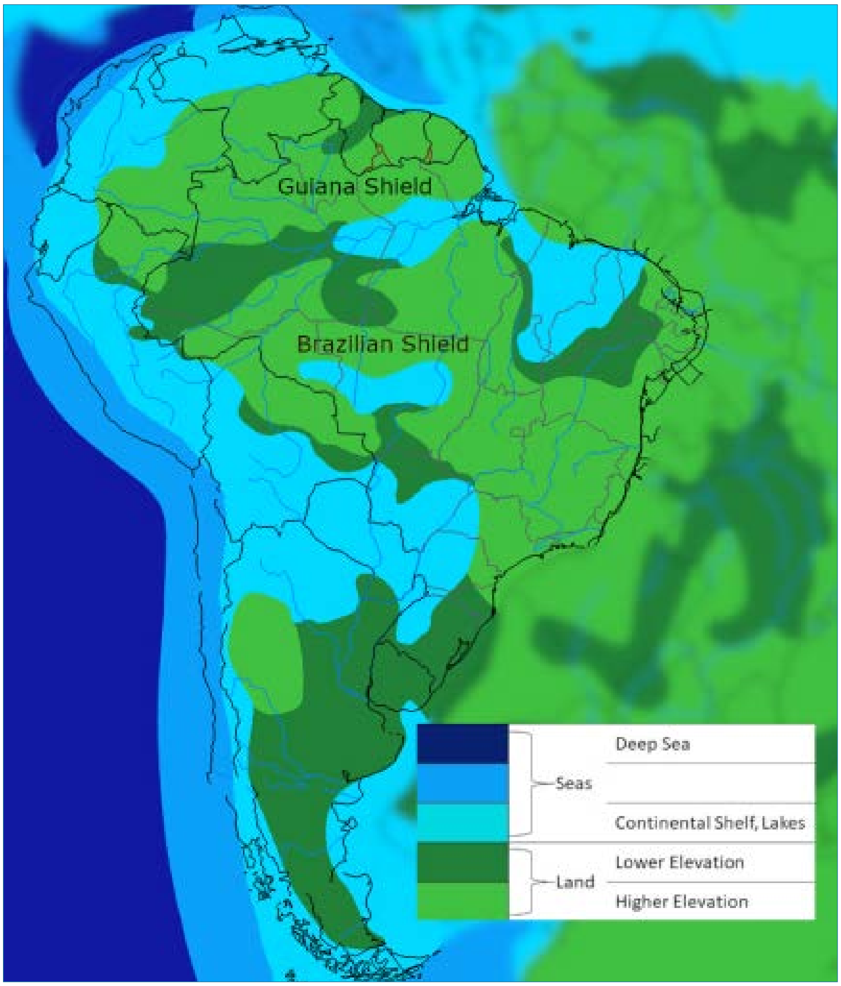

Figure 2. Pre-Flood map of South America showing interpreted environments. The Guiana and Brazilian shields are identified. The pre-Flood upland areas, which became the shields, are shown in light green and the lower elevation lowland areas in dark green. Courtesy of Davis J. Werner and ICR.

plants and animals to lower elevations as the water receded. In addition, these surges also transported marine plants and animals, producing a rich mix of biodiversity.

And as mentioned earlier, the Andes Mountains were actively rising at the same time, forming a barrier to the west. This scenario would have trapped many of these future fossils in swirling pools between the mountains and the pre-Flood uplands, depositing them in the Miocene sediments of western Amazonia. This model better explains the strange mix of plants and animals from fresh and saltwater environments we find fossilized together.

South American coal

Extremely large Cenozoic coal deposits directly point to a high Flood boundary (see Clarey, Werner, and Tomkins, this issue) and cannot be accounted for by localized post-Flood catastrophes. In South America, Cenozoic coal seams are the thickest and most extensive across the entire continent and comprise approximately one half of all coal deposits spanning all geologic ages.[15,16] The regional extent of South American Cenozoic coal deposits is also several times greater than the areal geographical extent of all other deposits from other geological ages.[16] Furthermore, the total tonnage of Cenozoic coal in South America is estimated to be much greater than that for any other geologic age or combination of ages.[15] Interestingly, most of the estimated tonnage of Cenozoic coal underlies the Amazon River drainage basin in Brazil, Peru, and Colombia—the region mentioned above in our discussion of an alleged inland Amazon Sea.[15] The remainder of the Cenozoic coal deposits appear to be fairly evenly distributed throughout the rest of the coal-bearing regions of the continent.[16]

Tying it all together with late-Flood runoff

The late-Flood runoff and transport model accurately predicts and explains the higher elevation ecosystem category of fossils we typically find in Cenozoic rock layers. In this model, plants that were ripped off the highest pre-Flood elevations along with animals living at higher elevations were moved and deposited in late-developing Cenozoic basins. These deposits are much too massive in both areal scope and depth to be attributed to localized post-Flood catastrophes as proposed in models that incorporate a premature Flood/post-Flood boundary at the Cretaceous-Paleogene. Thus, the Neogene-Quaternary (N-Q) boundary is the best choice to fit the emerging global geological and paleontological data.

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The fossil record is complete enough

Michael J. Oard

Ever since Darwin wrote the *Origin of the Species*, evolutionists have regarded the fossil record as vastly incomplete. To their mind, the fossil record is the actual record of past life in which evolution should be obvious. Darwin believed that the fossil record should be full of transitional fossils and blamed the lack of such fossils on the extreme imperfection of the fossil record:

> "But just in proportion as this process of extermination has acted on an enormous scale, so must the number of intermediate varieties, which have formerly existed, be truly enormous. Why then is not every geological formation and every stratum full of such intermediate links? Geology assuredly does not reveal any such finely-graduated organic chain; and this, perhaps, is the most obvious and serious objection which can be urged against the theory. The explanation lies, as I believe, in the extreme imperfection of the geological record."[1]

Numerous secular scientists after Darwin have continued to use this excuse that the fossil record is vastly incomplete. For instance, renowned evolutionist Stephen Jay Gould wrote:

> "All paleontologists know that the fossil record contains precious little in the way of intermediate forms; transitions between major groups are characteristically abrupt. Gradualists usually extract themselves from this dilemma by invoking the extreme imperfection of the fossil record."[2]

Most scientists have heard of the imperfection of the fossil record, and paleontologists

> "… have underscored and emphasized Darwin's point for the past 150 years by routinely highlighted incompleteness and bias. And if bias was not good enough at scaring off the biologists, we have added megabias."[3]

The fossil record is essentially complete

Scientists have had more than 160 more years to collect fossils. Evolution should be obvious within the fossil record by now. Steven Holland points out that the fossil record is imperfect in a sense, but really nearly complete. It is imperfect in that it did not record every organism that has ever lived. So, "all data sets are incomplete",[3] and he believes we need to "take a different path".[3]

First of all, we need to recognize that the imperfection of the fossil record is exaggerated:

> "Our exaggerated emphasis on the imperfection of the fossil record feeds the perception among scientists in general that the fossil record is an unusually poor data set. It isn't. … We already know much about the structure of the fossil record."[4]

Holland recommends that paleontologists should not emphasize the incompleteness of the fossil record any more, although not ignoring it completely.

Second, Holland contends that instead of concluding, as many do, that the fossil record is not worth considering, scientists should 'embrace' it along with the sedimentary record, and work with it. The fossil record is better than most scientists recognize, since "We know much about the structure of the fossil record."[5] Not only do paleontologists know the structure of the fossil record, but also that it provides a good record of species richness:

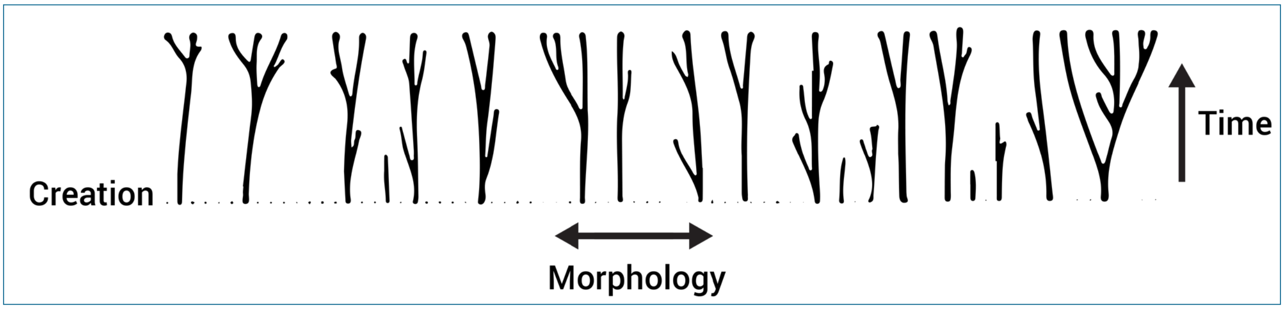

Figure 1. The creation orchard of life

> "Through her comprehensive examinations of live-dead comparisons, Susan Kidwell (2002, 2013) showed the fossil record contains a high-fidelity record of species richness and especially abundance, a pattern both unexpected and most welcome."[5]

Holland praises the fossil record as a record of past life:

> "As paleontologists, we have an extraordinary data set at our disposal, and we have the expertise to understand it. We have something that no other field of biology has—time, deep time—and we need to play to that strength. We have access to worlds far different from our own, with biotas, geographies, and climates unlike anyone has seen."[5]

I agree that paleontologists and scientists in general need to embrace the fossil record and accept the fossil record for what it is saying today. But doing so raises a conundrum for the evolutionist: the higher-fidelity the record of species richness the fossil record is, the less evolutionists can appeal to the incompleteness of the fossil record to explain away the morphological gaps between fossil taxa. So, if the fossil record is so good, why have these gaps not been filled after 160 years more of collecting fossils, if evolution is true? The lack of intermediates, the gaps, are not only real and universal, but they are even more glaring after so many years of digging up fossils.[6] Michael Denton documents that 100,000 taxon-defining novelties are "not led up to gradually from some antecedent form, and which remain invariant after their actualization for vast periods of time."[7] The glaring, universal gaps in the fossil record should easily be enough to reject evolution, but paleontologists and many other scientists rarely draw this conclusion, likely because of a previous commitment to naturalism and evolution.

The fossil record is nearly complete due to Flood burial

From a biblical creation point of view, the Flood buried the pre-Flood world. We would expect sudden appearance of different kinds of fossils followed by stasis, unlike what is expected for evolution. Therefore, we would expect the fossil record to be complete, except for that small number of new fossils that are being discovered every year. These fossils do not change the nature of the fossil record; it contains universal gaps that can be explained by the creation orchard of life (figure 1). The fossil record is just what is expected from a biblical perspective: an original creation of different kinds described in Genesis 1, with much variety within the kinds both at creation and at the end of the pre-Flood era.

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Finally, the dark side of Karl Marx revealed

The Devil and Karl Marx

Paul Kengor

Tan Books, Gaston, NC, 2020

Jerry Bergman

Karl Marx (1818–1883) is one of the most influential men of the last century. As a result, much has been written about him. OhioLINK (the *Ohio* *L*ibrary and *I*nformation *N*etwork's consortium of the State Library of Ohio, together with Ohio's college and university libraries) alone, lists 723 books about Marx, most laudatory, some objective, and a few critical. As Kengor observes, in a typical book and college class, one will hear "all Marx is a good Marx" (p. 35). He also notes that a few excellent biographies of Marx have covered the "sordid side of Marx … [a side that is] ignored by so many on the political left" (p. 35).

The biography by Paul Johnson (*Intellectuals: From Marx and Tolstoy to Sartre and Chomsky*) concluded that

> "Savagery is a characteristic note of his verse, together with the intense pessimism of the human condition, hatred, a fascination with corruption and violence, [plus] suicide pacts and pacts with the devil" (quoted on p. 37).

Kengor then gives some examples which eloquently illustrate Johnson's claim (pp. 37–53). From reading Marx's works, evidence supports the claim that he was mentally unbalanced. This view contrasts with what I learned in college about what was claimed to be Marx's brilliance, his concern for the exploited, and his goal to make the world a better place for all humanity.

Kengor's book is one of the few critical books that has carefully examined this sordid side of Marx. He found so much material, he had to condense it down to 462 pages. One focus was Marx's active antagonism to organized religion, particularly the Roman Catholic Church. Kengor also discussed in some detail Marx's acceptance of Darwinism as an important factor in his animus to Christianity.

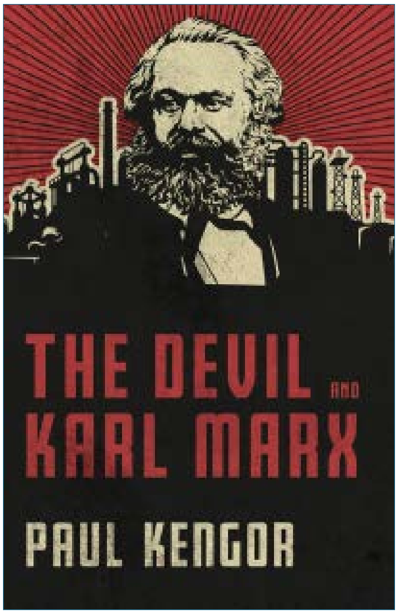
Professor Paul Kengor documents that no thinker in the nineteenth century has had so powerful an influence on mankind as Karl Marx, and no other man had more influence on Marx than Friedrich Engels (1820–1895; figure 1). As Kengor documented, a third person important to the work of Marx and Engels was Charles Darwin (1809–1882).

Kengor begins the book with a review of the lives lost due to communism. Noting the difficulty of obtaining an accurate tally, Kengor concludes that a total of one half billion is not an unrealistic number. Then he listed the countries that tried communism and which have failed, including the USSR, Cambodia, Cuba, Venezuela, and North Korea.

Marx's progression from Christian to atheist

Marx was baptized at age six and kept the faith at least until his initial college years (p. 60). When he completed high school, on his graduation certificate was written: "His knowledge of the Christian faith and morals is fairly clear and well-grounded."[1] Marx also penned literature praising Christians and Christianity. Union with Christ, he wrote, gives us

> "... an inner elevation, comfort in sorrow, calm trust, and a heart susceptible to human love, to everything noble and great, not for the sake of ambition and glory, but only for the sake of Christ."[2]



Kengor writes that although Marx was raised in the richly religious soil of his home town he later "would stomp upon that religious bounty rather than feed upon it as nourishment for his troubled soul" (p. 60).

His radical shift in thinking occurred after only a few years of university life. At the university of Bonn, Marx became increasingly critical of Christianity. His theology professor, Bruno Bauer (1809–1882), vigorously attacked the New Testament, denying the "historicity of Christ and portraying the Gospels as fantasy, as mythical inventions" (p. 13). From Bauer, Marx came to regard the miracles of the New Testament, and Christianity itself, as myths. He was only 19 then, a teenager. No doubt he learned about the claims that atheists still use today to discredit Christianity, claims that have been effectively refuted by many modern Christian apologists. Bauer

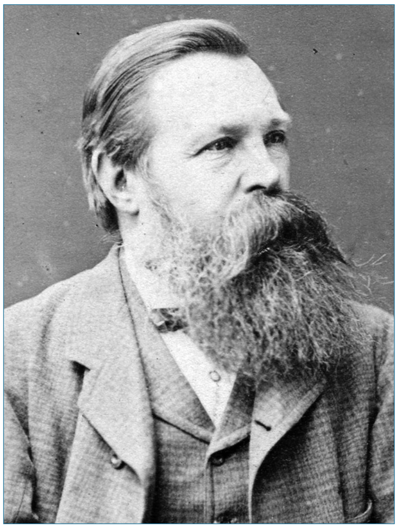


Figure 1. Friedrich Engels was Marx's main co-worker and the co-author of many of his writings. Engels' family were wealthy factory owners, and he was an important source of financial support for Marx.

soon became Marx's closest friend at the University of Bonn, frequently visiting the home of Bauer and his brother, Edgar (p. 14). At the end of his university studies, Marx viewed the Christian religion as one of the most immoral and evil of all existing religions. He wrote, "This heaven I've forfeited, I know it full-well. My soul once true to God, Is chosen for Hell" (quoted on p. 51).

Another man who greatly influenced Marx was Mikhail Bakunin (1814–1876). Bakunin was a Russian materialist and anarchist who viewed the myth of God as a belief effectively used to oppress others. As an evolutionist, he had a low view of Christianity, mocking God, writing "our first ancestors, our Adams and our Eves, if not gorillas, [were] very near relatives of gorillas" (p. 19). God was an "eternal egoistic solitude" creature who created Adam and Eve so that He "might have some new slaves" (p. 19).

The influence of Darwinism

Marx's Darwinian worldview influenced many of Marx's ideas. For example, the goal of communism was to evolve mankind to a level of full social and economic equality, when actually it was a totalitarian ideology committed to bringing about a massive change in humanity by altering human nature itself (p. 27).

Darwinism was an important ingredient that supported secularism, especially after 1859. And it was secularism that laid the foundation for atheism, then communism, that allowed it to flourish. Both Marx and Darwin sought to produce a unified science of mankind, which caused Marx to immediately realize the significance of Darwin's work. For Marx, the critical factor in his belief was secularism, which was rooted in religious skepticism. And a major pillar of religious skepticism was the writings of Charles Darwin. Marx especially admired Darwin for dealing a "grand blow for materialism and atheism" (p. 92).

Darwin undermined the major historical proof for God, the evidence for design in the natural world. Darwin's primary importance to Engels and Marx was to support materialism. In short, Darwin concluded that species were not immutable. Instead, all animals were descended from common ancestors going back to the original ancestor of all life. Different species were the result of gradual changes occurring over millions of years. Furthermore, God had nothing to do with this progression. The cause was natural selection.

Darwinism and rejection of the creation of Adam and Eve can lead to racism and, in Marx's case, extreme racism. As Kengor writes:

> "Karl Marx was a racist who cast freely with choice epithets aimed at blacks and even Jews … his awful statements about blacks and Jews … ugly views by Marx [were] littered throughout his personal and professional writings" (p 86).

A few examples included how Marx spoke of his own son-in-law, Paul Lafargue, the husband of his daughter Laura. Paul

> "… came from Cuba, born in Santiago … because Paul was Cuban, Marx viewed him as marred by 'Negro' blood in his veins, prompting Marx to denigrate him as 'Negrillo' and 'The Gorilla'" (p. 86).

Karl never let up his ridicule of Paul. In November 1882, 14 years after Lafargue and Laura married, Marx complained to Engels that Lafargue had all the flaws of Negroes including low intelligence. In November 1911, Marx's son-in-law, the 'Negrillo' Paul, died in a suicide pact with Marx's daughter, Laura. The importance of Marx in the communist movement is revealed by the fact that none other than Vladimir Lenin (1870–1924) spoke at Paul and Laura's funeral (p. 94).

Particularly loathsome to Marx was anyone who was part Jewish or African. Marx referred to his fellow German socialist Ferdinand Lassalle as a 'greasy Jew', 'the little kike', 'water-polack Jew', 'Jew Braun', 'Yid', 'Izzy', 'Wily Ephraim', 'Baron Itzig', and 'the Jewish Nigger' (p. 86). In a July 1862 letter to Engels, Marx confidently observed that his conclusion about Lassalle was as follows: "It is now perfectly clear to me that, as the shape of his head and the growth of his hair indicates, he is descended from the Negroes" (p. 87).

Marx's personal life reflected his anger and intolerant racist views. Four of Marx's six children preceded him in death, and all had tragic ends. The two daughters who survived him later committed suicide (p. 85). When Marx's wife, the vivacious Jenny, died her husband did not bother to attend her funeral (p. 91). When Karl Marx died, his co-worker, Engels, "gave the eulogy, invoking not God but Darwin" (p. 92).

Trotsky found his gods in Marx and Darwin

Born Lev Davidovich Bronstein to a wealthy Ukrainian-Jewish family in the Ukraine, leading communist Leon Trotsky (1879–1940) embraced Marxism in 1896 when he "found his gods in Marx and Darwin" (p. 118). Trotsky wrote, "Darwin destroyed the last of my ideological prejudices … about the world, and life and its origins." As a result, Trotsky rejected Genesis and accepted 'evolutionary theory', which he wrote:

> "… took possession of me completely. Darwin stood for me like a mighty doorkeeper at the entrance to the temple of the universe. I was intoxicated with his [Darwin] thought" (p. 118).

Trotsky moved into London in 1903 and there befriended a fellow communist, Lenin. He spent ten years working for the communist cause in Britain, Austria, Switzerland, France, Spain, and the United States. When Trotsky returned to Russia he became chairman of the Petrograd Soviet and played a key role in the November 1917 revolution that overthrew the new provisional government. After the death of Lenin in January of 1924 and the rise of Joseph Stalin, Trotsky was removed from his government positions. He was expelled from the Soviet Union in 1929 and began writing books and articles very critical of Stalin. As a result, he was assassinated with an ice axe in Mexico in 1940 at age 60.

The war against Christianity

The war against Christianity in Europe by the Nazis is well known, but less well known are the murderous results of communism in Russia. The path from Bauer, Darwin, and Marx led to the communist revolution in Russia and the massive slaughter of Christians. Respect for the Christian faith in the pre-communist Russia was rich and vibrant, even among the leaders (p. 119). After the October 1917 revolution,

> "… a full-throttle war on religion was underway … an open campaign of terror was launched against all religions, particularly against the Russian Orthodox Church … a policy of terror … felt by every religious faith" (p. 119).

Marx's friend and close co-worker Lenin's actions "against religion and the Church are astonishing in their diabolical ferocity and immorality" (p. 119).

One of thousands of examples of the massive slaughter of Christians occurred in 1918. In one small diocese, 47 clergymen were shot, drowned, or axed to death. The state confiscated land and church property, including schools. Religious faith was replaced by a new faith, Marxist-Leninism, which "became the new state religion" (p. 120). Religious instruction was forbidden, and children were encouraged to turn in their parents if they taught them about God. Marriage became a state ceremony and the prohibition against divorce was lifted, wreaking havoc on the Russian family. Children belonged to the state. Parents were to provide for their physical needs, while the state worked to train their mind to accept atheism and communism.

Most Russian church buildings were dynamited or turned into storage rooms. The ones that remained were monitored by full-time, state-employed 'church watchers' (p. 121). From the 40,000 churches in Russia, 150,000 priests, monks, deans, and bishops were sent to frigid Siberia or worse parts of the country. One ex-seminarian, Joseph Stalin (1878–1953), after he read Darwin as a seminarian student, became an evolutionist and atheist and made things even worse for the Christians. Of the 657 churches in Moscow in 1917, only about 150 remained by 1976. Kengor continues by documenting in sordid detail the communist attacks against the church in virtually every country they took over. Kengor includes a chapter on the persecution of the seminaries, churches, and clergy behind the Iron Curtain. The ideology of Karl Marx, Kengor explains, resulted in "sheer contempt for religion", which has continued today in all the countries controlled by a communist party (p. 302).

Summary

Materialism led to Marxism, which led to a holocaust that snuffed out the lives of some half a billion persons. All because of the work of one man, Karl Marx, whom many in academia venerate today. And a critical factor was the work of Friedrich Engels. Another critical factor was the writings of Charles Darwin and his theory of evolution, which, in the minds of many, negated the need for God to explain the origin of the physical creation.

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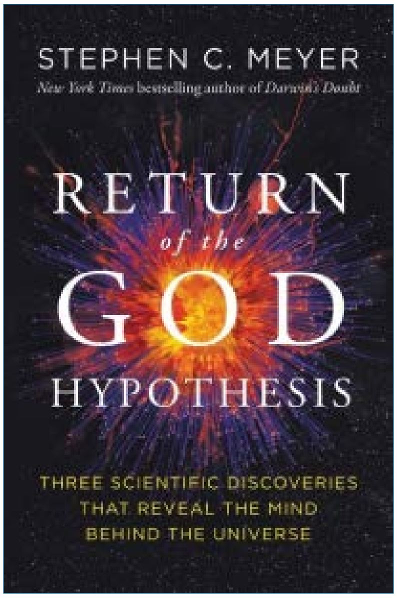
The existence of specified information in the universe points to a creator God

Return of the God Hypothesis: Three scientific discoveries that reveal the mind behind the universe
Stephen C. Meyer
Harper One, New York, 2021



John Woodmorappe

Author Stephen C. Meyer has a Ph.D., from the University of Cambridge, in Philosophy of Science. He is Director of the Center for Science and Culture at the Discovery Institute in Seattle. In this work, he delves into many subjects, but mainly philosophy of science, cosmology, and biology. I largely focus on the latter.

In this book, Meyer reports on many debates he has had with leading evolutionists. For this reason, the reader is assured that he has interacted with all the main arguments and counterarguments. The long-term follower of theistic scientific thought is reminded of Duane T. Gish, who likewise debated evolutionists and thereby sharpened his arguments.

The biblical worldview made modern science possible

The author points to the analysis of chemist Melvin Calvin on the origin of modern science:

> "Calvin notes that the monotheistic worldview of the ancient Hebrews suggested a reason to expect a single coherent order in nature and thus a single, universally applicable set of laws governing the natural world. By contrast, because animists, polytheists, and pantheists affirmed the existence of many spirits or gods, each possibly interacting with nature in different ways, they had no reason to think that natural phenomena would manifest uniformity and order. The ancient Hebrews, on the other hand, thought that, as Calvin put it, 'the universe is governed by a single God, and is not the product of the whims of many gods, each governing his own province according to his own laws'. Calvin, like many historians and philosophers of science, identified this belief in an order-loving monotheistic God as 'the historical foundation of modern science'" (p. 37).

Scientific discoveries because of, not in spite of, the religious beliefs of early modern scientists

Some critics have argued that religious belief is a drag on scientific thinking, effectively a science stopper, and that the achievements of early modern scientists only came when they separated their religious beliefs from their studies. Others have asserted that there is no relationship between science and the Christian worldview. After all, religion was dominant at the time, so it is hardly surprising that most scientists also were religious.

Meyer soundly rejects these kinds of thinking. He realizes that the presence of God was not incidental; it was part and parcel of the everyday scientific reasoning of the early modern scientists. He writes:

> "Nevertheless, many of the founders of modern science did not just assume or assert by faith that the universe had been designed by an intelligent agent. They also argued for this hypothesis based on discoveries in their fields of study. Johannes Kepler perceived intelligent design in the mathematical precision of planetary motion … . Robert Boyle insisted that the intricate clocklike regularity of physical laws and chemical mechanisms as well as the anatomical structure in living organisms suggested the activity of 'a most intelligent and designing agent'. Carl Linnaeus later argued for design based upon the ease with which plants and animals fell into an orderly groups-within-groups system of classification … . The tradition attained an almost majestic rhetorical quality in the writings of Newton" (p. 47).

Not a GOTG (God of the Gaps)

Unbelievers (and their compromising evangelical allies) sometimes sneeringly dismiss a Creator God as Someone that is invoked whenever a materialistic explanation is inadequate—until subsequent research shows that a materialistic explanation is adequate after all (figure 1). Is this objection validly applicable to Intelligent Design?

As a classic example of GOTG, unbelievers bring up Isaac Newton, who supposedly invoked the direct Hand of God, in *ad hoc* fashion, whenever he could not explain some aspect of planetary motion. Meyer actually re-examined Newton's *Principia* and found this to be untrue. It turns out to be a rationalistic legend. Newton did invoke God in a providential sense, but never as a gap-filler. As Meyer explains:

> "Third, though Newton affirmed these powers of God, he did *not* postulate occasional, special, or singular acts of God in place of a law-like description of planetary motion or to remedy irregularities in the laws of nature or to fix an unstable planetary system. Newton thought that God was responsible on an ongoing basis for the mathematical regularities evident in nature, not fixing irregularities or rectifying instabilities [emphasis in original]" (p. 429; see also p. 518).

Meyer provides the following analogy to rebut the canned GOTG contention that is nowadays used against the proponents of Intelligent Design. He comments:

> "Yet we would not say, for example, that an archaeologist had committed a 'scribe-of-the-gaps' fallacy simply because—after rejecting the hypothesis that an ancient hieroglyphic inscription was caused by a sandstorm—she went on to conclude that the inscription had been produced by an intelligent scribe. Instead, the archaeologist made an inference based upon her experience-based *knowledge* that information-rich inscriptions arise from intelligent causes. She did not base her inference *solely* on her judgment that no natural cause could explain the inscription [emphasis in original]" (pp. 416–417).

Does RNA rescue the evolutionists?

In living things, DNA is necessary to synthesize protein, and proteins are required to assemble DNA. So which came first? Evolutionists would have us believe that this chicken-and-egg question is circumvented by a long period during which non-living chemicals, capable of self-replication, had been subject to natural selection. Meyer elaborates: "The RNA-world hypothesis posits that life first arose from a process of chemical evolution that gained traction after self-copying RNA molecules putatively first made prebiotic natural selection possible" (p. 305). According to this thinking, the emergence of DNA and proteins was only the crowning achievement of this process. Is the foregoing scenario realistic, or is it more the product of evolutionistic wishful thinking?

Meyer (pp. 180–181) lists many fatal problems with the RNA-world hypothesis. The worst one is this: the RNA-world hypothesis presupposes the existence of sequence specificity and information; it does not explain its *origins* in the context of an unintelligent process! This brings the evolutionist back to square one, as pointed out by the author: "Yet explaining how the building blocks of RNA arranged themselves into functionally specified sequences has proven no easier than explaining how the constituent parts of DNA might have done so" (p. 181).

No such thing as a self-replicating molecule

Meyer unmasks a 'self-replicating RNA' experiment as follows:

> "The 'self-replicating' RNA molecules in this experiment did not copy a template of genetic information from free-standing nucleotides as protein machines (called polymerases) do in actual cells. Instead, in the experiment, a presynthesized *specifically sequenced* RNA molecule merely catalyzed a single chemical bond, fusing together two other presynthesized partial RNA chains. Their version of 'self-replication,' therefore, amounted to nothing more than joining two sequence-specific halves together [emphasis in original]" (p. 309).

The experiment clearly requires multiple cherry-picked intelligent processes to even make it work and does not even begin to explain the origins of biological design. Even then, the specially chosen RNA molecule is in no sense self-replicating. It, at most, causes two other *pre-selected* RNA molecules to join together. And even *that* has very limited relevance, if any, to any evolutionistic origin-of-life scenario.

What are we to make of this? The 'self-reproducing molecule', a pillar of evolutionistic imagination, is already dead on arrival. The self-reproducing molecule does not exist, and neither does the natural selection of molecules, let alone the prebiotic evolution of the first life. Meyer quips: "First, the process of natural selection presupposes the differential reproduction of already living organisms and thus a preexisting mechanism of self-replication" (p. 179).

Evolution does not explain the origin of novel biological information

Let's now assume that some form of life did come to exist by chemical evolution. Things do not get any better for the evolutionist. In fact, some evolutionists have admitted as much, as observed by Meyer:

> "Over the past three decades, many evolutionary biologists have challenged a key tenet of the neo-Darwinian synthesis, namely, the idea that small-scale microevolutionary changes can be extrapolated to explain large-scale macroevolutionary innovations. For the most part, microevolutionary changes (such

Figure 1. An intelligent designer of the universe is not a 'God of the gaps'.

> as variation in colour) merely use or express existing genetic information, while the macroevolutionary change necessary to assemble new organs or whole body plans requires the production of new genetic information. Recognizing this and other problems, in 2008 a group of sixteen evolutionary biologists met in Altenberg, Austria, to express their doubts about the creative power of the mechanism of random mutation and natural selection. They are known as the 'Altenberg 16' …" (p. 195).

Natural selection does not create biological novelty: the problem of specified complexity remains

One must not confuse the oft-quoted survival of the fittest with the arrival of the fittest (p. 482). Meyer thus summarizes the issue at hand:

> "As conceived from Darwin to the present, natural selection 'selects' or acts to preserve, those random variations that confer a fitness or functional advantage upon the organisms that possess them. But it 'selects' only *after* such advantageous variations and mutations have arisen … . All this means that natural selection does nothing to help *generate* functional DNA base (or amino-acid) sequences, that is, new genetic information … . Why a formidable challenge? Again, because random mutations *alone* must produce *exceedingly rare* functional sequences among a cast combinatorial sea before natural selection can play any significant role [emphases in original]" (pp. 323–324).

Computer programs do not demonstrate the unintelligent origins of biological information

The likes of atheist Richard Dawkins have written computer programs that purportedly show how natural selection is supposed to act on random mutations, over countless generations, to create biological information. They do no such thing. Far from it. The computer program constantly selects sequences against a final, *preselected* target. This includes iterations of random letters culminating in the phrase 'Methinks it is a weasel'.

Evolution has no such foresight and does not strive to any sort of final goal or outcome. Moreover, according to standard evolutionary theory, each step that is 'chosen' by natural selection must endow its bearer with a reproductive advantage. No computer program has even begun to show how each step, with or without culminating in a final predetermined outcome, is supposed to be advantageous to its 'bearer'. That is the essence of evolutionary theory, and the fatal flaw of 'evolution-demonstrating' computer programs.

Specified complexity in proteins

Proteins have distinctive folds, and it takes only a few mutations to destroy a protein fold, while many mutations are needed to transform one protein fold into another. This makes it virtually impossible for new protein folds to arise from evolutionary processes, as Meyer explains:

> "So just as a series of random changes to computer code will destroy the function of the software before a new program could arise, a small handful (typically between 3 and 15) of random changes to the amino acid sequence in a protein will destroy the stability of the protein fold well before enough mutations could accumulate to generate a novel fold. In fact, function-ready protein folds will degrade more quickly than English sentences" (pp. 319–320).

'Rewiring' of developmental gene regulatory networks (dGRNs) does not create novel animals

The dGRNs govern the timing and expression of genetic information during animal development. As Meyer explains, "These networks of genes and gene products function much like integrated circuits and ensure that the developing organism produces the right proteins at the right times to service the right types of cells during embryological development" (p. 311).

Some evolutionists have downplayed the role of new genes in the putative formation of new animal body plans and have instead focused on the supposed power of 'rewired' dGRNs in this role. This is especially claimed for the sudden appearance of novel animals during the Cambrian explosion.

Is 'rewiring' even feasible? Note that the dGRN cannot be subject to step-by-step testing of random mutations by natural selection, as demanded by evolution, and as explained by Meyer:

> "Yet all available observational shows that dGRNs do not tolerate changes or perturbations to their basic control systems … . Even modest mutation-induced changes to the genes in the core of the dGRN produce either no change in the developmental trajectory (due to a preprogrammed redundancy) or catastrophic (most often lethal) effects within developing animals. Disrupt the central control nodes and the developing animal does not shift to a different viable, stably heritable body plan. Rather, the system crashes, and the developing animal dies or, if it survives, is severely malformed" (p. 314).

So, we are right back to the 'hopeful monster' fantasy.

Ironically, not only does 'rewiring' not do away with intelligent design, but successful 'rewiring', were it to take place, requires just that! Meyer comments:

> "Any electrician or electrical engineer—indeed, anyone who works with actual circuitry and a power supply with current passing through the circuit—knows that successful rewiring requires well-informed decisions, that is, both information *and* intelligent design. What rewiring manifestly does *not* allow is *random* changes. That's a great way to burn down your house or blow out the mother-board of your computer [emphasis in original]" (p. 317).

The nylonase novelty that is not

Nylon, a man-made compound that does not occur in nature, was first made in the 1930s. There is now a protein (enzyme) that can break it down. So, we are told, an evolutionary novelty has arisen in just 40 years. Moreover, the new enzyme shows that new protein folding can arise, from blind evolutionary processes, even in an astonishingly short period of time.

Meyer deconstructs the foregoing evolutionary narrative. Just because nylon does not occur in nature does not mean that none of its components occur in nature, and some of these components may be vulnerable to attack by existing enzymes. So the nylonase capability may have long pre-existed the invention of nylon itself. In fact, that is exactly the situation at hand. A 'cousin' enzyme to the nylonase enzyme has been found to have weak nylonase activity. It differs from the nylonase enzyme by only two point mutations. So the nylonase enzyme is not even a novelty; it is a tweaking of a pre-existing capability. In other words, it is an optimization, not an innovation (p. 322). Far from being supportive of evolution, it begs the question about its origins. Thus, this trait may go back to creation. Finally, the optimized nylonase activity, the result of two point mutations, has nothing to do with any sort of novel protein folding.

Conclusion

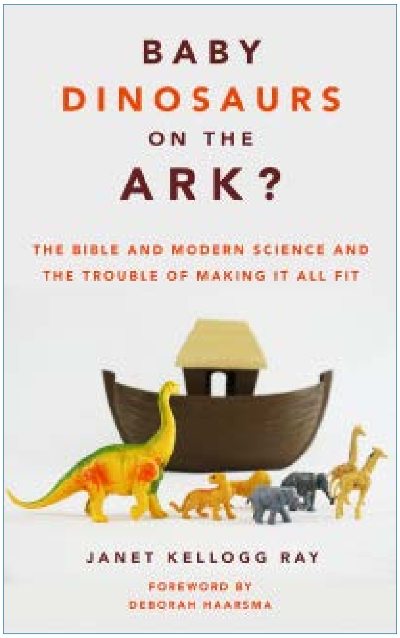
Meyer does not conclude that scientific observations, strictly speaking, prove the existence of God. Rather, it is a matter of probabilities. Consider the universe. Meyer remarks:

> "Moreover, as I've argued, the observation of extreme fine tuning confirms precisely what we might well expect if a purposive intelligence—indeed, a theistic or deistic creator—had acted to design the universe and life. We certainly have *more* reason to expect a universe fine-tuned for life (or a life-permitting universe that depends upon fine tuning) assuming theism or deism than we do assuming naturalism [emphasis in original]" (p. 274).

Evolutionists commonly display a condescending attitude towards the proponents of ID (Intelligent Design). Besides showing a great deal of intellectual arrogance, such an attitude is completely unwarranted. As for the scientific respectability of Intelligent Design, Meyer concludes:

> "Yet it is not only cosmology that has rendered the 'God hypothesis' newly respectable. As one surveys several classes of evidence from the natural sciences—cosmology, astronomy, physics, biochemistry, molecular biology, and paleontology—the God hypothesis emerges as an explanation with unique scope and power. Theism explains an ensemble of metaphysically significant events in the history of the universe and life more simply, more adequately, and more comprehensively than major competitive metaphysical systems, including not only materialism and naturalism, but also pantheism and deism. Again, this does not *prove* God's existence, since superior explanatory power does not constitute deductive certainty. It does show, however, that the natural sciences now provide strong *epistemic support* for the existence of God as conceived by Judeo-Christian and other traditional theists [emphasis in original]" (p. 298).

Dismissing biblical creation without engaging creationist arguments



Baby Dinosaurs on the Ark

Janet Ray

Wm. B. Eerdmans Publishing, Grand Rapids MI, 2021

Joel Tay

Baby dinosaurs on the Ark is one of several new books that is claimed to have been written by an ex-creationist who now embraces evolution. Belief in biblical creation is presented as anti-science, although there is very little interaction with actual creationist arguments. The book comes recommended by several big names in the theistic evolution community, such as Dennis Venema, Karl Giberson, John Walton, Thomas Oord, and the current President of *BioLogos*, Deborah Haarsma. Unfortunately, despite the high praises by notable theistic evolutionists and the claim to have been written by an ex-creationist, it is hard to escape the conclusion that the author isn't well informed about what creationists actually believe.

Whenever I write book reviews, I try to list some of the strengths of a book even if I disagree with the author's conclusion. This was exceedingly difficult to do with *Baby Dinosaurs on the Ark.* While there are significant errors throughout the book, the biggest issue I had was the author's inability to interact with arguments from biblical creationists. The uninformed reader is left hanging with the impression that biblical creationists do not have any answers to her objections.

This book consists of a collection of short, disjointed topics on what evolutionists believe, often skimming through a whole multitude of arguments without any significant depth. Topics range from genetics, geology, paleontology, human evolution, intelligent design, astronomy, and biochemistry.

Each topic follows a similar structure. Janet Ray starts off with a short story. She then explains what evolutionists believe and why they believe those things. This is followed by a very brief paragraph or two of what creationists believe, but the author almost always leaves out the reason *why* creationists believe those things. Biblical creation is then dismissed in one of these four ways:

First: Assert that evolution is science. Therefore, if you deny evolution, you are antiscience.

Second: An appeal to authority. Most scientists believe in evolution, therefore biblical creation has to be wrong; or biblical creationists don't publish in peer-reviewed secular journals.

Third: There is no mention of *why* biblical creationists believe what they do, leaving the reader with the impression that biblical creationists have never addressed the issue on hand.

Fourth: Creationists are dismissed as trying to 'fit the science into the Bible'. Biblical creation is then dismissed in a mocking tone without pointing to any actual contradiction in their worldview, nor does she engage with their arguments.

It came to a point where I wondered whether the author was really ignorant of creationist literature, or whether she was going out of her way to avoid interacting with creationist arguments. (As Proverbs 18:17 says, "The one who states his case first seems right, until the other comes and examines him.") This is especially unfortunate since most of her objections are really basic, such that anyone vaguely familiar with basic creationist literature would have been able to answer them.

Consider the following as examples of what I mean by 'basic'. Distant starlight is stated as a problem for creationists (pp. 64–68). Typical of the touch-and-go nature of her writings, she doesn't mention that creationists have several workable creation models, nor does she mention that the big bang itself faces a distant starlight problem (i.e. the horizon problem).

She does the same for other topics such as radiometric dating, the claim that micro-evolution over time leads to macro-evolution, that human and chimp DNA are 99% similar (a thoroughly discredited claim), homology, apemen, objections against a global Flood, rock layers, continental drift, ice core and radiometric dating. And she doesn't stop there: how all the animals could have fitted on Noah's Ark, why human fossils are never found with dinosaur fossils in the same layers, the Ice Age, how animals got to Australia, and marsupials, dinosaur artifacts, and dinosaur soft tissue.

There are many other topics covered in the book, but this is just a sampling of the type of 'basic' apologetic questions that you would not expect an evolutionist to raise if they were even vaguely well-versed in creationist literature. Unfortunately, an uninformed reader is likely to come away thinking that creationists have no answers to these questions, since she hardly begins to explain why creationists believe what they do. Any attempt to write a comprehensive rebuttal of all her mistakes would probably result in a book three times as long as hers. For this reason, I will only engage with a few selected examples of what she has written to give the reader an overall feel of the book.

P. fluorescens

The only example in the book where the author engaged an issue beyond what most could consider to be 'elementary' creation apologetics, was when she brought up the example of *P. fluorescens*. Ray acknowledges that natural selection only selects from genes already present (p. 37). Nevertheless, she claims that "microevolution events, over time, result in macroevolution" (p. 73). So, for evolution to happen, species must tinker with new combinations of genes. Unfortunately, but not surprisingly, Ray assumes that advantageous mutations are evidence for evolution (p. 35).

P. fluorescens is a nitrogen-fixing bacterium found in soil. Scientists knocked out a gene responsible for growing a flagellum. This caused the bacteria to lose their ability to swim. These immobile bacteria colonies had to be fed regularly, or they would have starved to death. When a graduate student forgot to feed the bacteria for a few days, most of the bacteria died. However, a few colonies survived. These bacteria were later found to have regrown a smaller but less efficient flagellum.

It turns out that *P. fluorescens* has a nitrogen-regulating protein that is around 30% similar to the protein for flagellum growth. A mutation resulted in the over-expression of this protein, allowing the bacteria to compensate for the missing flagellar protein. These mutants were able to reconstruct a small but functional flagellum. Ray took this as proof that environmental pressures drive evolution, and that this is an excellent example of how genes can be repurposed, or recombined, resulting in dramatic changes in a species.

Biblical creationists have no problems with such examples. Creationists have often argued that God has robustly engineered creatures to be able to adapt to new environmental niches. Moreover, most creationists believe that natural selection is an important part of the biblical model.[1] But if natural selection and the role of environmental pressures are consistent with both biblical creation and evolution, how can they be cited as proof for evolution?

What Ray does not tell us, however, is that the original research paper raises some interesting issues. For example, this 'repurposed protein' is supposed to have occurred randomly, yet for the noted phenomenon to have occurred, there had to be two different mutations occurring together in less than four days. Even if we assume that this is a chance mutation and not a design feature, we see that the resultant mutant now overproduces a protein involved in nitrogen regulation. The resultant mutant is not only described as less fit compared to original bacterium, but because the flagellum is tied to its excessive nitrogen production, the bacterium is no longer able to regulate nitrogen properly—if the protein production drops, it stops forming the flagellum and it dies. If it retains this overproduction and makes the flagellum, it survives, but it is severely handicapped without its ability to properly regulate nitrogen. The bacterium has 'devolved' in order to survive and has now lost its ability to regulate nitrogen! As the paper concludes, "Trans-acting mutations can contribute to gene network evolution, but as predicted, such mutations bear severe pleiotropic cost."[2] In addition, while homologous proteins may substitute for an existing function, they cannot be used to explain the origin of irreducibly complex biochemical pathways. Simply put, Ray's best argument for evolution turns out to be a case of 'devolution'.

Strawman and errors

Unfortunately, Ray takes the example of *P. fluorescens* as proof that common environmental pressures drive evolution (p. 39). This is extended to explain how the ichthyosaur, dolphin, and shark could have evolved so many similar traits despite being a reptile, mammal, and fish (p. 41). She uses this to explain how environmental pressures have caused similar-looking counterparts among both marsupials and mammals. E.g. Australia is home to many marsupials while the rest of the world is populated with placental mammals. Yet Australian marsupials do look similar to many placental mammals. Marsupial sugar gliders, for example, resemble placental flying squirrels (p. 41).

While she doesn't think that the look-alikes between marsupials and placental mammals are a problem for evolution, she claims that the dominance of marsupials in Australia is a problem for creationists. She writes:

> "Only one type of marsupial is found anywhere outside of Australia: the opposums of South and North America … . Australian mammals pose a difficult problem for creationists … in less than 4,000 years post-flood, one generic marsupial pair and one generic

> monotreme pair made their way across a vast ocean to repopulate Australia, including diversifying into the many species living today" (p. 102).

She then mocks the possibility that non-flying mammals could have spread to Australia by floating forests (figure 1) after the Flood, or that a post-Flood ice age could have lowered the sea levels, forming land bridges (pp. 102–103). Typical of her dismissal of biblical creationists, she concludes:

> "Consequently, the race to Australia was won by kangaroos in kayaks with their built-in baby wraps, while placentals were left behind dragging their tired and whiny toddlers" (p. 103)

As it is with all the rest of the book, she doesn't explain why creationists' explanations are wrong. Creationists are just brushed aside and ridiculed.[3]

Despite Ray's claim that biogeography is consistent with evolutionary theory, it is actually problematic for evolution. This problem is called *disjunct distributions*, and evolutionists have themselves appealed to floating forests and a lower sea level during the ice age(s) to rescue evolution.[4] Thus, Ray's dismissal of biblical creationists shines a spotlight on her lack of knowledge of both creationary and evolutionary scientific literature. Unlike evolutionists, creationists have an additional argument that evolutionists cannot employ—these creatures could also have been introduced by humans in the past.[5] As it turns out, Ray's mockery of biblical creation backfires on her.

Ray is also wrong to say that apart from opossums, all other extant marsupials are found in Australia. Extant marsupial creatures inhabit Indonesia, New Guinea, New Zealand, and even the remote Solomon Islands (E.g. the Northern common cuscus (figure 2), and the Sulawesi bear cuscus, and possums)—some introduced by humans. Furthermore, when we look at the fossil record, we find that marsupials used to be far more widespread. The remains of extinct marsupials have also been found in Africa (*Peratherium africanus*), Asia,[6] South America (*Thylacosmilus, Borhyaena, Cladosictis)*, and North America (*Stagodontidae*). In fact, this is a problem for evolutionists:

> "Living marsupials are restricted to Australia and South America … . In contrast, metatherian fossils from the Late Cretaceous are exclusively from Eurasia and North America … . This geographical switch remains unexplained."[7]

I am not aware of any reputable creationist who claims that all marsupials and monotremes in Australia came from one generic pair of each. It appears that for all the talk, Ray isn't familiar with biblical creation at all! Yet many such strawman arguments become the basis for ridicule in Ray's book. This is especially telling, since undergirding her narrative in her book is that she was an ex-creationist who became an evolutionist after seeing the light. In reality, the book demonstrates that her knowledge of creationist literature is astonishingly lacking.

Ray also wrongly asserts that Darwin was the first to propose a mechanism for evolution: natural selection (p. 34). She wrongly asserts that Darwin was the first to incorporate the idea of evolution over deep time, and claims that he was the first to propose a tree of life. This exposes Ray's unfamiliarity with the literature.[8]

She dismisses creationist illustrations depicting dinosaurs and people together, and likewise dismisses dinosaur stone figurines and artifacts from ancient human cultures. Instead, she points out that human fossils are never found with those of dinosaurs, and that this is a problem for creationists.[9] Claiming that there is no way to house 100 to 120 enormous dinosaurs for a year on the Ark together with food and water, she mocks the idea that baby dinosaurs or eggs could have been taken on the Ark (pp. 16–18). Creationists who use Behemoth, Leviathan, and dragons as examples of dinosaurs are likewise dismissed. We are not told what is wrong with having young dinosaurs on the Ark, before they went through their adolescent growth spurt. The whole thing is just mocked as yet another failed attempt to fit the science into the Bible.

Image: Piero "Positivo" Quadrini/Wikimedia Commons, CC BY-SA 4.0

Figure 1. Floating island La Rota in Posta Fibreno Lake, Italy

Naïve philosophy of science

Ray claims that when scientists speak of evolution as a theory, they do not mean that evolution is an untested hypothesis. Rather, "if we are to make a science term hierarchy, *theory* is at the top. Scientific theories rank *above* laws and facts because theories make

Image: Daderot/Wikimedia, CC0

Figure 2. *Phalanger orientalis*

sense of laws and facts" (p. 29). One can debate whether theory is higher than law, but indeed "evolution is just a theory" has long been on our list of *Arguments creationists should not use*—for that very reason.[10] That is, it is far too complimentary! Unfortunately, Ray asserts that the phrase "theory of evolution" means that evolution is foundational to understanding all of biology. "You may have questions about evolution, you may doubt or reject it, but you cannot validly label it as 'just a theory'" (p. 29). Throughout her book, science and evolution are lumped together as if they are synonymous, and creationists are portrayed as anti-scientific simpletons (p. 17).

Ray also rejects the idea that "facts must be interpreted and that the Bible is the only lens through which all facts should be filtered" (p. 45). Neither does she recognize that there is a crucial difference between historical science and empirical science. She writes:

> "Insisting on a young universe and a young earth requires dismissing chemical and physical principles routinely used in modern science and technology routinely used in modern science and technology for purposes other than determining age. Is it reasonable to trust the physics, chemistry, and mathematics in aeronautics and space travel and in every field of modern engineering, but disbelieve the exact same science when it tells us the age of the earth and universe? Insisting on a young earth discredits the fossil record, modern physical sciences, and archaeology, all in one fell swoop" (p. 75).

She claims that to deny evolution is to say that "science isn't just wrong. Science is an enemy" (p. 12).

> "While … the overwhelming majority of biologists accept evolution, there are working biologists (in the extreme minority) who reject it. When biologists reject evolution, however, it is for religious reasons, not a lack of scientific evidence."

She then quotes Todd Wood as justification:[11]

> "Evolution is not a theory in crisis. It is not teetering on the verge of collapse. … There is evidence for evolution, gobs and gobs of it. … There is no conspiracy to hide the truth about the failures of evolution. … Creationist students, listen to me carefully: There is evidence for evolution, and evolution is an extremely successful scientific theory … . It is my own faith choice to reject evolution" (pp. 45–46).

But why quote Todd Wood rather than Robert Carter, who would be more representative of the creationist movement at large?

Carter writes:

> "… most of us were once evolutionists and so we absolutely tested both theories. … we love science. We love thinking. … This is the reason we can embrace science and the Bible at the same time and without contradiction. And this is why we reject … deep-time naturalistic evolutionary theory."[12]

So why doesn't Ray quote Carter? Because doing so would undermine the narrative she is trying to push. Namely, that creationists are anti-science, and that Christians who love science also embrace evolution.

Theology

Ray claims that teaching evolution in church gets people talking about God. What she doesn't tell us, is that it not only gets people talking about God, but it also leads people away from the faith. In fact, Karl Giberson, the former vice-president of *BioLogos*, and one of the endorsers of this book, laments that telling his students that God used evolution caused them to become:

> "… so alienated from their home churches that they walked away, taking their enlightenment with them. … Many of my most talented former students no longer attend any church, and some have completely abandoned their faith traditions."[13]

Ray claims that she became an evolutionist through Kenneth Miller's writings.[14] She claims to believe every word of the Apostle's and Nicene Creed (p. 9), yet she also believes in an ancient universe, evolution, and the common descent of all life, including humans. There is no discussion of original sin, death before sin, or theodicy. Rather, Genesis is dismissed altogether as one of the "Ancient Near East text creation stories, of which there are several" (p. 57).

Ray claims that "a literal Genesis means a stand against the vast majority of modern science and scientists" (p. 182), and a stand against the science trusted for "medical care, disease research, agriculture, aviation, engineering, and energy. … If creationism is true … modern science collapses" (p. 182), and it would mean "it is within God's nature to mislead us" (p. 183). This would have been news to the creationist founders of modern science.

She claims that honouring Genesis requires recognizing its genre and listening to its ancient voice (p. 183). By this, she means that "When we read Genesis, we don't learn about modern science, but we do learn about God" (p. 184). "… the Bible is not an authority about the facts of modern science, it was never meant to be (p. 184)."

Ray claims that we do not have to "choose science or choose God" (p. 178). Why? Because, "Evolution theory says nothing about God or religion or any other world view" (p. 1). Ray rejects "all arguments of a universal flood, 'flood geology', or the descent of all life (humans and others) from a few on the ark" (p. 58). Even though she admits that "adding up the genealogies in Genesis" gives us an earth around 6,000 years old (p. 65), she asserts that Genesis is a theological story that says nothing directly about the age of the earth and universe (p. 64). Rather, Christians ought to "revisit the way we read Genesis" (p. 183). The Bible teaches us about "theology, not as science or a literal historical account" (p. 57). "The Bible gives us the answers to the *who and why* of creation; science answers the *how and when*" (p. 184). But Genesis actually goes out of its way to explain when (c. 6,000 years ago) and how (by God's command), and even in what order, contradicting evolutionary orders.

We see that Ray's attempt to address the conflicts between the Bible and evolution, always ends up dismissing Genesis as a mere story. Any attempt to reconcile biblical creation and science is ridiculed as 'fitting the science into the Bible'. In fact, the title of her book, *Baby dinosaurs on the Ark?: The Bible and modern science and the trouble of making it all fit*, does just that. It is a thinly veiled attempt at mocking how biblical creationists try to *force* science into the Bible.

The difference between Ray's approach to the Bible and that of the Apostle Paul shows clearly when she asserts: "What Adam and Eve *cannot* be, however, are the literal, genetic ancestors of all humanity" (p. 169). But even compromisers like William Lane Craig agree that some form of historical Adam, through whom sin entered the human race, is a clear biblical teaching.[15]

Despite her claim to be a practising Christian for whom "the Bible is viewed as authoritative for faith and life" (p. 58), it would seem that the opposite is actually true when it comes to interpreting Genesis.

Her denial of Adam and Eve as the genetic ancestor of all humans means that she has to reject the doctrine of Original Sin, i.e. Pelagiansm.[16] While she claims to be a practising Christian, Ray's treatment of Scripture falls short of the standards of the Chicago Statement on Biblical Inerrancy.[17] That is, she denies the inerrancy and infallibility of Scripture. Her hermeneutical approach of appealing to the genre of 'Ancient Near East creation stories' as a way of rejecting the historicity of Genesis, also falls short of the Chicago Statement on Biblical Hermeneutics.[18]

To put it bluntly, evolution, not the Bible, is her foundation for truth. Though this was not her intention of her writing the book, *Baby dinosaurs on the Ark* demonstrates how Ray's belief in evolution has unwittingly shipwrecked her faith.

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"The ICBI commentary adds, 'Though the Bible is indeed *redemptive* history, it is also redemptive *history* (emphasis in the original), and this means that the acts of salvation wrought by God actually occurred in the space-time world' (Article XII). With regard to the historicity of the Bible, *Article XIII in the commentary points out that we should not 'take Adam to be a myth, whereas in Scripture he is presented as a real person.'* … It adds, 'We further deny that scientific hypotheses about earth history may properly be used to overturn the teaching of Scripture on creation and the flood' (Article XII of the 'Chicago Statement'). *In short, the ICBI framers believed that using genre to deny any part of the historicity of the biblical record was a denial of inerrancy* [emphases added]." Geisler, N.L., *Explaining Biblical Inerrancy: The Chicago Statements on Biblical Inerrancy, hermeneutics, and application with official ICBI commentary*, Bastion Books, Arlington, TX, p. 11, 2013.
18. Article 19 of the Chicago Statement on Biblical Hermeneutics: "We deny that Scripture should be required to fit alien preunderstandings, inconsistent with itself, such as naturalism, *evolutionism*, scientism, secular humanism, and relativism."; Article 22 writes, "We affirm that Genesis 1–11 is factual, as is the rest of the book. We deny that the teachings of Genesis 1–11 are mythical and that scientific hypotheses about earth history or the origin of humanity may be invoked to overthrow what Scripture teaches about creation [emphasis added]."

Animal behaviour intelligently designed!

Animal Algorithms: Evolution and the mysterious origin of ingenious instincts

Eric Cassell

Discovery Institute Press, Seattle, WA, 2021

Philip B. Bell

The author of this enjoyable book from the Intelligent Design (ID) stable enjoyed a successful career as an aircraft systems engineer. Eric Cassell is also a past consultant for both NASA and the Federal Aviation Administration (US). A navigations systems expert, he is well qualified to have written *Animal Algorithms*, which probes the workings and origins of complex animal behaviours: feats of navigation, architectural constructions, complex insect societies, and more. Detailed references and endnotes for each of its eight chapters are found towards the end of the book, plus a general index.

Evolutionary writers refuse to consider ID explanations for life's diversity and complexity. ID advocates, conversely, have comprehensively and compellingly shown that a commitment to methodological naturalism "renders evolutionary theory not an inference to the *best explanation* but, less impressively, an inference to the *best allowed explanation*—in this case, the *best purely materialistic explanation* [emphases in original]" (p. 168). On the contrary, as the concluding sentence of this book puts it, "the design inference is not the end of science, as claimed by opponents of ID. Rather, it opens the door to a wider range of scientific investigation" (p. 206). By applying these tried and tested design principles to all sorts of animal behaviours, Cassell has made a unique contribution to the debate.

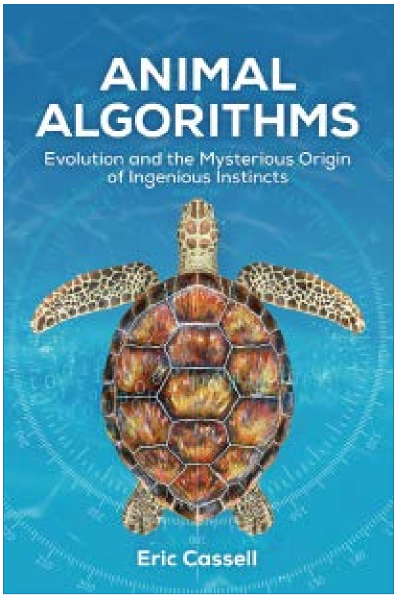
Why algorithms?

The word 'algorithm' immediately calls to mind computational programming. Algorithms are at the heart of many branches of mathematics and engineering, and are essential to modern everyday life:

> "Today we find algorithms being used all around us. Examples of algorithms are found in internet search engines such as Google, which … search the internet for any term that users query. Smartphones include algorithms in GPS route navigation, voice recognition, and various other applications. Route navigation applications employ complex algorithms to compute the most efficient route to the desired destination. In most cases, there are several possible routes, and the algorithm determines which one is likely to be the fastest. Such algorithms are, of course, never the result of a blind material process" (p. 162).

Therefore, it is apposite for ethologists (students of animal behaviour) to speak of algorithms in relation to such things as animal compasses (p. 47), bee navigation (p. 62), honeycomb construction (p. 125), and other complex programmed behaviours (p. 154).

The author uses the descriptor *complex programmed behaviours* (CPBs) in preference to talking of *instinctive* or *innate* behaviour. Many animal



behaviourists dislike the perceived teleological connotations of words like 'instinct' because of their aversion to design, purpose, and goals in biology—and Cassell wants his arguments to be considered on their scientific merits. Moreover, the term CPB limits the discussion to particularly striking examples of animal behaviour.

That information-rich algorithms underlie CPBs is undeniable. By exploring with his readers all sorts of fascinating CPBs, Cassell makes his case with copious references to the scientific literature. Just as attempts at elucidating instances of biochemical complexity demand that engineering design explanations are allowed—think *Darwin's Black Box* and other book titles in a similar vein—efforts to explain the origin of CPB algorithms arguably more so.

Of course, even comparatively simple forms of animal behaviour have a genetic basis.

As a zoology student in the mid-1980s, I well remember several lectures on the sea slug *Aplysia californicus* (figure 1), studying the basis of simple reflex responses to artificial tactile stimuli. When investigators prodded the animal, it responded

Figure 1. The sea slug *Aplysia californicus*

by withdrawing its gill and syphon into the body mantle. A slug that was repeatedly stimulated showed a progressive lessening of its response (termed habituation). In other experiments, *Aplysia* exhibited different simple behaviours, like dishabituation and sensitization. This pioneering work led to neuroscientist Eric Kandel (1929–) and two others sharing the Nobel Prize in Physiology or Medicine in 2000.[1]

Cassell observes that the simple habituation response in *Aplysia* "is accomplished through a network of approximately *three hundred neurons*, including sensory neurons, motor neurons, and interneurons [emphasis added]" (p. 153). If basic reflex behaviour is comparatively complex neurologically, "it is obvious that much more complex programmed behaviors correspondingly involve significantly more complex neural and related mechanisms" (p. 154). Quite! It is no wonder that evolutionists are mystified as to the origin of the underlying genetically coded algorithms and neurological controls for complex animal behaviours—navigation and migration abilities, nest building, hierarchical insect societies, and so on.

Moreover, when one considers just how miniscule the 'brains' of some of these animal marvels are (think: bees, ants, and termites), the unprejudiced must surely conclude with the author:

> "The optimization required to embed the algorithms in such small brains is best explained as the product of skilful engineering design" (p. 177).

Cassell refers to such "extraordinary mental feats" in small creatures with the delightful phrase "genius in Lilliput" (p. 15).[2]

Such conclusions are surely self-evident to advocates of ID, as well as to biblical creationists. Let us consider some of the many examples of CPBs reviewed in *Animal Algorithms.*

Complex programmed behaviours defy evolution

What is known about each type of CBP is, needless to say, the culmination of many dedicated scientific careers and decades of research in ethology. Selected highlights follow.

(i) Navigation and migration

Two chapters are devoted to the brilliance of animal navigation and migration. Chapter two details the following methods employed by various organisms: landmark navigation; dead reckoning (or path integration, where the animal keeps track of compass heading and distance travelled so it can compute a direct path home); a polarized light compass (determining the sun's position even on cloudy days); a celestial navigation compass (based on the positions of stars); and true navigation (a map sense and something akin to GPS). The latter is especially impressive and includes, in certain birds, the ability to detect the earth's magnetic field—both its intensity and (as research now indicates) its inclination angle, enabling the bird to establish its latitude. For example, the Manx Shearwater (figure 2) makes journeys of 6,000 mi (10,000 km) using a true map sense which is "an astonishing ten times more accurate than a commercial aircraft inertial navigation system!" (p. 56).

When creatures are navigating sizeable distances, the calculations are trickier because of the Earth's globe shape, so these animal navigators must be doing some sort of spherical geometry:

> "Spherical geometry is complicated by the fact that on a sphere there are no straight lines, so standard (Euclidean) geometry does not work. Human mathematicians perform the calculations using complex spherical trigonometry" (p. 48).

That animals accomplish with ease the sorts of tasks that normally fall to gifted and highly trained big-brained human beings is at once both astounding and humbling.

> "The precise specifics of how an animal's (sometimes tiny) brain performs such computations remain unknown, but again, it appears to involve *innate programming* [emphasis added]" (p. 48).

Explaining the origin of the genetic programming of complex migratory behaviours is indeed an eye-watering problem for evolutionists. For instance, consider the legendary migrations of monarch butterflies.[3] On their two-to-three-thousand-mile journey (which involves up to three generations of

Image: Abyssal/Wikimedia, CC-BY-SA-3.0

Figure 2. A Manx Shearwater, *Puffinus puffinus*, one of many impressive bird navigators

butterflies) they navigate using a sun compass, even under overcast skies. How much information would have to be encoded in an alleged evolving butterfly genome?

> "Comparisons of migratory monarch genomes with the genomes of non-migratory monarchs has [*sic*] revealed that more than five hundred genes are involved in migratory behaviour" (p. 66).

Attempting a naturalistic explanation of systems that so clearly bespeak design is calculated to befuddle the mind.

Compared to monarchs, bees navigate far shorter distances, but their home area is nevertheless "as much as 150 square miles around a nest." Their behavioural talents are impressive: "they use several methods of navigating, including visual landmarks, sun compass, and polarized light compass. Each is employed depending on the circumstances [e.g. cloudy or sunny]…" (pp. 59–60). Back at the hive, a scout bee's 'waggle dance' then communicates precise information to other bees—the compass heading and travel distance to suitable flowers. All this from a creature with a brain of just 950,000 neurons, compared to a human being's 85 billion! Cassell comments:

> "… it is unclear how a Darwinian process can be a plausible explanation. There is a suite of individual capabilities and behaviors involved (including navigation, data processing, mathematics, and communication), requiring *an engineering process* as well as the development of *computational algorithms*, which are encoded in the brains of honey bees [emphases added]" (p. 62).

As with monarch butterflies, the inference to design is clear. Programming of this sophistication and systems of such microminiaturization cannot be accounted for by a purposeless, blind step-wise process. While not mentioned by the author, it is now understood that honey bees have a solution to the fiendishly complicated 'Travelling Salesman Problem'. This is yet another indication of insect ingenuity, because software engineers have yet to achieve the computational performance required to solve this.[4]

Desert ants exhibit 'genius in Lilliput' too. Their brains are a quarter the size of honey bee brains, yet studies of their foraging trips have demonstrated an intrinsic path integration ability, something that is not learned or taught. Their repertoire of navigational competencies is mesmerizing:

> "Desert ants employ … visual landmarks, vector memories of route segments, and path integration. In addition, they use chemotaxis in close vicinity of a food source by the detection of odors. They also use a combination of sensor information sources for path integration, including a sun compass, biological clock, and two forms of odometers" (p. 63).

Research has shown that they are programmed to select whichever navigation method suits the particular circumstances; e.g. if "the environment is visually enriched, they will use landmark navigation; otherwise they will use path integration" (p. 64).

Cassell explains that experts in the field of animal migration acknowledge it involves a high level of integration of these 'instruments' and behaviours. All these systems are somehow encoded in the genomes of these butterflies, bees, ants, sea turtles, birds, and other animal navigators. This imposes a further insuperable constraint upon evolution. Accounting for any one navigation system is challenging enough. But how could a slow and gradual incremental process account for the integration of so many different systems? And the problems do not stop there, for, as Cassell notes:

> "There is some evidence for a role of epigenetics in migratory behaviour. … If both genetic and epigenetic mechanisms are necessary to control behaviour, this suggests that *multiple coordinated changes are necessary* for a trait before it can confer some advantage—precisely the sort of multi-component trait that challenges a Darwinian explanation [emphasis added]" (p. 78).

Quite how it is that so many precise, sophisticated, coordinated genome changes could occur through a blind, purposeless process is anyone's guess. Believing it occurred is not a crime, but it does not qualify as science. To conclude that the inference to design is a superior explanation is to enormously understate things.

Image: Peterwchen/Wikimedia, CC-BY-SA-4.0

Figure 3. Asiatic honey bee, *Apis cerana*

(ii) Complex animal societies

In chapter six, the author continues to regale the reader with fascinating facts and figures regarding CPBs of social insect colonies, notably bees, ants, and termites. We will continue to focus on the neurological and computational aspects here. Take bees for instance:

> "With honey bees … there is abundant evidence of *innate developmental programs* for physiology and behaviour related to age and in the service of labor. Also notable is the fact that the bees can perform various tasks in the division of labor, including foraging (which requires navigation and an ability to memorize numerous cues about flowers), finding new comb locations, building the comb, and cell cleaning and repairing [emphasis added]" (p. 93)

The neurologically wired programs underlying both a bee's individual behavioural traits and its ways of integration in the hive society are ultimately digitally encoded in the DNA. Incredibly:

> "A study of the highly eusocial Asian honey bee (*Apis cerana*) genome found 2,182 unique genes out of a genome consisting of 10,651 genes—about 20 percent of the total genome. In addition to these genes not being shared with other non-social insects, the closely related western honey bee (*Apis mellifera*) also does not share commonality with these genes. That is surprising, since it is believed the two species diverged from a common ancestor only one … or two million years ago" (p. 114).

A genomic analysis of *A. cerana* (figure 3) determined the average length of its genes to be 7,577 base pairs.[5] So for significant beneficial mutations to occur in over two thousand genes of this length would appear to pose a waiting time problem.[6]

Honey bees perform many vital tasks, such as choosing and synthesizing building materials for the comb, construction of the comb itself, repair and maintenance, and helping to control hive temperature. "All of these critical elements [for a thriving colony] are interdependent, meaning they arguably work as a kind of irreducibly complex system of behavioural systems" (p. 125). Cassell is surely correct in this assessment, to which we might well exclaim with Alice, "Curiouser and curiouser!"[7] Accounting for irreducible complexity of a system of irreducibly complex systems naturalistically propels an already hard job into the stratosphere. As with the case of animal migration, this interdependency and integration of so many programmed behavioural systems is a real killer as far as evolutionary theories are concerned, neo-Darwinian or otherwise.

Termites obviously differ from bees in many ways but have similarities in their eusociality.[8] Their impressive mound constructions are veritable cities in which they cultivate fungal gardens, cooperate to fend off intruders, and control ventilation to adjust moisture and temperature.[9] In fungus farming termites (Macrotermitinae) young termites ingest both gathered plant material and *Termitomyces* fungal spores. Then symbiotic gut bacteria help to partially digest the plant-fungus mix before it is defecated. The fungus continues to grow upon and break down new supplies of plant material which older worker termites are bringing inside. Upon reflection, this is a knotty problem for slow, incremental evolution:

> "In Darwinian terms this relationship [between termites, the bacterial community, and the domesticated fungus] is assumed to have developed through coevolution. However, this requires *the coevolution of three entirely separate genomes* (termite, fungus, and bacterium) to foster the symbiosis. This is an extremely complex relationship that involves numerous genes in each species [emphasis added]" (p. 101).

As Cassell justifiably comments, albeit rather downplaying things, it is "highly improbable" that such coordination of numerous gene mutations


Image: Pollinator/Wikimedia, CC-BY-SA-3.0

Figure 4. The nest of an organ pipe wasp, *Trypoxylon politum*. The different colours result from different muds being sourced to daub the next at different times.

in three independent genomes could have occurred.

In contemplating the suite of complex behaviours seen in such eusocial creatures, it is worth labouring an earlier point. Evolutionists attempting scientific explanations for the origin of social insect CPBs face a truly gargantuan task. We are not talking of a modest number of gene mutations here, rather:

> "It is now known that the transition to social behaviour requires hundreds or thousands of modified or novel genes and their expression through epigenetic mechanisms" (p. 119).

The answer lies in the algorithms! The level of complex and highly integrated programming existing in the micro-brains of eusocial insects screams intelligent design. Is ID a science stopper? Not so. It is those who insist upon unguided, naturalistic explanations for such wonders who are guilty of stifling true scientific investigation. As Cassell says, much later in the book, "Design theorists are free to simply follow the evidence" (p. 192), and such evidence as we've highlighted here points in no uncertain terms to intelligent design.

(iii) Animal architecture

This absorbing topic is the subject of chapter five, covering such creations as the nests of organ pipe wasps (see figure 4), weaver ants, and termites, the combs and hives of bees, and the webs spun by spiders. The author slips into using teleological language as he contemplates the latter:

> "Spiders are another of nature's master engineers. … For example, the golden orb-weaver spider has seven kinds of silk glands, with six spinnerets. Some is used for spinning webs, of course, but other types are used for wrapping prey and encasing eggs. Silk can be stronger than steel of the same thickness, can stretch more than rubber, and is stickier than most tape. … Despite great effort, humans have yet to produce anything functionally equivalent to silk" (p. 132).

Subsequent to the publication of *Animal Algorithms*, researchers at Johns Hopkins University have used fast-frame-rate infrared video to determine the entire web-building sequence in a small nocturnal spider species—the hackled orb weaver, *Uloborus diversus*.[10] Reflecting on their findings, team leader Prof. Andrew Gordus stated, "I think they're incredibly elegant, and it reminds me of watching a performer perform a dance."[11] All the sets of actions of the whole choreographed routine are executed in the same sequence by each *Uloborus* individual.

Clearly, the behaviours behind the hackled orb weaver's architectural productions are algorithmically determined, thus encoded in the genome.[12] As with the other CPBs already discussed, numerous genes are involved. This confronts all who wish to explain how spider webs arose naturalistically, or the origin of the silk itself. Cassell further observes:

> "After decades of failed attempts to provide a causally adequate explanation, one can be forgiven for concluding that we have no compelling reason to assume that a step-by-step evolutionary pathway … actually exists" (p. 134).

Much more could be said about this most interesting subject. The CPBs involved in animal architecture evidence sophisticated programming and the author rightly points out that the vague evolutionary just-so stories are not worthy explanations.

Final remarks

This review outlined the book's overall conclusions before laying out some of the many examples showcased by author Eric Cassell (chapters 2–5). The remainder of the book examines further conundrums facing those who attempt to explain the irreducibly complex systems of integrated CPBs exhibited in the enthralling field of ethology and demonstrate the superiority of ID over and against blind evolution (see table 1).

Space constraints prohibit discussion of all these points, but we will conclude with a brief mention of two of them. Firstly, the table indicates that Cassell sees ID as competing with blind evolution in explaining design flaws. However, his treatment of suboptimal design (pp. 197–198) does not adequately answer the Darwinian challenge that the waste, dysfunction, and cruelty observed in the natural world are incompatible with a benevolent, wise Designer. It is true that design flaws do not negate design hallmarks pointing to ID. Moreover, human engineers cannot achieve perfect design, if "perfection is understood as a result free of trade-off restraints" (p. 198). Nevertheless, the author restricts his discussion to animal behaviour in the *present* world. Within the Creation/

Table 1. Comparison of discriminating factors for two competing explanations for the origin of CPBs (copied from Fig. 7.1 of *Animal Algorithms*, p. 169).

Metric	Blind evolution	Intelligent design
Microevolution	✓	✓
Similarities across taxa	✓	✓
Design flaws	✓	✓
Abrupt appearance		✓
Engineering design		✓
Genetic change		✓
Origin of information		✓
Teleology		✓
Convergence		✓
Simple explanation		✓
Predictions & Retrodictions		✓

Fall paradigm taught in Scripture, this world is subject to the Curse, but the Creator faced no constraints in His original "very good" creation of living organisms (Gen. 1:31). In his brief treatment of "the problem of 'evil' animal behaviour" (pp. 198–203)—e.g. infanticide, cannibalism of offspring, siblicide (one offspring killing another)—the author confesses the challenge these things pose for benevolent design. Mere design will always be a weak answer to evolutionists who highlight ID's inadequate theodicy. As Cassell says, the only satisfactory answer to a theological challenge of this nature is one which "is provided by Christian theology and the idea of 'the Fall' and entrance of sin into the world. In this theology the appearance of sin results in death, disease, and other maladies."[13]

Secondly, how do evolutionists respond upon observing markedly similar behaviours in social insects, or comparable navigational behaviours across creatures as diverse as birds, marine vertebrates, and insects? They are forced to invoke convergence, time and time again. Yet appeals to convergent evolution are excuses for ignorance, for they say nothing about *how* these complex traits might have originated through neo-Darwinian means. Convergence implies that there is a biological inevitability in such CPBs arising in disparate animals. Not so, argues Cassell. Rather, "the evidence indicates it is not inevitable but contingent" (p. 143). For example, most groups of bees, wasps, and ants are not social. A CPB, by its very nature, is not something deterministic, but evinces top-down design—this bespeaks systems engineering, not blind evolution (Table 1).

The author has presented a strong argument for ID based upon scientific *knowledge* about CPBs and their algorithmic encoding in DNA. How is it, then, that so many scientists continue to argue against ID tooth and nail? "Such an aversion is due," argues Cassell, "to teleophobia, meaning an aversion or unwillingness to admit the existence of design or final causes in nature, since they fit uneasily within the naturalistic paradigm" (p. 179). In so doing, they violate the spirit of true science.

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Details in biblical creation and flood presentations

(Mis)interpreting Genesis: How the Creation Museum misunderstands the ancient near eastern context of the Bible

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Details, details, details (the parallel to real estate's location, location, location) count heavily in models and presentations by biblical scholars and scientists alike. The intrusion of one weak, contrived, or inaccurate detail can destroy the trust of recipients of those models or presentations. The explosion of the number of ancient texts discovered through archaeological excavations since the middle of the nineteenth century has spawned numerous debates over the role of ANE literature in biblical interpretation. Critics of biblical inspiration and inerrancy sometimes ignore archaeological evidence that confirms the historical authenticity and accuracy of the Scriptures. Some scholars tend to focus only on apparent contradictions. Objectivity has become a rare commodity among both Bible scholars and secular critics. Each tends to approach the text with a developed and concretized worldview and theological presumptions.[1] Indeed, established presuppositions can lead to the inclusion of questionable elements in creationist models and museum displays, as well as in the arguments of opponents to those presentations.

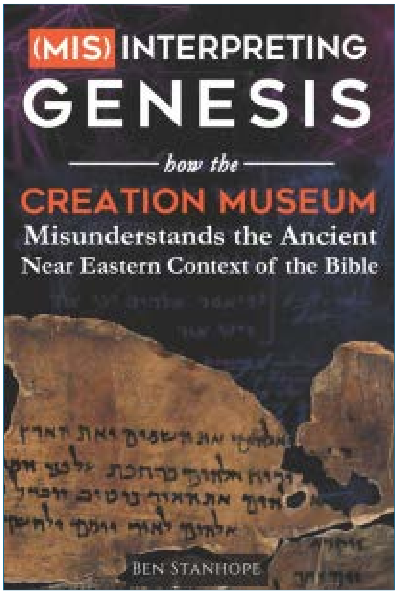
Thesis and compliment

In his "Introduction" (pp. 11–17), Stanhope admits to rejecting "much of the Creation Museum's theology" (p. 12) without getting into any specifics. Many questions (he lists nineteen, p. 13) have driven him to abandon any literal reading of the early chapters of Genesis. The thesis of *(Mis)interpreting Genesis* is that

> "... archaeological and linguistic discoveries about the Bible's original context clearly show that a great deal of mainstream young-earth interpretation of biblical creation texts is wrong" (p. 14).

That does not mean that he has totally rejected the young-earth viewpoint, however. On the one hand, Stanhope claims to be "in full agreement with the Creation Museum that old-earth interpretations that try to read millions of years out of the days of Genesis 1 are dismally unimpressive, and rather obvious attempts at contorting the text into conformity with modern science" (p. 154). But, on the other hand, he insists that "Genesis 1 is *clearly not* a sequentially accurate account of the origins of the material world [emphasis in original]" (p. 155), nor is it "an accurate account of the universes' [*sic*] chronological, material formation" (p. 171). He agrees that the Genesis account speaks of human beings as God's appointed vice-regents (p. 166), making the account distinct from other ANE literary productions. In fact, he compliments the Creation Museum for accomplishing "the finest job of any institution in making the issues involved dramatically tangible and clear to the public" (p. 15).

Iron sharpening iron



While Stanhope's views represent some significant differences from the young-earth interpretation of Scripture and the inspired character of Scripture, some of his criticisms must be taken to heart. The book's first section deals with the Creation Museum's saurian identifications for Leviathan (pp. 21–36) and Behemoth (pp. 37–45), as well as the "King James' Unicorns" (pp. 47–49) and Isaiah's mention of "flying serpents" (pp. 51–62). Relying upon parallel biblical references and pertinent data found within ANE sources, he questions identifying these last two creatures with an *Elasmotherium* and a flying dinosaur, respectively. Absolute identification of all four of these creatures remains unproven with the sole exception of the 'flying serpent'. It behooves all biblical scholars to admit to a lack of definitive data for leviathan, behemoth, and the so-called unicorns. Perhaps the best solution for the Museum would be to include carefully worded qualifying statements in their displays and related literature.[2]

More dinosaurs, dragons, and demons … oh my!

In the appendixes (pp. 243–299), Stanhope misses the opportunity to explain how ancient peoples communicated about biblical events through both oral and written media down through time. Many myths arose out of a kernel of truth involving an actual historical event told and retold until the event has taken on a different telling. Researchers must account for any purposeful skewing in the retelling for the purposes of self-advancement or political propaganda. Scholars must determine the actual historical roots and reworking of the narrative, since some retelling can be influenced by religious, cultural, or political viewpoints that might interfere with accurate oral and/or written transmission.

Stanhope mentions that the various cultural views of cosmology (specifically the concept of a solid sky) "comport with cognitive dispositions that are found to be anthropologically universal" (p. 283). However, he fails to explain how he reached that conclusion—he offers no evidence supporting that universality. Also, the potential use of metaphor across many cultures should be included in the discussion of transmission. In other words, just as we still speak of *the sun rising*, rather than *the earth turning* on its axis, all cultures using this language understand that it is an example of accommodation to the viewpoint of humans standing on the surface of the earth. No mature person gives the statement an overly literal meaning.

Many modern scholars automatically assume that ancient cultures were far too primitive, backward, or prescientific to use sophisticated figures of speech in daily conversation and written literature. Such provincial thinking denigrates and demeans the thinking and accomplishments of ancient peoples who have produced detailed histories and sophisticated literary products, as well as architectural marvels.

Different worldviews

Tackling Stanhope's criticisms of some Creation Museum displays requires a brief discussion of worldviews. Background, culture, education, experience, and faith can all contribute to forming one's personal worldview. Simply put, a personal worldview consists of a philosophy of life and how someone perceives the world. While groups of individuals may share a worldview, one factor (like faith) can make a big difference and set individuals apart from others with whom they might otherwise share much in common.

In the matter of origins, theologian and scientist alike must admit that no human witness was present at the beginning of the universe or of our planet. Since there were no human eyewitnesses and we are unable to replicate such immense events in the laboratory, everyone must exercise a certain amount of faith. In the attempt to deal with the matter of origins, two major worldviews must be distinguished. So it should come as no surprise to anyone that those who are outside biblical faith possess a different worldview than those who espouse that faith. Scripture and faith play significant roles in how believers evaluate a worldview.

However, some apologists, philosophers, and theologians hold that Scripture cannot be accepted as evidence—instead, Scripture must be subject to external evidence for the purpose of establishing its truthfulness. Such an approach emasculates biblical authority and subjects the Bible to external human authority—an autonomous authority exercised by fallen human beings. Such a situation is not new to the modern era—it has always been so since the fall of mankind. It does not mean that fallen humans cannot understand anything the Bible says. Rather, conflicting worldviews affect how one interprets the biblical text.

Stanhope assumes that the Hebrew writers of Scripture must have held to the same cosmology as all the pagan cultures surrounding them in the ANE (pp. 83–117). But, in addition to that problematic assumption, he reveals his antagonism to the doctrine of the inspiration of Scripture:

> "... if you believe in biblical inspiration, you are only setting yourself up for worldview fragility and biblical-exposure-anxiety if your definition of that doctrine only comes from pure theological theorizing" (p. 84).

For evangelicals the doctrine arises from, and is based solely upon, the biblical teachings themselves, not upon any human philosophizing or formulation. Even though he admits that "Genesis doesn't borrow its creation story from anyone" (p. 92), he insists that the writer of Genesis must conform to ANE cosmology. In other words, the Hebrew Bible writers and editors must, of necessity, be viewed as totally prescientific (in terms of modern science, at least).

Stanhope exposes his own overly literalistic interpretation of the biblical text when he argues that "we are wrong when we interpret the 'waters above' as anything other than a literal celestial ocean" (p. 116). In the course of his explanation, he ignores the use of metaphor by the ancient Hebrews and their neighbours. Arguing that the biblical writers really believed in a solid, metallic (or stone) sky from texts like Job 37:18, he assumes the writers and their readers understood metaphors literally (pp. 94–95, 103–104). That is demonstrably false. For example, the use of Job 9:6 and 26:11 in an attempt to prove that the Hebrew cosmology held to literal pillars upon which the earth sat fails to take into account Job 26:7's statement that God "hangs the earth on nothing". The "windows of heaven" (Genesis 7:11; 8:2; Malachi 3:10) likewise turns out to be merely a metaphor when we read 2 Kings 7:2, 19 and its revelation that even the military officer did not believe there were really any 'windows' in the sky.[3]

Continuing his assault on biblical worldviews, Stanhope offers alternative interpretations for Isaiah 40:22 ("circle of the earth"; pp. 120–123) and Job 26:7 (“hangs the earth on nothing”; pp. 124–126). He accuses young-earth creationists of “Filtering the text through modern science” (p. 123). It becomes increasingly evident that he himself, however, ‘filters’ the text through pagan literature. Presenting Nebuchadnezzar’s speech in Daniel 4:10–11 as though Daniel shared Nebuchadnezzar’s worldview, Stanhope ignores the fact that a biblical writer’s quotation of a pagan’s words does not require that the writer agree with what the unbelieving person has said. His bottom line: “the biblical conception assumes a flat earth” (p. 129). This reveals a gap in his knowledge of ANE history. Before a flat-earth viewpoint existed, the ancient Babylonians already considered the earth to be a sphere—indeed, the earth and the stars as a nested set of spheres. It was not until around 800 BC that they switched to a flat-earth viewpoint.[4]

J.J. Niehaus suggests that a

> “... use of the comparative method that places biblical narratives among the mythological or legendary donations of the world is flawed, because it assumes that biblical data are capable of such classification. It ignores (or rejects) the Bible’s claims about its own historicity.”[5]

Figure 1. Tel Arad’s 10th century BC shrine reveals an unbelieving worldview held by some Israelites.

The difference between the faith reader and the non-faith reader of Scripture often comes down to supernaturalism vs naturalism. Supernaturalism remains open to the miraculous; naturalism most quickly dismisses miracles and any reality of God as the Bible’s ultimate author.

Human beings forget, neglect, disobey, or skew what God has revealed to them (see figure 1). In the past, God chose to intervene in human history by means of special revelation. Without revelation mankind possesses no authoritative or dependable direction from their Creator, especially when it comes to matters of origins and of miracles. B.T. Arnold remarks that OT studies “have been dominated by evolutionary explanations for Israelite monotheism”[6] over the past three decades. Liberal biblical criticism is a living virus still infecting biblical studies with radical humanism and antisupernaturalism.

Biblical inspiration and interpretation

Addressing the matter of hermeneutics and the perspicuity of Scripture, Stanhope responds to those creationists “who claim that specialized technical knowledge is necessary to understand major elements of biblical scripture” (p. 217). He could have strengthened his argument by demonstrating that Christians up to the Reformation had no direct access to the Bible for personal study or reading (pp. 219–220), since the Roman Catholic Church had kept the Bible in Latin and under the sole interpretive authority of its priests. Stanhope correctly observes that the church ought to maintain “a healthy skepticism of scholars” and to critique their arguments (p. 224), while simultaneously not disparaging the role of scholars in gaining an understanding of the Bible. Indeed, “The golden age of Biblical interpretation is now” (p. 227), as long as we also understand that now is the platinum age of antibiblical criticism. Humility behooves both Christians and critics. Unfortunately, the latter too often exhibit the hubris of secular humanism.

The final chapter of the book addresses the matter of accommodation. Stanhope opens with a discussion of 1 Corinthians 10:14 for which he completely misunderstands Paul’s meaning (pp. 229–231). Elsewhere he has argued that many young-earth interpreters have focused on similar problems only to miss the actual meaning of the text itself (e.g. pp. 34, 207, 241). Instead of concluding that Paul “just assumes and indirectly affirms on canonical record, some idea about the Israelite wanderings that probably did not happen” (p. 231), why not respond (as he has elsewhere) that the ‘rock’ is pure metaphor or symbolism, not to be taken as the actual physical rock out of which God had given water? Likewise, he becomes so determined to demonstrate that a woman’s hair must be taken as an extreme sexual metaphor or euphemism that he ignores any evidence in the ANE world to the contrary (figure 2). All ancient cultures that prized a man’s long hair certainly

Figure 2. Stanhope takes a woman’s long hair in 1 Corinthians 10:14 as an extreme sexual euphemism.

were not making the hair an equivalent euphemism.[7]

The Genesis 1–2 creation account

“Reading Genesis like an Ancient Israelite” (pp. 63–213) forms the most extensive portion of the book’s contents. Here Stanhope argues that Genesis 1:1 consists of a dependent clause (“In the initial period in which God created the heavens and the earth”, p. 74) and that the elements of Genesis 1:2 “were already present before God began creating” (p. 75). According to him, those elements could have “been sitting around for five minutes, perhaps fourteen billion years” (p. 69). In other words, the biblical text is agnostic about the time of creation. Thus, Stanhope declares that the young-earth doctrine of recent creation has been “predicated on an incorrect translation of the first verse of the Bible” (p. 82).

Weaknesses exist in Stanhope’s arguments that contradict his claim of an ‘incorrect translation’ of Genesis 1:1. First, for every Hebraist he cites, there are just as many who insist on the independent clause translation (“In the beginning God created the heavens and the earth”)—with equally impressive academic qualifications. For example, Hershel Shanks (1930–2021), founder of the Biblical Archaeology Society, cited with agreement the popularizer of the Documentary Hypothesis, Julius Wellhausen, in calling it “a *verzweifelt geschmacklose* [desperately tasteless] construction, one which destroys a sublime opening to the world’s greatest book.”[8]

Second, the dependent clauses in three ANE texts, purported to deal with creation (*Enuma elish*, *Atrahasis*, and KAR 4; pp. 76–79), do not prove that the author of Genesis 1:1 must have followed their pattern. Third, the construction of the introductory section of Genesis 2:4–7 (p. 79) fails to prove that Genesis 1:1 must be taken as a dependent clause. Indeed, Stanhope totally ignores pointing out all the differences between the ANE ‘creation’ stories and the biblical creation account—as well as the differences between Genesis 1:1–3 and 2:4–7. An objective treatment requires such a comparative analysis.

Stanhope focuses on the presence of the number seven in the creation account. While there is no denying such a presence and intentional use, it demeans the ability of Moses to suggest that he did not compose Genesis with these numerical elements, but that it was inserted “after the Babylonians conquered Jerusalem” (p. 148; cf. pp. 156–157). If Moses penned Genesis, then it should come as no surprise that he recapitulated some of the elements from the creation account in his composition of the Tabernacle account in Exodus (cf. pp. 150–151) (figure 3). Given the significance of the Tabernacle to the Israelites’ faith, it should also not be a surprise that the author of 1 Kings would pattern his report of the construction of the Temple after that of the Tabernacle (cf. pp. 151–152). Stanhope agrees that the seven days of creation should be understood as literal days (pp. 152, 167, 169 n. 64), but insists on tying the creation account’s use of seven days to other ANE texts (pp. 152–155). He ignores the likelihood that the ANE parallels might have arisen out of the actual historical events themselves and the memory of their retelling even before Moses wrote Genesis. After all, Stanhope states that it is ‘implausible’ to view Genesis 1 as “directly borrowing from these texts” (p. 154). Later in the volume he makes the same statement with regard to ‘direct influence’ from Egyptian texts (p. 162). He explains that the concepts were merely “natural to the Hebrew’s own thinking as they were to other Semitic nations and the Mesopotamians” (p. 154). Unbelieving Hebrews might very well have shared the pagan worldview of the unbelieving non-Hebrew peoples around them, but that is very different from claiming that the godly and divinely chosen authors of Scripture possessed the same worldview.

Speaking about the Garden of Eden, the author first identifies his goal as demonstrating that “the Bible’s ancient Near Eastern context is our primary key for its accurate interpretation” (p. 132). Then he defines ‘the sons of God’ as supernatural beings comprising a council of ‘deities’ inferior to God (p. 134). He accepts a minority interpretation of John 10:34’s citation of Psalm 82:6 (p. 136 n. 9). Since Jesus identified the ‘gods’ in Psalm 82:6 as human judges,[9] it seems futile to try to interpret the text differently to identify those ‘gods’ as a supernatural divine council. Stanhope admits that Israel’s

Figure 3. A model representing the biblical Tabernacle in Timna Park, Israel

theology was unique, but "still shares many of the categories, symbols, and much of the language and conceptual framing of its surrounding context" (p. 143). While agreeing with this observation for some aspects of the Garden of Eden, one must be cautious to not stretch this principle. If a council of angels is involved in Genesis 1:26 (p. 164), that implies that mankind was created in the image of both God and angels—raising huge theological questions.

Death and violence in creation

An anachronism in Creation Museum staff-related presentations (modern watermelon being eaten by a *T. Rex*, pp. 189, 190, figure 20) becomes one of Stanhope's targets (pp. 188–190). In this case, he has not kept pace with change[10] nor provided his readers with evidence of the actual Museum display, which lacks any such anachronism (figure 4). He makes a better point when addressing the issue of "miraculous textually baseless solutions to resolve basic logistic issues" (p. 192). He does lay an equivalent charge at the feet of old-earth commentators who find "evasive ways to weasel our way out of the obvious meaning" of some biblical passages (p. 194). A major point revolves around the meaning of the Hebrew words *kabash* ('subdue') and *radah* ('rule') as used in Genesis 1:28 (pp. 194–99). Stanhope appeals to available sources supporting the association of violence (especially killing animals for food) or a potential struggle to control. However, he seems to ignore those scholarly sources suggesting neither term need include death or killing.[11] A key argument he offers directs readers' attention to the fact that the "origin of animal death and predation is never even hinted at" in Genesis 3, dealing with the curse upon the ground (p. 200). Opposing some young-earth views that meat eating (by humans) did not begin until after the Flood, Stanhope points to God's killing of an animal to clothe Adam and Eve in Genesis 3:21 and Abel offering the fat from his flock's firstborn animals in Genesis 4:2 (pp. 202–203). He also indicates that such sacrifices included priests and those offering the animals eating portions of the meat elsewhere in Scripture. He concludes that Genesis 9:1–5 presents prohibitive legislation, for which four other examples are listed (pp. 203–204).

Figure 4. Creation Museum's display depicting a dinosaur eating a melon (photo by Paul DeCesare July 2017, used by permission)

Next, Stanhope seeks to demonstrate that the use of biblical texts like Isaiah 11:1–9 fail to prove that death did not exist until after the Fall (pp. 205–208). Basically, he argues that those texts merely declare that at some time in the future God will so work that "predators will no longer plague humans *and their domestic property* [emphasis in original]" (p. 206). However, he glosses over the implications of "the lion will eat straw like the ox" by attributing the statement to an intentional hyperbole (p. 207).

Stanhope admits that Romans 8:19–22 raises a "more credible objection" (p. 209). Depending upon studies of rabbinic sources (presuming they are legitimate background to what the apostle Paul really meant), he says that he found nothing explicitly linking "the origin of animal death to Adam's fall" (p. 209). Isaiah 24–27 supposedly provides the biblical background for Paul's description of creation's decay, groaning, sighing, and mourning (pp. 210–211). Because of that Old Testament connection, Stanhope concludes that ‘the creation’ refers only to the ground and its plants (p. 211), not animal life. Again, however, he has selected a distinctly minority interpretation. The majority understand ‘the creation’ to refer to all subhuman life.[12] As a final statement regarding this issue of death before the Fall, Stanhope offers this palladium: “one need not necessarily abandon their young-earth views at all to agree with its [his] arguments” (p. 213).

The long lifespans of the patriarchs

Stanhope refuses to take the lifespans literally in the Genesis 5 and 11 genealogies (pp. 173–186). He focuses on the seemingly ridiculous idea of Eber (Abraham’s great, great, great, great grandfather) “still alive and kicking at Abraham’s death and even outlived him by 464 years (Gen 11:14–17)” and, according to Genesis 11:10–14, Shelah (Abraham’s seven times great grandfather) and Shelah’s grandfather both still living at the time Abraham died (p. 175).

The biggest issue involves the death of Terah, Abraham’s father, because the genealogy in Genesis appears to place Terah’s death thirty years after Abraham’s death.[13] In addition to the historical and textual issues, Stanhope points to the mathematical problems with taking the text literally: the numbers in the Genesis 5 genealogy “are all divisible by 5 or end in a 2 or a 7 (with the single exception of Methuselah whose age can be derived by adding multiples of 5 and 7)” (p. 178). One explanation he offers for this artificial composition of the Genesis genealogies involves “competitive historiography” to make one’s own culture’s heroes to appear superior to another’s heroes (p. 183). He argues that the artificial choice of numbers contrasts starkly with the “*actual random* numbers given for the reigns of Israel and Judah’s kings [emphasis in original]” (p. 184).

What kind of response might be proposed to Stanhope’s problems with taking the genealogical numbers literally? First, the seemingly odd ancestral inversion with the younger dying long before their elders comes as a direct result of the rapidly increasing decline in fallen humanity’s length of life. Second, the use of phrases like ‘in a good old age’ (Genesis 25:8) or ‘was old’ (Genesis 27:1; 35:29; 37:3) display an idiom relative to the expected lifespan of individuals rather than an absolute declaration in comparison to all previous ancestors. Third, the age of Terah is not supplied for each of his three sons, and the sons are not listed in their birth order (Genesis 11:26). Fourth, either Abraham was born when Terah was 130 years old or Terah actually died at the age of 145.[14]

A global flood?

When Stanhope says, “It’s historically outrageous to suppose a global flood in these centuries is supposed to have managed to blast out the Grand Canyon” (p. 185), he misunderstands the geological data presented by geologists like A. Snelling for a post-Flood formation of Grand Canyon[15] (figure 5). Stanhope fails to deal with other young-earth options to a 2300 BC date for the Flood. He makes a good point concerning a serious issue, but rejecting it so simply and categorically places him in jeopardy of sounding like he attempts to make some young-earth arguments sound—ignoring valid options and using ridicule and *ad hominem* arguments to try to silence the opposition.

Figure 5. Forming of Grand Canyon may be a post-Flood event

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3. This reviewer deals with this issue more fully in “Old Testament Evidence for a Literal, Historical Adam and Eve”; in: Mortenson, T. (Ed.), *Searching for Adam*, Master Books, Green Forest, AR, pp. 45–49, 2016.
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10. Staff at the museum report that a *T. Rex* head on a stand with wheels was formerly used as stage decoration, but has been relegated to storage. They made the right decision not to include that head with a modern watermelon in museum displays—long before Stanhope's criticisms.
11. See Wagner, S., כָּבַשׁ *kāḇaš*; in: *Theological Dictionary of the Old Testament*, rev. edn, Botterweck, G.J. *et al*. (Eds.), Green, D.E. trans., Eerdmans, Grand Rapids, MI, **7**:52–57; Zobel, H.-J., רָדָה *rāḏâ*; in: *Theological Dictionary of the Old Testament*, rev. edn, Botterweck, G.J. *et al*. (Eds.), Green, D.E. trans., Eerdmans, Grand Rapids, MI, **13**:330–336, 1995.
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14. Cf. Kidner, *Genesis: An introduction and commentary*, pp. 120–121: "Terah's age at death presents a difficulty, since it makes his eldest son 135 years old (26), whereas Abram was only 75 (12:4, with Acts 7:4). One solution is to suppose Abram to have been the youngest son, born sixty years after the eldest but placed first in the list in 11:26, 27 because of his prominence (like Ephraim before Manasseh). Another is to follow the Samaritan text, which gives Terah's age as 145 at death. This seems preferable, if only because Abram would scarcely have made the exclamation of 17:17 had his own father begotten him at 130." Hamilton, V.P., *The Book of Genesis, Chapters 1–17*, pp. 366–368, offers a more complete explanation.
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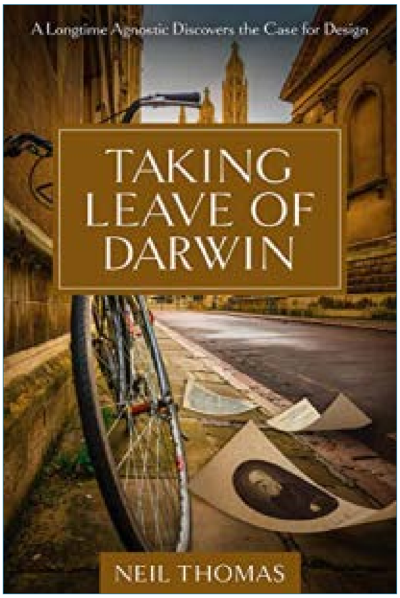
Leaving Darwin to go nowhere

Taking Leave of Darwin: A longtime agnostic discovers the case for design
Neil Thomas
Discovery Institute Press, Seattle, 2021



Lucien Tuinstra

Given that the publisher of *Taking Leave of Darwin* is prominent in the ID movement, it is likely that readers might have preconceived ideas about its contents. Throughout most of the book, the author keeps his cards close to his chest when it comes to his current worldview, and it is not until near the end that we can place Neil Thomas into a category.

A Reader Emeritus at the University of Durham, author Dr Neil Thomas studied at the universities of Oxford, Munich, and Cardiff. He has a wide variety of interests, including language, literature, and logic & rhetoric. Thomas has been a long-time member of the British Rationalist Association and has previously authored other books.

Taking Leave of Darwin is a thin paperback of 136 pages of text plus 14 pages of endnotes. The copious endnotes attest to it having been well researched, and the author has commendably managed to densely pack this wealth of information into a slim volume. Unfortunately, the author's frequent use of foreign expressions—mostly Latin, but also French and German—makes it abstruse at times. This is a shame, because it might turn off some of his readers, including perhaps those who might benefit from reading about the paradigm shift which occurred in the life of Neil Thomas: he now concludes that over the course of his life he has been conned!

Sandwiched between prologue and epilogue are six chapters, each starting with a pertinent quote setting the scene for the topic on hand. Chapter 1 gives some background about the theory of evolution, especially the views of Charles Darwin and Alfred Russel Wallace. Chapter 2 deals with Darwin's intellectual maturing from boyhood to adulthood and the immediate reception of *The Origin of Species*. The next chapter covers the longer-term impact of the book, including the response to Darwin's idea in more recent years. Fossil evidence and Darwin's *The Descent of Man* are also discussed. Chapter 4 turns to cosmology, as well as how bias can hinder progress in science. The fifth chapter details what the scientific method can and cannot do, while the final chapter brings everything together and reveals the personal journey of the author.

Accept magic?

The author helpfully presents the history surrounding *The Origin of the Species* and the controversy it caused. It is fair to say that Thomas has pierced its bubble of metascience and exposed the fallacious thinking of its contents. For example, in the prologue he talks about it apparently being “politically incorrect … to challenge the truth-status of *The Origin of Species*” (p. 11). Also, he has noticed “an alarming degree of bias” among specialists (p. 13), the ones who many people think are somehow free of partisanship.

He says it is generally accepted that *Homo sapiens* evolved from apelike ancestors, but to go on and insist we ultimately descended from microbes might stop a good number of people in their tracks (pp. 24–25). Darwinian natural selection (which he himself said would be better termed ‘natural preservation’, p. 17) was accepted to be capable of removing the weak; few ascribed creativity to it (p. 35). Thomas discusses the vocal tract differences of apes and humans and questions the evolution from one type to the other, because the brain has to develop in tandem with the vocal tract to drive any new mechanical features: “Synchronization of those two processes would of course point not to random evolution but to coordination and therefore design” (p. 68). He realises that simply adding time does not resolve the conundrum because he quotes from Jewish creationist Lee Spetner’s book *Not by Chance! Shattering the modern theory of evolution* (p. 74):

> “When one deals with events having small probabilities and many trials, one should multiply the two numbers to determine the probability. One should not just stand gaping at the long time available for trials, ignore the small probability, and conclude that anything can happen in such a long time. One has to calculate.”[1]

Thomas refers to the catch phrase ‘just like that!’ (p. 110) by the British comedian Tommy Cooper (1921–1984; figure 1) to describe how natural selection, in the minds of its advocates, is ostensibly endowed with an almost divine power. He shares a revealing quote by New Zealand professor Neil Broom,[2] from his book *How Blind is the Watchmaker? Nature’s design and the limits of naturalistic science*: “megatime becomes the instrument of creative change. It is used as a kind of magic wand, waved at appropriate points in the argument in order to accomplish quite remarkable feats of materialistic magic” (p. 86).

When Darwin published his *Origin*, it was well known—and attested by himself in the book—that the fossil record did not show gradual evolution. If evolution happened at all, some believed, it would have to be by ‘saltations’ (abrupt jumps) to jump the discontinuities, something espoused later by Stephen Jay Gould and Niles Eldridge under the banner of ‘punctuated equilibrium’—a view “that Darwin ruled out of account” (p. 64). Thomas describes Gould as the “insider’s insider to the world of evolutionary science … [who] irreverently described ‘the extreme rarity of transitional forms in the fossil record’ as ‘the trade secret of paleontology’” (p. 129). Quite!


Image: Colin Park / Statue to Tommy Cooper. / CC BY-SA 2.0

Figure 1. “Just like that!”—Tommy Cooper

Natural selection and its ‘ability’

Neil Thomas is not alone in noting Darwin’s appeal to artificial breeding to make his case for natural selection: “an odd stand-in for a mindless process” (p. 115). He continues to expose the fallacy of the reification of nature by questioning Darwin’s own words: “One might legitimately ask, how it is possible to ‘intently watch’ and ‘carefully select’ unintelligently?” (p. 116). Perhaps because, as he observed earlier, “Darwin tended to humanize nature even as he naturalized mankind” (p. 80). Thomas clearly recognizes that Darwin “could not appeal to the wonder-working mechanism of chance variation and natural selection until a self-reproducing biological machine had first arisen” (p. 50). The only natural way *that* could come about is by abiogenesis (aka chemical evolution), contrary to the Law of Biogenesis (Louis Pasteur) that life only comes from life. This is understood by Thomas who then expounds, “since recent advances in molecular biology show that the humblest bacterium contains more genetic information than the instruction manual for NASA space probes” (p. 51).

The author acknowledges another issue with the artificial versus natural selection analogy, and illustrates this with an (unreferenced) example:

> “Forty years of research and development [to introduce artificial hearts to patients] and forty billion dollars went down the drain. If such gargantuan efforts and expense could not fashion a functioning heart-substitute, it becomes all the more difficult to imagine a heart being constructed by the serendipity of random mutations and natural selection” (pp. 112–113).

He perhaps ought to have elaborated a bit more. Instead of simply stating that "decades ago … the fatalities topped 200", it would have been helpful to cite current progress involving this medical procedure. For instance, people with an artificial heart *can* live longer, albeit that currently it is for a maximum of two years.[3]

What about the debate revolving around neo-Darwinism as the explanation of life? Thomas has the impression that,

> "... if so many persons of such luminous intelligence and ingenuity have bent their minds to solving the problem, and have come up with only the most questionable of hypotheses, then perhaps there is a mystery that will never be wholly unravelled" (p. 123).

If these hypotheses are so questionable, as indeed he makes clear throughout his book, one wonders what Neil Thomas himself believes.

Belief and honesty

Clearly, the author has been, and continues to be, on a journey. The question is whether he is really willing to follow where the evidence leads, or prefers the mystery to remain. Surprisingly, he calls Richard Lewontin intellectually dishonest. However, Lewontin was famously candid when he admitted:

> "We take the side of science *in spite* of the patent absurdity of some of its constructs … *in spite* of the toleration of the scientific community for unsubstantiated 'just-so' stories, because we have a prior commitment, a commitment to materialism [emphases in original]" (p. 97).

Thomas is right in calling Lewontin out in his failure to follow where the scientific evidence leads, due to his materialistic commitment. Few atheists are so honest. The late Antony Flew abandoned his atheism for theism, which, according to Thomas, "seems to be the only conclusion which is unassailable on strictly logical grounds, however unwelcome that conclusion will seem to many readers, in whose number I count myself" (p. 126).[4] So says a lapsed agnostic and reluctant convert to the idea of God!

Figure 2. Where does the evidence lead?

And there you have it; Thomas does not want there to be "a supranatural intelligence" and he considers himself "a long-standing humanist with no allegiance to any revealed faith" (p. 146). He admits having disregarded some of his own assumptions (p. 127), but will he continue to travel the full journey to Christian theism? He thinks he knows and writes about where this would lead: "in the direction of an unknown (and potentially unknowable) source of intelligence outside of nature" (p. 143). As Thomas himself concedes, "Intellectual integrity was sacrificed on the altar of ideological commitment" (p. 118). But is Neil Thomas himself also wielding the knife that slays the offering?

Conclusion

Taking leave of Darwin gives a good overview of the history and current state of affairs when it comes to Darwinism, while at the same time serving as a roadmap of the journey the author has been on (and still is).

Neil Thomas calls the category of Theistic Evolution "deistic Darwinism" (p. 108), but where he would fit himself is not entirely clear. For all his scepticism of aspects of evolution, he is far removed from the biblical camp and the teaching of the age of the earth and Bishop Ussher's timeline of approximately 6,000 years (p. 23).

The book might be a helpful starting point for people who have an aversion to biblical creationist writing but are willing to probe the veracity of Darwinism. As this long-time agnostic author discovered, the case for design is strong. However, it's a shame that *Taking Leave of Darwin* doesn't take the reader to a more satisfying conclusion.

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Response to "Candidate site for Noah's Ark, altar, and tomb" by Griffith and White

I applaud Ken Griffith and Darrell K. White for their recent article on a potential Ark landing site in *Journal of Creation*.[1] It was truly a monumental effort. I particularly appreciated how they attempted to tie the genetic ancestry of specific crops and a style of culture to the general area, if not the specific site. Furthermore, I am pleased that they find value in a Neogene-Quaternary post-Flood boundary, which I have proposed rather extensively, especially for the entire region surrounding Turkey.[2] And I agree that the Ark would have likely rotted away if it had landed below 3,000 m in elevation. Furthermore, I also agree that the Zagros Mountains were likely not the Ark landing site, but for a different reason. Research has shown that the Zagros Mountains were not in existence at the necessary time for the Ark landing.[3]

However, I do have a few issues with several of their other interpretations. Many of these seem to be based on rather speculative circumstantial evidence and/or an over-reliance on extrabiblical sources. The Bible is the only reliable source of information for the timing of the Ark landing and its landing site.

Specific issues with their proposed site

On page 53 of their article, Griffith and White discuss the geology of their proposed landing location. Both their timing for the volcanism at Karaca Dag and their timing for the landing of the Ark seem a bit off target. The Bible is quite clear that the Ark grounded on Day 150 of the Flood year (Gen. 8:3–4). This was the same day the floodwaters reached their highest point (Gen. 7:24 and 8:3). If Karaca Dag is dated at 2.7–1.5 Ma in secular years (and the relative timing confirms this), it is primarily a Pleistocene (Ice Age) eruption, not a Pliocene eruption, making it closer in age to Mt Ararat, which is also mostly a Pleistocene volcano. This makes both of these volcanoes essentially post-Flood features and virtually excludes them from the list of possible Ark landing locations.[4]

The Bible tells us we need an Ark landing site that was in existence at the peak of the floodwaters, at about Day 150 of the Flood. My research has found that the high point (peak) of the floodwaters was at about the level of the K-Pg (K-T) boundary (in the secular geologic column) based on detailed studies of the stratigraphy across multiple continents.[5] And instead of Karaca Dag and/or Mt Ararat, I have proposed an alternative site, west of Mt Ararat, that also fits the criteria laid out in the biblical account.[4]

The crustal rocks in much of northeastern Turkey consist of highly metamorphosed Mesozoic sediments and oceanic crust that were caught between colliding plates during the Flood. Uplift of this crustal complex produced a prominent ridge—with 'ridge' here matching the Hebrew phrase 'mountains/hills of Ararat'—known as Kagizman Ridge.[4] This east–west ridge extends for over 160 km to the west of Mt Ararat, with some peaks standing over 3,000 m in elevation (figure 1). This topographic ridge seems to have developed at about the same time the rocks encompassing the K-Pg (K-T) boundary were being deposited globally, placing its formation on, or about, Day 150 of the Flood.[5]

The Ark may have settled on one of the higher peaks of Kagizman Ridge as the area was thrust upward, grounding the Ark. Later, receding-phase sediments and subsequent volcanic activity filled in the basins on the flanks of the ridge. Importantly, no new sediments were deposited on the crest of the ridge itself. In contrast, Mt Ararat and Karaca Dag likely didn't begin to form until well after Noah had vacated the Ark during the post-Flood Ice Age.

Secondly, Griffith and White's speculation that the Ark was cut into three pieces with one segment tipped over and rolled downhill is rather

Figure 1. Map showing the locations of Kagizman Ridge, Mt Ararat, the proposed site of Babel from an earlier *J. Creation* paper by Griffith and White.[8] Note the travel direction (white arrow) from the 'mountains of Ararat' to the Babel site, whether the Kagizman Ridge or Mt Ararat itself, is from the east. Image courtesy of ICR.

implausible. This would entail quite an engineering feat, especially with the limited number of humans available at that time. There are a multitude of alternative methods that would have allowed access to the Ark without sawing it completely through twice and moving the massive pieces. The second cut at 45° seems particularly suspect if not outright unbelievable. Much of the impetus for suggesting these monumental cuts and shifts of the Ark is based on the improbable interpretation that the gravels are in-place ballast stones from the Ark. Instead, these gravels could have arrived at the site in a multitude of ways. Without better analysis of the 'gravels' at the surface, and in the subsurface, it is difficult to jump to the solitary conclusion that these are ballast stones from the Ark.

Finally, on page 61, the second paragraph, the authors mention the possibility of finding 'bitumen' flakes below the surface, presumably from the Ark. This seems to reflect the assumption that the Ark was covered with an oil product. But I don't think there was any real bitumen or oil product prior to the Flood.

Unfortunately, the so-called 'pitch' covering the Ark is frequently used by critics as an argument against a global Flood. For example, evolutionary geologist David Montgomery insists that most sedimentary rocks could not have formed during the Flood because

> "... a literal reading of the Bible requires that such rocks already existed at the time of the Flood because bitumen, the pitch or tar Noah used to caulk the Ark (Genesis 6:14), comes from sedimentary rock."[6]

However, the Hebrew word used in this verse, *kopher*, doesn't literally translate as 'pitch'. Henry Morris III stated:

> "The word is used 17 times in the Old Testament, and is translated 'pitch' only in Genesis 6:14. Most of the time, *kopher* is translated with some term that represents money [italics added]."[7]

It seems more likely that *kopher* was some sort of expensive (hence the possible reference to money) sheathing or covering that was placed over the wood of the Ark. It may have been some type of tree resin, but was unlikely to have been a true oil product.

The first actual reference to what's likely true oil or bitumen is found in Genesis 11:3, in the narration about the building of the Tower of Babel. The Bible says, "They had brick for stone, and they had asphalt for mortar". The Hebrew word for asphalt is *chemar*, which is sometimes translated as bitumen, cement, or slime. So here, unlike the use of the Hebrew word *kopher*, the Bible is likely describing a tar or bitumen product, essentially a hydrocarbon formed by the Flood.

Overall, I am pleased to see some fresh thinking on the Ark landing site. New ideas are always good. However, the details provided in the Bible cannot be side-stepped. All suggested Ark landing sites must fit the biblical timeframe and be supported by the geologic timeframe. We need a site that appeared, or was in existence (geologically), around the peak of the Flood (Day 150) and is part of the mountains of Ararat. In my opinion, Karaca Dag fails this test.

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» Ken Griffith and Darrell White reply:

Ark sites are like football teams. Everybody has their favourite, but only one can win the championship. Our only objections to Dr Clarey's preferred Ark site are that the archaeology and plant biology don't seem to support it. That may change with new discoveries.

Geologists and archaeologists have one thing in common. They can both tell you the order in which things occurred, based on the stratigraphy. But they also tend to make the same error, which is to assume that because they know the order, therefore they know the date that something occurred. Dates require synchronisms in order to be confirmed. This is called calibrating the curve. Since the rocks don't come with labels and every place on Earth is different, geologists must be somewhat subjective in assigning any given formation a classification in the geological column.

Determining which strata in the geological column mark the midpoint and end of the Deluge is a highly speculative endeavour that has spawned decades of debate between creationists who agree the Flood was global. While we respect the geological models of Snelling and Clarey, the Ark site itself is the only data point for the midpoint of the Flood that could conclusively calibrate the models.

Karaca Dag is not a small volcano. The area which Clarey claims to be a post-Flood eruption, which the professional geologists classified as Pliocene (figure 1), covers 2,000 km^2 and extends all the way to the Tigris River. If Karaca Dag was actively erupting on such a scale in the centuries after the Flood, then the Prepottery Neolithic (PPNA) culture could not have

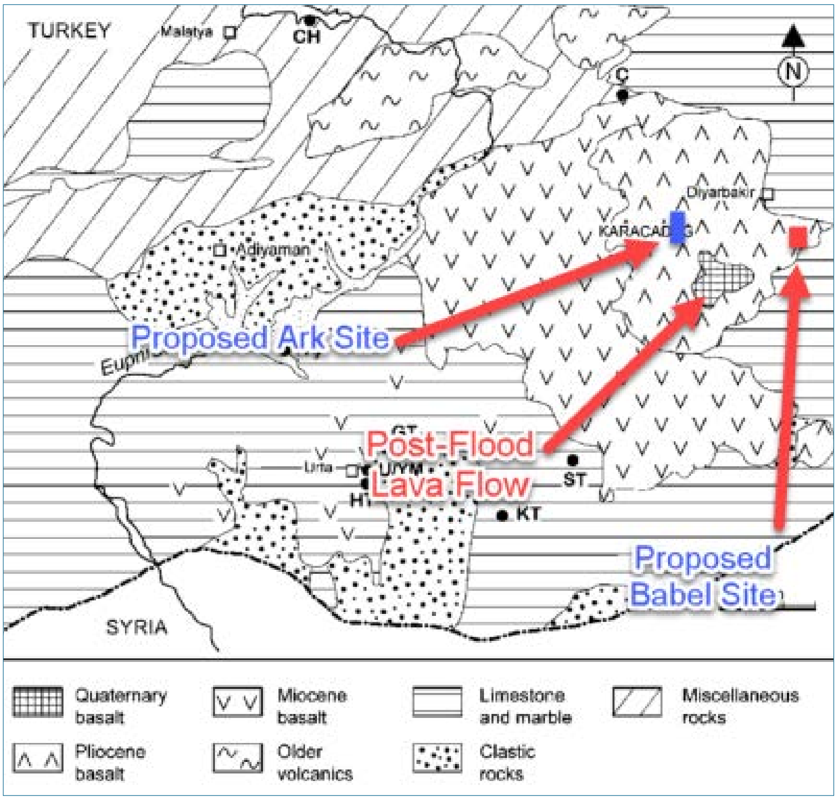

Figure 1. Geological map of Karaca Dag showing Pliocene Basalt (after figure 4 in Haldorsen *et al.*[1])

Image: Bjoertvedt/Wikimedia, CC-BY-SA-3.0

Figure 2. Prepottery Neolithic A distribution excludes Kagazman Ridge

lived and developed on its flanks. In our view, the only post-Flood eruption of Karaca Dag was the small cone on the east flank labelled as Quaternary basalt in figure 1.

The Ark itself should have left an archaeological signature. That signature would be the thousands of containers that carried the fresh water and food supplies not only for a family of 8, but for all of the animals (Genesis 6:21). Those containers would have been useful and valuable in a post-Flood world with no industry to make new ones. They would be passed down for at least a few generations, and thus carried outward from the site as the tribes migrated. The nearly indestructible remains of those containers should demarcate the region where humanity began after the Flood.

The Prepottery Neolithic A appears to be just such a signature. For some reason our ancestors learned how to farm, build stone houses, and make mud bricks; but they chose to use jars of stone instead of clay. These stone jars vary greatly in quality, but the best of them are as thin as cardstock and are made of materials as hard as diorite, well beyond the manufacturing capabilities of neolithic farmers. The smaller and more valuable the jars were, the further they would be expected to have travelled from the point of origin. Kagizman Ridge (figure 2) is outside the region of PPNA sites.

We agree it would not make sense to spend the time and energy on such a difficult task as cutting the Ark into sections unless there was something of great value inside that could not simply be removed by cutting a hole in the hull. That part of our hypothesis may be mistaken, and the layout of the site may suggest evidence of temples or other buildings built at a later time.

Our idea that the Ark remains lie under the school is the part of our thesis most likely to be wrong and is the easiest to test. However, a massive weight of historical, biological, and archaeological data points to the mountain Karaca Dag as the point of origin for post-Flood humanity.

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Jesuit accommodation in relation to biblical chronology and Chinese history

Andrew Sibley

The Jesuit missionaries developed a policy of accommodation in relation to Chinese religious and cultural practices in the 17th century. The Order further received permission in AD 1637 to use the Septuagint, instead of the Latin Vulgate, to try and harmonize the biblical chronology with Chinese history. Chinese history was believed to have extended back to nearly 3000 BC, and the historical accounts contain within them both creation and flood narratives that may loosely correlate with biblical history. How they correlate requires further research. Without getting into a discussion over whether the Masoretic Text or the Septuagint provide the better chronology, the Jesuit motivation for preferring the Septuagint was not entirely pure, being based upon an accommodation to non-Christian beliefs. The reception of Chinese history in the West, along with the discovery of indigenous people groups in the Americas, led increasingly secular academics to postulate that the biblical Flood may have been local, that not all humanity were related to Noah, or even related to Adam. The Jesuit policy of accommodation only encouraged the development of heterodox beliefs in Europe in the 17th century, including regarding biblical chronology.

The events of the Chinese Rites Controversy, which came to the fore in the 17th and 18th centuries, reveal that there was a desire among the Jesuit missionaries to accommodate non-Christian practices and beliefs with Christian sacred texts, and Catholic doctrine. The controversy arose because they found it difficult to make converts in China through an open approach, whereby Chinese converts were expected to fully replace Confucian rituals with Catholic rites. The Jesuits argued, in response to the problem, that many of the rituals were merely cultural and not religious (although in many animistic cultures honouring the dead descends into ancestor worship). A related controversy, which is the subject here, arose with regard to chronology. The China missionaries had gained permission from the Vatican in AD 1637 to use the longer chronology of the Greek Septuagint (LXX), instead of the Latin Vulgate that is based upon the Rabbinical Masoretic Text. The purpose was to try and harmonize Chinese history with the biblical accounts of creation and the Flood. While this move was within the bounds of orthodoxy, the motivation was not entirely based upon principle. While having apparent success in China, although perhaps only superficial, the policy weakened defences against biblical criticism and heterodox beliefs in the West in subsequent decades.[1]

While examining the role of the Jesuits, we should recognize their determination and courage, despite highlighting the problems with accommodation. We may also note that they were not the only ones seeking to reconcile the Bible with ancient texts in ways that potentially undermined Scripture. For example, Robert Fludd, and some members of the Royal Society in England, were influenced by Kabbalism and Hermeticism. Other writings kept alive into the early modern period included various works of Greek philosophy, Egyptian history, Hindu writings, and the Chaldean and Sibylline Oracles.[1]

Chinese rites controversy

The Jesuits received permission from the Vatican in AD 1637 to use the Septuagint in support of their mission work in China, as opposed to the Latin Vulgate.[2,3] This was for the purpose of overcoming an apparent anachronism between the Bible's chronology and Chinese history. The policy of accommodation with regards to Chinese tradition and history was first developed by Fr Matteo Ricci (figure 1). It was considered to be the most effective way of making progress for the Christian message.

The Chinese held to their culture, tradition, and history strongly, often with nationalistic fervour. The missionaries' aim was to first gain the acceptance of the *Literati*, the respected Confucian scholars, with the longer-term goal to establish Christianity in China. They did this by sharing Western science, dressing in Chinese clothing, and, in some instances, taking part in Confucian rites, which they regarded as cultural and not religious. However, the Confucians believed in venerating ancestors, which led to opposition from Dominicans and Franciscans to their policy of accommodation—hence the rise of the Chinese Rites controversy in the Catholic Church in the 17th and 18th centuries. The Catholic *Sacred Congregation for the Propagation of the Faith* agreed with the Dominican objections in a ruling of 1645, but agreed with the Jesuits upon appeal in 1656. The Vatican's position hardened in the early 18th century against accommodation. In a decree of 1704, and a Papal Bull of

Figure 1. Matteo Ricci and Paul Xu Guangqi, from *La Chine d'Athanase Kirchere de la Compagnie de Jesus: illustre de plusieurs monuments tant sacres que profanes,* Amsterdam, 1670. Plate facing p. 201. Ricci developed the policy of accommodation for the Chinese mission.

Image: Kircher, Athanasius, 1602-1680/CC BY-SA 3.0

1715, Clement XI banned the rites, and insisted that Catholics use the word *Tianzhu* 天主 (Lord of Heaven) for God. This replaced the traditional Chinese terms *Tian* 天 (Heaven) and *Shangdi* 上帝 (Supreme Emperor). The hard line of the Catholic authorities made relations with the Chinese rulers more difficult and led to the expulsion of Catholics from China. However, the policy was reaffirmed by Benedict XIV in 1742, even forbidding further debate. A relaxation was granted on 8 December 1939.[4,5]

Chinese and biblical chronology

In terms of unravelling chronology, the various approaches towards Chinese history were set out most clearly in several works in the 17th century. Jesuit priest Gabriel de Magalhães identified three opinions relating to the beginning of Chinese history in his major work *Nouvelle Relation de la Chine*, written between 1650–1668, and eventually published in 1688. Martino Martini's work *Sinicae historiae decas prima* was published earlier in Europe in 1658 (Martini had travelled to Rome from China over a period of four years, from 1650 to 1654). Philippe Couplet's work was also available from 1686. Attempts at harmonizing the biblical accounts with Chinese history continued through the 18th century.[6]

A number of Chinese texts were used for their historical accounts. Texts available included those from the Song dynasty (AD 960–1279), two important pre-Song texts, and later writing from the late Ming dynasty (AD 1368–1644), and the early Qing dynasty (AD 1644–1911). The Jesuits further relied upon later commentaries, some of which elaborated upon the shorter earlier texts. The first pre-Song text available was that of Sima Qian's *Shiji* (*Records of the Historian*), the first part including the first five sovereigns, including that of the Yellow Emperor Huangdi 黃帝. Later editions from the Ming dynasty included a pre-text, the *Bu Shiji*, essentially a short commentary on three earlier emperors. The second pre-Song text, *Zhushu jinian* (*Bamboo Annals*), dates from the tomb of Prince Xiang of Wei (318–296 BC), being discovered in AD 284, and copied in the fifth and sixth centuries. Among Song dynasty text is the *Shaowei Tongjian jieyao* (*Summary of the Comprehensive Mirror by Shaowei*) of Jiang Zhi (AD 1111), which includes the early period from Fuxi 伏羲; and the *Huangwang daji* (The Great Record of Emperors and Kings) from AD 1141, which begins its account with the mythical Pangu 盤古 (for a more complete discussion of Chinese sources see Standaert (2012)).[6] Pangu was considered a giant being asleep within an egg of chaos, with the pantheistic creation narrative taking place over periods of 18,000 years. The god-like being was considered the ancestor of the twin brother and sister, Fuxi and Nüwa 女媧.[7]

Magalhães outlined several approaches among Chinese scholars. Available were various speculative ancient mythologies, albeit not strongly supported by the Chinese scholars, which suggested Chinese history began tens or hundreds of thousands of years ago. Another opinion that was regarded as more historical related to accounts which began with the emperor Fuxi who was one of the five early sovereigns (figure 2a) and was believed to have reigned in Shensi province from 2952–2838 BC. The third view was that the first was Emperor Yao 堯 (figure 2b), who began his reign in 2357 BC. Yao was associated with a flood narrative. The Chinese history was then traced through 22 dynasties involving 236 kings over 4025 years (2357 BC to AD 1668, the time of Magalhães writing).[8] However, Magalhães' work was not published until after it had been brought back to Europe by Couplet two decades later.

Martino Martini (1614–1661) considered that Chinese history started with Fuxi in 2952 BC, although his detailed chronology began with the Yellow Emperor Huangdi in 2697 BC. This history consisted of identifying 45 cycles of 60 years each (sexagenary cycles), ending with Emperor Ai of Han (6–1 BC) around the time of Christ's birth.[9] Martini recognized that the flood in the time of Emperor Yao correlated broadly with the period of the biblical Flood (as

Images (a) and (b): CC BY 4.0

Figure 2. Painting of Emperor Fuxi (left), and Emperor Yao (right), by Kanō Sansetsu (1589–1651). Images dated to the Edo period, 9th year of Kan'ei (1632). Located in the Tokyo National Museum.

outlined in Ussher's chronology and the Vulgate), but along with the Jesuit missionaries he preferred the chronology of the Septuagint as a means of reconciling the accounts.[5,10] He only tentatively suggested that Yao, or Jao, maybe connected to Janus, a Greek flood survivor, and in some sources linked to Noah.[3]

The Greek translation of Genesis infers that the creation occurred around 5554 BC, and the Flood around 3298 BC. The worldwide biblical Flood occurred around 2348 BC, from the derived chronology of the Vulgate (from Ussher), with creation around 4004 BC.[11] The Latin text would give insufficient time for the Chinese chronology, if Chinese history were to be fitted in the shorter timeframe, and for the Chinese to be descended from Noah. Martini placed the biblical Flood prior to 3000 BC, with Chinese history beginning at Fuxi shortly afterwards. Magalhães placed the biblical Flood at 3152 BC, that is 200 years prior to Fuxi, utilizing the limited flexibility that the Septuagint gave him. Martini could not find any cause of a flood in the Chinese writing, nor find evidence within the texts to ascertain whether the flood was local or universal, which he thought supported such a viewpoint.

Martini further questioned whether the Chinese flood accounts and the biblical ones were identical, and expressed, with some certainty, that East Asia had been inhabited from before the time of the biblical Flood "… *extremam Asiam ante diluvium habitatam fuisse procerto habeo*". The Chinese chronology was supported by Jesuit astronomer Sabatino de Ursis; while residing in Peking he concluded that Emperor Yao was reigning in 2358 BC. This was determined from observations of the position of various stars and calculated backwards to the location mentioned in the Shu Ching (*The Classic of History*).

Against Martini's equivocation, John Webb, a 17th-century English scholar, argued more strongly that Emperor Yao should be identified with Noah, as the dates correlated reasonably well. Webb believed that Noah had in fact built the Ark in China, making the case that Mount Ararat was somewhere towards the east, and then the Ark landed there as the waters receded. His main preoccupation was to argue that the Chinese language was the primitive one that Adam had spoken. Georg Horn, a German theologian from Leiden, traced backwards from Yao and identified Fuxi with Adam, in his attempt to correlate the other biblical patriarchs with the list of Chinese Emperors.[3,12,13]

The Jesuit position was further outlined in 1686 by Philippe Couplet, with his work *Tabula chronologica monarchiae sinicae* (*Chronological Table of the Chinese Monarchy*) published in Paris in 1686; the purpose being to reinforce agreement between the Septuagint Chronology and the Chinese history. A year later he published some of the works of Confucius in Latin *Confucius Sinarum Philosophus*.[14] Couplet had spent 20 years in China, having been inspired by one of Martini's lectures to travel. An earlier work, dated to 24 December 1666, had been returned to Europe, but remained unpublished (*Prologomena ad Annales Sinicos, necnon Synopsim Chronologicam Monarchiæ Sinicæ*). While Martini had developed an uninterrupted chronology, Couplet left a gap in which the biblical Flood may fit. He thought that lack of the deluge account in Chinese history made interpretation difficult. Couplet's published work, in tabular form, began the Oriental chronology from Huangdi in 2697 BC, until the time of the Incarnation of Christ (the unpublished work began with Fuxi). The second work continued Chinese chronological account to the time of Couplet's writing.[6]

Impact upon Western thinking

As the attempt to harmonize Chinese history continued through the 18th century, the literal account of a global flood was undermined in Europe. Isaac Vossius, in his *Dissertatio de vera aetate mundi*, of 1659, argued that the biblical Flood was not universal, but only local, and that the Bible was only dealing with the events of the Middle East and not the whole of human society.[8,12] This debate also encouraged consideration of belief in pre-Adamic races. The problem of the existence of ancient Gentile people groups, such as the Africans, Chinese and Native Americans, and scepticism that ancient people could cross the oceans, was one of the reasons that led Isaac La Peyrère to argue for the existence of pre-Adamic people. The work, *Prae-Adamitae*, was published in Latin in 1655 and in English in 1656, and it was subsequently discussed by members of the Royal Society.[15] Giordano Bruno had intimated such a position in 1591.[16]

The desire to know more about Chinese history had reached as high as the French King Louis XIV, and Couplet had organized a questionnaire in Paris 1684, seeking further information about the Chinese history and chronology. Jesuit missionaries continued to try and harmonize the Chinese history with the sacred texts through the 18th century. However, reflecting the spirit of the times, Voltaire, in 1756, simply claimed the Oriental ones were older in his *Essai sur les mœurs et l'esprit des nations.* This completely undermined the integrity of Scripture.[6] While the policy of accommodation had been an attempt to further the Christian mission in China, the developing dialogue in Europe only played a part in undermining the revealed faith.

Summary

The Jesuit mission to China in the 17th century developed a policy that accommodated certain Chinese Confucian cultural aspects into their services. Furthermore, they received permission to use the Septuagint, with its longer inferred chronology, as opposed to the shorter period outlined in the Vulgate. While Christians may argue that this slightly longer chronology may fit within orthodox limits of biblical chronology, their motivation was not entirely based upon principle, but what was useful. It led to reliance upon the pagan Chinese chronology to inform Scripture, which is more problematic. The policy was discussed at length by Roman authorities and declared illegitimate for two centuries, from 1704 until 1939. While the policy may have had some success in gaining respect from the Chinese authorities in the short term, it is arguable that in the long term it was counterproductive.

In relation to this accommodation, the discovery of ancient cultures in East Asia and in the Americas led some academics to consider the possibility that not all people groups had experienced the Flood, or that some men and women may not be directly descended from Noah, or Adam and Eve. Western pride also led many scholars to think erroneously that Europeans were the first to cross continents. The campaign for accommodation in China may seem to have been only a small step, but it helped to open the door for heterodox beliefs to arise in Europe, including the development of belief in deep time. As discussed in a couple of other papers, during the 18th century Jesuit-trained academics conducted a similar process of accommodation in relation to Hindu practices and chronology. This is the Malibar rites controversy, which further contributed to the European development of belief in a more ancient history of the world.[17]

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The evolution of the human urinary bladder

Jerry Bergman

The urinary bladder is a vital system for waste removal employed in virtually all terrestrial tetrapods. A literature review was conducted to evaluate the evolutionist claims concerning its development. The review found that not only is there no evidence of its evolution, but the problem is so difficult that even just-so stories were not found. Two very different urine excretion systems exist, and no evidence was located to support the postulate that the simple system in fish evolved into the far more complex system existing in mammals. Furthermore, both systems were designed to effectively deal with the elimination needs of the organism in which they are employed.

Waste control is of vital importance in all living organisms. With rare exceptions, all terrestrial tetrapods have a urinary bladder, which stores urine and enables its release under voluntary control.[1] Many animals, such as fish, release urine as it is produced. Humans and most mammals, birds, reptiles, and amphibians can store it to some extent and release it when the appropriate opportunity arises. Many animals use this ability to mark their territory, a communication system that requires bladder control.

The urinary bladder, often referred to simply as 'the bladder', stores urine produced in the kidneys until its disposal by urination. In humans and a number of other vertebrates, this hollow muscular distensible organ (figure 1) rests on the pelvic floor. Urine enters the bladder from the kidneys via the ureters and exits via the urethra. The typical human bladder holds between 300 and 500 ml (10.14 to 16.91 fl. oz.) of liquid before the urge to empty is triggered, but it can hold considerably more. In contrast, most invertebrate animal life-forms have no means of control over releasing liquid waste. It is released into the environment very soon after it is produced. Many vertebrates (see shortly) lack a bladder, their ureters instead opening into a cloaca that also holds fecal matter.

The anatomy of the human bladder

The urinary bladder is an integrated system consisting of muscular tubes called 'ureters', which propel the urine forward from the kidneys to the bladder by a set of coordinated wave contractions called 'peristalsis'. This enables the urine's movement forward from the kidneys regardless of the body's position; standing straight up, or lying horizontally. The bladder is divided into a broad *fundus* located at the top, the main part called the *body*, an *apex* at the bottom and a *neck* where the urine is drained into the urethral orifice.

The bladder's inner lining, the *mucosa*, consists of special epithelial cells called 'transitional epithelium'. This layer can stretch as the bladder expands and protects the other layers from the effects of urine if it is too acidic or too alkaline. Next is the *submucosa*, made of connective tissue in which there are nerves and blood vessels. Beyond this is the *muscularis*, the central structure which is made up of three layers of muscle fibres. The superior (top) part of the bladder is covered outside with a *serous membrane* which is continuous with the peritoneum that lines the abdominal cavity generally. It protects the bladder against friction between it and the organs in proximity to it. The lateral (side) and inferior (bottom) parts of the bladder are surrounded by a layer of fibrous connective tissue called the *adventitia*.

The bladder walls are able to greatly expand due to a series of thick mucosal folds called 'bladder rugae'. These folds look like wrinkled skin when the bladder contracts, which causes it to assume a pyramidal shape. When filled with urine, the bladder expands, causing it to resemble a balloon. The urinary bladder wall is normally 3 to 5 mm thick, but, when distended, thins to less than 3 mm.

The muscularis of the bladder wall is constructed from smooth muscle fibres arranged in spiral, longitudinal, and circular bundles to form the required shape, allowing the bladder to empty when necessary. The muscularis is also known as the detrusor muscle. It remains relaxed when the bladder is filling, but contracts to force urine out of the bladder and into the urethra when the bladder is full.[2]

At the bladder neck there is a smooth triangular region called the *trigone*, formed by the two openings of the ureters and the internal urethral orifice opening into the urethra. This contains muscle fibre that form a sphincter. This acts like a valve, so that, when contracted, it prevents urine from leaking into the urethral tube and out of the body. In males, the neck of the urinary bladder is contiguous with the prostate gland such that the first part of the urethra travels through the centre of the prostate.

To function, the entire system requires a set of arteries and veins, and nerves coordinated by the brain and other parts of the nervous system. Lacking this complete system, or any part noted above, the bladder will not function properly, or at all.

The waste-control function in all living organisms is of vital importance.[1] Urine primarily consists of nitrogenous wastes, including ammonia, urea, uric acid and creatinine, plus toxins, drugs, hormones, salts, and hydrogen ions.[3] Due to the potential lethality of these substances if allowed to build up, the complex system of urine removal described above is critical.

Urinary bladder systems in reptiles

All turtles, tortoises, and certain lizards, such as the Gila monster, have a urinary bladder designed to recycle urine through their body to reuse, and hence conserve a significant portion of the water in urine.[4] Most other lizards also possess a urinary bladder,[5] but legless lizards, often called 'snake-lizards', lack a bladder and use a cloaca through which urine flows out of the creature's body as soon as it's produced. All snakes lack a bladder; thus, their urine is also emptied directly into the cloaca for elimination.[6] Given the design of snakes and their mode of life, the advantages of this design are obvious.

Alligators and crocodiles have kidney and excretory systems similar to those in other reptiles, except they do not have a bladder.[7] Certain other reptiles possess a midventral wall in the cloaca, which opens into a urinary bladder. Beuchat, in his survey, reported that a urinary bladder is present both in all tuataras and all chelonians. In all fish, birds, and most reptiles, the urinogenital ducts and the anus both empty into the cloaca. This posterior orifice is not only the opening for the digestive and urinary tracts, but also the reproductive tract.[1,8] Thus, a clear contrast exists between animals that possess a urinary bladder and those that lack it. Furthermore, the presence or absence of a urinary bladder does not form the logical ranking from lower life-forms lacking a urinary bladder to higher

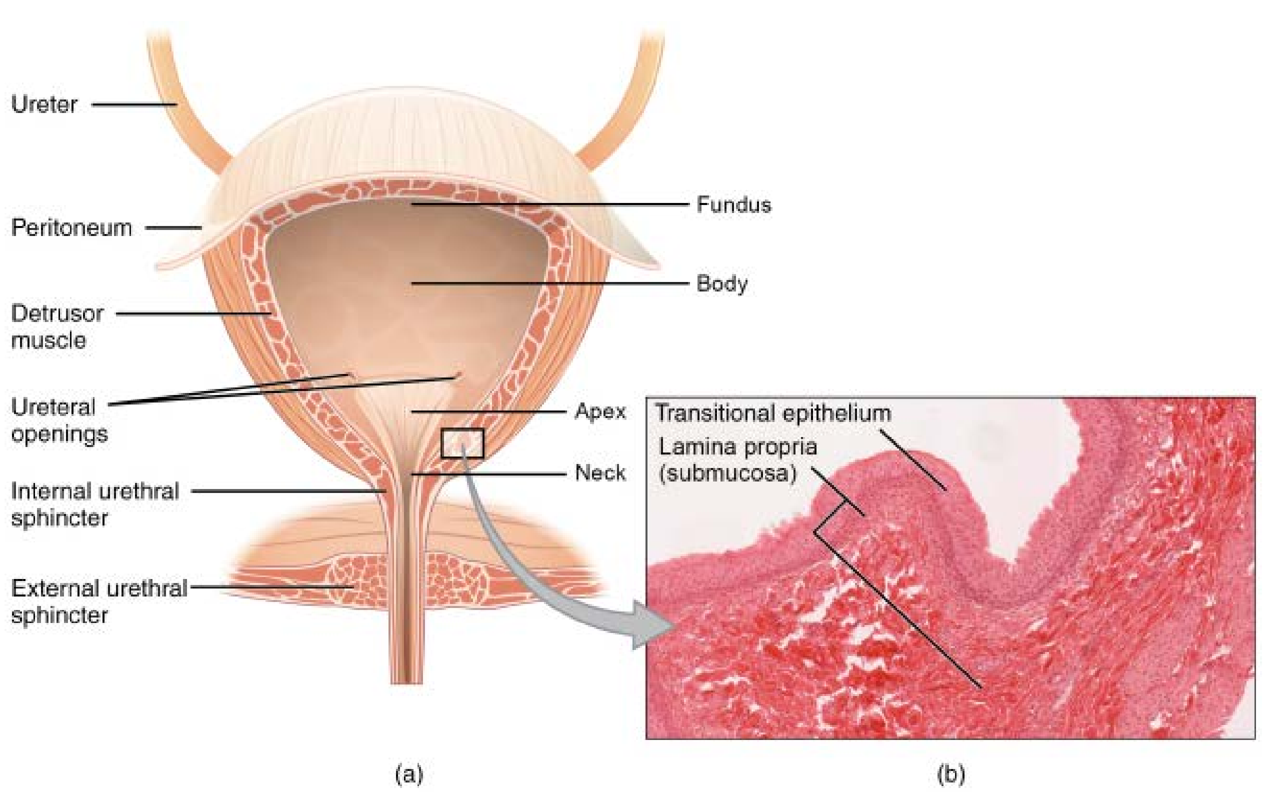

Image: OpenStax College/Wikimedia, CC-BY-3.0 [modified]

Figure 1. The human male urinary bladder (a), displaying transitional epithelium and part of its wall (b)

forms possessing it. Beuchat concluded that phylogenic (evolutionary) generalizations cannot be made from the existing data.[8]

Evolution of the bladder

Animals either have a urinary bladder system or lack one. Consequently, the challenge to evolutionists is to attempt to bridge this gap by short steps, each one a step that allows the animal to effectively eliminate toxins so as to prevent internal toxicity. In short, the evolutionary question to be answered is: "How can this organ evolve from a thin-walled structure in fish to the complex urinary bladder existing in mammals?"[1] Some major design differences exist in urinary bladders, so some evolutionists have postulated that it evolved twice![9] The just-so story proposed is that the area anterior to the cloaca expanded slowly until a balloon-shaped structure developed—which proceeded to evolve all of the many structures seen today in the human bladder as outlined above.

Internet searches using the phrase 'evolution of the urinary bladder' produced mostly articles on the *development* of the human bladder in the embryo. Even books such as *Understanding Human Anatomy Through Evolution*, in spite of a detailed discussion of the human urinary bladder, mention not a word about its possible evolution.[3] The author did mention the "ability to concentrate wastes and control water loss was crucial to the evolution of terrestrial animals such as humans", but not a word on *how* it could, or did, evolve.[3] Lieberman likewise ignored the topic of its evolution in his book on human evolutionary biology, a field in which he is a professor.[10] Wilder discussed its function but completely ignored its evolution.[11]

Romer & Parsons speculate that since the bladder evolved very early in evolutionary history it has disappeared in animals that evolved later which do not, today, have the organ. Specifically, in a few lizards, snakes, crocodilians and birds (except ostriches), evolutionists claim that the entire bladder system has totally disappeared.[12] In these cases, urine is poured directly into the cloaca and then exits into the environment. Theories about how or why it disappeared were not mentioned by Romer and Pearson in their chapter.[13]

A study by McCarthy and McCarthy was one of the few exceptions that did not ignore the evolution problem. After noting that almost all terrestrial tetrapods have a urinary bladder with a storage function, but many marine and aerial species lack a urinary bladder, or have only a very small storage capacity, they postulate that this difference in bladder morphology:

> "… indicates it has evolved from a thin-walled structure used for osmoregulatory purposes, as it is currently used in many marine animals. It is hypothesized that the storage function of the urinary bladder allows for an evolutionary selective advantage in reducing the likelihood of successful predation. Random walks simulating predator and prey movements with simplified scent trails were utilized to represent various stages of the hunt: Detection and pursuit."[1]

Disagreement exists about this proposal. McCarthy and McCarthy's model was not based on incremental change from a lack of bladder to a fully functional bladder, but contrasted the functionality of a storage bladder under voluntary control vs a continual excretion of waste. The concern here is the evolution of the bladder, not the evolution "from an osmoregulatory organ to one of storage".[1] The function of the bladder is controlled release of urine, and a bladder that continually releases urine lacks this function. By allowing the release of urine at select locations and intervals, the urinary bladder serves to reduce the likelihood of soiling the area where the animal sleeps and spends much of its time.[9]

In spite of evolutionary proposals by McCarthy and McCarthy about 'selective pressure', an unbridgeable chasm exists between the simple tubes used in invertebrates and the far more complex urinary-bladder system used in virtually all vertebrates. No direct evidence of the evolution of one system into the other exists, nor have any viable just-so stories been proposed to explain the evolution of the simple invertebrate urinary system into the complex vertebrate kidney-urinary system.

The common reason evolutionists present for the lack of evidence to bridge this chasm is that soft tissue is usually not preserved in the fossil record. However, there have been numerous discoveries of fossils in which the structure of soft tissues, such as the brain and internal organs, or even the whole creature in the case of jellyfish and cephalopods, has been beautifully preserved. In recent years there has, in addition, been the discovery of non-fossilized tissues (i.e. intact, thus still soft and elastic when demineralized, with identifiable proteins), mostly in dinosaur bones[14] and a handful of other specimens.[15] These may motivate the search for, and further research on, other types of soft tissue.

Another problem with leaning on the soft-tissue preservation difficulty to explain the lack of evidence is the fact that thousands of so-called 'living fossils' exist that are believed to be anatomically close to their claimed multiple millions-of-years-old designs. Thus, if bladder evolution occurred, evidence of it should exist in living animals that bridge the two very different systems. Romer and Parsons highlight the problem, noting fossils have a "paleontologic record [that] is ambiguous and open to controversy".[16]

Summary

All life either has a bladder system or lacks a storage-and-controlled-release urinary system. To work properly the bladder system requires all of its components to operate. How one system could gradually evolve into the other system by a slow and gradual means via mutations and natural selection is almost totally ignored in the literature. Even just-so stories are almost unknown. The rare attempts to postulate a possible evolutionary path are little more than suggestions and speculation and are often readily admitted as such. The evidence supports the conclusion that the first bladder was a fully developed functional system that had to operate at a high degree of effectiveness and efficiency in order for the animal to survive.

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Pre-Tejas volcanism in North America: challenge to Hydroplate Theory

Edward Isaacs

The extensive geologic history of volcanism is a centrepiece of nearly all secular and diluvial global tectonic models except Hydroplate Theory (HPT). Proposed in 1972 as a comprehensive explanation of the Genesis Flood, HPT purports to explain 25 major features of Earth. However, despite ubiquitous volcanic deposits throughout the stratigraphic record, HPT has largely ignored volcanism in favour of supercritical water. It relegates continental volcanism to the latter stages of the Genesis Flood, following the formation of most major mountain belts. This diminishes HPT's explanatory value for the vast pre-Cenozoic volcanic deposits of North America.

Ever since geologists determined basalts were congealed lavas, volcanism has been a focus of global tectonic and geodynamic models. Its extensive record has been interpreted as evidence for gradual processes through deep time, yet research has demonstrated its cataclysmic nature.[1] This emphasis on volcanism has been extended to most diluvial models, with the exception of Hydroplate Theory.

Proposed by Dr Walt Brown in 1972, Hydroplate Theory (HPT) claims to explain 25 features of Earth,[2] including the distribution and nature of modern volcanoes such as those that form the Ring of Fire.[3] Rather than postulating volcanism fuelled by a viscoelastic mantle, HPT sets forth a unique set of initial conditions, including an interconnected shell of supercritical water separating an upper granitic crust from solid basalt basement. This supercritical water would become the driving mechanism of the Flood, leading HPT to predict little volcanic activity prior to its Continental Drift Phase late in the Flood.[4] Initiated by up-buckling of the Mid-Atlantic Ridge, this phase's rapid lateral relocation of the continents drove the continents into their present positions. Their rapid deceleration produced major mountain belts such as the Rocky Mountains and initiated continental volcanism like the Columbia River Basalts of the Pacific Northwest.[5] However, HPT's focus on late-Flood volcanism ignores the volume of volcanic deposits preceding the Cenozoic Tejas megasequence rocks in North America produced during and following the Continental Drift Phase. Understanding these pre-Tejas volcanic rocks is imperative to any global tectonic model.

Hydroplate Theory: a tectonic synopsis

HPT proposes Earth was created with an interconnected shell of water 1.6 km thick, dividing a 100-km-thick granite crust from a basalt basement and solid mantle (figure 1). Continuous lunar tidal pumping[6] caused the subterranean water to reach supercriticality,[7] which helped maintain the pre-Flood rainless hydrology for approximately 1,600 years until the Genesis Flood.[8]

At the onset of the Flood, crustal failure produced linear cracks in the granite through which the supercritical water erupted as the 'fountains of the great deep' of Genesis 7:11 (figure 2a). The purported fountains fuelled the 40 days of intense rain, the inundation of the continents, and further expansion of the linear cracks. After the first 40 days, the rising floodwater covered the fountains (figure 2b),[9] although subterranean water continued to flow onto the surface of the granite crustal fragments (hydroplates).

Erosion of hydroplate edges continued until portions of the basalt basement up-buckled from the lack of overlying pressure, creating the Mid-Atlantic Ridge. This lowered mantle pressure beneath the Mid-Atlantic Ridge, shifting the subsurface from the Pacific Basin towards the uplifting Mid-Atlantic Ridge. Lubricated by the remaining supercritical water, the hydroplates slid laterally off the rising Mid-Atlantic Ridge towards the deepening Pacific Basin until the supercritical water dissipated and friction halted the hydroplates (figure 2c). Termed the 'Compression Event' (CE), this rapid deceleration produced mountain belts such as the Rocky Mountains in North America, while the friction generated by the hydroplates generated magma, fuelling volcanic eruptions such as the Columbia River Basalts. As Brown states:

> "Friction at the base of skidding hydroplates and below sinking mountains generated immense heat, enough to melt rock. Crushing produced similar effects, as broken and extremely compressed blocks and particles slid past each other. The deeper the sliding, the greater the pressure pushing the sliding surfaces together, so the greater the frictional heat generated.

Where heat was most intense, large volumes of rock melted. High-pressure magma squirted up through cracks between broken blocks. Sometimes magma escaped to the Earth's surface, producing volcanic activity and 'floods' of lava outpourings, called flood basalts, as seen on the Pacific floor and the Columbia and Deccan Plateaus."[4]

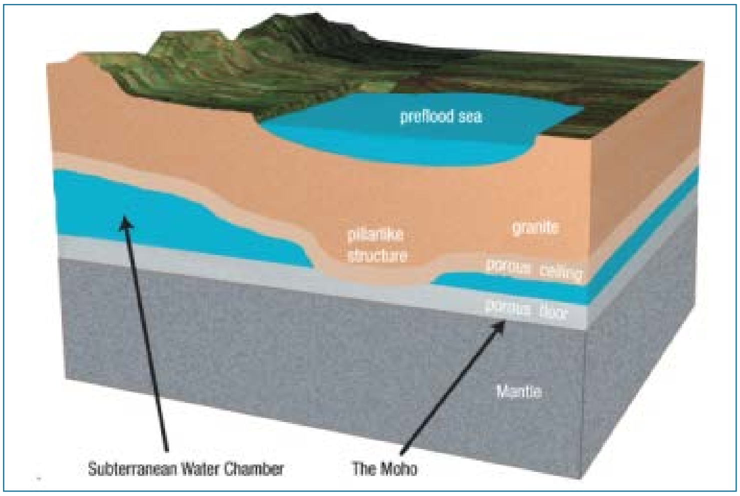

Figure 1. Depiction of Hydroplate Theory's proposed crustal structure before the Genesis Flood. Observe that the granitic crust and underlying subterranean chamber rest upon the solid basalt basement and mantle. Image from Brown, ref. 2, figure 55 on p. 126.

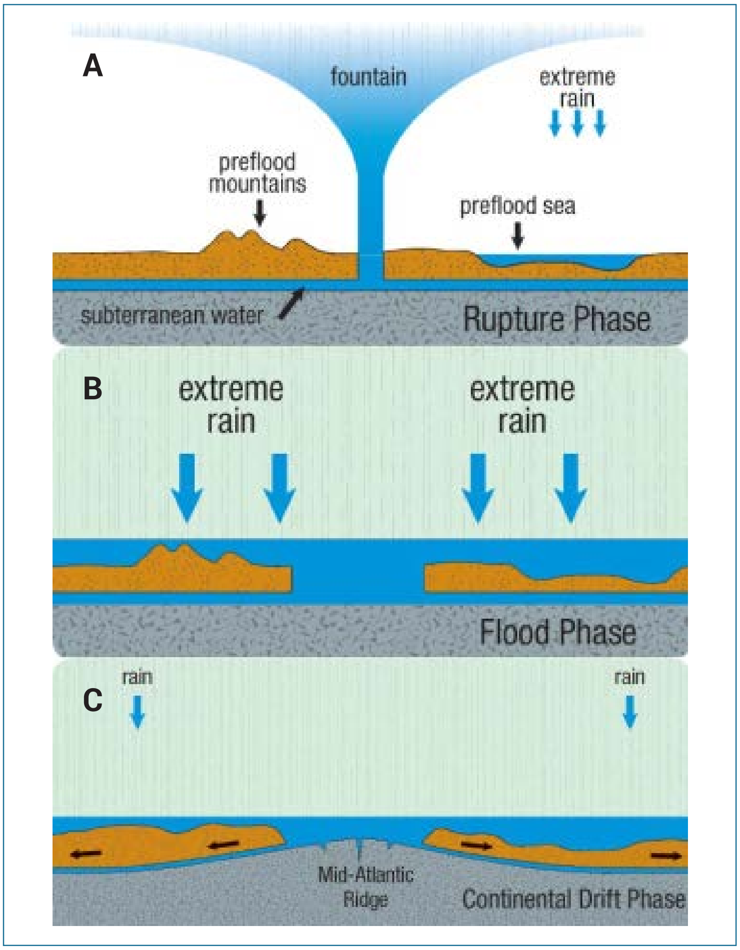

Figure 2. HPT postulates the Flood proceeded in three primary phases: (A) the Rupture Phase, begun by crustal failure and the fountains of the great deep; (B) the Flooding Phase, during which the subterranean water was released onto the continents; and (C) the Continental Drift Phase, initiated by the formation of the Mid-Atlantic Ridge. Collage produced from Brown, ref. 2, figures 57, 60, and 64, pp. 127, 131, and 133.

The liquefaction submodel

Stratigraphy has historically been inextricably linked to tectonic paradigms. The plate tectonics renaissance of the 1960s brought a revolutionary perspective on how sedimentary environments respond to tectonics.[10,11] HPT also provides a unique stratigraphic paradigm in its liquefaction submodel. It proposes that diluvial strata were produced by repeated wave-induced continental-scale liquefaction that sorted grains into graded successions.

As the fountains inundated the continents, pre-Flood regolith and eroded granitic crust were deposited atop the hydroplates, which were 'fluttering' in response to water hammers being generated in the subterranean chamber. This caused tsunami-like waves to travel across the hydroplates. The increased pressure beneath crests and decreased pressure beneath the troughs gradually sorted sediments into roughly homogenous units, which would have continued until the hydroplates grounded on the basalt basement during the CE. This rapid deceleration also caused the sediment on the hydroplates to decelerate and compress, releasing massive amounts of water that further stratified the sediment. Brown explains:

> "Likewise, each decelerating granite hydroplate acted on the bottom sedimentary layer riding on the hydroplate. Sedimentary layers, from bottom to top, acted in turn to decelerate the topmost layers. As each water-saturated layer decelerated, it was severely compressed—similar to suddenly squeezing a wet sponge. Sediments, forced into a denser packing arrangement, released water. Sedimentary particles were crushed or broken, so their fragments filled the spaces between particles, releasing even more water. The freed water, then forced up through the sediments, caused massive liquefaction. As the sedimentary

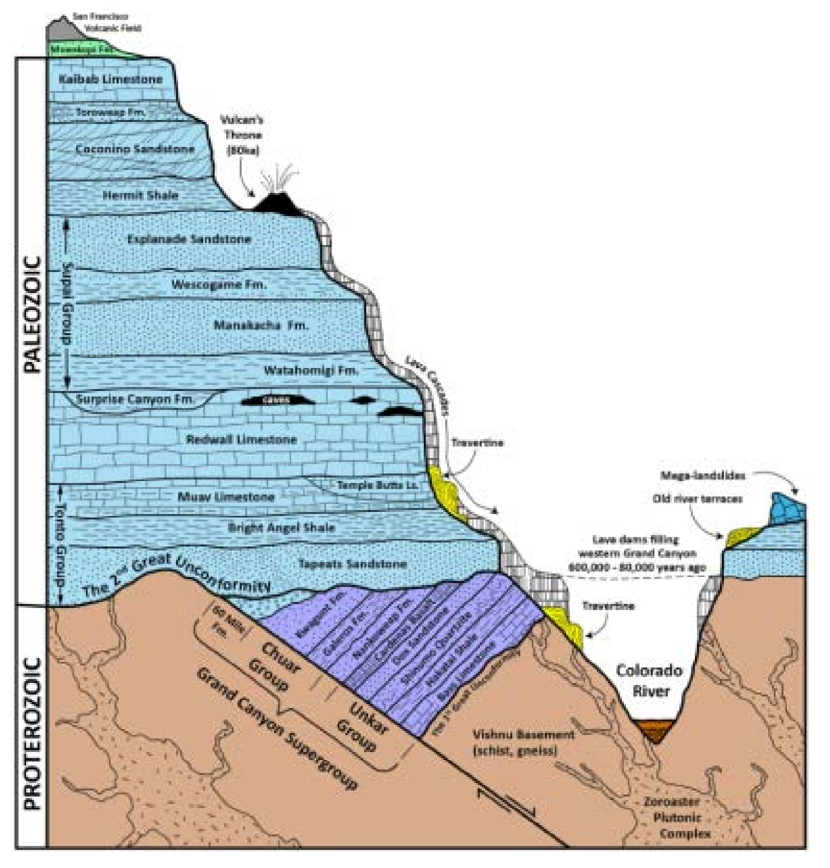

Figure 3. The Grand Canyon's Precambrian stratigraphy is dominated by the deformed Grand Canyon Supergroup intruded by Zoroaster Granite and overlain by the Great Unconformity and horizontal Phanerozoic sediments. Hydroplate Theory postulates that the Great Unconformity represents the past slippage plane that divided the horizontal Paleozoic strata from the tipped and bevelled Grand Canyon Supergroup below. Within the Grand Canyon Supergroup is the Cardenas Basalt of the Unkar Group, yet Hydroplate Theory postulates that continental volcanism did not begin until *after* the Continental Drift Phase and the deformation of the Grand Canyon Supergroup, indicating that HPT does not predict the presence of lava at this point of the Flood. Reproduced from Gootee.[30]

> layers decelerated and compressed, they became more and more fluid. Eventually, some layers were so fluid that slippage occurred above them, as in our [example] deck of cards. Below that level, extreme compression and liquefaction caused fossils to float up and collect at this watery level where sliding was taking place."[12]

This reorganization of the sedimentary fabric produced vast sedimentary sheets across the current continents, but beneath the primary slippage zone the strata were compressed and tipped diagonally:

> "As slippage began during the compression event, layers below the slippage plane continued to compress to the point where they tipped. The sliding sedimentary block above the slippage plane beveled off the still soft tops of the tipped layers."[13]

Brown illustrates this instance at the Grand Canyon (figure 3), suggesting that the Great Unconformity represents such a slippage plane, dividing the horizontal Paleozoic strata from the underlying tipped and bevelled Grand Canyon Supergroup.[13]

A comprehensive stratigraphy?

While traditional stratigraphy sees strata forming by a host of processes in various environments,[14] HPT focuses on liquefaction to explain most of Earth's sedimentary deposits, making few predictions for rigorous field studies. Creation educator J.D. Mitchell applied HPT to John Day Fossil Beds,[15] but most of his interpretations were similar to traditional stratigraphy or were general answers offering little more insight. As such, HPT has yet to demonstrate a practical field stratigraphy.

Nonetheless, HPT does allow some predictions. First, sediments should be found near the stratigraphic level at which they were initially deposited. Brown said the fossil succession found within the stratigraphic record was produced by the relative buoyancy of animal carcasses, but sediment grains would have densities closer to each other than to carcasses. Therefore, grains would not rise to the surface during liquefaction but instead would be concentrated near the level where they were deposited, creating graded deposits and cyclothems as proposed by Brown.[16] Thus, the presence or absence of a substance (e.g. lithic or mineral) in the stratigraphic record should reflect the processes active at the time a cyclothem or sequence was being deposited and initially sorted.

Second, volcanics should be overrepresented in the most recent rocks. After all, HPT proposes that volcanism began only during the waning phases of the Genesis Flood after most strata had already been produced. Brown states that the first major volcanic outpourings on North America were the Columbia River Basalts following the formation of the Rocky Mountains during the CE at the close of the Continental Drift Phase.[9] This implies volcanism initiated in North America in the Tejas megasequence (Paleogene and Neogene), the highest of seven primary unconformity-bounded series of

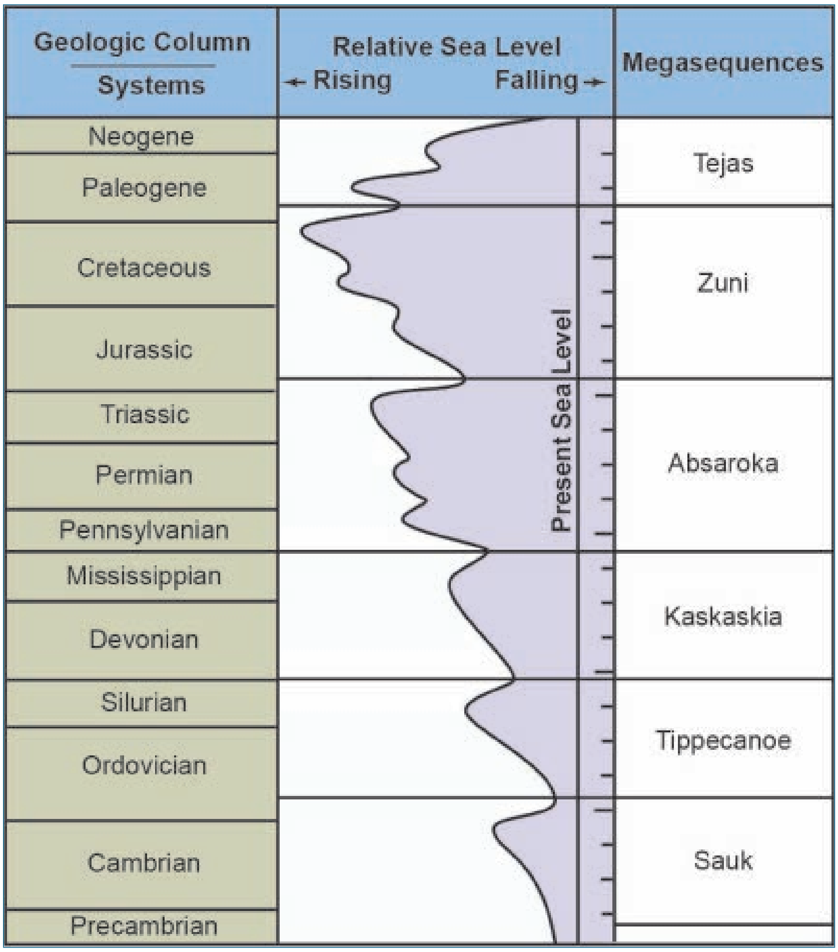

Figure 4. Earth's Phanerozoic stratigraphy has been categorized into six unconformity-bounded sedimentary packages termed megasequences with one additional Neoproterozoic megasequence not shown. Because HPT's Continental Drift Phase would correlate to the uplift of the Rocky Mountains during the Tejas Megasequence, one would expect little to no volcanism recorded prior to the Tejas Megasequence, yet many examples have been catalogued to the contrary. Courtesy of the Institute for Creation Research.[21]

strata (figure 4). Therefore, pre-Tejas volcanism should be small to non-existent in North America.

Third, volcanic deposits should rarely, if ever, contain interbedded or overlying sedimentary strata. After massive liquefaction in the CE, the grounded hydroplates would have lost the flutter that produced wave-induced liquefaction and thus the requisite process for stratification. Instead, the subsequent outpourings of flood basalt would be surficial in nature or overlain by ungraded deposits. This would be far different than the stratified deposits formed earlier in the Flood.

These predictions allow us to test the expectations of HPT against the stratigraphic record. Because sediment grains would be concentrated in cyclothems near the stratigraphic level where they were initially deposited, HPT would expect little to no evidence for volcanism before the CE and subsequent outpourings of flood basalts, which would not be interbedded with or overlain by stratified sediments. Therefore, volcanics should be most commonly present as surficial rocks above the basement of orogens such as the Rocky Mountains, which had formed during the CE. Conversely, extensive volcanics older than the Rocky Mountains (and thus the Tejas megasequence) would conflict with HPT predictions.

Pre-Tejas volcanism in North America

Based on geological and geophysical data collected from boreholes, site investigations, and published fieldwork, Clarey and his colleagues have catalogued the nature and extent of much of the stratigraphic record into seven continental-scale unconformity-bounded sequences of strata, termed megasequences.[17] While some have argued that megasequences are based on the Geologic Column,[18] considered by some HPT advocates as a 'mental abstraction',[19] these megasequences can test HPT on a continental scale because they provide a broad generalization of the actual rock record. Furthermore, they generate a frame of reference anchored to events like the uplift of the Rocky Mountains (Tejas megasequence), which in turn can be correlated to HPT's Compression Event (table 1).[20] Thus, 'pre-Tejas' rocks, correlating with rocks predating HPT's Compression Event, can test HPT's predictions and the rock record.

The seven megasequences cumulatively comprise the bulk of strata on most continents. In North America, the lowest megasequence is a diminutive 'pre-Sauk' comprised primarily of clastics and volcanics, followed by the Sauk, Tippecanoe, Kaskaskia, Absaroka, Zuni, and Tejas megasequences, respectively, which also increase in volume and amount of volcanic contribution. Volcanic rocks comprise 18% of the Tejas megasequence (17,800,000 km^3 [21]), the last and most extensive of the seven megasequences. Only a small portion of the 3,200,000 km^3 of volcanic rocks is represented by the Columbia River Basalts, which occupy merely 210,000 km^3.[22]

The pre-Tejas megasequences, correlating to HPT's Flood Phase in North America, each contain 1–7% volcanics. This totals approximately 1,750,000 km^3 of volcanogenic strata,

Table 1. Synopsis of major periods and associated activities postulated by Hydroplate Theory (reproduced from Isaacs[29])

HPT Period	Geological events
Creation	God creates Earth's pre-Flood structure (basalt basement rock overlain by interconnected water channels and granitic crust).
Pre-Flood Period	Subterranean water becomes supercritical within a decade of Creation.
The Flood: Rupture Phase	Crustal failure allows subterranean water to jet out (fountains of the great deep) and inundate the continents. Crack encircles Earth in two hours.
The Flood: Flood Phase	Subterranean water continues to inundate the continents as floodwater rises, causing wave-induced liquefaction.
The Flood: Continental Drift Phase	Mid-Atlantic Ridge (MAR) buckles upward forming antipode Pacific Trenches. Continents slide away from the MAR.
The Flood: Compression Event	Mountains form from the collisions and halting of the hydroplates during the Continental Drift Phase while massive liquefaction sorts the fossil record.
Recovery Phase	Floodwater recedes from the continents, ending the Flood. Continents begin to stabilize as the Ice Age begins. Phase continues to the present.

over half the volume of volcanics in the Tejas megasequence. As can be seen along the North American Midcontinent Rift System[23] or the Cordilleran Margin,[24] these can be both lava flows and volcaniclastics.

Too much volcanism before the Compression Event

Extensive pre-Tejas volcanism in North America challenges HPT because it predates the CE (see table 1). Many pre-Tejas volcanic rocks have been deformed and/or folded in mountain belts such as the Appalachians or Rocky Mountains, supposedly produced during the CE, such as the Cardenas Basalt.[25] A member of the Grand Canyon Supergroup, the pre-Sauk Cardenas Basalt must have been tilted and bevelled along with the Shinumo Sandstone and other beds allegedly inclined during the CE.[26] Similarly, volcaniclastics are often stratified and can contain fossils associated with their stratigraphic position, thereby requiring liquefaction. For instance, the rich fossiliferous Two Medicine Formation in central Montana contains interbeds of residual ash despite being folded into the Willow Creek Anticline during the Laurentide Orogeny or Compression Event of HPT.[27] This pales in comparison with the immense Ordovician ash-fall tephra folded in the Appalachians,[28] yet such residual ash deposits are found throughout the North American stratigraphic record, requiring extensive volcanism before HPT's Compression Event.

HPT cannot explain this extensive pre-Tejas volcanism. After all, HPT requires both flows and volcaniclastics to occur near the stratigraphic level they were produced at, providing a datum on the initiation of volcanism within the stratigraphic record. Because HPT's solid mantle cannot provide a source of magma to the hydroplates, it must assume that magma came from frictional heating of the hydroplates during the CE when the hydroplates collided with obstacles or ground upon the basaltic basement. At no other time is enough friction generated. Prior to this, the hydroplate could only make contact with the basalt basement as a pillar at rest or as a fluttering edge, which would only have pulverized the hydroplate edge as it was lubricated by the near-frictionless supercritical fluid. Thus, with no mechanism to produce magma, HPT has no explanation for the vast volcanic outpourings predating its CE.

Conclusions

Though volcanism is central to most modern tectonic and geodynamic models, HPT stands alone, relying on supercritical water as the driving force of the Genesis Flood. This forces HPT to focus on recent volcanism. Despite the distribution of modern volcanic activity being one of its claimed strengths, HPT fails to explain the extensive volcanic record of the pre-Cenozoic.

While HPT's liquefaction submodel does not provide a comprehensive stratigraphy, several primary assumptions can be identified to test HPT. Because sediments should be found at the stratigraphic horizon at which they were formed, volcanism should be found only in late Flood rocks and be overlain by, or interbedded with, little to no strata. HPT claims the Columbia River Basalts mark the initiation of North American volcanism during deposition of the Tejas megasequence following the CE. However, the volume of North American pre-Tejas volcanic rocks challenges this assumption. Stratification by alleged liquefaction, deformation by mountain building, and deformation by the CE indicate that these pre-Tejas volcanic rocks cumulatively preceded the CE. Without a connection to a viscoelastic mantle or a means to generate magma through friction, HPT cannot account for the presence of so much early Flood volcanism prior to the CE.

HPT's inability to explain the volcanic record questions not only its liquefaction submodel but the entire paradigm. To be considered a working model for the Genesis Flood, revision of HPT is necessary to defend its tenets and accurately portray geohistory.

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7. The supercritical phase is when a fluid is "at a temperature and pressure above its critical point, where distinct liquid and gas phases do not exist". Supercritical fluid, en.wikipedia.org/wiki/Supercritical_fluid, accessed 1 January 2018.
8. For details, see "Did It Rain before the Flood? What Generated the Preflood Mist?"; in Brown, ref. 2, p. 477.
9. "After 40 days and 40 nights, the avalanche of rain (*geshem*[4] rain) stopped, because the layer of water rising on the earth reached a tipping point and suddenly poured into and suppressed the high jetting of the fountains of the great deep. [See "The Water Prevailed" on page 493.] However, high-pressure, subterranean waters continued to gush out and add to the rising floodwater. On the 150th day, floodwaters covered all preflood mountains. Then, the floodgates were closed by the hydroplates slowly settling onto the chamber floor, pinching shut the outward flowing water." Brown, ref. 2, p. 491.
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19. For instance, see Mitchell, ref. 15, pp. 92–104.
20. See table contrasting biblical chronology to that proposed by Hydroplate Theory in Brown, ref. 2, p. 490. At the climax of the Flood at day 150, Brown states: "Hours later [after Mid-Atlantic Ridge uplifted], the massive hydroplates decelerated and crashed; they were crushed, thickened, buckled, and heated in a powerful *compression event* [emphasis in original; brackets mine]."
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With over a decade of study to his credit, ***Edward Isaacs*** *is a keen student of the sciences, focusing on the geological processes of the Genesis Flood and ensuing Ice Age. As a creation researcher and educator, Edward is an ambassador of Logos Research Associates.*

Parametric design—evidence of creation

Michael Milroy

Evolutionary theory proposes that the apparent design seen in nature is the result of natural stochastic (chance-driven) selection processes. Nevertheless, mechanical engineers do not design by chance. Instead, they use parametric software, which allows them to specify constraints, relationships, and dimensions of the objects they design. This is similar to what we see in organisms, which are functionally and proportionally constrained ('symmetry'), have relational and balanced dimensions, and additional finely tuned parametric characteristics. This strongly suggests that organisms, like engineered systems, are designed for function and purpose, and did not evolve through blind natural processes.

There are two central premises to evolution:

1. According to Darwin, evolutionary changes are "formed by numerous, successive, slight modifications".[1]
2. According to Dawkins, things only appear to be designed. He said: "Biology is the study of complicated things that give the appearance of having been designed for a purpose."[2]

The first of these premises has lost credibility following Behe's books on irreducible complexity, which show the improbability of multiple complex new coordinated parts developing simultaneously in an organism.[3] For the second premise, this paper examines the shapes, symmetries, proportions, and fits of parts of organisms and concludes that these reflect indisputable design aspects that dwarf modern design methodologies. And that biological structures such as the skeleton require design capabilities that are mathematically staggering.

There is a lengthy book by Scottish mathematical biologist D'Arcy Wentworth Thompson (1860–1948), titled *On Growth and Form*. The book covers the mathematics underlying biology. The author was not a creationist, but neither was he an evolutionist. Wikipedia states "the book is weakened by Thompson's failure to understand the role of evolution and evolutionary history in shaping living structures".[4] It is no surprise that a scientist who studies biology has difficulty understanding how evolution can explain the design he sees in nature.

Parametric design, the most modern methodology

A common misperception is that the DNA in the egg and sperm determine the characteristics (phenotype) of a new organism. But zygote development is controlled not by the genome alone, but by everything that is in the zygote. So, the basis for zygote development is cellular, not genomic. "The zygote genome has no control over the laying down of its own body plan!"[5] Not only is the basis cellular, but the cellular control of the development spans two generations. "The mother thus places the germ cells for her grandchildren in a safe place within her child until it is time for them to develop!"[5]

While we have learned a lot about how embryonic development proceeds, much of how its cells do this and what the individual letters in the DNA in those cells do to define and control the 3D shape of tissues and bones is a mystery. (While development is under cellular control, the genome appears to carry most of the cells' information, so this paper will refer to the genome as the information source for organisms). The various alleles of a gene can specify different adult sizes of tissues and bones, but most aspects of the shape probably are not assigned to a gene with alleles. (It is not likely that the genes that control the shape of one's teeth would have alleles for every cranny and protrusion). This paper proposes that the 3D shape information may be held in the genome in a parametric fashion, where the DNA encodes the parameters digitally in a manner analogous to a parametric computer-aided design (CAD) program on a computer.

Modern parametric design is exemplified by the popular CAD software Solidworks™ used today by mechanical engineers. There are several aspects to parametric design:

1. The size and shape of parts (e.g. dimensions, curvature, and surface shapes) are specified by variables (parameters). Patterns of holes or protrusions can also be specified to reduce file sizes.
2. The parts are constrained to fit with other parts in a specified manner (e.g. an eyeball needs to be just slightly smaller than the socket it fits in, legs need to be the same length as other legs, a bird's upper beak must be the same length and width as the lower beak, and the two beak halves must be of comparable depth and must mate perfectly). These relations are also parameters.
3. The parts are constrained to meet design criteria that limit variations in the part itself (e.g. the left leg bone must be the mirror image of the right leg bone, beak shell thickness in the larger beaks must be adequate to crunch the

hardest seeds, and beaks need to be symmetric left and right). There are a few exceptions to the symmetric beaks, like the crossbills within the genus *Loxia*.[6] See also the problems with cross-beak chickens.[7]

Figure 1 shows a Solidworks™ model of a crude 'animal'. One dimension controls the length of all four legs. Another dimension controls the diameters of all four legs, as the rear legs are constrained to be 1.5 times the diameter of the front legs, as shown by the equation in the Modify box on the right. The left legs are constrained to be mirror-images of the right legs, both for position and size. One dimension controls the length of the head, which in turn determines the jaw length, constrained to be ⅓ of the head length. The width of the lower jaw will always match the width of the upper jaw. Just a few dimensions can control a lot of other dimensions, allowing changes to our 'animal' that maintain its viability. The software makes it easy for the engineer to make variations in the model, which explains its popularity.

Parametric design produces a compact file size, important when parts are numerous and complex, as they are in animals. It also can scale parts in size by varying a single parameter, which mimics the growth of an organism. One thing that Solidworks™ does not have is a feature to control the start of growth, rate of growth, and end of growth of parts. For example, bones start to grow in an embryo at a certain stage, then increase in size until adulthood. The rate of growth is species-dependent, slow for humans, faster for chimps, and very fast for steers (one year to maturity). Our teeth on the other hand, grow in full size (the enamel's width and length is fixed once the tooth breaks out of the gum), but are sequenced over 20 years to appear when there is room in the jaw.

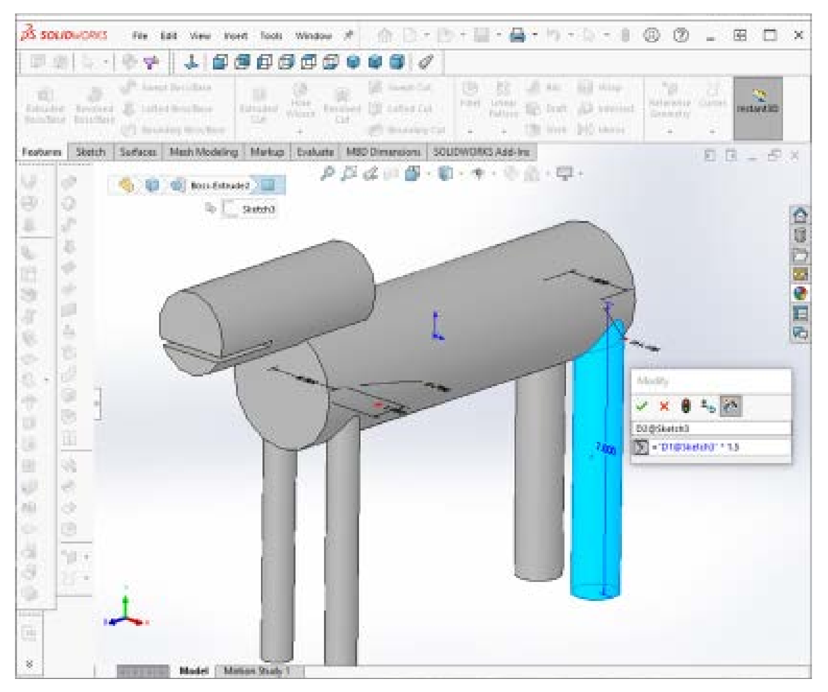

Figure 1 Solidworks™ model of an 'animal'

Alternatives to parametric design

Modelling without parametric capability

3D shapes used to be modelled by mechanical engineers on computers using non-parametric solid and surface models. As the models were input to the computers, the engineer would have to specify the size and shape of solids (composed of entities called 'primitives', such as cylinders and spheres) and surfaces (defined by entities like numerous cross-section curves) at the start, and then further changes were not possible. Design relationships within the part or relationships to other parts could not be specified. If the engineer wanted a ball and socket arrangement, the two parts were defined when they were input to the computer. The engineer would enter the dimensions as fixed values. Later, if the size of one part changed, then the mating part had to be recreated from scratch. Changes could not be made to just a few lines, as this often would affect large sections of the model. This made work for the engineer slow and frustrating. This dramatically changed when parametric modelling became available in the 1990s.

Biological systems cannot be using this non-parametric form of design data storage, as the parts cannot be grown from infancy to adulthood with fixed parameters. This also applies to embryological development. Specific cells are not predestined to become specific parts of the body. Instead, switching patterns, stressors, and chemical gradients dictate how any cell will develop in its relationship to its neighbours.

Modelling as a cloud of data points

Another model that can define 3D objects is a data-point cloud, where numerous data points are specified on the surface of the part. Triangles are typically used to join the points and create surfaces. Biological systems cannot be using this form of design storage, as copious amounts of data are required to model parts, and smooth surfaces such as ball joints are difficult to model, and (as for the solid non-parametric model), the parts cannot be grown from infancy to adulthood with fixed parameters.

Therefore, in an analogical fashion to parametric design modelling, this paper proposes that the 3D shape information is held in the genome in a parametric fashion.

Evidence for the parametric design nature of the genome's data storage

Size variations over time and in related species or breeds

While much of the parameter storage in the genome is still a mystery, in many cases alleles have been identified that specify particular characteristics, like leg length, beak length and depth, fur length, skin colour, etc.[8] We have been designed (not by chance) so that large-scale variations like skin colour among a kind or species are controlled by just a small number of genes. This in itself is evidence of design. But the proof of design is most obvious by considering the way that size varies between species or breeds, and also over time as an organism grows. Design is also evident in the way that part constraints and relationships are maintained when variations occur between species or breeds, and as the organism grows.

Finch beak variations in related species and over time

Consider beaks in the various Galápagos finch species. Originally, these finches all descended from a pair of finches that came off the Ark. The Galápagos finches produced—and they are still able to do so—new beak sizes and shapes in just a few generations under the control of either genes and/or epigenetics. Epigenetics is a recent discovery which does not require changes in the genome (hence mutations are irrelevant), yet allows traits to be passed on.[9] Beak shape is also under the control of a gene,[10] and its shape changes in ways that show pre-engineered design variation in the genome.[11] However, in this paper, the evidence for design is shown not in genetics, but by showing that chance cannot be responsible for the changes.

Figure 2 shows some of the Galápagos finches. Design is evident because there were *no evolutionary missteps.* That is, no exception to the following was ever observed: in every generation, all the upper and lower beaks, whatever their size and shape, still matched each other. If the upper beak was extra deep, so was the lower beak. If the upper beak was wide, so was the lower beak. The curves of the beaks where they met each other remained the same, while the upper profile of the upper beak changed, as did the lower profile of the lower beak. The lengths of the two halves always matched, and the beak's left/right symmetry was maintained. As the birds grew from infancy to adulthood, the growth of the two halves was consistently matched. Did this happen by evolution? Not a chance (pun intended). If evolutionists wish to contest this, they must explain how the parametric design in the genome arose from nothing, from when its ancestor supposedly had no beak.

Design evidence from another beak

Figure 3 shows the beautiful, curved beak of the adult pied avocet, along with the stubbier beak of a pied avocet chick. Note the variable curve of the adult's bill, and the precise fit between the upper and lower beak halves. The width and depth of the two halves match beautifully. Likely dozens of parameters would have to be precisely matched to create this bill. The parameters must also be matched while the beak grows and changes shape rather markedly, an impossible task for evolution working by chance mutations. No transitional fossils exist that show this problem with beak development. In fact, no intermediate fossils exist! This is the well-known punctuated equilibrium problem, which is the mystery of the missing transitional forms throughout the fossil record.[12]

Human teeth

Human teeth require a huge number of parameters to define their topology and growth sequence. As babies, we grow 20 primary teeth in a sequence as our jaws grow. As with all other animals, our teeth are symmetrical on the left and right side, and are specialized for use (incisors, canine, and molars). The teeth 'magically' appear as space becomes available for them. They all grow to the same length, and

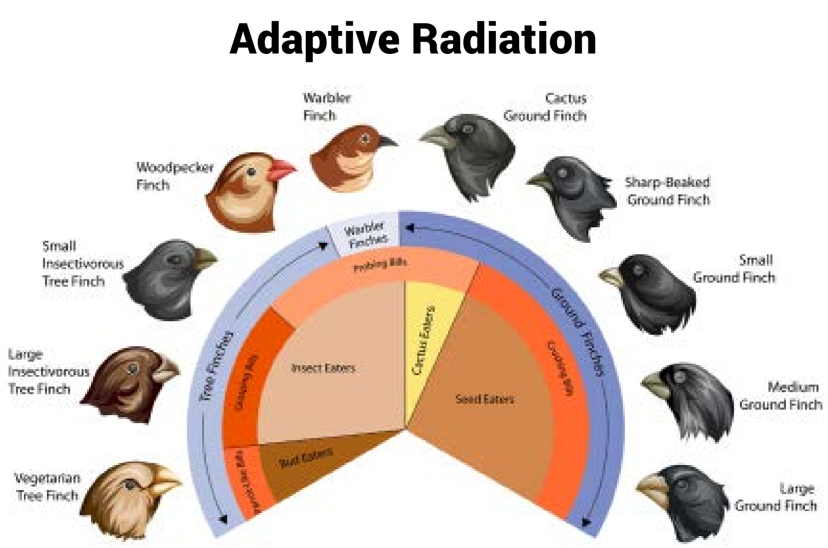

Figure 2. Adaptive radiation of Galápagos finches

Figure 3. Pied avocet adult and chick showing mature and immature beaks

mate nicely with the opposing teeth (this is a generalization; some of us need braces, perhaps because of mutations in our genome, a result of Adam's sin). This all seems very obvious, because that is what we usually see. But evolution says that the processes guiding this development originally came about by selection acting on chance mutations. How is it that most animals exhibit these common characteristics (teeth fitting jaws and mating with opposing teeth)? Where are the fossils of all the animals with deformed teeth that evolution was trying to fix? (Actually, there are numerous exceptions which make things even *more* difficult for evolution, like the elephant having just four molars that are replaced six times over the elephant's life by new ones that slide in from the rear).[13]

As we continue to grow, 32 permanent teeth appear in a sequence as space becomes available. These teeth probably utilize a different biological program from the primary teeth, as there are a different number of teeth, and the timing is different. The permanent teeth are shown in figure 4. As with our primary teeth, the adult teeth are specialized for use (incisors, canines, premolars, and molars). The fit between the teeth is precise, usually just enough to slide a piece of floss between. How do the teeth know to grow to just the right size? How do the upper teeth line up so neatly with the lower teeth? If each tooth required 22 parameters (a very conservative guess) to define its position, shape, and size (along with an appropriate number of roots), then for our 20 primary teeth and 32 permanent teeth we'd need (20 + 32) x 22 = 1,144 parameters; a big number to have found by chance and selection. But that does not include the complication of choosing the precise time at which to grow the teeth! Incidentally, chimpanzees have 32 permanent teeth, too, but the timing and the shapes are completely different than in humans.[14] So the number of parameters evolution must find is unchanged.

Other evidences of design

Inter-related fit of parts is evidence of design.

In evolution, there is no way that one part knows what size the mating part is. For example, eyeballs exactly fit sockets. (One might argue that the eyeball just grows until the socket is filled, but what about the bug-out eyes of animals like the tarsier?) In the skeleton, ball and socket joints exactly fit each other. In the skull, foramina (holes) neatly fit the nerves and blood vessels that pass through them.[15] Again, these fits are maintained throughout the growth of the organism.

Mirrored parts

Homology in evolution teaches that similar bone structures in different organisms 'prove' that one developed from the other or from a common ancestor. But evolution cannot explain how a mutation that changes the shape of a bone on the left side would be matched by a change on the right side. There are no mirrors in DNA. Do not think of the mirroring as a task that a simple algorithm could do for the whole body. Skin, fingernails, muscle, tendons, bone, cartilage, and blood vessels all need to be mirrored. However, other organs like the heart and appendix must not be mirrored. Could the algorithm that mirrors the fingernails work on the tendons? Not likely.

Dog breed sizes

Researchers recognize that most of today's more than 400 breeds of domestic dogs have only arisen in the past 200 years or so as the products of artificial selection.[16] Dog breeds come in many sizes, but all four legs on a dog are the same length, illustrating a parametric constraint. As a dog grows, the legs are always right for it. If evolution was doing this by chance, the front legs might be short and the back legs long, or the left front leg might be longer than the others. Similarly for all the parts of the dog (like the skeletal balls and sockets), which always appear in a size appropriate for the dog. (It could be argued that sausage dogs have disproportionate legs, but their necks are also short, maintaining

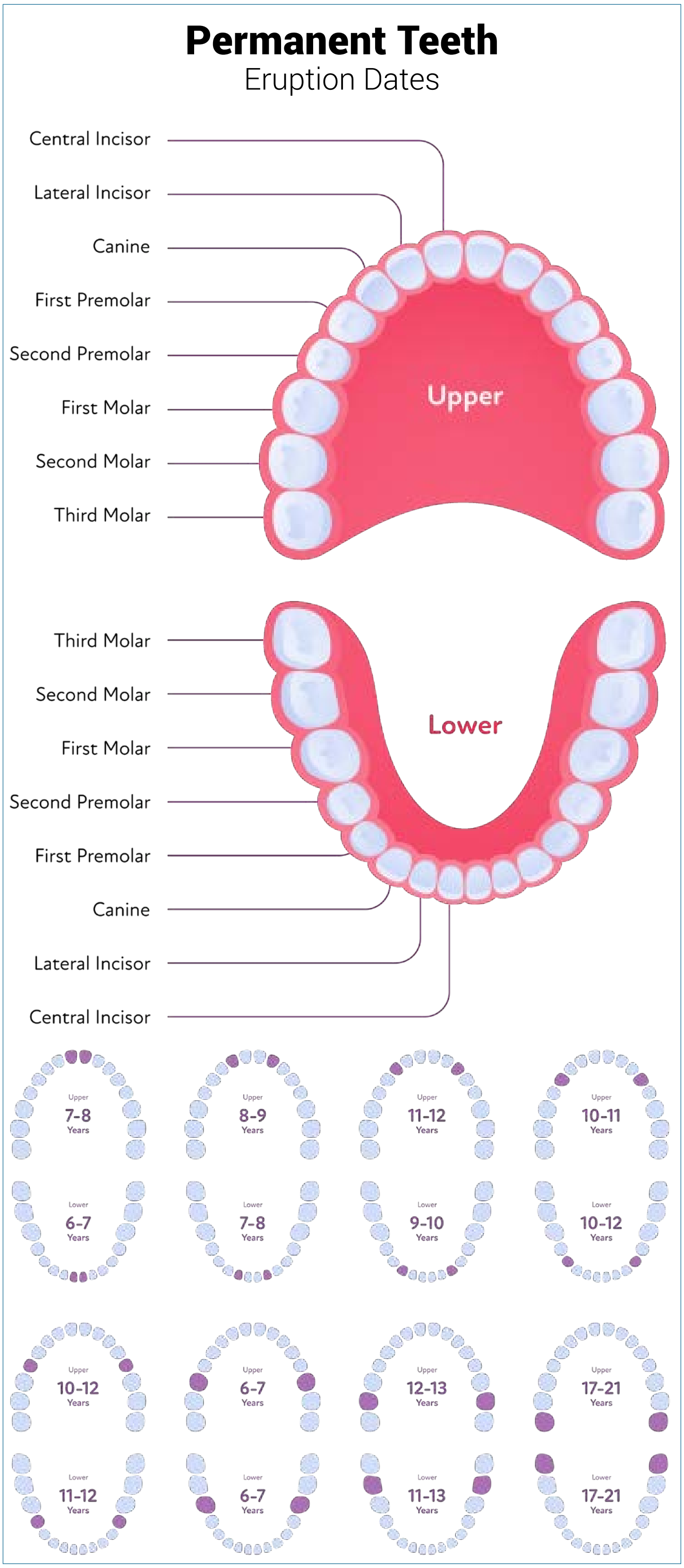

Figure 4. Type and sequence of our permanent teeth

an overall proportionate look). Colouration also comes in a huge variety, but patterns are varied, distinct, and colour-coordinated for each species (e.g. Dalmatian, white husky, golden retriever, corgi). Teeth in upper and lower jaws fit together whether jaws are wide, long, or short (for the most part, though inbreeding can produce bad hips and undershot jaws). How could evolution pack all this diversity into an original wolf-like creature if it needed to arise in stepwise function by mutations? For most of the diversity of the dog breeds to occur in 200 years, evolution would have had to be working at a fantastic rate. If it was evolution, where are all the harmful mutations, which even evolutionists admit would greatly outnumber the beneficial ones?[17]

Automatic adjustment of parameters?

Bones automatically increase in density when stressed. It is possible that the body has sensors that automatically adjust other parameters in the body. There is so much we don’t know about how bodies develop.

Parametric complexity

The term ‘parametric complexity’ for biology is coined here to describe the huge amount of data needed to specify the 4D (3D plus time) topology of an organism. The term was chosen to be similar to the term ‘irreducible complexity’, which has been so devastating to evolutionary theory. In this section, the mathematical improbability of evolution will be shown.

Consider the number of parameters needed to define the 33 vertebrae in the spine of a human. If you have seen a replica of the spine you were probably fascinated by the way each vertebra interlocked with its neighbour, permitting some rotation and bending while ensuring that excess movement is limited and the spinal cord is protected.[18] Figure 5 shows a human spine and a detailed view of one of the lumbar vertebrae. The interlocking mechanism in the vertebra is hard to figure out from the picture, but it is obviously precise and intricate. It would not be easy to create a parametric model of this in a CAD program like Solidworks™, because of the complexity of the shape. Every facet, bump, and curve requires additional parameters to define it. As the part cannot be constructed with simple geometric solids like cylinders and extruded shapes, the part model would have to be modelled

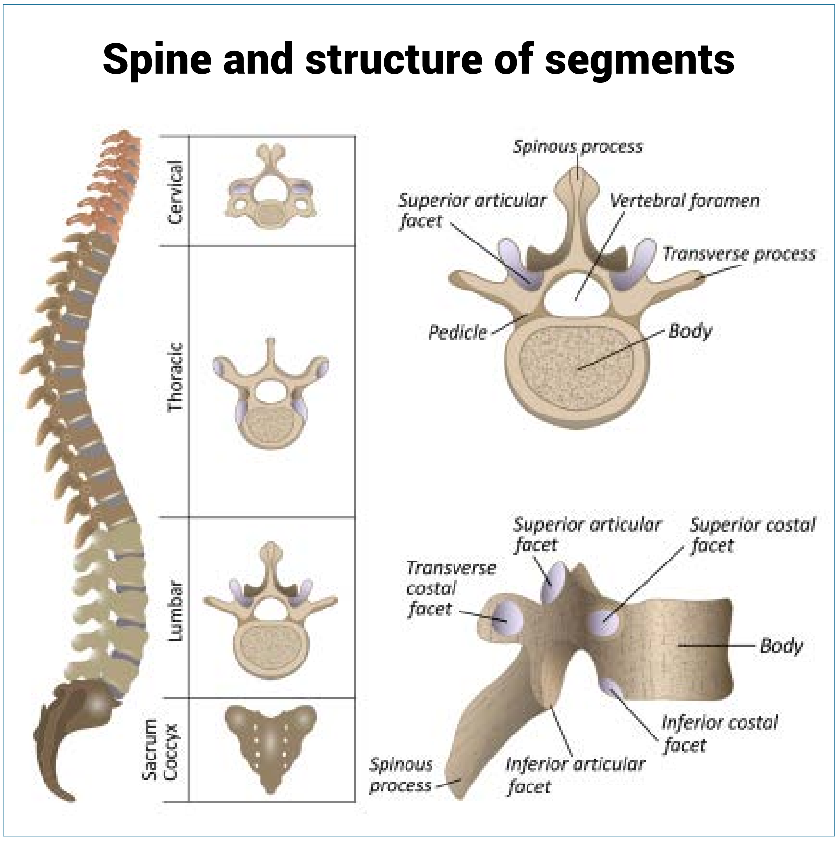

Figure 5. Human spine, showing detail of a lumbar vertebra

using surfaces, which could be as simple as triangles covering the part. There are three parameters required to specify each triangle (one x, y, and z coordinate for a corner of each triangle, typically only one corner needs to be defined). It would take at least 30 triangles (90 parameters) to make a very crude approximation of the left half of a vertebra, plus 1 parameter to specify that the part is mirrored. To be ultra-conservative, let's assume that the shape could be specified in the genome with 50 parameters.

For the spine to evolve, evolution must find 50 parameters for each of 33 distinctly different vertebrae. This is 50 x 33 = 1,650 parameters that must be found by chance. But if the spine is evolving from a chimp-like ancestor we will already have many of these parameters correct, so assume that just 20% of the parameters must be adjusted, giving 1,650 x 20% = 330 parameters.

So, could this be done by 330 beneficial mutations? Not even close! Each parameter is not just a binary digit like a 0 or a 1. If it was in Solidworks™, it would be a floating-point number, requiring four bytes for a single precision float. Let's be conservative and say that we must find a parameter that is within one of a possible 256 values, which can be specified with eight bits. Then it would require 330 x 8 = 2,640 mutations to respecify the spine. (Actually, each base pair in the genome can take on one of four values, twice what a binary bit can, but then it would require more 'luck' to find the correct base pair value).

Is defining the spine as simple as getting 2,640 beneficial mutations? Again, this understates the problem. The places where the mutations are required are buried in a mass of other base pairs that make up the hugely complex genome. As was stated before, most of the genome's function is a mystery.

If an incorrect parameter is found during evolution's trial and error search (which will happen more than 999 times out of a 1,000 since beneficial mutations are rare), the organism must be selected against (by death) and a new parameter tried. If we gave evolution a huge concession and said that there was a 100% chance that a valid mutation would occur every time natural selection went to work, and magically fix itself in the entire population instantly, it would still take 2,640 generations to evolve the spine, or about 52,000 years if a generation is 20 years.

If we consider Haldane's Ratchet,[19] which showed that the deleterious mutations (which are more numerous than the beneficial ones) multiply and fix in the population faster than the beneficial mutations, then evolution has a hopeless task. And the spine is just a small part of our body. If we are evolving from a chimp-like ancestor, we also need a lot of time to evolve our teeth (as shown already), then there is our bigger brain, our lack of hair, our hands with a larger thumb,[20] our arched feet,[21] and the list goes on. Evolution has a lot of work to do, and it has no time to make mistakes. As Haldane's Ratchet shows, the mistakes destroy the human race faster than natural selection can improve it.

But there is yet more to the mathematical improbability! The parameters must be scaled in size over the growth of the organism, from infancy to adulthood, and this scaling must be correctly timed. Each vertebra must maintain its interlocking relationship as the spine grows. This makes the evolutionary story even more implausible.

With parametric design, mechanical engineers make designs that are not nearly as complex as the human body. When a new feature needs to be added to the model, many times the parametric relationships to existing parts are lost. These relationships have to be deleted and new relationships created. How could evolution delete and create new relationships each time a new feature arose?

The purpose of this paper was not to show that the genome stores its topology information in parametric form, only that there are similarities. Nor was its purpose to show that a human spine is quite different from a chimp's (it is!). This paper was written to show that the evidence of design in the genome is stunning. We have *no idea* how the genome is able to specify complex interconnected shapes that maintain their relationships from infancy to adulthood. One thing is certain, evolution's explanation of chance mutations with natural selection is not an explanation.

Conclusion

The genome specifies 3D topology in a manner something like a parametric design system, contrary to evolutionists' assertions that design is not involved. This is demonstrated by the variations in finch beaks and dog breeds, which always change in ways that preserve the organism's ability to function. This is not something explained easily as having arisen by evolutionary chance mutations, which would frequently produce deformities, not functional organisms. The concept of 'parametric complexity' was introduced, which shows the huge number of parameters that must be precisely specified over the growth of an organism. Clearly, the genome shows evidence of design by God, of whom it is said: "Do you not know? Have you not heard? The Lord is the everlasting God, the Creator of the ends of the earth. He will not grow tired or weary, and his understanding no one can fathom" Isaiah 40:28 (NIV).

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Can ligating homochiral polypeptides explain the origin of homochiral biomolecules?

Royal Truman

In a series of papers, the α-helical coiled coil protein folding motif was generated by ligating 15- and 17-residue peptide fragments. This formed a 32-residue template able to mould additional fragments of the same chirality autocatalytically. Autocatalysis in a racemic mixture of fragments generated almost only all D or all L 32-residue peptides. It has been claimed that this may explain the origin of homochiral biomolecules. However, providing a steady supply of large already homochiral fragments having the necessary primary sequences to the carefully designed system will not occur naturally. Furthermore, the system only works because the end of one of the two fragments was first chemically activated to a thiobenzyl ester.

A distinctive feature of biology is the autonomous synthesis of multiple copies of enantiomerically pure biomolecules. For over a century immense effort has been devoted world-wide to finding naturalistic mechanisms able to generate polypeptides consisting of only L-amino acids and nucleotides containing only D-sugars.

A few examples of self-replicating molecule schemes have been devised.[1–3] Most rely on hydrogen-bond donor and acceptor interactions of nucleic acid base-pairing. Since RNA is a complicated molecule, many organic chemists do not believe the enantiopure nucleotides could have been made reliably and in the huge amounts necessary in a plausible prebiotic context.[4–6] But one encounters claims in the literature that short D- or L-peptide chains favour further chain extensions leading to enantiomerically pure polymers. Professor Ghadiri at the Scripps Research Institute is the key figure associated with these experiments. He has designed a peptide-based auto-catalytic replicator based on residues of the same chirality.[4,7]

Siegel advertises a key publication by Ghadiri in *Nature* rather dramatically claiming that “Ghadiri *et al.* use a peptide system to demonstrate how ‘homochirality’, or single-handedness, may have evolved in biological molecules.”[8] He did not write that this research provided some insights or possible analogies but that this may indeed be how homochirality arose naturally.

Many others have also referred to Ghadiri’s work as significant in explaining the origin of homochiral biomolecules. Cintas wrote that “In a recent study, Ghadiri *et al.* suggest that peptides consisting exclusively of D or L amino acids will only replicate on templates of the same handedness.”[4] Statements like these lead to the impression that individual D-enantiomer amino acids or small peptides will be selectively added to peptide chains once a small homochiral template chain is available.

Ghadiri and his colleagues have candidly admitted:

> “The origin of homochirality in living systems is often attributed to the generation of enantiomeric differences in a pool of chiral prebiotic molecules, but none of the possible physiochemical processes considered can produce the significant imbalance required if homochiral biopolymers are to result from simple coupling of suitable precursor molecules.”[7]

I thoroughly agreed with this assessment. But has a breakthrough now been discovered by them after over a century of fruitless attempts?

α-helical coiled coil peptides

The experiment design of Dr Ghadiri’s work was based on a well-known protein folding motif, the α-helical coiled coil (figure 1).[9–12] In this structure two or more α-helices intertwine using non-covalent interactions.

About 10% of all biological proteins display this motif.[13] Coiled coils can have parallel or antiparallel arrangement, and they can be formed by intrachain interaction of the same subunit, or by interchain bonds between distinct polypeptide chains.[14] α-helical coiled coils range in length over two orders of magnitude. They are known to form rods, segmented ropes, barrels, funnels, sheets, spirals, and rings, using anywhere from two to more than 20 helices in parallel or antiparallel orientation.[15] The simplest version consists of an identical pair of parallel α-helical peptides that wrap around each other with a slightly left-handed superhelical twist.

A distinguishing feature of α-coiled coil peptides is the heptad repeat motif $(abcdefg)_n$. Looking down the α-coil structure reveals a series of vertically aligned amino acid residues, figure 2.

The *a* and *d* residues comprise a hydrophobic core surface between the complementary α-coils, forming a knobs-into-holes type packing.

Figure 1. The α-helical coiled coil motif consists of two or more intertwined α-helices.

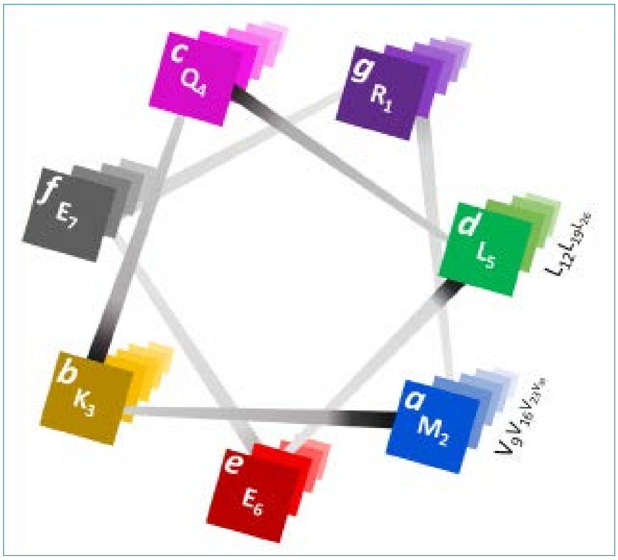

Figure 2. One member of an α-helical coiled coil dimer, which join at the *a* and *d* positions. Viewed from above, with three to four residues aligned beneath each heptamer position. Capitalized are standard 1-letter amino acid abbreviations; subscripts are their position in the primary sequence of the peptide. Figure based on work reported in reference 16.

Design of the autocatalytic peptide system

In these studies, the 32-residue templating peptide was based on the leucine-zipper domain of the yeast transcription factor GCN4.[17] The individual monomeric peptides are typically random coils in water, but form α-helices when aggregated. The researchers reasoned that if a 32-residue peptide were split into two shorter fragments these could be chemically ligated into a full-length intact peptide which could act as an organizing template for additional copies of the two shorter fragments.[17]

Ghadiri's studies used the primary sequence shown in [1] or sometimes a slight modification of it.[16]

```
Sequence: RMKQLEEKVYELLSKVACLEYEVARLKKLVGE[1]
Heptad:   gabcdefgabcdefgabcdefgabcdefgabc
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The sequence [1] differs from GCN4 in six residues. Two tyrosine residues were placed to facilitate spectroscopic quantitation using HPLC-UV, and alanine and cysteine residues were placed at the ligation site on the solvent-exposed surface. An asparagine was replaced with valine (N16V) to allow autocatalysis through one- and/or two-stranded α-helical template structure(s). The ligation site was astutely designed to lie on the solvent-exposed surface of the α-helical structure to avoid interference with the hydrophobic recognition surface.[17]

The interhelical recognition surface between the two peptide replicators is dominated by both hydrophobic packing interactions and electrostatic interactions (especially between the residues E_6 and R_1).[17] The residues K_3, Q_4, and E_7 are exposed to the solvent and should be more tolerant to substitutions.[16]

One full-length α-helical monomer serves as a template to mould the shape and location of both peptide subunits.[17] Optimal placement of each peptide end which is to be ligated thus accelerates amide bond formation. One peptide is a 17-residue fragment, E, with the electrophilic end preactivated as a thiobenzyl ester (figure 3). The sulfhydryl of the cysteine is more nucleophilic at neutral pH than all other side chain moieties, ensuring that the correct reaction occurs.

The 15-residue fragment N contains an N-terminal cysteine which serves as the nucleophilic partner. The experiments were carried out in dilute neutral aqueous solutions: 100 mM 3-(N-morpholino)-propanesulphonic acid (MOPS), 2M NaCl, 1% v/v BnSH, at pH 7.5.[7,17]

Both the E and N fragments consisted entirely of homochiral amino acids. The L-enantiomer chains were labelled E^L and N^L; the D-enantiomer chains, E^D and N^D. When equimolar proportions of these four peptides were condensed by forming an amide bond, four templates (T) were generated: either homochiral (T^{LL} and T^{DD}) or heterochiral (T^{LD} and T^{DL}) (figure 4). T^{LL} and T^{DD} were generated preferentially. T^{LL} templates autocatalytically accelerated the reaction of E^L with N^L faster than the heterochiral (T^{LD} and T^{DL}) templates do.[7] As further evidence of the selective templating effect, E^L, E^D, N^L, and N^D were added to a high concentration of pure T^{LL}, which led to a high predominance of T^{LL}.

Fragment E: Ar-RMKQLEEKVYELLSKVA-COSBn
Fragment N: CLEYEVARLKKLVGE-$CONH_2$
Fragment T: RMKQLEEKVYELLSKVACLEYEVARLKKLVGE

Error correction is claimed

Experiments showed that a single residue change from D→L or from L→D can prevent self-replication, since this disrupts the perfect α-helical structure, probably causing steric interference in the residue side chains.[18] This was demonstrated as follows.[7]

Three nucleophilic peptide versions of N^L were synthesized, each having just one L-residue replaced by its enantiomer: N^L_{dLeu26}, N^L_{dArg25}, and N^L_{dCys18}. The first two 'mutants' were designed to test the effects of one residue with the wrong chirality within the informational complementary hydrophobic recognition interface (N^L_{dLeu26}) and the non-informational solvent-exposed helical surface (N^L_{dArg25}). Reaction mixtures using equimolar amounts of E^L and either of these two mutants produced only background rates of the corresponding fragment condensation products T^{LL}_{dLeu26} and T^{LL}_{dArg25}, i.e. with no autocatalytic effect.

The third 'mutant' N^{LL}_{dCys18} was expected to have a minimal effect on the stability of the developing helical fragment or on its interactions with the template. Reacting equimolar amounts of E^L and N^L_{dCys18} displayed only a small rate enhancement in the formation of product T^{LL}_{dCys18} (1.3 times over the background rate).

Unexpectedly, all three of the template mutants accelerated production of the homochiral replicator T^{LL} when 'non-mutated' E^L and N^L were combined.[7]

This was presented as an example of error correction[19] leading to reliable replication, but a better insight is that only the enantiopure E^{LL} template works properly. A more amenable finding for evolutionary purposes would have been a series of peptide sequences displaying increasing rate enhancement with ever fewer disruptive residues of the wrong chirality. That would have offered a more plausible path for chance to produce the optimal templating sequences, starting with slightly functional sequences having mixed D and L residues.

In another experiment, a very conservative chirality-conserving alteration was made. Alanine was substituted for a leucine at position 26 in the nucleophilic peptide fragment, which prevented self-replication.[17]

Another study showed that electrostatic substitutions at the solvent-exposed position could decrease the initial rate of peptide fragment condensation by more than 3 orders of magnitude.[20] This further emphasizes the limited number of acceptable alternative residues per position competent to produce α-helical coiled coils.

Autocatalytic peptide network stabilized against errors

Ghadiri and colleagues have devoted much effort attempting to show that their carefully designed system has prebiotic relevance. We are informed that

> "The peptide-based systems described are the first examples of self-organized chemical networks that display characteristics essential for evolution: sequence-selective reproduction and dynamic error correction."[19]

The authors reiterated their claim that loss of autocatalysis due to single residue replacement represents 'error correction'.[19] Two additional series of experiments were performed, involving four peptide fragments: the native electrophilic E and nucleophilic N fragments, which when ligated produce the optimized template T; and fragments E_{9A} and N_{26A} having one alanine of the same chirality replaced. Four potential templates can form:

$$E + N \rightarrow T \qquad [2]$$

$$E + N_{26A} \rightarrow T_{26A} \qquad [3]$$

$$E_{9A} + N \rightarrow T_{9A} \qquad [4]$$

$$E_{9A} + N_{26A} \rightarrow T_{9/26A} \qquad [5].$$

The results of experiments to identify catalytic and autocatalytic effects are summarized in figure 5.

The doubly modified product $T_{9/26A}$ is catalytically inactive. Mutant templates T_{26A} [3] and T_{9A} [4] do not auto-catalyze their constituent peptide fragments,[19] and the intact template T never catalyzes ligation involving a modified peptide.

Furthermore, the single-residue-modified templates T_{26A} and T_{9A} catalyze the ligation of E with N, generating additional T, which further autocatalyzes ligation of E with N.[19]

All these reactions accelerate ligation of E with N, and none of the modified peptides. The authors claim this leads to error-correcting self-organized autocatalytic cycles, which collaborate to produce the native sequence T.[19] They reference key publications by Eigen on his notions of hypercyclic networks.[21–23]

Ghadiri *et al.* discovered by accident a scheme which contradicts the 'error-correcting' effect. E with a mutant N_1 produced a replicator R_1, and E with N_2 produced R_2, which cross-catalyzed each other. By judiciously adjusting the initial concentrations of R_1 and R_2, it is possible to set up a 'hypercyclic network' where R_1 and R_2 can coexist, at least for some undetermined number of cycles.[24]

The oscillating effect in relative concentrations occurred between two 32-residue peptides merely differing at one position, but the authors refer to it as a hypercycle. In genetic systems complex subsystems of completely unrelated biomolecules are indeed linked; for example, the production of mature t-RNAs and aminoacyl-tRNAs-synthetases. A true prebiotic hypercycle must produce raw materials autocatalytically and feed these into consuming autocatalytic reactions. Nothing like that was demonstrated in this work.[24] Peptides E and N were not generated through an integrated process but were simply made available as needed by an intelligent chemist.

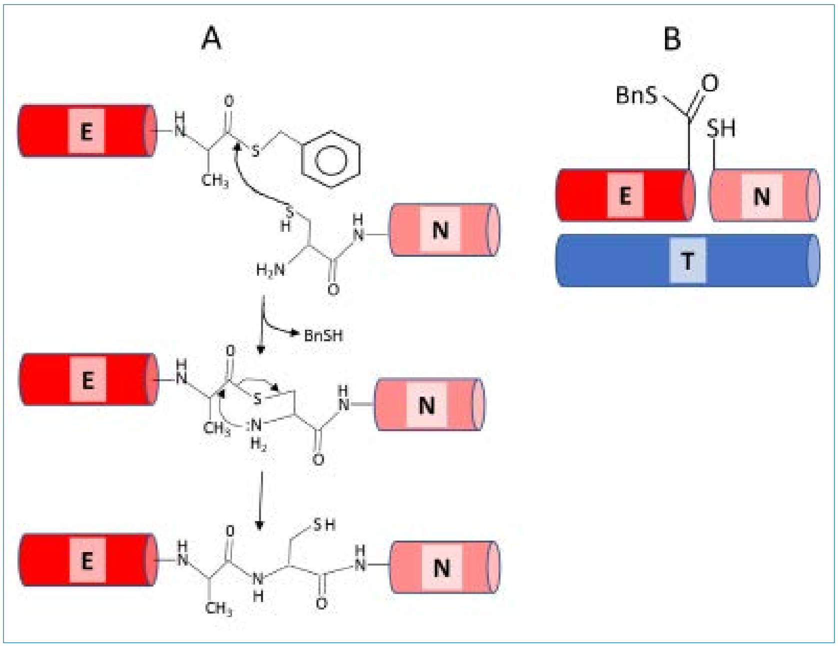

Figure 3. Ligation mechanism between the activated *C*-terminus of the electrophilic peptide fragment E and cysteine of the nucleophilic peptide fragment N (Bn means benzyl). A) Full mechanistic details. The intermediate thioester rearranges rapidly to produce the native amide bond. B) Simplified view of the ligation of E with N. Modification of figures found in reference 16.

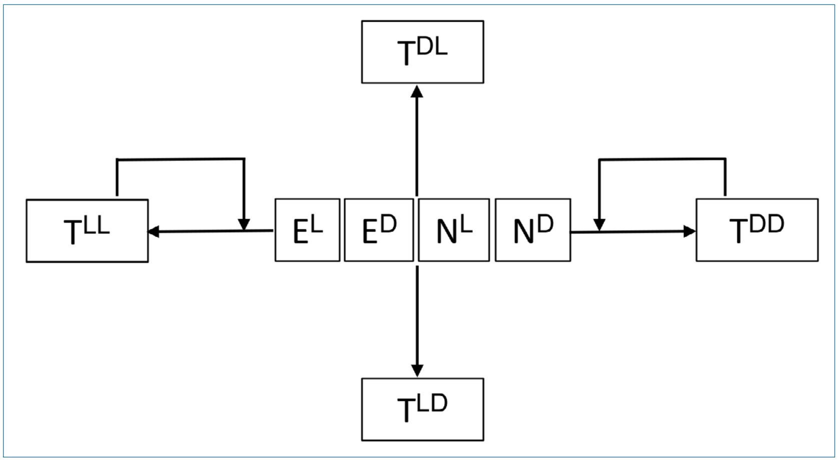

Figure 4. Condensation of enantiomerically pure L- or D-peptide fragments E with L- or D-peptide fragments N produces primarily the homochiral templating products T^{LL} or T^{DD} and very little of the mixed version T^{DL} or T^{LD}. Modification of a figure found in reference 16.

Usage of 'errors' misleading

What do Ghadiri *et al.* mean by 'errors'? Errors in biological genetic systems are clearly understood, referring to mutational defects which ultimately damage the host organism. This occurs because an important multicomponent process is damaged. But the researchers wrote, "Here we describe autocatalytic peptide networks that stabilize themselves against errors by subjugating the mutant population for the synthesis of the wild-type peptide."[19] Here 'error' simply means a modification in peptide sequence leading to slower autocatalysis. Is this correct biologically or for abiogenesis purposes? Is everything which accelerates a process, e.g. cancerous cell growth, beneficial for living systems and to be selected for?

Biological systems are all about regulation, starting and stopping enzymatically catalyzed biochemical reactions at the right time and place, generating products in the appropriate concentration range. A runaway uncontrolled process leading to a single chemical compound is the opposite of what is needed.

"Subjugating the mutant population" invokes Darwinian thinking but has no relevance to the rich variety of DNA-, RNA-, and protein-error-correcting molecular machines which are encoded on genomes. These correct specific flaws in the individual biomolecules, such as replacing mismatched nucleotides on DNA or chemically tagging a misfolded protein to be enzymatically degraded. The 'correction' claimed merely reflects faster reproduction of one sequence vs. slower ones, although there is no reason to assume that the faster one is what would be needed along a random naturalistic trajectory leading to living systems.

Autocatalysis made possible through a designed system

In a key 1997 paper, Ghadiri and colleagues emphasized the word design multiple times when discussing these experiments and never referred to evolution. When alluding to the purpose and value of their research, they state correctly that applications in the future "would first require the ability to rationally design informational self-reproducing and self-replicating molecular systems."[16]

They should have emphasized the need for intelligent conception by pointing to facts their work revealed. Only the use of enantiopure fragments and the resulting templates provided reliable peptide catalytic cycles. The findings an evolutionist would have hoped for were not obtained, namely a wide variety of functional sequence alternatives linking non-functional to ever better autocatalytic sequences.

Despite having used a highly effective templating sequence, after 170 minutes almost 15% side products were obtained.[16] If this kind of system were to arise naturally it would operate for only a few iterations and then discontinue like the other experiments based on RNA or DNA Ghadiri and his colleagues criticized.[7]

The templates did not facilitate addition of only individual D or only L amino acids, nor were the E and N sequences selected from among a vast pool of alternatives present. The homochiral E and N peptides which were made available must have been large to have molded with a specific template and would have been provided in the same molar proportion. No effort was invested to extrapolate to very dilute unstirred concentrations of E and N having a relative proportion of, for example, <1:10,000, which is very plausible given the extreme sequence specificity of the two fragments. Autocatalysis would have been insignificant and have soon consumed the less available fragment.

Likelihood of a random sequence leading to an α-helical coiled coil

In free nature a large concentration of 32-residue homochiral peptides with the correct primary sequence will not arise at the same time and location. Under plausible aqueous natural conditions, peptides 15 to 17 residues long having any specified sequence would be present in at best negligible concentrations.[25]

Suppose somehow only the 20 proteinogenic amino acids were present in only the L-enantiomer form. We will ignore the >99% other potential contaminants. Only a tiny subset of all $20^{32} \approx 4.3 \times 10^{43}$ possible sequences based on twenty proteinogenic amino acids would serve the intended templating purpose. The coiled coil dimers must pack together in a specific knobs-into-holes manner.[26] Every seventh residue must be aligned vertically along the α-coil to produce a suitable hydrophobic surface at which to dimerize, figure 2. Each turn will have approximately 3.5 residues, with the heptad positions *a* and *d* forming a hydrophobic surface on one side of the helix.[27]

As a minimal requirement the canonical seven-residue repeat must contain hydrophobic (H) apolar residues at positions *a* and *d* and polar (P) residues elsewhere, generating the pattern (H•P•P•H•P•P•P).[28] But this pattern can lead to dimeric, trimeric, or anti-parallel tetrameric conformations. The parallel, dimeric coiled coils exhibit strong preferences for specific hydrophobic amino acids at the five *a* and four *d* positions.[27] Loss of function for coiled coils has been shown to occur often even when similar hydrophobic residues are used.[29,30]

The primary sequence is very constrained, since coiled coils are stabilized by both intrachain and interchain interactions. A leucine repeat is often found at the *d* positions and a preponderance of β-branched amino acids (valine, isoleucine, or leucine) at the *a* positions since this favours dimer formation due to packing considerations.[27] Asparagine is often also found at the *a* positions, which directs dimerization by forming buried hydrogen bonds.[27]

In addition, whether hydrophobic residues will support the coil structure depends on the other hydrophobic residues they interact with on the same or the partner molecule. Sauer *et al.* found that many combinations of hydrophobic residues were nonfunctional,[31] and Ransone *et al.* reported that mutating two or more leucine residues prevented formation of the heterodimer.[30] Indeed, it has been demonstrated that disruptions to the coiled coil structure occur irrespective of whether the mutated residue lay in an inner *a*/*d*, adjacent *e*/*g*, or outer *b*/*c*/*f* position.[28]

Hodges *et al.* have demonstrated that leucine residues at the *a* and *d* positions contribute more than other hydrophobic residues tested (Ile, Val, Phe, Tyr, and Ala) to the stability of the coiled coil.[32] Replacing a single Leu by the very similar residue Ala at *a* positions decreases stabilization of the dimer on average by about 3.3 kcal/mol and 2.0 kcal/mol at *d* positions.[33] In general, mutations using less hydrophobic residues tend to be more deleterious for protein stability at more buried positions.[34–37]

Thus, not every combination of eight possible hydrophobic residues (alanine (A), valine (V), leucine (L), isoleucine (I), proline (P), phenylalanine (F), methionine (M), and tryptophan (W)) can be used at the *a* or *d* positions. For example, multiple bond-bending proline residues or bulky phenylalanines or tryptophans would prevent effective packing. Therefore, we estimate that positions *a* and *d* should have no better than about 3/20 probability per residue position of having an acceptable residue by chance in the E or N sequences.

For the non *a* and *d* heptad positions, theoretically around 5/20 of the residues might work in some positions, being polar and non-charged (serine (S), threonine (T), tyrosine (Y), asparagine (Asn), glutamine (Q)). (Chemists don't all agree on how to classify cysteine (C), and histidine (H) is polar and often charged). This is surely an overestimate, since multiple bulky side chains could interfere with packing.

Salt bridges formed by the interaction between positively (lysine, K or arginine, R) and negatively (aspartate, D or glutamate, R) charged amino acid side chains can help hold an α-loop together, but if in the wrong positions would twist the coil out of register. Interaction of residues having the same charge would destabilize the structure. Interhelical salt bridges between residues, especially at the *e* and *g* positions, may be necessary to stabilize the structure in some sequence variants.[15,38] However, at the wrong locations covalent disulfide bonds could hinder forming the coiled structured by affecting how the side chains interact. Similar considerations apply to histidine, tyrosine, phenylalanine and tryptophan, which can form weak hydrogen bonds.

Formation of a covalent disulfide bond between two cysteine residues can ensure or hinder that the two α-helices

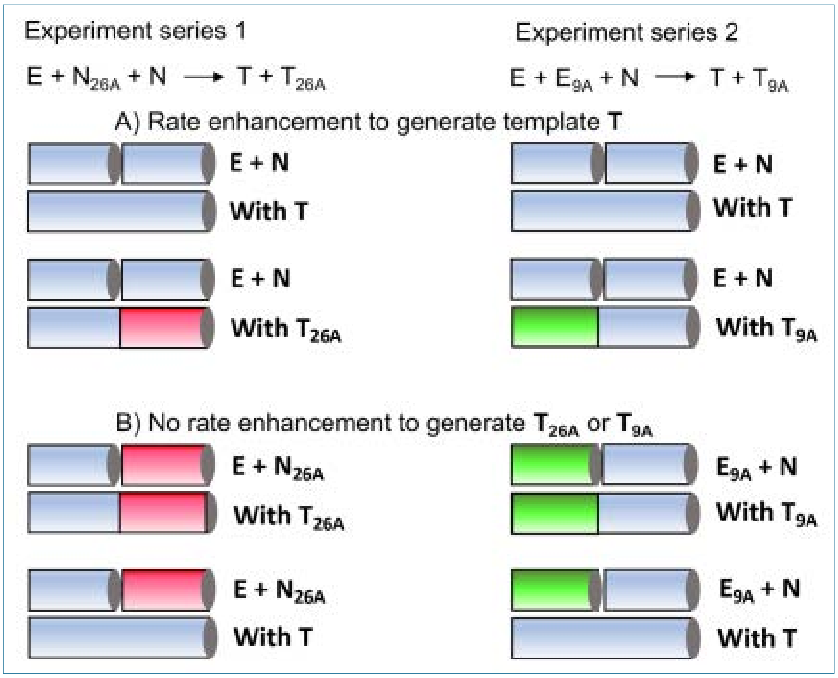

Figure 5. Catalytic effects of template variants. The optimized sequence is shown in blue, variants in other colours. See main text for discussion. Modification of a figure found in reference 19.

are in a parallel and in-register alignment to produce the coiled-coil structure. The amount of stabilization of protein structure contributed by a disulfide bond is around 1 kcal/mol but, depending on distance and angle, can be higher.[39]

Summary of the hurdles to produce the system naturally

1. Only a miniscule number of linear peptides large enough to produce this autocatalytic system would have existed in water, with two having to be exactly 15 and 17 residues long.[25] Call the number of candidate peptides with suitable length r_{15} and r_{17}.
2. r_{15} and r_{17} must consist of only L-residues ($p = ½$) and have suitable primary sequences ($p \approx ¼$). The joint probabilities would be roughly $(½ \times ¼)^{15}$ and $\sim (½ \times ¼)^{17}$, respectively. A template cannot form unless both fragments exist. This demands that $r_{15} > 1 / (⅛)^{15} \approx 3.5 \times 10^{13}$ and $r_{17} > 1/ (⅛)^{17} \approx 2.3 \times 10^{15}$ copies of peptides of correct lengths must be formed.

   Under plausible prebiotic scenarios this seems unlikely. But including the next constraint removes all doubt.
3. The electrophilic end of the r_{17} must be preactivated, for example as a thiobenzyl ester, but not the other peptides, which could react with the N fragment. The probability is for all practical purposes zero.

Constraint (2) does not consider the relative proportions of amino acids present when proposing a factor of ¼ (i.e. 5⁄20) per residue position, but seems reasonable. Valine and leucine would have indeed been more plentiful, facilitating formation of the hydrophobic surface. However, they would then also be more likely to be found at positions where hydrophobic residues are not desired. The most plentiful amino acid claimed to be formed by natural processes, glycine, is rarely used by an α-helical coiled coil. And non-proteinogenic α, β, γ, δ, and ε amino acids can also form naturally and are delivered to Earth by meteorites; so far more than 20 alternatives would compete at each residue position. We also neglected side chain reactions involving their amino and carboxylic acid groups, intramolecular ring formation, and all oxidation and other possible destructive reactions.

It is true that the templating effect produces more T^{LL} and T^{DD} than T^{DL} and T^{LD}, and perhaps sufficient enantiopure E and N variants had been generated. Suppose all the amino acids used at each position had an L/D abiotic ratio of 1/0.55, an absurd assumption. Then only 1 out of 7,844 of the N would be enantiopure ($1/0.55^{15}$), and 1 out of 25,931 of the E sequences ($1/0.55^{17}$). The more numerous activated 'wrong' E would still react together, with or without partial templating enhancement.

Suppose, hypothetically, that one template (T) appeared somewhere during tens of millions of years despite factors (1) – (3). Now an additional pristine E and N fragment must not only overcome these overwhelming constraints, but this time in addition must do so right next to T before it degrades. A flood of interfering racemic peptides with incorrect sequences of various lengths, not just fifteen and seventeen long, would surround these new correct E and N peptides. Furthermore, isolated single-stranded helices like T are unstable in aqueous solutions.[40,41] Therefore, very little time would be available before T, E, and N would both hydrolyze and racemize.

Expecting this first T to autocatalyze a copy of itself is unrealistic. But to be relevant for origin-of-life purposes, this would have to occur countless times at the exact same location!

Significance for extant life

Variants of the 32-residue sequence do exist within some biological proteins, encoded for on DNA. The researchers made no attempt, however, to explain how their peptide autocatalytic system could have converted into a genetic system, with the α-helical coiled coil motif now found in many proteins with unrelated primary sequences.

The fascinating experiments were inspired by existing biological protein structures so cleverly designed that no one would have thought up the autocatalytic scheme without them. But ligation of E with N only occurs thanks to first converting to a highly reactive thiobenzyl ester, so the autocatalysis could *not* have arisen naturally. Templating merely accelerates the process by optimally moulding the reactants together. Essentially the authors demonstrated that if optically pure E and N were mixed with no contaminants present, properly activated in a laboratory, a chemical bond would form. Nothing resembling a solution to the origin of homochirality in a genetic system has been demonstrated.

The researchers did demonstrate that L- or D-only residue sequences interact more effectively with a peptide template of the same chirality, an unsurprising result, but the peptides were already homochiral. The unstated implication is that obtaining homochiral peptides E and N would be more likely than a full homochiral 32-residue peptide by chance. But E and N must be present at the exact same location concurrently, and only the homochiral version of E must be preactivated.

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Does paleontology nullify geological arguments for the location of the Flood/post-Flood boundary? Setting the record straight

Michael J. Oard

The location of the Flood/post-Flood boundary is a key component of a sophisticated Flood model. One proposal is for a late Cenozoic boundary. Others challenge that position by pointing out that numerous genera cross various late Cenozoic stratigraphic boundaries, implying that such paleontological successions preclude a late Cenozoic boundary. Before addressing their arguments, an ongoing misinterpretation of my position is explained.

After decades of research in Flood geology, the location of the post-Flood boundary still remains controversial. The impasse is largely between advocates of a Cretaceous-Paleogene (K-Pg) boundary, who rely primarily on paleontology, and advocates of a late Cenozoic boundary, based on a broader range of geological criteria. Arment[1] and Ross[2] have argued that a late Cenozoic boundary is implausible because it requires representative baramins of mammals to have made a round trip, migrating first to the Ark, then back to the same locations, in order to create the fossil successions observed today. Ross has further argued that the highest biostratigraphic 'break' in the fossil record corresponds to the K-Pg boundary.

If a pre-Flood supercontinent, like Rodinia, is assumed, 'post-Flood' North American mammals would have had to have left from the location of the star in figure 1a and walked to the Ark. Ross puts the Ark, with a question mark, in the Middle East (figure 1b), but we do not know where the Ark was built. Ross argues that after the Flood these same mammals would have had to travel east across the Bering Land Bridge to return to North America (figure 1c). Similarly, Arment describes Australian marsupials travelling to the Ark, only to return after the Flood.[1]

Before delving into the specifics of their fossil mammal arguments, a few issues need clarification. First, critics seem to have misunderstood my position on the Flood/post-Flood boundary and my use of the geological column. Second, they also seem to ignore the plethora of geological arguments that indicate the boundary is in the late Cenozoic. They have two straw man arguments: (1) that mammals lived before the Flood, where their Cenozoic fossils are found and (2) the mammals had to migrate from their fossil locations to the Ark.

Misunderstanding the late Cenozoic boundary

Arguments against the late Cenozoic boundary fail to understand that position. The source of this apparent blind spot is possibly a rigid commitment to uniformitarian stratigraphy, rather than a Flood-based one, such as Walker's.[3] Ross assumes the late Cenozoic boundary is universal at or near the Pliocene/Pleistocene boundary, or, in paleontological terms, the Blancan/Irvingtonian NALMA stage.[2] Arment better represents it by covering a range of possibilities: (1) the Oligocene/Miocene, (2) the Miocene/Pliocene, and (3) the Pliocene/Pleistocene. However, he resorts to Ross's straw man argument at times, assuming 'late Cenozoic' is the same as Plio/Pleistocene. In both cases, the misunderstanding probably rests on an absolute adherence to uniformitarian chronostratigraphy.

My position has been clear for many years.[4] Uniformitarian stratigraphy approximates a Flood column, no more. I reject the strict global synchroneity of the geologic column. Thus, a 'late Cenozoic' boundary may be in the Miocene, Pliocene, or Quaternary, *depending on the location*. That is why I proposed a wide range of *field* criteria to define it. Clarey's position is that the boundary is in the late Cenozoic but mostly close to the Pliocene/Pleistocene boundary of the geological column.[5] Snelling noted: "On the basis that a global flood has occurred, there can be no assuming whatever that the fossil-bearing strata must be dated according to the uniformitarian scheme."[6] That is why I emphasize local, broad, empirical criteria. 'Late Cenozoic' is only a loose and convenient approximation.

Ignoring the geological criteria

Ross,[2] Arment,[1] Whitmore,[7] and others fail to appreciate the power of a boundary built from a wide range of empirical

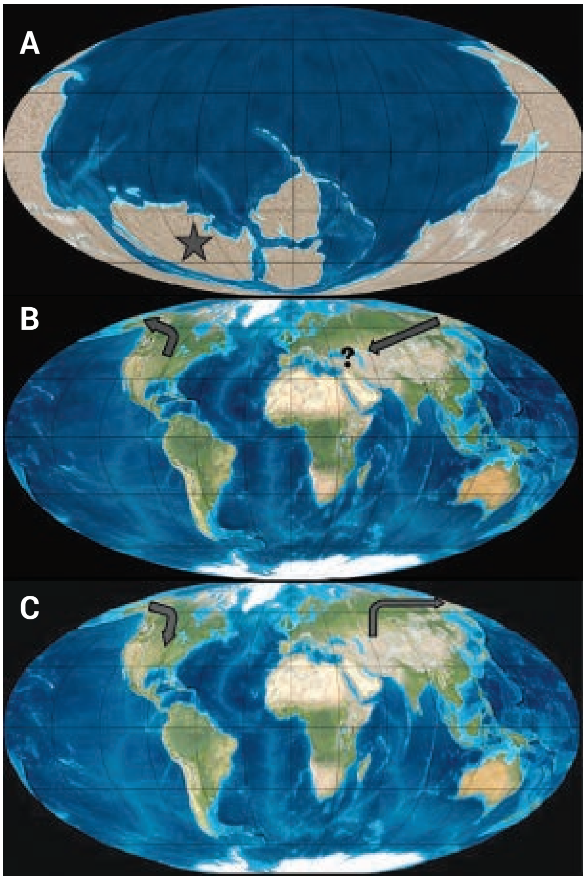

Figure 1. Illustration of the animal ‘round trip’ argument. Continental configurations for: A. Rodinian-like supercontinent with a star for the location of North America, B. near-modern configuration with arrows depicting potential migration path out of North America to an unknown pre-Flood Ark location, and C. modern with arrows depicting required post-Flood migration path to North America (from Ross[2]).

evidence. Ross[5] amplified his paleontological argument and dismissed the numerous other geological criteria as “a set of disparate observations”.[8] Arment ignored the powerful argument from Cenozoic coal:

> “Regarding Oard’s hand waving with Miocene coal, I can only reiterate that the method I am proposing applies to specific fossil beds and may not be suitable for broad stratigraphic brush strokes. So unless Oard finds a coal seam with an imbedded *Lampropeltis* [snake], I don’t see a problem.”[9]

The geological arguments

Specialist arguments are valuable for their depth but can be misleading because they cannot account for contrary data. Something as significant as the post-Flood boundary must satisfy many specialties; this is the basis for a range of geological arguments. My 33 evidences[10] (table 1) cover a wide range from different fields of the earth sciences,[11] which have been amplified in the *Journal of Creation*.[12–16] These have been applied to the Yellowstone super volcanic eruptions,[17,18] the mammals in the High Plains sediments,[21] formations along the Arctic coast of Canada and Alaska,[19] and the Ashfall Fossil Beds State Historic Park in northeast Nebraska.[20]

Clarey reinforced these and added at least two more.[9,21,22] First, the massive early Cenozoic (Paleocene) Whopper Sand is thick and widespread in the Gulf of Mexico, indicating deposition involving powerful, wide currents, interpreted as the onset of the receding phase of the Flood. How can post-Flood catastrophes deposit this sand in the deep Gulf of Mexico? Second, the traditional landing site for the Ark, Turkey, is surrounded by vertically continuous uninterrupted Cenozoic marine strata from the Cretaceous level to the top of the Miocene and even Pliocene in places. How could the animals and humans have exited the Ark if it was still completely surrounded by water?

Saving the K-Pg boundary thesis requires addressing all these lines of evidence. Moreover, a broad range of evidence is usually superior because any one line can be misleading without appropriate context. For example, it is generally true that Ice Age fossils are not permineralized, while Flood fossils often are (number 8 in table 1). But there are exceptions, such as the many discoveries of original dinosaur proteins and tissues from the Flood. Ross and Arment need to address the entire range of evidence, not simply paleontological boundaries.

Whitmore and Garner do address much of the geological evidence (figure 2).[23] However, many deposits of unparalleled extent (number 2), global and regional unconformities (number 3), and others are continued after the Flood. Their K-Pg boundary position requires extremely large and energetic post-Flood catastrophes and fails to show how table 1 criteria, such as thick, widespread coal, could have formed after the Flood.

Persuasive geological criteria

Global deposits of Cenozoic coal are powerful evidence. Advocates of the K-Pg boundary must explain them, including the 60-m-thick seams of nearly pure, sub-bituminous coal in the Paleocene and Eocene of the Powder River Basin of northeast Wyoming and southeast Montana.[24] Some of these coal seams cover large parts of the basin, which extends approximately 190 km east–west and 320 km north–south (figure 3). The thick Smith/Big George seam covers an area of about 120 km north–south and about 65 km east–west.[25]

There are also thick coal seams in the Miocene, such as the Latrobe coal in southeast Australia.[13] Current theories of coal formation require that it be buried under thousands of metres of sediment. If true, and if bituminous and anthracite coal is now at the surface, like in several seams in the powder River and Appalachian Basins, it implies not only deep burial, but *the subsequent erosion of all that sediment*. How could these be from post-Flood catastrophes?

Another persuasive geological argument is the existence of Cenozoic salt deposits. The very late Miocene Messinian salt deposits beneath the Mediterranean Sea cover about one million km^2 and average 1 km thick. These, in turn, are covered by about 1 km of Pliocene and Quaternary sediments. Both the chemical sediments and the overlying sediments are difficult to explain absent the Flood.

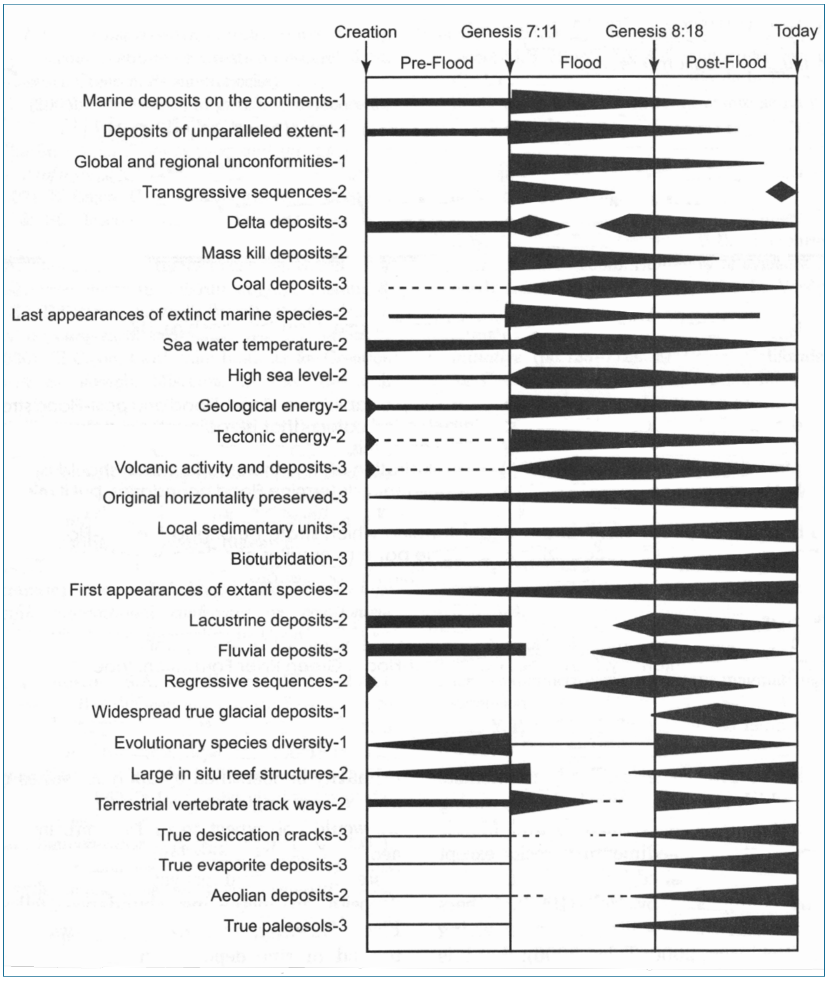

Figure 2. Whitmore and Garner's pre-Flood, Flood, and post-Flood criteria.[27] The importance of each criterion is shown by the thickness of the horizontal line during the time period. The number following each criterion is a ranking of the importance within a Flood model (1 being the most important).

Why use the geological column?

Part of the boundary disagreement lies on how the uniformitarian geologic column is viewed. Many Flood geologists, including the K-Pg boundary advocates, use its global chronostratigraphic (relative age) column as mostly absolute. They see it as a history of burial of organisms in the Flood and post-Flood period.[26] Even many who agree with a late Cenozoic boundary make this assertion.[27] Whitmore lumped me in with some others when he claimed that I did not believe in the geological column: "Some creationists have denied the reality of the geological column (Oard 2010a, 2010b; Reed and Froede 2003; Woodmorappe 1981)."[28]

Whitmore may be correct regarding the others, though a more thorough explanation of that position is available,[29–33] but seems to misunderstand my published position. I have long held to a *general* order of the fossils and strata corresponding to the geological column, but question its precise *global* synchronicity.[34,35] The rock record is highly nonlinear, with great deposition during the first 150 days of the Flood, followed by great erosion after Day 150.

Reconciling the Flood with the uniformitarian template, I have concluded that the Cenozoic is highly diachronous.[36,36] In other words, some Cenozoic rocks formed as the Flood rose, some formed as the Flood receded, and some may have formed after the Flood. For instance, the Cenozoic in the Rocky Mountain valleys and High Plains of the United States likely represents deposition during Walker's Inundatory Stage, because of the massive erosion of the top of the valley fill (table 1, number 20 and table 2) and tracks of mammals.[37] However, most of the Cenozoic continental shelf deposition occurred during the Recessional Stage. These sediments are primarily dated by microorganisms, not the mammals of the Rocky Mountain valleys.

Oceanic sediments have not yet been analyzed in any depth by creation scientists, but since secular scientists find ice rafted debris (IRD) in early Cenozoic strata around Antarctica,[38,39] they hence dated the Antarctica Ice Sheet as developing in the early Cenozoic. This ice sheet is from the post-flood Ice Age.[40] If the IRD are truly ice rafted, then it is likely that at least some 'early and late Cenozoic' sediments on the ocean bottom are post-Flood. If so, the Cenozoic cooling curve for the oceans could be post-Flood.[41]

Table 1. Summary of evidences for a late Cenozoic boundary. The strength rating refers to the end-Cretaceous difficulty in reconciling these datasets.

Sedimentary rock evidences	**Strength**
1. Huge volume of Cenozoic sedimentary rocks	Strong
2. Thin, widespread Cenozoic sedimentary layers	Moderate
3. Consolidated Cenozoic sedimentary rocks	Moderate
4. Deposition of widespread or thick Cenozoic 'evaporites'	Strong
5. Cenozoic phosphorites	Weak
6. Formation of Cenozoic carbonates	Moderate
7. Tremendous Cenozoic continental margin rocks	Strong
Organic evidences	
8. Cenozoic mineralized fossils	Moderate
9. Thick, pure Cenozoic coal seams	Strong
10. Cenozoic amber	Strong
11. Oil and natural gas formed during the Cenozoic	Moderate
12. Large, pure microorganism skeletal layers during the Cenozoic	Moderate
13. Lack of mammals buried in the Flood but millions afterwards	Strong
14. Cenozoic fossil order and massive, numerous extinctions	Moderate
Tectonic evidences	
15. Huge Cenozoic vertical tectonics	Strong
16. Tremendous horizontal plate movement during the Cenozoic	Moderate
17. Cenozoic ophiolites	Moderate
18. Cenozoic metamorphic core complexes	Weak
19. Cenozoic ultrahigh-pressure minerals	Moderate
Geomorphological evidences	
20. Huge Cenozoic erosion of the continents	Strong
21. Erosional escarpments formed during the Cenozoic	Moderate
22. Tall erosional remnants, like Devils Tower	Strong
23. Widespread Cenozoic planation surfaces	Strong
24. Long-distance, transport of hard rocks during the Cenozoic	Strong
25. Cenozoic deep valleys	Strong
26. Cenozoic pediments	Moderate
27. Cenozoic water and wind gaps	Strong
28. Cenozoic submarine canyons	Moderate
Climatic evidences	
29. Cenozoic mid- and high-latitude warm climate fossils	Strong
30. Cenozoic volcanic winter	Strong
31. Cenozoic meteorite or comet impacts	Weak
Miscellaneous evidences	
32. Cenozoic accelerated radiometric decay	Strong
33. Cenozoic Middle East geology	Strong

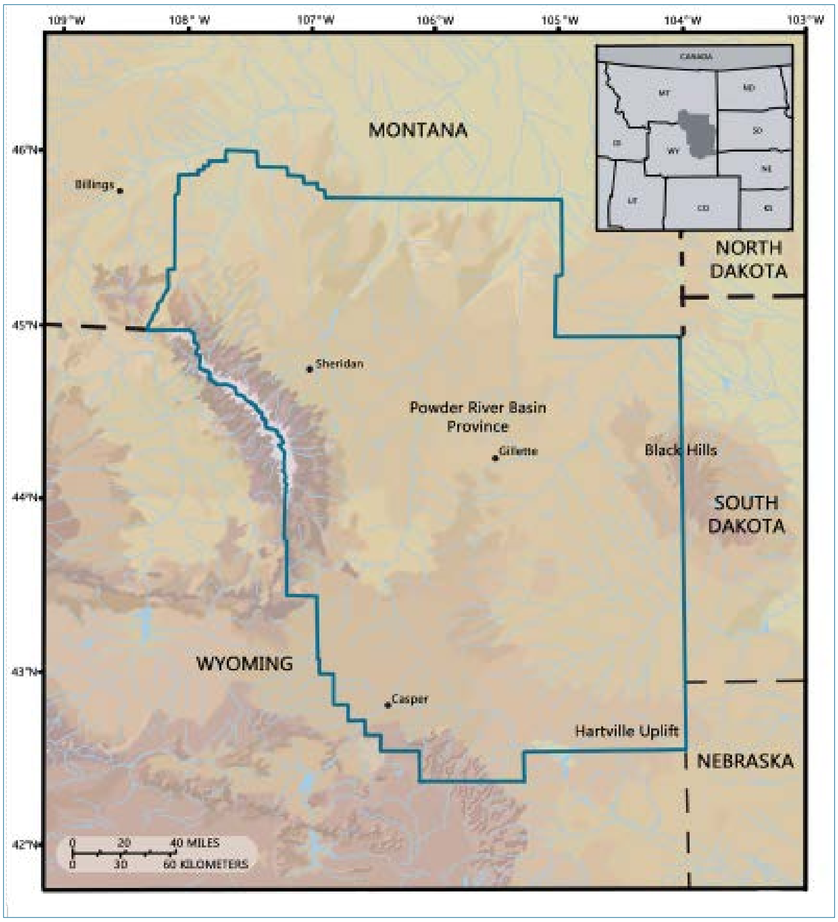

Figure 3. Map of the Powder River Basin in northeast Wyoming and southeast Montana, USA (drawn by Melanie Richard)

I have previously stated that I believe the Paleozoic and Mesozoic generally follow a global chronologic sequence in the Flood:

> "Although the general sequences of Paleozoic to Mesozoic seem valid, the periods within those eras may not represent an exact sequence, since the Devonian in one place may be deposited before the Cambrian in another."[42]

Since the Paleozoic and Mesozoic seem to correspond with Walker's Inundatory Stage, there is general agreement between the accepted geologic column and Walker's way of viewing the strata for these two episodes of the Flood record.

Whitmore argues for the validity of the chronostratigraphic timescale as a record of biblical history by referencing sheet formations, covering wide areas.[43] He cites the Coconino Sandstone and its equivalents in the Rocky Mountains and High Plains. However, this area constitutes only about 20% of the North American continent. Widespread strata do not demand the timescale. I also note these strata:

> "Paleozoic and Mesozoic strata can form large sheets over extensive areas such as the Great Plains, but they are generally broken and tilted in the mountains in the western United States, except for the Colorado Plateau."[48]

More compelling is Snelling's use of the well-behaved, little deformed strata of the Grand Canyon and the Grand Staircase.[31] However, this must be followed up with convincing evidence of the *global* synchronous nature of these rocks with their uniformitarian equivalents, including marine sediments.

Did Ark mammals live before the Flood where their Cenozoic fossils are found?

The assumption of an equivalence between the geologic column and the Flood record does not excuse the straw man arguments from paleontology. Ross and Arment argue that pre- and post-Flood fauna lived in the same locations, requiring round trip migrations to and from the Ark to the same place; unless this is what they think I believe. Ross does allow for the possibility that the North American mammals could have been transported exceptionally far *en masse*, but they are still confined to North America.[2] Regardless, two of each baramin had to trek long distances from where their Cenozoic fossils are found to the Ark, assuming either the same continental geography before the Flood as today or a supercontinent (see figure 1).

There are numerous problems with this line of argument. First, we don't know the geography, topography, or bathymetry of the pre-Flood world. Snelling adequately answers this and other misunderstandings:

> "As a matter of fact, if the Flood was global, pre-Flood geography would have been totally different from that of the present earth, since the tectonic forces unleashed during the Flood, and the massive erosion of the pre-Flood geography followed by deposition of great thicknesses of fossil-bearing sedimentary layers, would have guaranteed a total reshaping of the geography and topography of the earth's surface. In the second place, no one can prove that the kangaroos and the other Australian marsupials were confined to Australia *before* the Flood. And if not, then none of the

Table 2. Minimum erosion of Rocky Mountain basins and High Plains of North America based on erosional remnants, listed from north to south.[52–54] Total erosion likely was much more, especially on the High Plains, where erosional remnants are limited and/or of low altitude.

Location	Amount of erosion
South-central Saskatchewan	100 m
Northeast Montana (Flaxville Plateaus)	100 m
Northwest Montana, southeast Alberta	730 m
Near Great Falls, Montana	375 m
Near August, Montana	800 m
East-central Montana	435 m
Southwest North Dakota	300 m
Western North Dakota	160 m
Bighorn Basin, north-central Wyoming	430 m
Powder River Basin, northeast Wyoming	470 m
Wind River Basin, central Wyoming	700 m
Southeast of Wind River Basin	850 m
Southeast Wyoming	270 m
Great Divide Basin, southwest Wyoming	640 m
Fossil Basin, southwest Wyoming	600 m
Western Nebraska	440 m
Northeast Utah	540 m
Northwest Colorado	560 m
North-central Colorado	610 m
Central Colorado	1,520 m
South-central Colorado	1,500 m
Southeast Colorado	180 m
Northwest Kansas	120 m
Northwest New Mexico	760 m
North-central New Mexico	1,000 m
East-central New Mexico	310 m
Northwest Texas	180 m

> chosen pairs of marsupials would have had to "hurry" to get from Australia to the Ark during the decades that it was under construction. In fact, it is possible that kangaroos and other marsupials may have been living in the same region as Noah [emphasis in original]."[10]

Ross assumes the Rodinia supercontinent (figure 1a), although Genesis 1:9,10 does not require a supercontinent. If there was, God could have easily directed fauna to the Ark.

Second, Cenozoic mammals could have been transported long distances to their fossil locations, as Ross admits. If the animals were floating, they could have travelled far from where they lived before the Flood; they could have travelled from some other 'continents', wherever they were before the Flood. Cenozoic fossil locations are not necessarily the locations from where they migrated to the Ark. Transport is suggested by the disarticulation and destruction of many fossils; many Cenozoic mammal fossil finds are scraps of jaws and teeth, like those of the early Cenozoic strata of the Bighorn Basin, north-central Wyoming, USA.[44] They likely travelled some distance before being buried.

This highlights the problem of 'biocorrelation', the dating of fossils by their 'stage of evolution'.[45] This requires not simply correctly assessing features as 'primitive' or 'archaic', or 'specialized' or 'advanced'. Having only fragments increases the uncertainty of such methods, even granting evolution. Sometimes, just finding the fossil scrap in 'older' strata is all that is needed to judge the feature as primitive:

> "Willwood fossil mammals are important because they include representatives of archaic groups, *more characteristic of Paleocene faunas*, coexisting with some of the earliest known members of extant higher taxa [emphasis added]."[46]

The lack of consistency is amazing. When paleontologists found Cretaceous marine dinoflagellates with early Cenozoic mammals, they labelled the marine fossils as 'reworked'.[47] This strategy is frequently used.

Third, transport of animals after the Flood could have occurred on log mats.[48] Indeed, in some cases it is the only plausible explanation, even for some larger animals. For instance, moderate sized ground sloths from South America are also found in the West Indies, and log rafting seems to be the only logical way of transport. Finally, there could have been representatives of all the baramins *close* to the Ark before the Flood that were not buried and fossilized there, as indicated by Snelling, above. Fossils are a partial record of the past, not a complete one.

Cenozoic mammals did travel from the Ark to all the continents

The real challenge of the 'round trip' argument is that well-known problem of biogeography and the dispersion from the 'Mountains of Ararat'. It is a large subject. It is also worth noting that it is a larger problem for evolutionists. Creationists must explain extant and extinct fauna, including Ice Age animals. There are five possible mechanisms of

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Figure 4. *Brontotherium hatcheri* fossil skeleton from the National Museum of Natural History in Washington D.C.

mammal migration: (1) land bridges, (2) island hopping, (3) log mats, (4) human transport, and (5) divine providence.

K-Pg boundary advocates have greater problems. In addition to dispersion, they must explain the rapid and significant diversification of Cenozoic fauna in the short time between the Flood and the Ice Age, as well as their migration, increase, burial, and fossilization. Wise has even advocated rapid saltation (extremely rapid evolution) where four-legged mammals somehow turned into whales within this two-century timeframe![49,50] Furthermore, some are buried by thousands of metres of sediment. All this would have had to have happened in about two centuries. To increase the problem, deposition and fossilization was followed by deep erosion—up to 1,520 m of sediment are eroded in the Rocky Mountain Valleys and High Plains of the United States (table 2).[51] The erosional debris is *not* found in nearby floodplains, but on the continental margins. This would require regional scale post-Flood currents. A Flood explanation is more reasonable.

Furthermore, K-Pg boundary advocates must explain why hardly any mammals died and were buried in the Flood, but millions died, were buried, and fossilized afterwards. In addition, the order of appearance and disappearance of numerous mammals at various times within the Cenozoic occurred globally at the same time. Brontotheres are like rhinoceroses but with unique horns (figure 4). They appear in the late Paleocene and go extinct at the end of the Eocene. How is this explained in the post-Flood world?

Summary

Advocates of a K-Pg post-Flood boundary seem to misunderstand their opponents' arguments. This partially stems from too much reliance on the uniformitarian chronostratigraphic timescale as a global and precise measure of biblical history. It is better to assess the location of the boundary at individual geographic locations using a wide range of physical field evidence. This evidence strongly suggests that the Cenozoic is often diachronous.

Furthermore, the 'round trip' argument is a straw man that distracts from the force of the multiple lines of geologic evidence presented by advocates of a late Cenozoic boundary. Two of each baramin of the Australian marsupials and North American mammals did not have to migrate to and from the Ark. The real issue is post-Flood dispersion and more general issues of biogeography. Those should occupy our paleontological focus.

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Developments in paleoanthropology no. 2

Peter Line

This paper continues the theme begun in 2021 of discussing some of the fossil finds and/or developments in paleoanthropology from a creationist perspective. This includes the naming of a new species, *Homo bodoensis*, as well as the discovery of a juvenile skull, attributed to *Homo naledi*, from the Rising Star cave system of South Africa. New fossil pieces from the lower back of *Australopithecus sediba* are also discussed, as is a new study on fossil footprints from Laetoli Site A, Tanzania. Lastly, the Omo fossils and their redating are examined.

Homo bodoensis and the muddle in the middle

On 28 October 2021 Roksandic *et al.* published an article in the journal *Evolutionary Anthropology* titled: "Resolving the 'muddle in the middle': The case for *Homo bodoensis* sp. nov. [sp. nov. means new species]"[1] The Middle Pleistocene (apparently now renamed 'Chibanian'), dated as a period between supposedly 129 to 774 thousand years ago (ka), is said to be important because it allegedly "saw the rise of our own species (*Homo sapiens*) in Africa, our closest relatives, and the Neanderthals (*Homo neanderthalensis*) in Europe."[2] The article from The University of Winnipeg went on to state:

> "However, human evolution during this age [the Middle Pleistocene] is poorly understood, a problem which paleoanthropologists call 'the muddle in the middle'. The announcement of *Homo bodoensis* hopes to bring some clarity to this puzzling, but important chapter in human evolution."[2]

Marshall commented:

> "Roksandic and her colleagues want to make sense of the muddle. They argue that all the African fossils previously called *H. heidelbergensis* or *H. rhodesiensis* should be thought of as one species, *H. bodoensis*. This species, they argue, eventually gave rise to ours."[3]

Furthermore, as stated by Marshall, Roksandic *et al.* "say *H. heidelbergensis* fossils found in Europe can all be reclassified as early Neanderthals, and that fossils from the eastern Mediterranean that don't quite fit any of the species could represent interbreeding."[3] Roksandic *et al.* suggested:

> "… the poorly defined and variably understood hominin taxa *Homo heidelbergensis* (both sensu stricto [*sic*] and sensu *lato*) and *Homo rhodesiensis* need to be abandoned as they fail to reflect the full range of hominin variability in the Middle Pleistocene."[4]

For *Homo heidelbergensis* sensu lato to be abandoned you cannot have the species existing in Asia. Hence, the authors also suggested that the "assignment of the Asian, particularly Chinese, archaic hominins into *H. heidelbergensis* should be abandoned", as "the Middle Pleistocene Asian fossils, particularly from China, likely represent a different lineage altogether."[5]

As indicated, Roksandic *et al.* introduced a new Middle Pleistocene 'hominin species' that they said "represents the direct ancestor of *H. sapiens*", and proposed "that this new species be based on the Bodo skull and thus be named *Homo bodoensis*."[6] The Bodo 1 partial cranium (see figure 1; cranial capacity ~1,250 cc) is not a new discovery, having been found in Ethiopia in 1976, and is dated to allegedly about 600 ka.[7] It has previously been variously classified as "close to the *Homo erectus-Homo sapiens* transition", *Homo sapiens rhodesiensis*, archaic *Homo sapiens*, and *Homo heidelbergensis*.[8] Apart from Bodo 1 (the holotype), other specimens in the proposed *Homo bodoensis* hypodigm include "Kabwe 1 (Broken Hill), Ndutu, Saldanha (Elandsfontein), Ngaloba (LH 18), and potentially Salé in Africa", as well as the Ceprano cranium from Europe.[9]

The species name, *Homo heidelbergensis*, has been around for over a hundred years, being first associated with the Mauer mandible from Heidelberg, Germany.[10] However, there has been persistent taxonomic confusion associated with *Homo heidelbergensis*, a species name not taken very seriously until approaching the end of the twentieth century.[10] As an example of this lack of seriousness, no mention of the name *Homo heidelbergensis* is found in the text of a chapter (by Pilbeam) titled 'Middle Pleistocene Hominids', published in 1975.[11]

Fast forward to 2021, and the name *Homo heidelbergensis* is so common that prominent Christian philosopher and writer (and also evolutionist) William Lane Craig has suggested that Adam and Eve may "be plausibly identified as members of *Homo heidelbergensis* and as the founding pair at the root of all human species."[12] Craig regards Genesis 1–11 as "Hebrew mytho-history", narratives that "need not be read as literal history", and believes that "Adam plausibly lived sometime between around 1 mya to 750 kya".[13] In his book Craig also wrote, "surely we can get used to the

Figure 1. Cast of the adult Bodo 1 *Homo heidelbergensis* from Bodo, Ethiopia. It was recently announced as the holotype for the newly proposed species *Homo bodoensis*. (Photo: Peter Line)

idea that Adam and Eve looked like *Homo heidelbergensis* rather than us."[14] I have no issue with Adam and Eve being 'robust' humans,[15] and hence possibly looking like *Homo heidelbergensis*. However, Craig's acceptance of evolution (including human evolution), with its eons of death and suffering before sin, as well as some of his other views for example, that Adam lived at least 750 ka and that Genesis 1–11 "need not be read as literal history", makes his take on Adam untenable from a biblical perspective and impossible from a scientific viewpoint.[16] For more detail on Craig's book see the review by Jonathan Sarfati.[17]

While quoted as agreeing with these authors [Roksandic *et al.*] that "*heidelbergensis* has been used as a rag-bag term for too long", paleoanthropologist Chris Stringer, from the Natural History Museum in London, is reported (by Ashworth) as believing that "the paper may not end the issues it aims to solve."[18] According to Stringer:

> "Regarding *Homo bodoensis* as the Chibanian ancestor of the *Homo sapiens* lineage has its problems, … as my and other research suggests that the facial shape of the Bodo skull is derived away from the ancestor of *Homo sapiens*, which was probably more like that of another relative, *Homo antecessor*."[18] [i.e. the authors appear to be saying that the Bodo face is too different from what it would likely look like if it was the ancestor of *Homo sapiens*; instead the face of *Homo antecessor* is more like what they would expect.]

Stringer also commented that one of the authors of the Roksandic *et al.* paper (presumably Xiu-Jie Wu) "has also just published another paper suggesting that a fossil from Hualongdong in China is also a Chibanian ancestor for *Homo sapiens*, which may well add further to the muddle!"[18,19]

For as long as the fossil specimens are interpreted using an incorrect model (evolution), 'the muddle in the middle' will remain in a confusing state. Whether they are called *Homo heidelbergensis*, Neanderthals, 'archaic' *Homo sapiens*, *Homo bodoensis*, or some other name, the fossil specimens assigned to these categories do not represent evolutionary 'apemen' stages between *Homo erectus* and modern *Homo sapiens*. Rather, they were fully human, that is, descendants of Adam and Eve, as also were the fossil specimens assigned to *Homo erectus*. As such, they belonged to various subgroups of the same species, *Homo sapiens*, whose individuals were capable of interbreeding with one another. The few differences were caused by factors such as human variation, genetic drift, as well as environmental influences. That some fossil specimens exhibit a mixture of traits from different human subgroups may well be explained by interbreeding between the different human subgroups. This can give rise to appearances that are sometimes blended in general character, and at other times mosaic.

Child of darkness

'A child of darkness' was the ominous title of the media announcement on 4 November 2021 about a new juvenile skull (nicknamed Leti) discovered in the Rising Star cave system of South Africa in 2017.[20] Delivering the announcement was Lee Berger from Wits University (University of the Witwatersrand), the project leader. Berger has delivered impressive finds in the past, so this would be quite a letdown for anyone expecting something similar this time. As evident from the reconstruction of the Leti skull, most of it (black—see figure 2) is missing.

Based on dental eruption, it was suggested "Leti would have been about 4 to 6 years old when she died if she matured like a human", although it was acknowledged that it was not known whether Leti was male or female.[20] It was noted that the skull was found alone, and that no "remains of its body have been recovered."[20] There was also no mandible (lower jaw) recovered, so the fossil skull can be more precisely described as a fossil cranium.

The fragmented fossil cranium, consisting of 6 teeth of the maxilla (upper jaw) and 28 cranial fragments, was stated by Brophy *et al.* (who described the remains in a paper) to be "consistent with a single, immature individual" (designated the U.W. 110 individual), with the dental morphology said to support attribution to *Homo naledi*.[21] Given the location of the find, this attribution is likely correct.

Figure 2. A reconstruction of the skull of Leti in the hand of Professor Lee Berger (Image Credit ©: Wits University)

I have previously discussed *Homo naledi* individuals.[22,23] They were likely *erectus*-like post-Babel humans, so descendants of Adam. Several of them possibly suffered from a developmental pathology known as cretinism, common in regions with iodine deficiency in the soils. About the Leti cranium, Brophy *et al*. wrote:

> "The largest cranial fragment is part of a cluster of ten bones designated as U.W. 110-13. It is a frontal bone fragment including a portion of the right orbit, a small adjacent portion of the frontal squama, and the superiormost part of the interorbital pillar."[24]

Not surprisingly, no accurate estimate of Leti's cranial capacity was possible, but it was stated that

> "… the radius of curvature of the endocranial surface at bregma is comparable to immature hominins with endocranial volumes in the 450–650ml range, such as the Taung specimen and the endocranial volume predicted for the newly described DNH134 specimen attributed to *H. erectus* … . This young juvenile *H. naledi*, with its right first permanent molar in gingival eruption, would be predicted to have 90–95% of its brain growth completed … . This is compatible with the known range of adult *H. naledi* endocranial volumes at 480–610cc … ."[25]

It was stated that the Leti cranium "was found in an extremely remote passage of the Rising Star Cave System, some 12 meters beyond the Dinaledi Chamber, the original site of discovery of the first *Homo naledi* remains that were revealed to the world in 2015."[20] The cranium was said to have been found in an extremely narrow passage (15 cm wide by 80 cm in length), its fragmented remains "found on a shelf of limestone about 80cm above the present cave floor."[20] It was also mentioned that

> "With no signs of carnivore damage or damage made by scavenging, and no evidence of the skull having been washed into the narrow passage, the team does not know how Leti's skull came to rest, alone, in such a remote and inaccessible part of the system."[20]

In the second paper on the find, describing the context, Elliott *et al*. said that they had not been able to find any alternate entrance into the Dinaledi Subsystem (which includes the Dinaledi Chamber), with the Chute (a 12-metre-high fracture in the dolostone) being the only route in.[26] On finding remains like Leti within the Dinaledi Subsystem, the authors stated:

> "The presence of fossil material within extremely constricted passages as far as 40m from the Chute appears inconsistent with gravity-driven accumulation of bodies or skeletal elements from beneath this entrance into the subsystem."[27]

Hence, the main issue raised by the find is how Leti and the other *Homo naledi* specimens ended up in the inaccessible and cramped spaces of the cave. It remains a mystery, although the authors hypothesized that "it is likely other members of its species were involved in the skull reaching such a difficult place."[20]

When initially publishing on the finds in 2015, the then Berger team considered how the fossil material got into the Dinaledi Chamber, with occupation, predator accumulation, and water transport hypotheses considered unlikely, but mass mortality or death trap and deliberate body disposal scenarios considered plausible—the latter explanation preferred by the authors.[28] They stated that

> "Based on current evidence, our preferred explanation for the accumulation of *H. naledi* fossils in the Dinaledi Chamber is deliberate body disposal, in which bodies of the individuals found in the cave would either have entered the chamber, or were dropped through an entrance similar to, if not the same as, the one presently used to enter the Dinaledi Chamber."[29]

On the issue of how the fossil material got into such a remote place, after the more recent Leti announcement, Michael Marshall wrote in *New Scientist*:

> "Leti's skull was found in a narrow fissure that is almost impossible to access. For that reason, the team argues that the skull was placed there deliberately, as a form of funerary practice. Presenting their findings at a virtual press conference, the researchers said it is evidence that hominins have been performing funerary rights [*sic*] for hundreds of thousands of years—even hominins with brains much smaller than ours."[30]

The suggestion that 'hominins' have been performing funerary practices (i.e. practices associated with burial) for hundreds of thousands of years is purely based on belief in evolution, not on any empirical evidence. Concerning burial practices, one can think of easier ways of disposing of bodies than crawling through the narrow and remote corners of the Rising Star cave system. In fact, it is hard to think of a more difficult way. Hence, I have reservations about such a hypothesis. However, if it was some sort of a religious practice then it need not necessarily make sense to us and/or be practical.

In my first article on *Homo naledi*, after the remains were first revealed in 2015, I speculated on how the remains had ended up in the Dinaledi Chamber.[31] One suggestion was that the people classified as *Homo naledi* may have been forced into the chamber and left there to die. Perhaps the *Homo naledi* individuals were forced to crawl in there whilst alive because of disease, or punishment for something, and then were blocked from exiting the cave system (hence, left in there to die). Perhaps further work on the site will shed more light on this mystery.

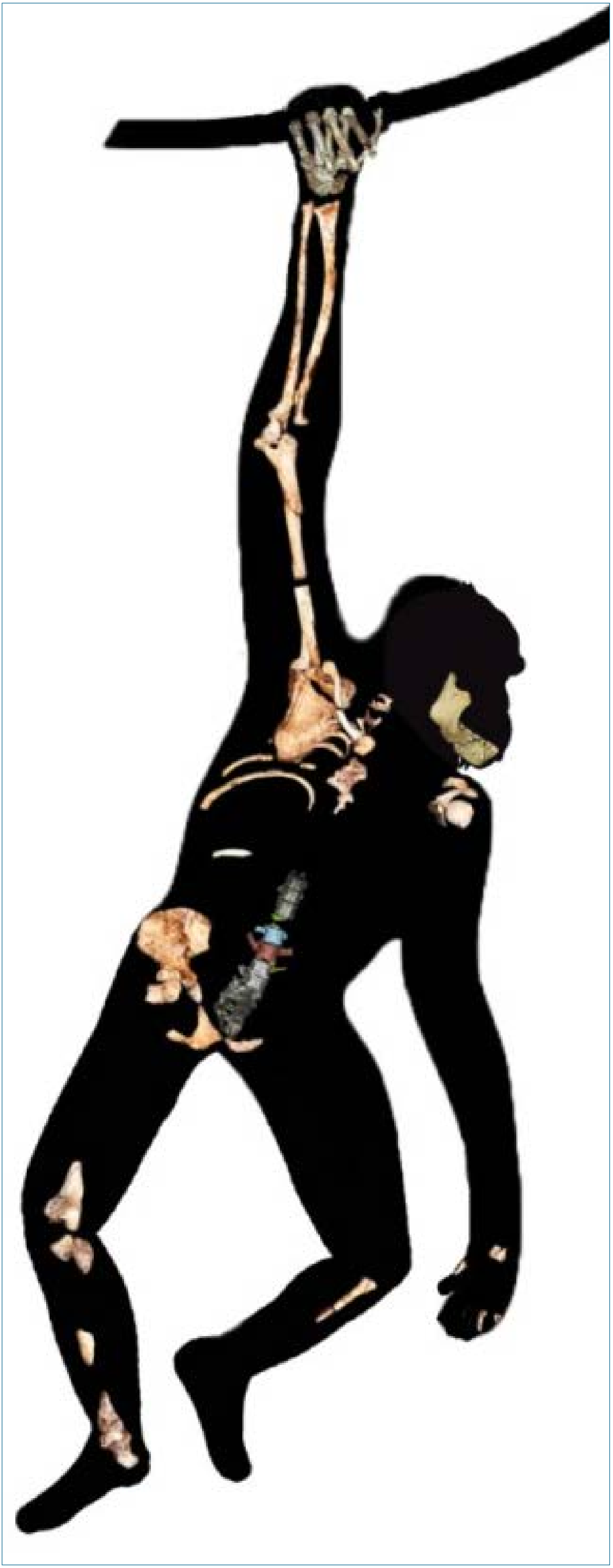

Figure 3. *Australopithecus sediba* silhouette showing the newly found vertebrae along with other skeletal remains from the species. Note that the newly found vertebrae are coloured. (Image (& Caption) Credit ©: NYU & Wits University)

Australopithecus sediba gets a lower spine

November 2021 was a busy month with respect to new fossil announcements for Lee Berger. Having announced the *Homo naledi* Leti discovery (see above) about three weeks earlier, Berger went on to promote the publication by Williams *et al*. (on 23 November 2021) of new fossil pieces (lumbar vertebrae) from the lower back of *Australopithecus sediba* (see figure 3).[32] These new fossils, from Malapa, South Africa, were said to "fit together with the previously discovered MH2 fossils, providing a nearly complete lower spine."[33] MH2 is the partial skeleton of an adult individual (likely female), which was first reported on in 2010.[34] Although its catalogue number is MH2, the 'female skeleton' has been nicknamed 'Issa' by the researchers.[35] The *Australopithecus sediba* fossils, including MH2, are dated to supposedly ~2 Ma.[36,37] According to Williams *et al*.:

> "Analysis of the fossils suggested that MH2 would have had an upright posture and comfortably walked on two legs, and the curvature of their lower back was similar to modern females. However, other aspects of the bones' shape suggest that as well as walking, *A. sediba* probably spent a significant amount of time climbing in trees."[33]

News releases about the new find by New York University (NYU) and Wits University, institutions involved in the research, were titled "Ancient human relative, *Australopithecus sediba*, 'walked like a human, but climbed like an ape'".[35,38] However, according to one of the reviewers of the paper, that *sediba* engaged in "human-like bipedalism" had not been demonstrated:

> "Line 47: I agree based on the morphology of the fossils, that *A. sediba* used its lower back in a kind of bipedalism. However, the mosaic of features shown in the lower back tells us that we should be cautious to affirm that was a 'human-like bipedalism'. The authors should find another way to define it, human-like

> bipedalism (which is an obligated or complete bipedalism) is not demonstrated here."[39]

The authors of the paper appear to have agreed with the reviewer that human-like bipedalism had not been demonstrated, nor was likely, leaving one to wonder why the headline included the false claim that *Australopithecus sediba* "walked like a human":

> "We understand the point the reviewer makes here and think our use of 'human-like' was misunderstood. We clarify that we do not think MH2 or any early hominin engaged in modern human-like bipedalism. Instead, we were mainly referring to 'human-like' bipedalism to contrast with ape-like bipedalism. Our comparisons of MH2 to modern humans are done because we are the only extant hominins for which we can gather large samples to compare to fossil hominins. We fully agree that MH2 and other early hominins were not fully modern human-like in bipedalism; in fact, we suspect that many modern human adaptations have to do with endurance walking and even running, which would be absent in tree-climbing early hominins like *A. sediba*."[39]

As I have mentioned in another publication, when comparing some of *Australopithecus sediba*'s mix of characteristics, as presented by Colin Barras in *New Scientist* in 2013,[40] the ape-like ones (small brain, shoulders and long arms suited for climbing, conical rib cage and weak heel) appear to indicate unambiguously that it was an apish primate.[41] Its supposed 'human-like' features, on the other hand (expansion of prefrontal cortex, small teeth, precision grip suited for tool use, pelvis, knee and hip for upright walking), are more ambiguous in interpretation.[41] For example, as I reported in the *Journal of Creation* in 2021, a study found that efficient thumb opposition was not a characteristic of *Australopithecus*, including the *Australopithecus sediba* MH2 specimen.[42,43] Hence, this throws doubts on any alleged "precision grip suited for tool use".

On the gait of *Australopithecus sediba*, based on analysis of the adult female MH2 skeleton, paleoanthropologist William Kimbel commented that the "proposed 'hyperpronation' of the foot and extreme inward rotation of the leg and thigh suggest an ungainly bipedal stride that might have made it into Monty Python's 'Ministry of Silly Walks' sketch."[44] Hence, if *Australopithecus sediba* walked upright it was likely not as a human, but more likely in a strange, non-human, manner. Also, as discussed in 2021, the finding that apes/primates in Europe were likely built for some form of bipedalism and/or upright posture, yet were not hominins, is a real blow to the idea that bipedalism equals hominin (i.e. apeman).[45] Why, then, would bipedal features in the australopithecines from Africa mean they were hominins? Hence, the argument of evolutionists that the australopithecines were hominins because they were in some way bipedal collapses.

Laetoli site A footprints

Footprint tracks at Laetoli, Tanzania, were first discovered in 1976, but as described by White and Suwa, the "most significant discovery of hominid tracks" occurred at Laetoli Site G in 1978.[46] Publications soon followed in both *Nature* and *National Geographic*.[47,48] According to paleoanthropologist Russell Tuttle, who studied casts of the best individual prints from the Site G footprint trails:[49]

> "The 3.66-Ma footprint trails at Laetoli in Tanzania are the earliest definitive evidence for obligate hominid bipedalism. In all observable features of foot shape and walking pattern, the three creatures that made the trails are indistinguishable from modern habitually barefoot human beings walking at a leisurely pace … . Indeed, if the prints were undated or if they had come from a younger time period, they probably would be designated *Homo*. … . That they were accomplished bipeds is beyond dispute because their regularly placed footprints (n = 69) extend over 27 meters of relatively open habitat with no hand impression anywhere along the trails."[50]

In 2016 Masao *et al*. reported on "hominin tracks unearthed in the new Site S at Laetoli and referred to two bipedal individuals (S1 and S2) moving on the same palaeosurface and in the same direction as the three hominins documented at Site G."[51] They noted that the "main metrical features of the S1 and S2 tracks (footprint length and width, step and stride lengths) are larger than the G1–3 equivalents".[52] These more recently discovered footprints, at Site S, are said to be the same age (supposedly 3.66 Ma) as the ones at Site G, the two sites being 150 metres apart.[53] Masao *et al*. tentatively suggested "that the new footprints can be considered as a whole with the 1970s ones",[54] i.e. part of the same group. Discussing the implications of the new Laetoli footprints, the authors stated:

> "The impressive record of bipedal tracks from Laetoli Locality 8 (Site G and the new Site S) may open a window on the behaviour of a group of remote human ancestors, envisaging a scenario in which at least five individuals (G1, G2, G3, S1 and S2) were walking in the same time frame, in the same direction and at a similar moderate speed. This aspect must be evaluated in association with the pronounced body-size variation within the sample, which implies marked differences between age ranges and a considerable degree of sexual dimorphism in *Au. afarensis*."[55]

Image: Ellison J. McNutt, Kevin G. Hatala, Catherine Miller, *et al.* /Wikimedia, CC BY 4.0 (modified orientation)

Figure 4. Footprint of an unknown species from Laetoli Site A (left). Human-like footprint from Laetoli Site G (right).

In December 2021 McNutt *et al*. published a study on footprints from Laetoli Site A. These prints were discovered in 1976, but at the time they were only partly excavated before falling into obscurity.[46,56] In 2019, McNutt *et al*. "located, excavated and cleaned the site A trackway," the Site A footprints previously dated to supposedly 3.66 Ma, the same date as the footprints at Sites G and S.[57] The authors reported that the "footprints at site A are readily distinguished from those at site G, indicating that a minimum of two hominin taxa with different feet and gaits coexisted at Laetoli."[57] From their analysis, McNutt *et al*. concluded:

> "… the site A footprints were made by a bipedal hominin with a distinct and presumably more primitive foot than *A. afarensis*. The gross shape of the foot is chimpanzee-like, with slight hallucial divergence and perhaps some midfoot mobility. However, the site A individual was walking bipedally with a narrow step width indicative of either a valgus knee, adducted hips, or both. This combination of foot morphology and gait kinematics inferred from the preserved footprints precludes them from having been made by *A. afarensis*."[57]

In a *Nature* companion article on the Site A footprints, Melillo commented that the "footprints themselves are oddly wide and short, and the feet responsible for their creation might have had a big toe that was capable of thumb-like grasping, similar to the big toe of apes."[58] See figure 4 for a comparison of footprints from Site A and Site G. Melillo also remarked that

> "It seems that two possibilities remain as probable explanations for the site A prints. They could have been created by a hominin species other than *A. afarensis* (perhaps the same as that represented by the Burtele foot). Alternatively, they could have been created by an *A. afarensis* individual walking in an atypical manner other than that tested in the study by McNutt and colleagues."[59]

The most logical and simplest explanation of the above footprints is that the Site G and S footprints belonged to true humans (i.e. descendants of Adam and Eve), and likely consisted of a group made up of both adults and children (accounting for the difference in size of the tracks). This is consistent with previous analysis (by, for example, Tuttle, mentioned above) that the Site G footprint "trails are indistinguishable from modern habitually barefoot human beings walking at a leisurely pace".[50]

However, the Site A footprints likely were from australopithecines, perhaps *Australopithecus afarensis*, but one cannot be sure of this. As discussed in the *Australopithecus sediba* section, above, and elsewhere,[45] that some australopithecines were able to walk bipedally in some way is not an issue for the Creation Model. It seems that the owner of the Site A footprints walked in a very strange bipedal manner, as it involved cross-stepping,[60] "in which each foot crosses over the body's midline to touch down in front of the other foot".[58] Evolutionists do not want to assign the Site A footprints to *Australopithecus afarensis*, as from their perspective that would indicate it was more 'primitive' than previously thought. Many (or most) evolutionists consider the Site G and S footprints as having belonged to *Australopithecus afarensis*. Hence, to them the Site A footprints must have been made by a 'hominin' more 'primitive' than *Australopithecus afarensis*. However, it is by 'consensus' that the footprints at Site G (and, by implication, at Site S) were assigned to *Australopithecus afarensis* by evolutionists, because of the supposed age of the prints, as indicated by Melillo:

> "After heated debates in the 1970s to 1980s, most palaeoanthropologists [*sic*] reached a consensus that all fossil bones and footprints dated to the middle Pliocene epoch (roughly 3.7 million to 3 million years ago) represented the hominin species *Australopithecus afarensis*. This species was the earliest hominin known at that time and the presumed ancestor to all later hominin species. However, fossils discovered in the past two decades challenge the hard-won consensus … ."[58]

Doing science by 'consensus' is not very scientific. Essentially, as humans are not supposed to have existed as far back as 3.66 Ma on the evolutionary timescale, the Laetoli footprints are not recognized as belonging to humans by evolutionists, even though (as at Site G) they are acknowledged as being "indistinguishable from modern habitually barefoot human beings" (see full quote by Tuttle, above).[50]

Melillo stated (see above) that the Site A footprints may perhaps have been "created by a hominin species other than *A. afarensis* (perhaps the same as that represented by the Burtele foot)."[59] DeSilva *et al*. acknowledged that the "Burtele foot possessed at least a moderately abducent hallux and some grasping ability with the big toe."[61] The Burtele foot

(BRT-VP-2/73), found in allegedly 3.4 Ma deposits in the Woronso-Mille study area of Ethiopia, would be contemporaneous in time with *Australopithecus afarensis*, yet was not assigned to that or any other taxon.[62] It is said to be "too primitive to belong to *A. afarensis*."[63]

Some associated foot bones of *Australopithecus afarensis* exist, although many have been found in isolation.[64] A composite *afarensis* foot skeleton from the Hadar 333 locality is said to show a "human-like rearfoot and midtarsal region, but long, lateral phalanges."[66] However, evidence that the foot of *afarensis* had a longitudinal arch appears to be lacking, based on examining the fossil foot bones, and similarly the evidence of a non-grasping adducted hallux is very ambiguous; the evidence seeming to instead indicate "some hallucal abducence,"[65] hence allowing some mobility of the hallux (big toe).

Evidence of a longitudinal arch (and adducted hallux) appears to be based on the Laetoli fossil footprints, but, as even DeSilva *et al*. note, even some evolutionists do not believe these footprints belong to *Australopithecus afarensis*, as they are "too human-like".[66] DeSilva *et al*. note that these evolutionists (including Tuttle) instead propose "that they were made by an as-of-yet undiscovered hominin with a more human-like foot".[66]

According to Tuttle, the hallux of the Laetoli 'hominid' Site G foot "is aligned with the lateral four toes, and the interdigital gap between it and the second toe is quite human", and the "G prints evidence a medial longitudinal arch."[67] In some respects, DeSilva *et al*. found the *Australopithecus afarensis* foot to be quite human-like, but their analysis depended, at least in part, on the Laetoli footprints having been made by *afarensis* (and not by humans), as admitted by them, as follows:

> "Nevertheless, the wealth of data from the Hadar foot bones and the Laetoli footprints form a general picture of the *A. afarensis* foot (assuming of course that the Laetoli 'G' and 'S' prints were made by *A. afarensis*)."[68]

One suspects that if the supposed age of the Laetoli footprint-bearing stratum had not been dated so 'early' (3.66 Ma), but much more recent, then evolutionists would be saying humans made them, but they cannot do so with the current attributed date as that would collapse their human evolution storyline. It is interesting how most evolutionists accept the Laetoli G footprints as belonging to *Australopithecus afarensis*, even though some consider them 'too human-like' to belong to *afarensis*. Yet, they reject the Burtele foot, as well as the Laetoli site A footprints, as belonging to *Australopithecus afarensis*, because they are considered 'too primitive' to belong to *afarensis*. If findings tend to be interpreted to only support the human evolutionary narrative, then are we dealing with science or a belief system?

It is also an example of the faulty logic and circular reasoning that so pervades this field. If fossil footprints are ruled out from belonging to humans essentially because of an alleged early date, then of course no fossil footprints of humans will ever be found to contradict the evolutionary timeline. In this case, after arbitrarily ruling out the possibility of fossil footprints belonging to humans in the supposed time period 3 to 3.7 Ma, some evolutionists then use this as proof that any human-like footprints (e.g. those at Site G) allegedly dated to this period were not made by humans, but rather by some australopithecine 'hominin', in particular *Australopithecus afarensis*.

The Omo fossils and their redating

Three adult skulls (Omo I, Omo II and Omo III) of various completeness, as well as a partial skeleton associated with one of the skulls (Omo I), were found and recovered in the Omo River region of South-West Ethiopia in 1967, by a team led by Richard Leakey.[69] Michael Day did the initial descriptions of the remains. The Omo I skull was described as having an incomplete vault, and the Omo II skull (1,435 cc) as consisting of an almost complete calvarium (lacking the face and part of the base).[70] The fragmentary nature of the remains of the Omo III skull was said to "preclude any real assessment of its affinities at this time, but what resemblance it has lies with the more modern of the first two Omo skulls."[71] The Omo I skull is the more modern in general form, being more lightly built (although its vault is still considered "robust by modern human standards"), and said to be "reasonably compared with both the Swanscombe and Skuhl skulls."[72] The Omo II skull was said to be similar in many features to the Solo skulls (i.e. the Indonesian Ngandong *Homo erectus*), and "to a lesser extent, the Broken Hill skull, the Vertessöllös occipital, the Kanjero skulls, and even indeed *Homo erectus*."[71]

The sites of the Omo I and II finds are said to "both come from the same level, a minor disconformity in the upper third of Member I, Kibish Formation [figure 5]."[73] Omo II is said to have been "found on the surface", whilst Omo I was "recovered from a siltstone".[74] The original date assigned to these Omo fossils was 130 ka in 1967, based on the decay of uranium atoms in oyster shells, but according to Frank Brown "that date should always have been taken with a pinch of salt".[75] This comment was made after the publication of new results, in 2005, "regarded as far more robust" by the BBC article reporting on the redating.[75] The new date, obtained by ^{40}Ar/^{39}Ar dating of feldspars, narrowed the age to between supposedly 104 and 196 ka, and with additional geological

Image: John Fleagle/Wikimedia, Public domain.

Figure 5: The Kibish Formation in southern Ethiopia, the location where the Omo fossils were discovered.

evidence, Omo I and II were said to be "relatively securely dated to 195 ± 5 kyr old".[76] According to the authors of the study this made "Omo I and Omo II the oldest anatomically modern human fossils yet recovered."[76] This aligned well with the then popular Out of Africa Model of modern human origins, which proposed that modern humans (*Homo sapiens*) evolved in East Africa, and that this occurred supposedly about 200 ka.[77] The relatively recent collapse of the Out of Africa Model, or at least parts of it, has allowed evolutionists to propose models whereby modern humans allegedly evolved from 'archaic humans' earlier than 200 ka.

According to a very recent study, the Omo I remains (and by implication Omo II) must be older than a colossal volcanic eruption that occurred allegedly 230 ka.[78] A research team dated pumice samples from a volcanic ash layer above where the fossil material was found, and argued that the Omo I fossils, being found deeper than this volcanic ash layer, must be greater than 230 ka.[78] Although the volcanic ash above Omo I was too fine-grained to be directly dated, the researchers were able to link the chemical fingerprint in this ash to a major eruption of a volcano (Shala), located 400 km away, identified as the source of the ash.[79] The researchers, using the ^{40}Ar/^{39}Ar dating method on pumice samples collected from Shala, obtained "a new minimum age for the Omo fossils of 233 ± 22 kyr", and commented that the "challenge remains to obtain a robust maximum age for Omo I." [80]

Both the potassium-argon (K-Ar) and argon-argon (^{40}Ar/^{39}Ar) methods have pitfalls,[81] and so the above ^{40}Ar/^{39}Ar ages are not accepted here. Aside from this, that these types of fossils keep getting redated indicates uncertainty about the dates by the evolutionists themselves, as why redate them otherwise. As an example of the uncertainties regarding the dating of 'hominin' remains, according to Brasseur, "55 years and 36 absolute datings later, considerable uncertainty remains regarding the potential age of Sangiran's extensive and deep fossiliferous strata."[82] For more examples of fossils being redated see Line.[83] In some instances, though, one gets the feeling that the redating is just to 'find' a date more suitable for some human evolution model. According to Vidal *et al*:

> "Our new age constraints are congruent with most models for the evolution of modern humans, which estimate the origin of *H. sapiens* and its divergence from archaic humans at around 350–200 ka … ."[84]

That there are several models for the evolution of modern humans indicates the uncertainty existing in this field since the collapse of the popular Out of Africa Model.[85] However, why should anyone take the latest speculations in the newer models, all based on the big assumption that evolution is true, any more seriously than in the earlier debunked model?

Both Omo I and Omo II were referred to as anatomically modern humans in the study by McDougall *et al*.[76] According to a coauthor of the study, anthropologist John Fleagle, "no scientist has been bold enough to suggest Omo II is anything other than *Homo sapiens*".[86] Discussing features that have prompted a comparison of Omo II to *Homo erectus*, paleoanthropologist Philip Rightmire, on the greater than 1,400 cc cranial capacity in Omo II, stated that it was "surely higher than would be expected in any member of that taxon [referring to *Homo erectus*]."[87] I have previously commented on the tendency, by evolutionists, to rule out crania from belonging to *Homo erectus* essentially because of a large cranial capacity, and how this is an example of circular reasoning.[88] That is, after arbitrarily ruling out crania with large cranial capacities as belonging to *Homo erectus*, this is then used as evidence that there are no *Homo erectus* crania with large cranial capacities. While acknowledging that analysis supports the assessment that the partial skull and skeleton of Omo I is anatomically modern, Pearson writes that "the preserved basicranial [base of the skull] details of Omo II recall the anatomy of *Homo erectus*, and Stringer (1974) found that it clustered with Ngandong in multivariate space."[89]

From a creation viewpoint, both Omo I and Omo II were descendants of Adam and Eve. Omo II has a cranial capacity slightly above the modern human average but shows affinity with fossil specimens classified as *Homo erectus*, whereas Omo I identifies clearly with *Homo sapiens*. Hence, they may have belonged to various subgroups of the same human species, *Homo sapiens*, as discussed earlier, with any morphological differences just reflecting variation within the biblical human *kind*. That Omo I and II appear to have lived contemporaneously and were found in the same general area (a few kilometres apart), indicate that they may even have lived together as part of a local human tribe.

Conclusions

While the ‘Middle Pleistocene’ fossil specimens are interpreted using an incorrect model (evolution) ‘the muddle in the middle’ will remain in a confusing state, and adding the name *Homo bodoensis* to the mix will not bring more clarity.

The main issue raised by the Leti find is how it and other *Homo naledi* specimens ended up in the inaccessible and cramped spaces of the cave. To me, the most logical explanation is that the people classified as *Homo naledi* may have been forced into the chamber and left there to die.

Based on new fossil pieces (lumbar vertebrae) from the lower back of *Australopithecus sediba*, headlines in the media claimed *sediba* “walked like a human, but climbed like an ape”. However, if *Australopithecus sediba* engaged in bipedalism it was likely in a strange, non-human manner.

The most logical explanation of the Laetoli footprints appears to be that the Site G and S footprints belonged to true humans, but the Site A footprints belonged to australopithecines, perhaps *Australopithecus afarensis*, but one cannot be sure of this.

The Omo fossils, redated for the second time, are given a minimum earlier date of allegedly 233 ka, which aligns the anatomically modern Omo I skull with newer evolution models of modern human origins, However, questions. remain concerning the reliability of such dates or redates. Also, the contemporaneous *Homo-erectus*-like Omo II cranium does not fit the evolutionary scenario.

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Australian marsupials: there and back again?

Michael J. Oard

To determine whether fossil fauna formed during or after the Flood, we need the location of the Flood/post-Flood boundary at each site. Correlation of local boundaries is currently imprecise because the geological column is not precise during the Cenozoic. Arment challenged the late Cenozoic boundary model based on his analysis of multiple genera of Australian marsupials that crossed three uniformitarian epoch boundaries. However, the key to determining the boundary is to encompass many kinds of rock and field evidence. Uniformitarian geologists initially dated marsupials as Pleistocene, but then pushed back their 'age' by a subjective method called 'biocorrelation', which depends on 'the stage of evolution'. The age of marsupials has thus been stretched back to the late Oligocene. The geology of Riversleigh, Australia, suggests that the animals lived in caves or fell into sinkholes early in the Ice Age. Then the caves were unroofed by acid rain. In central Australia, the marsupial fossils are associated with pluvial lakes from early in the Ice Age.

Numerous questions of biogeography are still unsolved for both uniformitarian and creation scientists.[1] Creation scientists must explain how the terrestrial animals dispersed from the Ark. However, this requires determining the Flood/post-Flood boundary at each location; to tell which fossils were buried during the Flood and which, after. Global uniformitarian boundaries may not be identical at each location,[2] so the Flood boundary has no uniformitarian equivalent.[1] That is why I suggest different locations can show a boundary in the Miocene, Pliocene, or even in the early- to mid-Pleistocene of the late Cenozoic.

Arment's fossil challenge

Arment[3] concluded that the post-Flood boundary in Australia was not in the late Cenozoic and does not contradict a boundary at the uniformitarian K/Pg boundary: "So, if the K/T boundary is postulated as recording the end of the final stage of the Flood, there is no data here that contradicts that."[4] He challenged the late Cenozoic boundary, arguing that many genera cross several uniformitarian stratigraphic boundaries, including the early to late Cenozoic. These are 61 marsupial genera that cross the Pliocene/Pleistocene boundary, 31 that cross the Miocene/Pliocene boundary, and 46 that cross the Oligocene/Miocene boundary—the line between the early and late Cenozoic. He concluded that since there are marsupials dated as early Cenozoic, then the late Cenozoic boundary model is wrong because too many lived both before and after the aforementioned boundaries.

Arment claims that one implication for a late Cenozoic boundary is that the marsupials needed to migrate to the Ark from Australia. However, this is unlikely.[2] But he is correct that the marsupials had to migrate from the Ark to Australia after the Flood. To estimate the probability of each marsupial genus migrating to Australia and not any other continent, Arment starts with the odds of arriving just in Australia as 1/6. He excludes Antarctica and makes Europe and Asia two continents.[5] He also assumes that the fossil genera are not found on other continents, which may not be true. More and more fossil surprises are found with further collecting (see below). Since the chance of one genus migrating to Australia is one in six, the odds of all the boundary-crossing marsupials making it to Australia has to be 1/6 to the power of the number of genera. Arment is assuming that the odds of each genus is 1/6, but it is possible that the each genus is not independent of other genera. Since marsupials coalesced in Australia and practically nowhere else, there may have been some reason why marsupials stayed together when migrating, making them interdependent. For all three boundaries, this becomes $(1/6)^{61}$, $(1/6)^{31}$, and $(1/6)^{46}$, respectively. These are astronomical odds, and he suggests that the post-Flood boundary cannot be in the late Cenozoic.

Arment's challenge answered

An accurate assessment of the boundary requires examining all the field evidence at each site. This can be difficult and time consuming. I have not examined the Australian sites and rely on literature descriptions. But I would argue that there is substantial evidence that marsupials from the late Oligocene to the present are post-Flood. This would place the post-Flood boundary at Arment's location just below the late Oligocene, or the very late early Cenozoic.

I believe the boundary is usually in the late Cenozoic, but, as described above, it can vary with place. If these locations show a boundary that extends *locally* into the Oligocene, arguing for a global, uniform correlation to the uniformitarian column is an unwarranted leap.

Arment is correct that the boundary at the sites he examined is below the Late Oligocene, according to uniformitarian dating. His conclusions apply to the marsupial fossil sites, but *not* to other sites in Australia or on other continents. Why these marsupial sites are an exception to the column is found in the unique dating method used by uniformitarian scientists.

There is a biostratigraphic break in Australia

If we expect a clear stratigraphic break or discontinuity to show the post-Flood boundary below the late Oligocene at the fossil sites, we will not be surprised that there is a gap of 25 Ma in the uniformitarian timescale until the marsupial fossils found in the Tingamarra Local Fauna at Murgon, southeast Queensland.[6] The dates for this site have been variously estimated, ranging from late Oligocene to late Paleocene,[6,7] suggesting that the uniformitarian dating of these sites is a rough estimate. The site is now dated as early Eocene.[8] Besides marsupials, there are many other types of animals, such as turtles, crocodiles, frogs, snakes, bats, birds, and a condylarth-like placental mammal,[9] if the descriptions are accurate. A condylarth is considered an extinct type of herbivorous placental mammal from the early Cenozoic.[10] This appears to be the earliest Cenozoic fossil site in Australia.

The Murgon site in Australia is not unique; marsupials, as well as placental mammals, are found on *all* the continents in the Cretaceous and early Cenozoic,[8] and were likely laid down by the Flood. The duck-billed platypus monotreme, once thought unique to Australia, has been found in the Paleocene of South America and Antarctica.[11] For the following discussion, all references to marsupials of Australia include only those found in and after the late Oligocene.

Why are marsupials dated to the late Oligocene?

The Australian sites assigned to the late Oligocene, Miocene, and Pliocene have been dated in a subjective manner called biocorrelation, which is based on an assumed 'stage of evolution'. They rarely can be radiometrically dated, since the local faunas are isolated, and there are few, if any, igneous intrusions or volcanic ash layers. Until 2016, there were only a little more than a half dozen widely dispersed radiometric dates associated with Tertiary marsupial fossils in Australia, including Tasmania:

> "Australia is one of the last continents to have a securely dated framework for the evolution of its Cenozoic terrestrial biotas. Until now, the vast majority of Australia's mammal-bearing deposits have been dated by biocorrelation, anchored by little more than half a dozen radiometric dates for the entire continent."[12]

One of these is a Rb-Sr date of 25 Ma on illite clay reported in 1983 from the Etadunna Formation, but the details of the dating had not been published as of 1993,[13] and the date is tentative as of 2016.[12]

Image: Uwe Dedering/Wikimedia, CC-BY-SA-3.0

Figure 1. Colour-coded elevation map of Queensland, Australia, showing the location of Riversleigh

Riversleigh initially dated as Pleistocene

An example of the dating uncertainty is Riversleigh—the main fossil marsupial site in Australia. It is a World Heritage Area, located near the Gregory River in northwest Queensland (figure 1).

The fossils are found in a 100 km^2 (39 mi^2) area with over 200 sites described as of 2006, with more sites added year after year.[14] Most of the fossils are unique to Riversleigh, but some are found elsewhere, and are used to help date those sites. Besides marsupials, a platypus, numerous bat species, various rats and mice, crocodiles, fish, frogs, turtles, lizards, snakes, various types of birds, lungfish, insects, arthropods, gastropods, and other invertebrates have been found,[14,15] including the unique marsupial mole.[16] The fossils occur in the soft Carl Creek Limestone, overlying Proterozoic siliciclastic rocks and Cambrian marine limestone and chert.[17]

When the Riversleigh fossils were first discovered, about 1900, they were dated as Pleistocene:

> "First, Cameron [in 1900] was convinced that the rocks that produced these fossils were no older than Pleistocene in age, i.e. less than 2 million years old, and many deposits of this age, even then, were known from Australia."[18]

The Riversleigh fossils were not considered 'old' until about 1950: "Before the 1950s, the marsupial record of the continent was generally believed to have no great antiquity."[19] They are now pushed back to the late Oligocene.

It is interesting that the Pleistocene date fits well with biblical expectations. The Pleistocene is the uniformitarian ice age period, and largely corresponds to the post-Flood Ice Age. Most terrestrial areas show a single glaciation event; it is data from deep ocean sediments and the hypothetical Milankovitch mechanism that have pushed the number of supposed ice ages to 50.[20,21] In areas not affected directly by the Ice Age, Pleistocene sediments are usually post-Flood. As an example of Pleistocene sediments likely from the Flood, hundreds- to thousands-of-metres thick strata is found in some basins.[22] For instance, the South Caspian Basin, northeast of Iran, is about 450 km (280 mi) in diameter and has a total thickness of about 27,000 m (88,500 ft) of sedimentary rock, most of it Cenozoic.[23] The top 10,000 m (32,800 ft) is regarded as Pliocene and Pleistocene.[24] Knapp *et al*. believe that the sedimentation rate was 2,000 m per million years for the past 5 Ma,[23] and if the Pleistocene was 2 million years long, that would mean 4,000 m of sediment accumulated during the Pleistocene.

Marsupial dates pushed back older than the Pleistocene by 'biocorrelation'

Numerous Pleistocene marsupial sites occur in Australia[25] with many of these marsupial families alive today. The number of pre-Pleistocene sites is small, around a dozen. I believe these sites are also post-Flood and have been misdated. The basis for misdating is an assumption of evolution as a valid correlation mechanism.

After 1950, paleontologists began calling features of the fossils, mainly teeth and jaws, 'primitive', 'derived', or 'advanced'. These terms were used in an evolutionary sense, and so implied younger or older dates. Kangaroo fossils, mostly teeth, from the Namba Formation in central Australia were judged to be 'extremely primitive'. Thus, the fossils were judged 'old' based on their 'stage of evolution'.[26] Uniformitarian scientists called this method *biocorrelation*.[27] Jones *et al*. inform us:

> "Unfortunately, the deposits that contain most Australian mammals are not readily dated in this way [by radioactive dating], and so other techniques and processes must be used.
>
> "One of these is called biocorrelation. Because of the large number of dated horizons in other areas of the world and in some places within Australia, it is sometimes possible to relate otherwise undated horizons containing fossils to a dated horizon somewhere else on the basis of shared fossils. Palaeontologists have used biocorrelation to date many Australian fossil mammal deposits."[28]

Since there are hardly any marsupial sites on other continents, paleontologists typically compare the sites only from Australia. These other sites have been also dated by biocorrelation: "Approximately 99% of the 360 fossil assemblages analyzed are classified using this method [biocorrelation]."[29] The procedure is subjective:

> "The principles and practices of stage-of-evolution biochronology are not formally encoded, but have developed through an evolving 'consensus of usage'."[30]

Biochronology is the method of correlating the fossils in time, while biocorrelation is the process of correlating fossils only. Recently, paleontologists have obtained several radiometric dates, but it is likely these radiometric dates were selected to fit previous biocorrelation 'dates'. U-Pb ages were determined on speleothems from unroofed caves at Riversleigh.[25] A hint that radiometric dates are fitted to previous beliefs was shown by Ayliffe *et al*.:

> "Despite the current widespread enthusiasm for sophisticated new numerical techniques used in analyzing existing data sets, major advances are likely to be slow and incremental, because they are reliant on field-based studies involving detailed analysis of sites conducive to multiple dating techniques."[31]

Radiometric dating has changed a few of the stages of evolution dates, such as that of the Riversleigh site of Rackham's Roost. It was previously dated as early- to mid-Pliocene based on the stage of evolution,[32] but now it is dated early Pleistocene, based on the U-Pb method on speleothems.[25]

Marsupials in the Etadunna Formation and/or its stratigraphic equivalent, the Namba Formation, of central Australia have also been dated by biocorrelation.[33] Stirton and others dated the Etadunna Formation as late Oligocene back in 1961, based on biocorrelation.[13,34] All the marsupial sites seem to use this method: "Another method in common use, at least until a more precise method can be found, is the assessment of the relative stage of evolution."[28] The Kangaroo Well Local Fauna of central Australia was also dated by biochronology.[35] A new site in the Northern Territory even used assumed evolutionary connections between different assemblages to extract a date in this manner:

> "The age of the assemblage can therefore only be assessed in terms of the relative stage-of-evolution of its members compared to their mostly closely related forms in other Local Faunas … ."[36]

Thus, ages of Australian marsupials are largely based on circular reasoning and evolution. The geological context may have helped persuade paleontologists that these sites are pre-Pleistocene. Riversleigh fossils were found in unroofed caves (see below), and those from central Australia are associated with pluvial lakes. The unroofing of caves and the drying of pluvial Lake Eyre would appear to take much time but can be explained by processes during the Ice Age.

Australia is probably the last continent with solid radiometric dates for its Cenozoic terrestrial biotas. Until now,

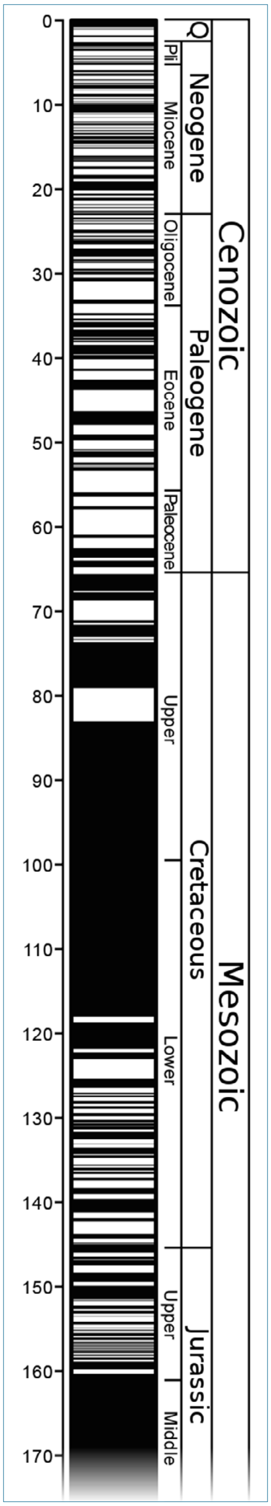

Figure 2. The standard magnetic timescale from the mid-Jurassic to the present. Dark areas are normal and light areas, reversals. The long black band is the Cretaceous normal superchron.

they have been dated by biocorrelation, anchored by a few scattered radiometric dates for the entire continent.[37] So the migration of dates from the Pleistocene to the Pliocene, Miocene, and even the late Oligocene, was accomplished by the subjective, non-standardized biochronology method that assumes evolution.

Biochronology is input to other areas of the world

The idea for biochronology in Australia actually got its start in North America by Stirton and others:[38]

> "The lack of formality [of biochronology] has an historic irony, for the development of codes governing other branches of stratigraphy owes much to studies of the thick, mammal-rich, non-marine sediment of the North American interior where stage-of-evolution biochronology originated … ."[39]

It is also used to date fossils in South America:

> "Most biostratigraphic sequences in Patagonia and elsewhere in South America have been based on the evolutionary stage and taxonomic representation of 'ungulates' (archaic endemic herbivores or southern ungulates) and/or marsupials."[40]

Paleomagnetism reinforces biocorrelation

Long *et al*. also have used paleomagnetism as a dating tool.[28] But a hiatus or a period of rapid sedimentation can affect a local paleomagnetic profile, making it easy to be off a reversal cycle. Because time is an unknown, any section can be made to fit the secular polarity chart (figure 2). Thus, paleomagnetism must be 'anchored' to other dating methods; it is not an independent dating method and hence is subjective:

> "Magnetic polarity zones, however, are not in themselves uniquely diagnostic, and without the aid of additional stratigraphy indicators, correlation of magnetic zones in terrestrial sequences is problematic. For example, differences in depositional rates, and/or diagenetic histories between two areas, or the presence of subtle unconformities, can result in an unrecognizable mismatch of polarity zones."[41]

Moreover, even in a particular normal interval, numerous 'excursions' occur. A paleomagnetic excursion is defined as a brief period of less than 10,000 ka during which the geomagnetic pole almost reverses. For instance, 10 polarity reversals and 27 excursions supposedly occurred in the past 2.6 Ma, the Quaternary, with seven excursions in the Bruhnes normal polarity chron.[42] With so many reversals, as shown on figure 2, combined with even more excursions, even small hiatuses or slight increases in sedimentation would throw off the dating. Worse, an unexpected paleomagnetic sequence can be explained by 'previously undetected' changes in sedimentation.

In the case of Australian marsupials, the subjectivity of using evolutionary changes to assign dates; reworking; and using nomenclature to obscure similarities between organisms from different countries, regions, and assumed ages are some of the reasons for skepticism of biostratigraphic correlations over long distances. It is also why I do not take the uniformitarian Cenozoic fossil ages as globally synchronous. The Upper Cenozoic seems to be highly diachronous within biblical earth history.[2]

Another boundary fluctuation

Uniformitarians want the public to consider the timescale as absolute, but they adjust dates and even stages at will. Simply noting the differences between the 2004 and 2016 scales shows that.[43,44] This 'insider' flexibility is seen in pushing the Antarctic Ice Sheet into the early Cenozoic. It had once been assigned to the late Pliocene/Pleistocene.[45] Then scientists found what they considered ice-rafted debris (IRD) in early Cenozoic deep-sea cores off Antarctica.[46,47] Those dates were likely from marine microorganism biocorrelation. Since IRD implies icebergs, which implies an ice sheet that reaches the ocean, the age of the ice sheet increased by a factor of ten:

> "Increasing the duration of the Ice Age by a factor of about 10 greatly increases the stress upon the creation scientists, who must compress the events of 15 m.y. into 4,000 y. of post-Flood time."[48]

The Antarctic Ice Sheet is now believed to have initiated between 32 and 42 Ma, and reached equilibrium at 15 Ma.[49] So, in regard to the Antarctic Ice Sheet, the post-Flood boundary would be near the uniformitarian Eocene/Oligocene boundary. The boundary is typically Miocene or younger. But if evolutionists change their dating of events that obviously mark the boundary and creationists rely on uniformitarian stratigraphy, we should expect the boundary age to bounce around, regardless of the field evidence that shows the location of the boundary.

Image: Huygens/Wikimedia, CC-BY-SA-2.0

Figure 3. Typical landscape at Riversleigh, northeast Queensland, Australia

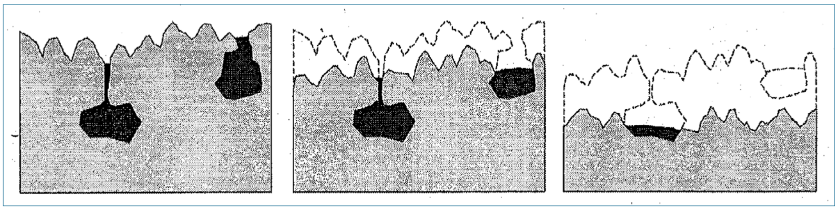

Figure 4. Schematic of the progress from cave and crevasse fills to unroofing caused by the dissolving of the surrounding limestone, leaving the deposit at or near the surface (from Arena *et al.*, 2014, figure 6, p. 34. Used in accordance with federal copyright (fair use doctrine) law. Usage by CMI does not imply endorsement of copyright holder).

How can early Cenozoic IRD be explained?

In the case of Antarctica, how do we explain ice-rafted debris (IRD) in biblical earth history? There are several possibilities. First, it is possibly not true IRD. At the end of the Flood, receding waters would have transported coarse sediments into the oceans (e.g. the Whopper Sand[50]). Coarse sediments can also be moved along the ocean bottom by currents or mass flows. Second, if the debris is IRD, then the host sediments are post-Flood, regardless of the uniformitarian age.

The study of ocean bottom sediments is a relatively new part of earth science. Creation scientists have not yet examined them closely and confidently explained them in biblical earth history. This must include evaluating the dating systems for ocean bottom sediments and any correlations to continental sediments. Ocean sediments are predominantly dated by microorganisms. Like terrestrial biostratigraphy, it relies on the assumption of evolutionary changes in those organisms.

Geological evidence that Riversleigh marsupials are post-Flood

Despite the uniformitarian ages, Australian fossil marsupial sites can be explained by the Ice Age.[51–53] The 35 criteria that determine the Flood/post-Flood boundary[2] do not seem to apply to the Riversleigh fossil sites. The fossil sites appear to be mostly near ground level with little relief (figure 3).

But other criteria indicate the sites are likely post-Flood. First, undeformed fossils are found in the soft limestone.[17] Some are articulated. Second, the fossils originated as deposits from crevasses and caves in the karst bedrock and are often found in flowstone, a type of speleothem. Third, numerous bat fossils occur with bat guano, better preserving them.[28,54] It is difficult to envision bat guano surviving the violence of the Flood. These lines of evidence suggest that the site is post-Flood, although dated into the Oligocene.

These fossil locations are out in the open because the caves were ‘unroofed’; the top has dissolved and the walls have widened (figure 4).[17] Similar caves are found elsewhere:

> “The occurrence of surface outcrops of deposits originally formed in cave interiors, also referred to as ‘unroofed caves’ (Mihevc, 1996), has been recognized as a common occurrence on the surface of karst terrains, particularly in the ‘classic’ karst terrains of Europe ... . Such deposits had previously been interpreted as clastic fluvio-lacustrine deposits formed by surface processes … . Denudational surface lowering is now widely recognized as a common process responsible for the attrition of enclosing solution-prone rocks with consequent exposure of cave deposits that include speleothems, detrital fills, biogenic deposits and phreatic flow deposits … .”[55]

Uniformitarian scientists believe unroofed caves are old, based on present-day erosion rates.

Image: Tentotwo/Wikimedia, CC-BY-SA-3.0

Figure 5. Colour-coded map of South Australia, showing the locations of Lakes Eyre and Frome today

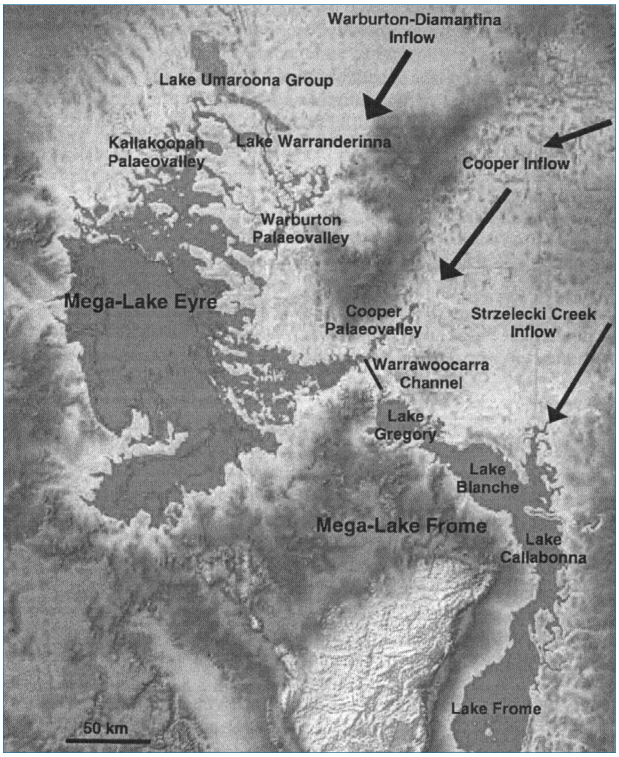

Figure 6. Mega-Lake Eyre and Mega-Lake Frome, based on paleo shorelines. The two megalakes were once connected through the Warrawoocarra Channel (from Webb, 2010, figure 2, p. 314.[63] Used in accordance with federal copyright (fair use doctrine) law. Usage by CMI does not imply endorsement of copyright holder.). The lake basin is assumed to be from a highstand during the Quaternary, which likely corresponds to the water level during the wet early post-Flood Ice Age.

Geological evidence from central Australia likely post-Flood

Marsupials are also found in northern South Australia, within the ancient lake basins of Lake Eyre, Lake Frome (figure 5), and other nearby lakes. These lakes may have once been joined (figure 6). Fossils have been found in the correlative Etadunna and Namba formations. The Etadunna was once dated at 15 Ma, but jumped to about 25 Ma, based on biocorrelation and paleomagnetism.[34] The fossils are believed to be in lake and river deposits, which suggests post-Flood, if the paleoenvironmental interpretation is correct. Other areas in central Australia, such as the Kangaroo Well and Pwerte Marnte Marnte Local Faunas, are also likely post-Flood, though dated lower in the Cenozoic by biocorrelation.[35,36]

Marsupials related to the Ice Age

Moreover, the geology of the sites is best explained by the Ice Age. At Riversleigh, limestone caves could have formed during the Flood.[56] Marsupials and other animals arriving early in the Ice Age may have lived in the caves. This was a time of mild winters, cool summers, and heavy precipitation due to high evaporation from the warm ocean.[51] The area could have been similar to a tropical rainforest,[15] although plant fossils are mysteriously rare.[57] This could be because the limestone created a high pH, and plants are best preserved in acidic conditions.[58] Uniformitarian scientists claim that northern and central Australia had an early- to mid-Miocene monsoon climate, but climate models cannot duplicate it.[59]

Immediate post-Flood volcanism created aerosols, which in turn caused acid rain. It could have dissolved the karst and exposed the cave fill within a few centuries. This timing suggests rapid animal migration from Ararat. Caves would offer shelter. Many of the animals that died in the caves could have been covered by ‘soft’ limestone, or flowstone. Others may have fallen into sinkholes. Then the area was denuded by heavy acid rain, dissolving cave roofs and walls (figure 4). In the mid to late Ice Age, volcanism decreased, the oceans cooled, and the climate transitioned to warmer summers and cooler winters.[60] Uniformitarian scientists put this climate change mainly in the Miocene, although they claim that the Pleistocene climate oscillated between wet and dry, likely influenced by Milankovitch theory's claims of multiple Pleistocene ice ages.

In central Australia, pluvial lakes covered a large area (figure 6) during the early to mid-Miocene: "Several lines of evidence suggest that one or more inland water bodies of considerable size existed in central Australia."[61] If the current playa Lake Mega-Eyre were raised 25 m (82 ft), based on its 'Quaternary depth', it would combine with Lake Mega-Frome to form an immense lake in central Australia.[62]

The enclosed basin of this lake likely was initially filled during the Flood, as shown by marine foraminifera.[34] Heavy early Ice Age rain maintained the lakes and resulted in rapid sedimentation. Marsupials were buried in lake and river sediments. During the mid to late Ice Age, the pluvial lakes dried, and marsupial fossils are found in the lakeshore sediments of those dying lakes.

Conclusions

Arment is to be applauded for tackling the vexing problem of biogeography for the Australian marsupials. However, evidence shows that strata now assigned as late Oligocene, Miocene, and Pliocene were dated by the questionable method of biochronology. Secular scientists frequently move dates, such as pushing the age of the Antarctic Ice Sheet back to the Eocene/Oligocene boundary. Radiometric dates for these fossil sites were not published until after 2015, and, based on typical practice, seem to have been cherry-picked to fit the 'known age'. All the marsupial sites in Australia, except Murgon, are likely from the Ice Age. That would push the post-Flood boundary a little 'deeper' with respect to the geologic column at these sites. However, those dates are much less significant than the cumulative field evidence. Arment's concerns are vitiated, and the perceived need for improbable two-way migrations voided.

Finally, I need to emphasize that the boundary just below the late Oligocene *only* applies to these fossil sites and not uniformly across Australia. Neither does it apply to other continents, since each continent and each site must be viewed on its own merits.

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Earth's upper mantle viscosity may be lower than assumed

Michael J. Oard and Nathan Mogk

The deformation of the lithosphere and asthenosphere is assumed by uniformitarian scientists to be very slow. The key measure of the resistance of the deformation of the solid earth is viscosity. When a load, like ice, is added to the surface of the earth, the surface is pushed down. When the load is taken off, the surface rebounds upward. Eastern Canada and Scandinavia are currently rising because of the melting of the Laurentide and Scandinavian ice sheets. Based on the assumed deep-time history of the Ice Age, uniformitarian geologists calculate a fairly high upper mantle viscosity of around 3–10 x 10^{20} Pa·s. However, calculations at many locations have shown a much lower viscosity for the asthenosphere, including pluvial lakes Bonneville and Lahontan, southeast Alaska, Iceland, and post-seismic earthquake motions in various areas. Regardless of the many complications and assumptions that go into viscosity estimates, it is safe to say that the viscosity and rheology of the upper mantle vary considerably. In biblical earth history, with a short timescale and a different Ice Age history, the upper mantle viscosities would be lower by at least a factor of five. This would imply deformation is faster and operates over shorter-length scales than commonly believed. This would be true in both a catastrophic plate tectonics and an impact Flood model.

Several creation scientists are attempting to produce a comprehensive global Flood model, but all models need work.[1] Such a Flood model is important because it would tie a lot of observations and deductions of the earth together that should be superior to uniformitarian models. We could also solve many other earth-science challenges by placing the challenges within the real framework for numerous earth processes—the Genesis Flood. One of those main processes involves deformation and tectonics. How fast does the earth deform by horizontal and/or vertical forces on the lithosphere? This question is of great practical importance as many people live in areas with seismic risk.

Secular scientists believe in very slow lithospheric deformation, partly based on their assumptions of deep time. On the other hand, any Flood model must postulate rapid deformation during the Flood—within a year or so.

What is viscosity?

Viscosity is "The property of a substance to offer internal resistance to flow."[2] The higher the viscosity, the more resistant to flow. Dynamic viscosity is in units of force x time divided by area or in SI units newtons x sec per m^2 or pascal seconds (Pa·s). Viscosity of natural materials, particularly solids, can be so large that only the order of magnitude is considered. The viscosity of water is about 10^{-3} Pa·s, while solid rock is on the order of 10^{20} Pa·s. A change from 10^{19} to 10^{20} Pa·s is an increase of 10 times the resistance to flow.

The viscosities in this paper will be applied to solid rock in the field of rheology, "the study of the deformation or flow of matter."[3] The viscosity is an important variable determining the flow or strain by an applied force. Strain is essentially the fractional change in thickness resulting from an applied force per unit area, or stress.

Earth's interior

The earth's interior is made up of layers of differing composition: crust, mantle, and core. The upper mantle and crust are fixed to each other and behave similarly mechanically, and together are called the lithosphere. Beneath the lithosphere is the asthenosphere, a low seismic velocity zone of unknown thickness. Lower seismic velocities likely correspond to higher temperature, and therefore lower viscosity layers. The origin and nature of the asthenosphere is very complex and debated.[4,5] It could be a layer of partial melt, increased water content, a compositional change, a temperature change, or a combination. Most believe it is a layer of partial melt.[6] But this is a simplification, since the asthenosphere is often missing beneath continents.[7] But a low velocity zone or zones, not necessarily the asthenosphere, have been detected below continents. The lithosphere/asthenosphere boundary can be sharp or diffuse. The depth of a low velocity layer can be variable, with poor lateral continuity.[8] The seismic velocity is greater in the lithosphere than in the asthenosphere, and thus the asthenosphere will more easily flow when a load is added to the surface of the earth, such as an ice sheet.

Another observation supporting the distinction between lithosphere and asthenosphere has been that earthquakes

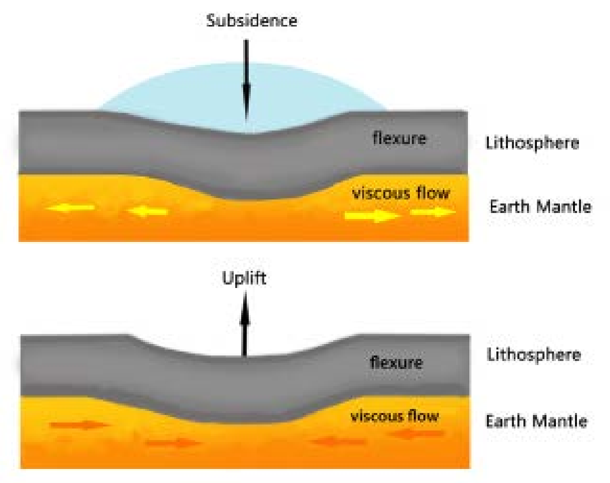

Figure 1. Glacial isostasy (drawn by Mrs Melanie Richard). In the top diagram, the ice pushes the lithosphere down, but after the ice melts, the lithosphere slowly rebounds upward.

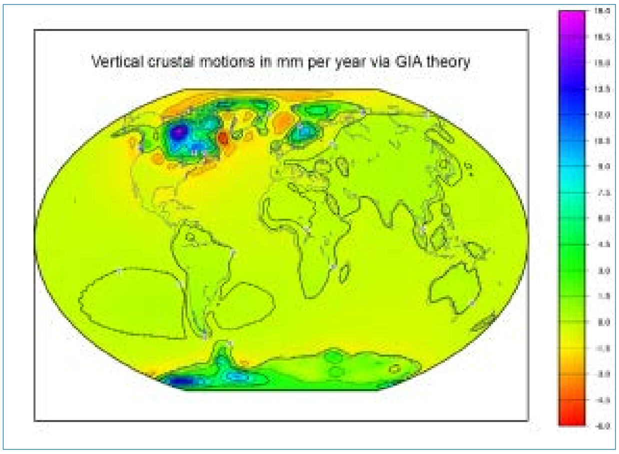

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Figure 2. Rate of lithospheric uplift due to post-glacial rebound. Note two centres of uplift for the melted Laurentide Ice Sheet corresponding to two ice domes.

caused by brittle failure of the rocks can occur both in the upper crust and the upper mantle.[9] However, with improved technology and higher resolution seismic networks, it is being recognized that the entire crust can be seismogenic (prone to earthquakes),[10] and the upper mantle may not significantly contribute to the strength of the lithosphere. This new understanding may undermine many of the rheological estimates done in the past.[11]

When modelling the earth's interior for glacial isostatic adjustment (GIA) studies, researchers commonly use PREM (Preliminary Reference Earth Model) derived from seismic data.[12] PREM is a 1 D average for the whole earth with depth of such variables as density and elastic structure.[13] Of course, it does not catch the horizontal variability of the upper mantle, and so may be a poor earth model to apply in some areas.

The assumed viscosity of the upper mantle based on Ice Age history

Isostatic depression and rebound is believed to be proportional to the density difference of the ice and the crust/upper mantle. Uniformitarian scientists commonly assume that the ice is about ⅓ the density of the crust and upper mantle.[14] So, for every 3 m of ice, the crust and upper mantle would have been pushed down about 1 m. During the build-up of ice, the rock of the crust and upper mantle is depressed and flows to the edges of the ice build-up, where rock accumulates and pushes the land up as the 'forebulge'. When ice melts, the depressed area slowly rebounds (figure 1) while the forebulge sinks, depending upon the rheology in the particular area.

Uniformitarian scientists assume that the thickness in the centre of the two ice sheets was about 3,000–4,000 m. So, the isostatic depression would be around 1,000–1,300 m in the centre of the ice sheet. Scandinavia and eastern Canada are observed to be isostatically rebounding (figure 2). Figure 3 shows a blow-up glacial isostatic rebound for Scandinavia. The shoreline of the northern Gulf of Bothnia of the Baltic Sea has been measured to be rising at about 1 cm/yr (figure 4), while the forebulge over the southwest United Kingdom is sinking (figure 5). The Hudson Bay area is also rising about 1 cm/yr,[15] leaving a series of shoreline terraces (figure 6). The highest estimated marine elevation in Scandinavia is 250 m.[16] Much of southern Finland was underwater right after the ice melted (figure 7). It is unknown how much rebound is left. Some have thought that some of this remaining uplift could be due to tectonic forces[17,18] or due to mantle convection.[19] However, this is unlikely, and likely difficult to know, since the areas of glacial isostatic and the proposed tectonic uplift are in the same locations.

Based on the isostatic rebound around the centre of the former Scandinavian and Laurentide Ice Sheets, uniformitarian scientists have calculated Earth's rheology:

> "Much of what is known about the rheology of Earth's deep interior has been inferred from modeling vertical motions caused by waxing and waning of ice sheets and recorded by marine shorelines."[20]

Early workers assumed a high viscosity of the upper mantle, which depended upon the uplift history and the estimated amount of isostatic rebound remaining. In 1941, Gutenberg estimated a viscosity of 3 x 10^{20} Pa·s, assuming the remaining uplift was only 20 m, while Vening Meinesz, in 1937, estimated a viscosity of 3 x 10^{21} Pa·s, assuming the remaining uplift is 180 m.[21]

Dividing the upper mantle up into the lithosphere and asthenosphere in later models resulted in a lithosphere viscosity of 0.7–1.0 x 10^{21} Pa·s and an asthenosphere viscosity of 7.0 x 10^{19} Pa·s, using an asthenosphere thickness less than 150 km and a very thick Scandinavian Ice Sheet.[22] The assumed thickness of the past ice sheet determines how much rebound should occur in the models, which vary.[23] However, there is a question of whether the asthenosphere even exists under Scandinavia. Because of the rheological assumptions, various models obtain different results.[24] Assuming no asthenosphere, the upper mantle viscosity beneath Scandinavia is 3–10 x 10^{20} Pa·s.[23]

The earth's mantle viscosity based on GIA modelling has been debated for many decades and especially depends upon model parameters and ice sheet history.[25] Lau *et al.* state: "Inferences of mantle viscosity using glacial isostatic adjustment (GIA) data are hampered by data sensitivity to the space-time geometry of ice cover."[26] With no asthenosphere below Scandinavia, the mantle viscosity is believed to slowly increase downward from an upper mantle value of about 3 x 10^{20} Pa·s.

Researchers are realizing that the upper mantle structure and viscosity vary considerably in the horizontal direction across the earth, and that GIA research over Scandinavia or Hudson Bay cannot determine the viscosity over the remainder of the earth.[27] Lithospheric thickness varies considerably, ranging from zero over mid-ocean ridges to about 280 km over Australia, North America, and northern European cratonic settings. The viscosity can vary by six orders of magnitude. Recent determinations in other areas of the world reinforce this (see below). This shows that a detailed, accurate ice model is crucial for GIA modelling and interpretation: "Thus, a well calibrated, detailed ice model is indispensable in GIA modelling."[28] The viscosities should be recalculated for Scandinavia and Hudson Bay region using biblical time and Ice Sheet variables.

The viscosity calculated from Lakes Bonneville and Lahontan shorelines

Earth scientists usually assume the Earth's upper mantle viscosity is similar to what they found with GIA studies of the melted ice sheets. The calculations made for Scandinavia and eastern Canada should apply only to those areas. But there are numerous indications that the earth's viscosity is much lower at many other locations.

Lake Bonneville was an Ice Age pluvial lake, one of dozens, that filled the Great Basin of the southwest United States in the vicinity of Great Salt Lake, Utah. It was about 350 m deep and about twelve times the size of Great Salt Lake.[29] The depth compares to the present average depth for Great Salt Lake of 3.7 m. Lake Bonneville had a volume of 10,300 km^3, near that of Lake Michigan. Shorelines are obvious and abundant (figure 8). Lake Bonneville fell about 100 m due to the Bonneville flood.[30] Then the rest of the lake evaporated, leaving behind salt and other minerals, creating the Bonneville Salt Flats of northwestern Utah (figure 9). The flats are used as a speedway for testing cars and attempting to set speed records.

The ancient shorelines of Lake Bonneville were among the first features in the late 1800s that indicated the earth responds to surface loads. Geologists G.K. Gilbert noticed the shorelines were bowed upward where the water was deepest. A recent analysis of Lake Bonneville uplift indicated the shorelines were bowed up more than 70 m in the centre. Using an updated uniformitarian lake chronology resulted in a best fit model with a thin elastic part of the upper lithosphere of 15–25 km and an asthenosphere viscosity about 10^{19} Pa·s.[31] An earlier estimate by Bills *et al.* had found a viscosity of about 4 x 10^{17} Pa·s from 40 km to 150 km depth.[32] These upper mantle viscosity estimates are more than 2 orders of magnitude less than the earlier assumed global average upper mantle viscosity estimated from the GIA for the past ice sheets.

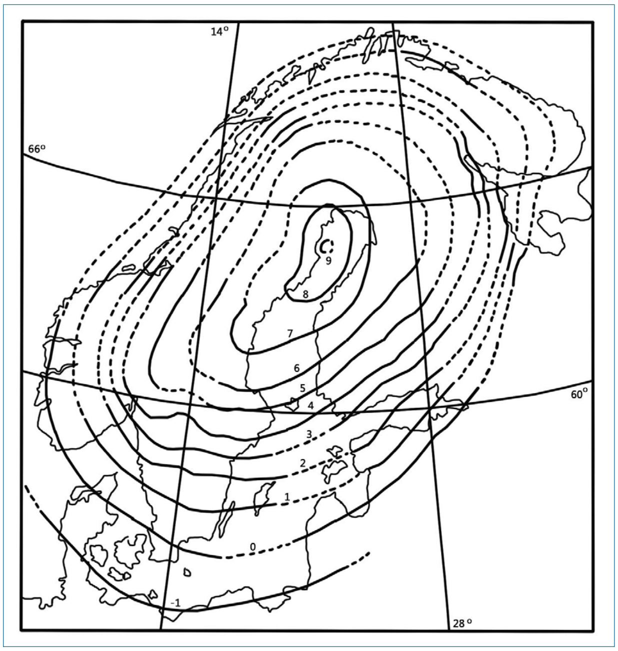

Figure 3. Map of post-glacial uplift in Scandinavia (1892–1991) in mm/year[57]

Figure 4. Sea level fall in the northern Gulf of Bothnia along the northeast Swedish coast, showing the location of sea level in 1846 and the amount of fall since then

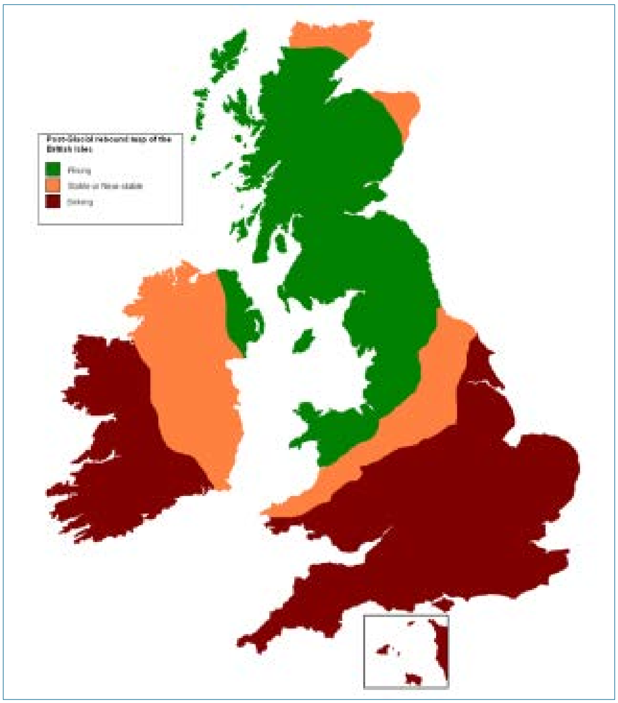

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Figure 5. A map of post-glacial rebound on the British Isles, showing where land is still rising and where land is sinking due to the collapse of the forebulge

Image: Mike Beauregard/Wikimedia, CC-BY-2.0

Figure 6. Layered beach ridges caused by isostatic rebound on Bathurst Inlet, Nunavut are an example of post-glacial rebound after melting of the Laurentide Ice Sheet after the last Ice Age.

One problem with this calculation from the point of view of biblical history is that deep time is built in, for instance by assuming Lake Bonneville existed 30–10 ka years ago. This age will influence the calculations, and the viscosity in biblical earth history would be lower in this area.

Lake Lahontan, western Nevada and a small part of California, USA, was another Ice Age lake in the Great Basin. Its shorelines were bowed up about 22 m.[33] Preliminary models indicate that the upper mantle viscosity beneath the former lake was about 10^{18} Pa·s and that rebound only lasted 300 years. Just like with calculations of Lake Bonneville isostasy, deep time is built in. So, within biblical earth history, the viscosity should be lower. A more recent calculation of Lake Lahontan uplift, but including earthquakes in western Nevada and adjacent California, USA, gave an asthenosphere viscosity of 5 x 10^{18} Pa·s.[34] However, the two-sigma uncertainty ranged from 5 x 10^{17} Pa·s to 5 x 10^{19} Pa·s because of uncertainties about Lake Lahontan.

Modern-day ice melting calculations

There are measures of upper mantle viscosity that contain few, if any, assumptions. These indicate an even lower asthenosphere viscosity, for at least those locations.

Practically all glaciers in the world have receded, and are currently receding, because of global warming, which has been only about 1°C, much of which can be attributed to natural processes.[35] Therefore, some glaciated areas have lost much ice over the last few hundred years, since the end of the Little Ice Age. For instance, Glacier Bay, Alaska, had an ice stream that had flowed all the way to the entrance of the bay by 1794, as observed by Joseph Whidbey on the ship *Discovery* during the Vancouver expedition. In 1879, naturalist John Muir observed that the glacier had retreated 77 km up to the end of the bay, losing an estimated 3,030 km^3 of ice, enough to raise sea level 8 mm. This retreat actually occurred before the end of the Little Ice Age in 1880 and before humans were adding significant CO_2 to the atmosphere.

Recent GPS measurements of Southeast Alaska, including the high St Elias Mountains, have shown that Southeast Alaska is uplifting at about 3 cm/yr.[36] It is believed that the onset of deglaciation of the St Elias Range began in 1880. Remarkably, GPS has also discovered seasonal and year-to-year variations of uplift rate based on annual temperatures and snowfall differences. The viscosity based on 55 km thick lithosphere and a 230 km asthenosphere resulted in a viscosity of 3 x 10^{19} Pa·s. Earlier estimates found a viscosity an order of magnitude less with a thinner asthenosphere of 110 km. There is a trade-off between the assumed thickness of the asthenosphere and the viscosity. The thinner the asthenosphere, the lower the viscosity and vice versa.

The viscosity below Iceland

All glaciers on Iceland advanced during the Little Ice Age (LIA). Glaciers were further advanced during the LIA than during the Great Ice Age caused by the Flood,[37] probably due to Iceland being surrounded by warm water for most of the time of the Great Ice Age, retarding glaciation. The largest glacier on Iceland, Vatnajökull, has been melting since the end of the LIA in about 1890 and the area has been rebounding upward. From this uplift, the asthenosphere viscosity has been variably estimated at 5 x 10^{17} Pa·s,[38] 1–2 x 10^{18} Pa·s,[39] 5 x 10^{18} Pa·s,[40] 4–10 x 10^{18} Pa·s,[41] and 1 x 10^{18} Pa·s – 5 x 10^{19} Pa·s.[42] Other researchers have estimated an asthenospheric viscosity as low as 7 x 10^{16} Pa·s.[39] These estimates are quite variable and probably depend upon the particular upper mantle model, the exact melting and uplift history of Iceland, and the mathematical solution to the equations. These low viscosities are much less than would be assumed from Scandinavia: "The sub-lithospheric [asthenosphere] viscosity has a maximum value of ~1 x 10^{19} Pa·s, about 100 times less than the commonly accepted value for the upper mantle."[43] The low viscosity is likely attributed to a fair percentage of upper mantle melt.

Earthquake viscosity measurements

When an earthquake strikes, the rapid co-seismic movement of the rupture relaxes during post-seismic relaxation, depending upon the viscosity of the upper mantle. The movements can be observed by GPS and other geodetic mechanisms in real time, so no assumptions of deep time enter in. The viscosities of the asthenosphere are sometimes measured to be very low. For instance, based on earthquakes in the northwest Pacific, the asthenosphere viscosity was estimated at 5 x 10^{17} Pa·s.[44] GPS discovered that after the 2002 M7.9 Denali, Alaska, earthquake, the viscosity was as low as 10^{17} Pa·s for two weeks.[45] A viscosity of 8 x 10^{18} Pa·s for a depth of 220–660 km was calculated for the great 2004 Sumatra–Andaman earthquake with a transient viscosity of 1–4 x 10^{17} Pa·s.[46,47] The great 2011 Tohoku-oki earthquake off Japan is believed to have shown a transient viscosity of around 2.5–5.0 x 10^{17} Pa·s with a steady state viscosity of 1.8 x 10^{18} Pa·s to 1.0 x 10^{19} Pa·s.[48] Based on earthquakes in the Mojave Desert of California, relaxation viscosities were 10^{17} Pa·s but may be as low as 10^{16} Pa·s.[49]

Some researchers suggest that the low transient viscosity may have been stress induced. Viscosities related to earthquake motion are much lower than those deduced from GIA studies:

> "Transient rheologies have also been suggested by other geodetic studies of postseismic deformation at times scales of a few days to decades … . For instance, *Pollitz et al.* [1998] inferred a steady state viscosity of 5 x 10^{17} Pa·s for the oceanic asthenosphere. This is in agreement with the value of the transient asthenospheric viscosity in the present model, and indicates again the existence of a LVZ [Low Velocity Zone] in the shallow mantle. Other studies in tectonically active continental regions … yield similar estimates of the steady state viscosity in the upper mantle, and they are generally much lower than those derived from postglacial rebound studies."[50]

The much lower viscosity deduced for earthquakes, melting of glaciers in mountains, and the other areas that were estimated are believed to be locations where the viscosity is low, possibly due to water and/or melt. It is difficult to know how representative these viscosities are for the asthenosphere in more stable areas, such as the US Midwest. But part of the reason these viscosity estimates are much lower than those derived from GIA of the past ice sheets could be that deep time is assumed in the latter.

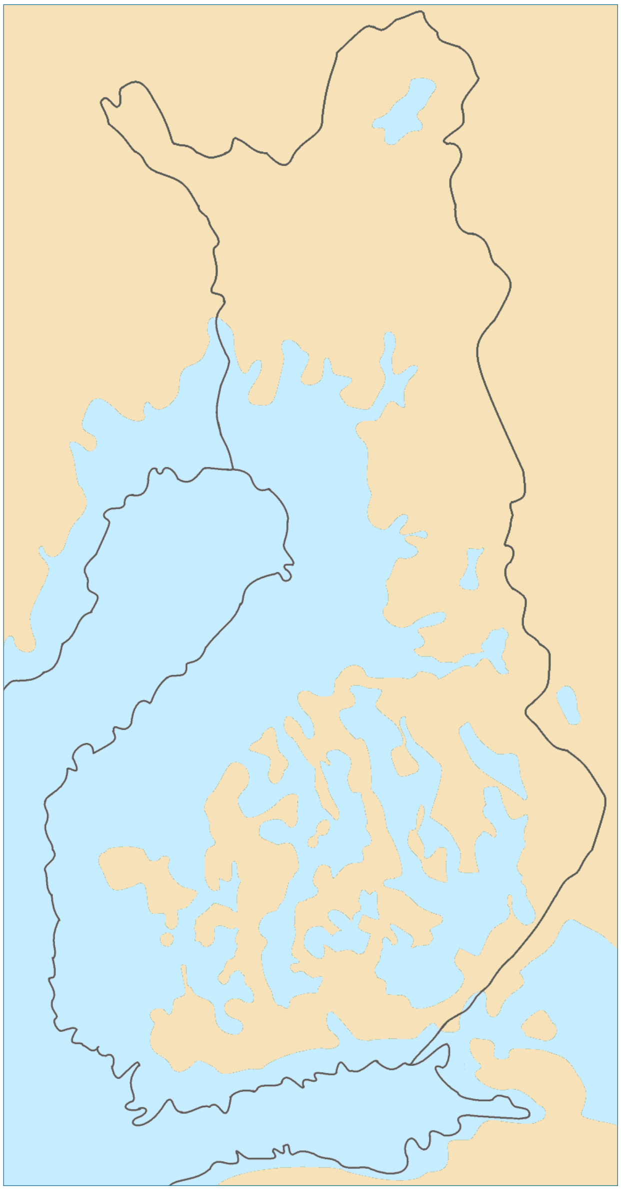

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Figure 7. The coastline of Finland after the last ice age, about 11,000 years ago, before glacial rebound

Creation science applications

From the point of view of biblical earth history, the ice sheets were about 40% as thick as those postulated by uniformitarian scientists.[51,52] Moreover, deep time is built in, with the ice sheets melting from 21 ka to 7 ka,[12] while in the biblical model they melt at about 4,000–3,800 years ago. So, the viscosity determined by GIA models would very likely be much less in biblical earth history than calculated

Figure 8. Lake Bonneville shoreline at base of mountains north of Salt Lake City, Utah

Figure 9. Bonneville Salt Flat, northwest Utah

by uniformitarian models. Equations calculated with biblical Ice Age variables show the viscosity below the former ice sheets is lower, with a decrease that is proportional to the time since glaciation. Following the derivational approach of Turcotte and Schubert,[53] a simple two-dimensional half-space model of isostatic rebound, not taking into account flexural rigidity, can be derived, which yields a relation where initial displacements of the crust decays exponentially according to a characteristic relaxation time:

$$\pi_r = \frac{4\pi \nu}{g\lambda},$$

where ν is the kinematic viscosity of the mantle, and λ is the wavelength of the displacement feature. As can be seen, the mantle viscosity is linearly related to the relaxation time of the system. Simple as it is, for the size of Fennoscandia and the secular uplift time of 21 ka, this model yields results in close agreement with Simons and Hager.[54] Given the approximate available relaxation time in the biblical timeline of the Ice Age, this same model gives a mantle viscosity which is lower by a factor of five for Fennoscandia, since the available relaxation time in the biblical model is lower than that in the secular model by the same factor.

The newly emerging research regarding the relative strengths of lower crust and upper mantle would also imply that isostatic rebound happens at faster timescales[55] and is more localized to individual tectonic blocks than has previously been assumed.[56]

Regardless, it is likely that the viscosity and the rheology of the Earth's mantle are much lower in many other regions than just where the past ice sheets melted. Moreover, they vary horizontally and vertically. Could there be a cause of such variability resulting from Flood events? Could the upper mantle have been created with variable viscosity and rheology? Lower viscosities would result in faster folding and deformation of rocks, whether the Flood was caused by catastrophic plate tectonics, impacts, or both.

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Racemization of amino acids under natural conditions: part 1—a challenge to abiogenesis

Royal Truman

Three-dimensional structure is a minimum prerequisite for protein functions. I show that even for optimized amino acid sequences under ideal laboratory conditions only 5–10% randomly distributed D-amino acids would prevent polypeptides composed of L-amino acids from forming a stable structure in water. Parity violation and selective degradation of one amino acid enantiomer by circularly polarized light could not have produced the necessary L-amino acid excess. Carefully designed experiments to amplify an initial enantiomeric excess using partial sublimation, crystallization separation techniques, isolation of eutectic mixtures, chiral minerals, and chiral auxiliaries are not plausible naturalistic solutions for the origin of large enantiopure peptides.

Professor Bada pointed out, in 1991, that "Currently, considerable controversy exists about the source of the organic compounds necessary for the origin of life on Earth."[1] Only a limited variety of organic molecules would have formed and in at best only trace quantities given the insignificant amount of reducing gases thought to have been present in the early earth.[2–5] The alleged frequent impacts of objects 10–100 km in diameter on the early earth would have pyrolyzed all organics present and prevented the origin of primitive organisms.[5] Furthermore, the annual source of amino acids (AAs) into the oceans from micrometeorite and cosmic dust which survived pyrolysis during atmospheric passage would have been $< 3 \times 10^{-15}$ g/l per year.[1] The maximum accumulation time would have been about 10 million years, since the entire oceans would have circulated through the hydrothermal vents during this time period, completely destroying AAs. Bada concluded that the maximum concentration of AAs in ancient oceans would have been only about 10^{-8} g/l, which corresponds to a concentration of $\sim 10^{-10}$ M, using an AA average molecular weight of about 110 daltons.[1]

In this 4-part series I will document laboratory data to help quantitatively evaluate abiogenesis scenarios. Future papers will rely on these to make my critiques more precise.

The homochirality problem

All proteinogenic AAs except glycine can exist as D or L enantiomeric forms, which are non-superimposable mirror images of each other (figure 1). Since Louis Pasteur's discovery of chiral crystals in 1848, scientists have been searching for a naturalistic origin for the homochirality of biomolecules. Homochirality refers to the use of almost exclusively L-AAs to form proteins and of D-sugars (figure 2) for RNA and DNA polymers.

Enantioselective synthesis of chiral molecules has been researched intensively for two centuries, providing deep understanding and techniques for medical and industrial purposes. The rewards are high. Knowles, Noyori, and Sharpless won Nobel prizes in 2001 for their work on chiral catalysis. But for abiogenesis purposes the conditions must be naturalistic and not expertly designed.

The efforts to find a naturalist explanation of homochirality in biochemistry was summarized by Professor Quack at the ETH Zürich university:

> "We think that no clear answer to the question of the origin of biochemical homochirality exists at present or is to be expected in the near future. Minimal conditions for such an answer would be that 1) in each possible mechanism for a desired selection all possible control experiments for proving the opposite outcome must be carried out and 2) the precise mechanism by which the effect leads to a selection of homochirality must be theoretically understood. To our knowledge none of the numerous suggestions existing today come even close to satisfying these minimal requirements."[6]

In the same paper Quack added:[6]

> "Each time some new effect for some perhaps possible mechanism in chiral selection comes up in the literature, this is quickly praised as the 'solution to the problem' (sometimes with cautious remarks in very small print) in the popular science press. There was a considerable amount of speculation in relation to the early findings of the stabilization of L-amino acids and D-sugars by parity violation.[7–11] These results were, however, refuted by recent theory."[12–25]

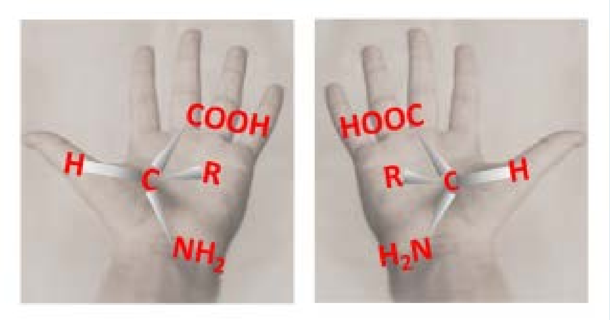

Figure 1. All proteinogenic AAs except glycine can exist as D- or L-enantiomeric forms, which are non-superimposable mirror images of each other.

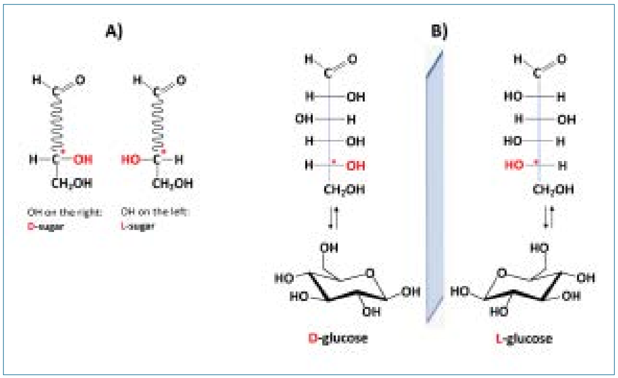

Figure 2. Nomenclature of D- and L-sugars. **A)** Using a Fischer projection locate the chiral carbon (C*) farthest from the carbonyl group (C = O). When the OH group is on the right side it is a D-sugar, otherwise an L-sugar. **B)** D- and L-linear and cyclic glucose.

He illustrates with an example:[6]

> "The alleged excess of L-amino acids found in meteorites is a fairly typical case with 'proof' and 'refutation' being repeated more than once."

I am planning to publish a detailed analysis of the key proposals elsewhere. The overview below will prepare the groundwork for understanding how rapid and inevitable AA racemization, covered in part 2, further discredits all of them under naturalistic conditions.

I. Potential sources of enantiomeric excess

Two approaches are used to attempt to explain the symmetry breaking: *parity violation* in otherwise identical molecules; and *selective degradation* of one enantiomer by circularly polarized light.[16] These hypothetical proposals lead to an enantiomer excess (ee)[17] much too small for abiogenesis purposes.

Parity violation

In nuclear physics, the weak interaction is one of the four fundamental interactions, and involves the interaction between subatomic particles, which produces β-decay of atomic nuclei.[18] Unlike the other fundamental interactions (gravitation, electromagnetism, and the strong interaction), it violates parity, i.e. symmetry rules.[19] The so-called z force interacts between the electrons and the atomic nucleus and can differentiate between right and left. This energy is called the parity violating energy difference (PVED).[20]

Enantiomeric excess of an L amino acid, ee_L is defined as (L – D) / (L + D). In practice, it is usually expressed as a percent. A tiny parity-breaking energy difference on the order of 10^{-14} J mol^{-1} could theoretically produce ≈ 10^{-15} % ee_L in a proteinogenic amino acid (AA).[16] This is based on parity differences in the weak interactions observed during radioactive decay of polarized ^{60}Co nuclei.[6,20–22] For biomolecules, *ab initio* theoretical calculations of the parity-violating energy difference predict that left-handed AAs and some D-sugars are more stable.[23] Symmetry violation cannot be unequivocally proved empirically, being below the current levels of detection.

Different computational techniques lead to different values, and so does the choice of conformation of molecules,[20] whereby the motivation is focused on finding and reporting the highest energy differences possible. Additional *ab initio* calculations by Mason and Tranter, in 1983, suggested a slightly larger energy difference.[20,24–27] They concluded that the parity-violating stabilization of an L-peptide, relative to the corresponding D-peptide, in the α-helix or the β-helix conformation is at most ~ –2 x 10^{-14} J mol^{-1} per amino acid residue, which suggests an enantiomeric excess of some 10^6 L-peptide molecules per mole (i.e. 6.0 x 10^{23} molecules) of racemate in thermodynamic equilibrium at ambient temperature.[28] This effect is still much too small for any chemical relevance.[29] The energy difference estimates for hydrated glyceraldehyde relevant for producing sugars range between 0.5–2.6 x 10^{-13}J mol^{-1}.[20]

Another method developed by Quack *et al.* called configuration interaction singles—restricted Hartree–Fock (CIS-RHF) to calculate parity violating potential E_{pv} also led to slightly higher values than the widely used SDE-RHF (single determinant excitations—restricted Hartree–Fock) method. This predicted an ee_L of ≈ 10^{-14}% for alanine, valine, serine, asparate, and glyceraldehyde.[30,31] These miniscule effects are contingent on the calculation technique used, and clearly there is a motivation to find and report examples of symmetry violation, although Quack and others have denied an energy preference in the case of L-alanine.[20]

To put things in perspective, Quack warns that[6]

> "The *de lege* (parity violation) community often expresses the belief that, because we know for certain that there is some preference at the molecular level that is caused by parity violation, there must 'somehow' be a connection to the evolution of biomolecular homochirality at the next higher level of organization. Such an argument can be easily refuted."

Selective degradation of one enantiomer by circularly polarized light

Theoretical considerations have led to the proposal that one enantiomer could be predominantly degraded by circularly polarized light (*CPL*), leading to an enrichment (under optimized conditions not expected to arise naturally) of ≈ 0.1% ee D or L, depending on the light source.[6,16,32,33] This can occur when a racemic mixture of molecules with sufficiently small excited electronic state barriers to enantiomer inversion is irradiated with CPL at a suitable wavelength.

The production of optical activity through CPL might occur through different mechanisms such as (i) the preferential decomposition of one enantiomer of a racemic mixture, (ii) asymmetric photosynthesis, or (iii) photo-interconversion of the enantiomers of a racemate.[34–36]

Selective degradation of leucine enantiomers on film

Chiral solid-state amino acids might have been exposed to circularly polarized vacuum ultraviolet (VUV) electromagnetic radiation before arriving on Earth. Meierhenrich *et al.* experimented with solid-state D,L-leucine 1-µm-thick films deposited on a MgF$_2$ window. These were irradiated with left circular polarized synchrotron radiation (l-CPSR) and right-CPSR (r-CPSR) at 170 and 182 nm in various experiments, inducing photochemistry via the (π^*, π_1)-electronic transitions.[37] Leucine was selected since it has the largest anisotropy factor g ($g = \Delta\varepsilon/\varepsilon$) among proteinaceous amino acids and therefore should provide the largest ee. This single-photon electronic excitation of AAs led to destructive photolysis, mainly by decarboxylation. Therefore, irradiating D,L-leucine with r-CPL (circularly polarized light) at the right wavelength was expected to produce an ee of the surviving L-leucine, and vice versa.[37]

A major drawback of direct photochemistry with CPL is that extremely low ee values are obtained unless a high-intensity source is utilized. After 70% photodecomposition, the highest ee reported was + 2.6% D-leucine when irradiating with only r-CPSR, but only at precisely 182 nm.[31,37] Remarkably, irradiation with l-CPSR, also at 182 nm, produced an ee of only 0.88% L-leucine.[31,37] The symmetric overabundance of the 'wrong' D-enantiomer is not very satisfying, and the authors attributed the difference to inexactitudes in the experimental setup. Table 1 summarizes their results. In three of the four experimental conditions the 'wrong' D-leucine is formed in excess, since at $\lambda = 170$ nm r- and l-CPSR both preferentially destroyed L-leucine.

What would happen naturally? The slight difference in absorption by D- or L-AAs has been shown experimentally to reverse at different wavelengths.[38] AAs would be exposed to a range of wavelengths, and a mixture of left and right-handed CPL sources will randomize the effect, tending to cancel out any ee.

Table 1. Enantiomeric excesses (averaged over three to six samples) obtained after irradiating D,L-leucine with l-CPSR (circular polarized synchrotron radiation) and r-CPSR[37]

Sample	λ [nm]	Irradiation	ee (d-leucine) [%]	CI$_{95}$[b]
1	182	l-CPSR	-0.88	0.28
2	182	r-CPSR	2.60	0.16
3	170	r-CPSR	0.75	0.36
4	170	l-CPSR	0.48	0.48

[b] CI$_{95}$ = confidence interval at 95%.

II. Enantiomeric amplification

There is consensus in the pro-evolution community that there is no known process able to produce the necessary highly pure L-AAs required for abiogenesis purposes. Instead, much effort is being devoted in laboratory methods to 'amplifying' small excesses of L-enantiomer AAs. The concept is to concentrate one enantiomer and physically separate it from the other in some restricted location. Note, however, that this *automatically enriches the mirror enantiomer* elsewhere.

Partial sublimation

Partial sublimation of racemic AAs at very high temperatures can sometimes separate some D- and L-AAs.[39–41] However, D- and L-amino acids which are separated by a few millimetres could easily remix, especially once dissolved in water.

Separation of crystals

Some DL racemic crystals of AAs are less soluble than the pure D- and L-crystals, so, if one enantiomer is present in excess, the liquid phase can be enriched by carefully crystallizing out the racemic DL- form.[42–45] This can be enhanced by taking advantage of the fact that stabler, larger pure D- or L-crystals sometimes form when that enantiomer is present in higher proportion.[42–46] Viedma and others have argued that in a few rare cases a small initial ee$_L$ of some AAs could be concentrated. The L-form crystals can form preferentially, benefitting from the larger number of initial L-crystal seeds made available by the researcher.

Under special conditions, this can be enhanced for some AAs using a carefully designed continuous abrasion-grinding process, which breaks smaller crystals preferentially.[43,47,48] However, forming L-enantiomer crystals would automatically enrich the solution phase in the D-enantiomer, quickly hindering formation of more crystalline L-form. Therefore, Viedma added a substantial amount of an appropriate aldehyde to a highly concentrated AA in an aliphatic acid such

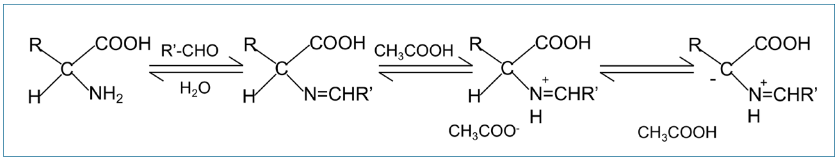

Figure 3. Racemization mechanism of amino acids with an aldehyde under acidic conditions[51]

as acetic acid at a high temperature.[49] Racemization thereby converted the excess D produced in the solution phase to L-form,[50] via the mechanism shown in figure 3. Protonating the imine produced by reacting AA with aldehyde is followed by proton abstraction from the *α*-carbon atom by the acetate anion, leading to the key planar carbanion intermediate which permits racemization.[50]

Suitable aldehydes presumably would have been present in adequate concentrations according to various abiogenesis scenarios, including influx from extra-terrestrial sources. But it is implausible that AAs with an excess of L-form would place themselves in a suitable hot mineral acid environment fortuitously co-located with an appropriate aldehyde, over and over, to produce a variety of L-amino acids in large quantities. Importantly, without intelligent organization the overall outcome would be devastating for naturalistic abiogenesis: faster indiscriminate racemization of *all* proteinogenic AAs. Viedma's solution provides yet another means to accelerate racemization throughout nature. The chemists who developed these laboratory and manufacturing enantiomer separation techniques before Viedma make no claim of relevance to abiogenesis.[50] (Traditional laboratory procedures, which can also be done in neutral or weakly alkaline conditions, use an aldehyde with a metal ion which forms a chelate compound with the initially formed Schiff base.[16])

Instead of removing DL-racemic crystals from an aqueous solution, Viedma showed, in 2001, that racemic aspartic and glutamic amino acid aqueous solutions can be made to crystallize as conglomerates under special supersaturated conditions. In conglomerates, D- and L-crystals form which are physically separated. The effect can be enhanced by partially immersing porous fire brick in the solutions to allow capillary rise.[52] Viedma does point out the obvious, that the spontaneous resolution mechanism over time will produce an equal number of opposing resolutions, with no net enantioselectivity.[52]

Among all proteinogenic AAs, asparagine and threonine form conglomerates spontaneously, which are pure separate D- and L-crystals.[28,53] For preferential crystallization to work, the homochiral interactions must be stronger than heterochiral interactions at the interface crystal–mother liquor. In theory, an excess of one enantiomer could be separated as a pure crystal.[54] Of course, for origin-of-life speculations an eternally frozen crystal of L-amino acid would serve no purpose. It would have to dissolve in water to form peptides at some point, racemizing to D-form and mixing with racemic amino acids from the environment.

Separation using the eutectic point of mixtures

Specific proportions of mixtures sometimes liquify/solidify at a lowest temperature called the eutectic.[55] Some combinations of amino acid enantiomers are indeed less soluble at various temperatures than pure D- or L-enantiomers, allowing separation in laboratories if done carefully.[56–58] Remixing occurs upon dissolving in water again, of course.

Use of chiral minerals

Some chiral minerals, such as quartz, can exist as dextro- and levorotatory enantiomorphic forms. But even carefully optimized laboratory experiments by Bonner *et al.* could only generate low ee values such as 20% for D alanine.[59–62] Extensive examination has shown, however, that D- and L-quartz are present in equal amounts worldwide, so once again no net enantiomeric preference would result.[63,64]

Use of chiral catalysts or auxiliaries

An approach to form L-AAs in excess involves mediation by chiral catalysts or chiral auxiliaries. This does not address the origin of their own optical purity, of course. One proposal involves the Strecker reaction using a mixture of D-pentose.[65] Breslow chirality transfer reactions via transamination have also been suggested.[66] However, the enantiomeric excesses of the products are much lower than that of the molecules from which they are transferred and would have to be co-located at the reaction location. For example, to obtain even a small excess of an AA, the fraction of pure sugar present had to be unrealistically high in one series of experiments.[65] Furthermore, some D-sugars increased, and others decreased the ee of the AAs tested, randomizing the net outcome.[65]

Breslow *et al.* found that non-proteinogenic α-methyl AAs found on meteorites could transfer their chirality during the synthesis of normal AAs.[66] (The α-methyl AAs differ from biological ones by having a methyl instead of hydrogen attached to the α-carbon.) However, they obtained the wrong products in excess (i.e. D-AAs) and had to experiment extensively to obtain the opposite outcome desired.

Their solution required using one equivalent of cupric sulfate, one equivalent of sodium pyruvate or sodium phenylpyruvate, and 4 equivalents of 96% pure L-α-methyl amino acid dissolved in water and vigorously stirred. All the reactants would need to be co-located in unrealistically high concentrations. (Anhydrous copper (II) sulfate is found naturally but as the very rare mineral chalcocyanite). The optimized and unrealistic special conditions finally led to L-phenylalanine with 37% ee and L-alanine with up to 20% ee.

This experiment illustrates a principle encountered in virtually all abiogenesis work. Researchers set up the precise laboratory conditions which force the outcome desired, often terminating the reactions before the inevitable wrong things then take over. We saw above that Viedma's proposed addition of aldehydes would facilitate racemization of AAs throughout free nature, the last thing naturalists wish to demonstrate. Breslow introduced a high concentration of Cu^{2+}, which, we will point out in part 2, accelerates amino acid racemization in water everywhere.[67] Again, the opposite to what naturalists wish to demonstrate. Such special-purpose-designed intervention in abiogenesis papers is ubiquitous; one must always carefully examine the experimental details.

III. Minimum homochirality to form polypeptide structure

What proportion of D-residues could a protein tolerate and remain functional? 5% of an average sized 300-residue protein represents fifteen positions. Large proteins with one or multiple secondary structures such as α-helices and β-sheets (figure 4) offer many ways to be rendered nonfunctional through L → D replacements. Most functional proteins would not tolerate fifteen randomly occurring residue inversions. The percentage tolerable will decrease with increasing protein size. A 3,000-residue protein would be worthless long before 150 randomly located residue replacements occurred.

A collection of random-sequence racemic peptides would not provide the reliable three-dimensional structures necessary for life-like chemical activities. Neglecting the need for having the correct sequences, about what proportion of the AAs would need to be L-enantiomers? To provide a minimum structure for something functional to occur, at a minimum one secondary structure (α-helix or β-sheet) would be needed. We will use experimental data available to see what ee_L would be needed to produce the simplest realistic β-sheet reliably. Some have suggested that α-helical L-peptides can cope with some D contamination,[69] but this leads to distorted and unstable α-helices.[70] In any event, evolutionists claim β-sheet structures arose first,[70] and we have the necessary detailed experiments to perform some mathematical analysis. In aqueous solution, short amphiphilic peptides do not generally possess a complete helical structure, so surfactants or liposomes are needed to help form alpha helices as small as 12 or 13 residues. In one experiment a helix structure for $(\text{Leu-Asp-Asp-Leu})_n$-Asp could be induced with the appropriate concentration of Zn^{2+} for peptides between 13 and 25 residues, but the sensitivity to L → D substitution was not determined.[71]

Brack and colleagues showed, in the 1970s, that $(\text{Leu-Lys})_n$ β-sheets are very sensitive to the incorporation of about 5% D-isomer and will only form fleetingly at ambient temperatures with *seven or more* of the correct homochiral residues in a row. Even this was only possible under optimized conditions, such as including the right coordinating metals and an aqueous media with high ionic strength.[71–74]

Salt ($NaClO_4$) concentrations had to be set as high as possible to produce these structures but not so high as to cause precipitation. It is very difficult to dissolve large poly(Lys-Leu-Lys-Leu) molecules, known to be fully in the β-form in salted solution.[74] Based on his observations, Brack concluded that large soluble β-sheets won't arise naturally, even when a small excess of one enantiomer is present, since the side chains would be forced into the plane of the β-sheet, generating conflicting steric contacts.[74]

Brack pointed out that some proteinogenic amino acids have been identified in the Murchison meteorite: Glycine, Alanine, Proline, Leucine (Leu), Isoleucine, Valine, Aspartic acid (Asp) and Glutamic acid (Glu).[73] Notice, however, that Lysine (Lys), used in the study above, was not found, and Leu was only present in trace amounts, rendering the relevance to abiogenesis reasoning doubtful. Our review of the literature on meteorites confirmed that Asp and Glu were reported in all the key studies we examined, but no Leu nor Lys, for example in three Antarctic CR chondrite meteorites, EET 92042, GRA 95229, and GRO 95577[75]; Tagish Lake meteorite samples[76]; Sutter's Mill Carbonaceous Chondrite;[77,78] and Aguas Zarcas.[79]

Brack *et al.* then examined other oligomers of varying sizes, whereby Leu continued to be used (being a very effective hydrophobic residue and optimal to form β-sheets) with an equimolar amount of Asp, Glu, or Lysine (Lys) as the hydrophilic residue. Water-soluble β-sheets using $(\text{Glu-Leu})_n$ and $(\text{Asp-Leu})_n$ chains could be produced when prepared properly. In pure water large poly(Glu-Leu) exists only as a random conformation. Adding NH_4^+ ions to a final 0.1 M solution converted it to water-soluble β-sheets due to shielding of the charged side chains by the salt. Monovalent cations, such as Li^+, Na^+, K^+, Rb^+, or Cs^+ ions, were not suitable for this purpose.[73] However, divalent cations Ca^{2+}, Ba^{2+}, Mn^{2+}, Co^{2+}, Zn^{2+}, and Hg^{2+} did induce β-sheets if the metallic ion / Glu ratio did not exceed 0.3 to 0.5. Mg^{2+} ions led to less soluble β-sheet structures, and CdS, which was also tested, precipitated with the polypeptide.

For the smaller oligomer $(\text{Glu-Leu})_9$, steady addition of increasing amounts of $CaCl_2$ from 0.1 to 0.3 equivalent increased the formation of β-sheet, but 0.5 equivalents totally precipitated the peptide. The smaller $(\text{Glu-Leu})_2$ oligomer is very soluble in salts but never produced any β-structure under any conditions tested.[73] Addition of 0.5 equivalent of

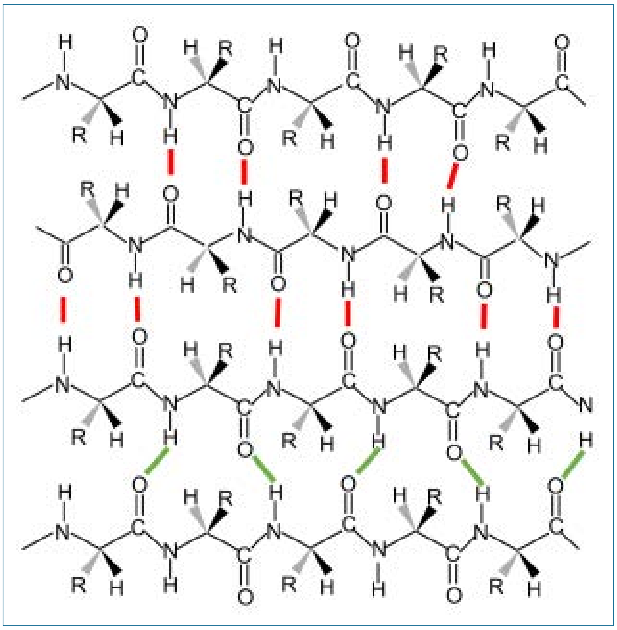

Figure 4. Schematic representation of a four-strand *β*-sheet. Hydrogen bonds are identified with red lines when the strands are antiparallel and green lines for parallel strands connecting the hydrogen and receptor oxygen. Based on an example from ref 68.

$CaCl_2$ to very large poly(Asp-Leu) also induced formation of a β-sheet.[73]

Notice that these peptides use an equal proportion of Leu and the hydrophilic partner. Is this reasonable? In an extensive study of the Murchison meteorite, reported in 2017, Koga and Naraoka found Asp, Glu, and Leu but no Lys.[80] To avoid the uncertainties introduced by considerable contamination from terrestrial L-enantiomers, we will consider only the reported concentrations of the D-form to calculate the relative proportion of Asp / (Asp + Leu) and Glu / (Glu + Leu) in the Murchison meteorite report. The former was 0.79 and the latter was 0.80. Therefore, the proportion of sequences having the minimum of 7-residues with a correct pattern (Leu-Glu-Leu-Glu-Leu-Glu-Leu) would be about 0.2^4 x $0.8^3 < 10^{-3}$.

10^{-3} is an overestimate of the average homochiral proportion which would form, for several reasons. Multiple copies would be needed for abiogenesis purposes, and if the necessary AAs were fortuitously available in some isolated environment, the Leu would be steadily consumed, making each new copy ever less probable. If β-sheets were to form using the residues Asp and Glu, then matters are statistically even worse.[80] Now the proportion with the right pattern would be about 0.1^4 x $0.9^3 < 10^{-4}$. Disruption by insertion of occasional glycyl is also known to decrease dramatically the tendency to form β-structures,[81] and Gly was about twenty times more abundant on the Murchison meteorite than the other L-proteinogenic AA. All this ignores the fact that the laboratory conditions necessary to produce the oligomers would never occur realistically.[82]

Nevertheless, Brack's work provides important insights to estimate how pure L-AAs must be for a polypeptide to possess a structural feature reliably, a minimum prerequisite for functionality.

Our goal is to determine how pure L must be to generate a seven-residue L-only pattern (Glu-Leu)$_3$-Glu by chance, with at least 50:50 odds.[83] For [L] = [D], $p(L) = 0.5$ we obtain $0.5^7 \approx 0.008$. A reliable supply of minimally functional β-sheets won't be produced from an amino acid mixture. Increasing the proportion to $p(L) = 0.9$ one obtains $0.9^7 = 0.48$, and now almost half the sequences would be L-AA and thus suitable in principle to generate a β-sheet.

$p(L) = 0.9$, meaning 90% L-AA in this abiogenesis environment, is not enough on average, since it only results in occasional and fleeting formation of a smallest-possible β-sheet under exceedingly unlikely conditions. We use other work published by Brack to illustrate. Asp side chains are more effective than Glu in forming β-sheets,[71] and (Asp-Leu)$_5$, (Asp-Leu)$_{10}$, and (Asp-Leu)$_{15}$ in water did not produce β-sheets at all. Cationic metal ions can interact with acidic side chains to inhibit charge repulsions, but no β-sheets were observed even if NH_4Cl, $CaCl_2$, or MgCl2 were added to (Asp-Leu)$_5$ and (Asp-Leu)$_{12}$.

β-sheets did form partially for (Asp-Leu)$_{15}$ in the presence of 0.5 molar equivalents Ca^{2+}/Asp residue, 1 equiv Mg^{2+}/Asp, or 0.3 equiv Fe^{3+}/Asp. Only addition of ~ 0.4 equiv Zn^{2+}/Asp was found to induce a complete random coil to β-sheet transition in the large (Asp-Leu)$_{15}$, but no β-sheet for (Asp-Leu)$_5$ and with (Asp-Leu)$_{12}$ only partially.[71]

The latter provides the data we need. Asp and Leu are optimal residues to form β-sheets and 0.4 equiv. Zn_2/Asp is an optimal condition, yet β-sheets only form partially. (Asp-Leu)$_{12}$ represents 24 L-residues; let us arbitrarily assume that two could be replaced by D-residues to favour the naturalist position in oligomers with optimal pattern (X-Leu)$_{12-1}$, where X = Asp, Glu, or Lys. The environment would require an L-proportion of ≈ 97% (i.e. $0.966^{20} = 0.50$). For comparison purposes, β-sheets in biological proteins consist of four to ten residues and are formed from three or more strands.[84]

Conclusions

No matter how an excess of L-AAs might be produced or resolved ('amplified') in some location, Bada points out that[85]

> '… racemization places an important restraint on any proposed mechanisms for the origin of optically active amino acids on Earth since racemization would rapidly convert any optically active amino acids back into an optically inactive or racemic mixture."

The concentration of AAs in a primitive ocean would have had to be very low, on the order of 10^{-10} M.[1] I propose that the presence of only 5–10% D-amino acids, or this amount of L → D conversion in peptides of size 20 or fewer residues, would prevent reliable secondary structures from forming, a minimum requirement for abiogenesis models. However, none of the proposed naturalist sources of ee$_L$ proposed could produce anywhere near this level of purity.

In part 2, I will examine how fast amino acid racemization occurs. I will consider the effect of acceleration through chelation with dissolved metal ions like Cu^{2+}; temperatures above 0° C and occasional intense heating from volcanos or meteorite impacts. Initially pure L-AAs and those found in peptides would racemize quickly, and we now realize this needs to occur for only 5–10% of the material to render it worthless for abiogenesis models.

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The multiple 'Adams' of Scripture

Jim Hughes and Shaun Doyle

Jesus is the Last Adam (1 Corinthians 15:45). Many commentators also refer to Jesus as the 'second Adam', largely due to proximity between the titles 'second man' and 'Last Adam' in 1 Corinthians 15. However, we argue that this is an invalid interpolation into the text. The term 'second Adam' does not appear in the Bible. Moreover, it masks both the theological richness of 1 Corinthians 15 and the history of redemption. Jesus is not the only character besides Adam to have been given the commissions Adam was given in Genesis 1 and 2. Jesus is the last of *several* Adamic figures, and He ends the line because He succeeded where all the others failed. Moreover, God's replication of the Adamic vocation to multiple people throughout the history of redemption indicates these commissions and promises were anchored in a literal, historical Adam.

Jesus is the Last Adam (1 Corinthians 15:45). But did any other 'Adams' came before him? At least one, of course: the first Adam. But were there others who filled the Adamic role laid out in Genesis 1–2? In 1 Corinthians 15:45–47, there is an important contrast. Drawing on Genesis 2:7, Paul calls Adam 'the first man Adam', but he refers to Jesus in two different ways: Jesus is 'the last Adam' (v. 45) and 'the second man' (v. 47). Some think, therefore, that 'second man' is a synonym for 'second Adam',[1,2] since as a 'second Adam' Jesus is the firstborn of the new creation.[3] However, we must respect Paul's precision—he calls Jesus 'the last Adam', not the 'second Adam'. The term 'second Adam' does not appear in the Bible. Moreover, a review of biblical figures central to the history of redemption shows that the first Adam was not the only person given the Adamic commissions before the last Adam. We find that Jesus was the last in a *series* of 'Adams' whom God commissioned in much the same way as He commissioned the first Adam.

Adam: God's first priest-king

Genesis 2:7 neither names Adam nor calls the 'man' God made from the dust the 'first' man. However, Paul makes that connection clear by adding the two words 'first' and 'Adam' to his quote of Genesis 2:7 in 1 Corinthians 15:45: "Thus it is written, 'The *first* man *Adam* became a living being [emphases added]'" (figure 1). Paul clearly believed that the 'man' made on Day 6 of Creation Week in Genesis 1:26–27 was the same man God made in Genesis 2:7. This is perfectly consistent with how Jesus, according to Mark 10:6–8, read Genesis 2 as an expansion of specific events on Day 6 of the Creation Week.[4]

Adam was a special man. He was the first ever human, and he is the father of us all: "And he made from one man every nation of mankind to live on all the face of the earth" (Acts 17:26).[5] As such, he was given a special role. God gave him, with Eve, dominion over the earth: "And God blessed them. And God said to them, 'Be fruitful and multiply and fill the earth and subdue it, and have dominion over the fish of the sea and over the birds of the heavens and over every living thing that moves on the earth.'" (Genesis 1:28). Though this applied to Adam *and* Eve together, Adam was given the first task of exercising dominion over the earth by naming the animals (Genesis 2:19–20). Adam thus was given rule, and had a primacy of authority even among humans, since he is the one from whom all other humans have come. This all suggests Adam was the first king over creation.

The Garden of Eden was also special. God's special meeting place with Adam was like the later tabernacle and temple.[6] The golden lampstand in the tabernacle and temple likely symbolized the Tree of Life.[7] The eastern gate to the Garden was guarded by cherubim (Genesis 3:24) just as the tabernacle entrance faced East (Exodus 27:13–16, Numbers 3:38) and both the tabernacle and temple were guarded by cherubim (Exodus 25:18–22; 26:31; 1 Kings 6:23–29). Furthermore, Adam was commissioned to 'serve and obey' God (Genesis 2:15–16). The same sort of commission, using the same words, was given to the priests and Levites who served in the tabernacle and temple (Numbers 3:7–8; 8:25–26; 1 Chronicles 23:32; Ezekiel 44:14).[8,9] These points indicate Adam met with God and served Him in the garden 'tabernacle'.[10] They indicate Adam mediated God's presence and blessing in creation. This suggests that Adam was the first priest.

Thus, we suggest Adam was a priest-king: he ruled as a king over creation and served in God's garden in Eden as a priest served in the tabernacle and temple. But He failed in his role. He sinned by eating from the Tree of the Knowledge of Good and Evil, which God told him not to eat from. And so, sin, decay, and death came into the world and infected the human race (Romans 5:12).[11] And the whole world was subjected to futility (Romans 8:20–22).[12] Man had made

οὕτως καὶ γέγραπται, Ἐγένετο ὁ πρῶτος
ἄνθρωπος Ἀδὰμ εἰς ψυχὴν ζῶσαν, ὁ
ἔσχατος Ἀδὰμ εἰς πνεῦμα ζῳοποιοῦν.

Figure 1. The Greek Text of 1 Corinthians 15:45 (UBS) shows that Jesus is called the *last* Adam, not the second Adam

himself futile, so God made the world he was set over futile and thrust Adam from His special presence in the Garden.

Noah: A new Adam for a new beginning

After Adam, things only got worse as his corrupted 'likeness' (Genesis 5:3) spread. His first son murdered another son (Genesis 4). All but the best of his sons was beset with death (Genesis 5). And the earth eventually became full of violence and evil (Genesis 6:5, 11). So, God decided to destroy the earth with a Flood. "But Noah found favor in the eyes of the Lord" (Genesis 6:8).

Judgment would come on the old world, but a new world would arise afterwards. God would start again with Noah as a new 'Adam' for a new world.[13] So, as God brought the animals to Adam for him to name (Genesis 2:19–20), He brought them to Noah to save on the Ark (Genesis 6:19–20). And after the Flood, when Noah came out of the Ark, Noah took up a priestly role and offered up acceptable sacrifices to God (Genesis 8:20) (figure 2).

In response, God reiterated to Noah the blessings he gave to Adam (Genesis 9:1–7). God told Noah and his sons to "be fruitful and multiply". God gave them the kingly role of dominion over the animals. Although this time they were not commanded to take dominion; they were *promised* dominion. And this time the animals were given to them to eat, as plants were in Genesis 1. And, in light of the violence that existed before the Flood, new commands were given: no eating blood, and no shedding the blood of man.

But a new promise was also given: God would never again send a flood to destroy all flesh. The rainbow reminds us of God's promise. Indeed, this promise indicates that, whatever floods have happened since, none have been so severe as to "destroy all flesh". And only a *global* flood could destroy all flesh. Thus, Noah's Adamic role reminds us that the Flood must have been global. The promises God gave after the Flood show that it was a new beginning for all creation.

Indeed, there are many literary parallels between Noah and Adam that suggest that Noah is a 'second Adam':

- Each is a father from whom all mankind is descended.
- God's bringing the animals to Noah for transport in the Ark (Genesis 6:19–20) is reminiscent of his bringing them to Adam for naming (Genesis 2:19–20).
- Once the animals were on board the Ark, Noah was responsible for their preservation, fulfilling an element of man's covenantal sovereignty originally assigned to mankind through Adam (Genesis 1:26).
- God made a covenant with each of them—the Covenant of Creation[14] with Adam and the New World Covenant with Noah (Genesis 9:9-17)—and each acted as a human mediator who represented all of mankind.
- Each was given an earth, devoid of humans, and a command and a blessing to multiply and fill it with inhabitants (Genesis 1.28; 9:1).
- Both had a relationship with the ground. Adam was created of the ground, and his name is derived from the Hebrew word for 'ground'. In Noah's case, the word 'soil' (Genesis 9:20 where he is called 'a man of the soil') is the same word translated elsewhere as 'ground' or 'land' (e.g. Genesis 6:7, 20).
- Both had duties related to tending plants from which they could consume the fruit (Genesis 2:15; 9:20). Adam tended the garden that God had planted (Genesis 2:8) and Noah planted a vineyard (Genesis 9:20).
- Both committed sins related to consuming fruit. Adam ate the forbidden fruit from the Tree of the Knowledge of Good and Evil (Genesis 3:7). Noah became drunk consuming a by-product of the fruit of the vine (Genesis 9:21).
- The shame of nakedness was associated with their sins (Genesis 3:7, 10–11; 9:21).
- Their nakedness had to be covered by others (Genesis 3:21; 9:23).
- Both had to toil to maintain their livelihoods from the cursed ground.
- Both of their personal sins introduced conflict into their families—Cain murdered Abel (Genesis 4:8) and was banished from his brothers (Genesis 4:12), and Canaan (Noah's grandson) became a slave to his brothers (Genesis 9:25–26).
- Both had sons (Cain and Ham) who committed sins, which became defining sins for their age.
- Both had immediate descendants who were cursed (Genesis 4:11; 9:25).
- Both lived for almost a millennium—Adam, 930 years; Noah, 950 years.
- The eventual death of each, as the result of the Curse (Genesis 2:17), is reported with similar words "all the days" (Genesis 5:5; 9:29).
- Despite their sin, both walked with God (implied in Genesis 3:8, and 6:9) and both believed God and took Him at His word (implied in Genesis 3:20 and 4:1, and 6:22).

Figure 2. *Noah's Sacrifice* by Daniel Maclise (1806–1870). Noah's sacrifice was a priestly act mirroring the priestly vocation of Adam.

- Both knew that God required shed blood and animal sacrifices as a type for the ultimate Atonement which man needs to cover sin (Genesis 4:4; 8:20).
- Both were blessed by God, with the same blessing (Genesis 1:28; 9:1).

Even though Noah is not called a 'second Adam', he acted in such a capacity. But, like Adam, Noah also failed. Noah planted a vineyard, and then got drunk and naked. His son Ham acted inappropriately with his father in his nakedness (the text does not specify clearly how).

Abraham: A new Adam for a new promise

Noah's descendants, however, became worse again. Instead of filling the earth as God told them to do, they stayed put, built a city, and began building a tower 'to make a name for themselves' (Genesis 11:4). So, God scattered them. He confused their languages, and so divided and humbled mankind. So, humanity spread, but we also splintered. We became divided, and different nations arose.

So, into a divided world, God again called another who might fill the Adamic role for a new beginning—Abraham. The commission of Genesis 1:28 was reiterated to Abraham in Genesis 12:1–3, as Beale explains:

> "The commission of Genesis 1:28 involved the following elements:
>
> 1. 'God blessed them';
> 2. 'be fruitful and multiply';
> 3. 'fill the earth';
> 4. 'subdue' the 'earth';
> 5. 'rule over … all the earth' (so Gen. 1:26, and reiterated in 1:28).
>
> The commission is repeated, for example, to Abraham: (1) 'I will greatly *bless you*, and (2) I will greatly *multiply your seed* … (3–5) and *your seed shall possess the gate of their enemies* [= 'subdue and rule']. And in your seed all the nations of the earth shall be *blessed* …' (Gen. 22:17–18)."[15]

Moreover, kings would come from Abraham (Genesis 17:6, 16; 35:11). And this promise was universal in scope, involving "all nations of the earth". With Noah, some of these facets became implied promises of dominion, while others remained commands ("be fruitful and multiply"). But for Abraham they *all* proved to be promises. God would fulfil all of them.

Abram also took on a priestly role. He travelled to Canaan as commanded (Genesis 12:1), and while at the tree of Mamre in Shechem, "The Lord appeared to Abram and said, 'To your offspring I will give this land.' So he built an altar there to the Lord, who had appeared to him" (Genesis 12:8).

However, Abraham was not the last Adam, either. Consider the enigmatic account of Melchizedek:

> "After his [Abram's] return from the defeat of Chedorlaomer and the kings who were with him, the king of Sodom went out to meet him at the Valley of Shaveh (that is, the King's Valley). And Melchizedek king of Salem brought out bread and wine. (He was priest of God Most High.) And he blessed him and said,
>
> > 'Blessed be Abram by God Most High, Possessor of heaven and earth; and blessed be God Most High, who has delivered your enemies into your hand!'
>
> And Abram gave him a tenth of everything" (Genesis 14:17–20).

As one biblical author pointed out: "It is beyond dispute that the inferior is blessed by the superior" (Hebrews 7:7). Abram, the new Adam, was blessed by Melchizedek, who interestingly was priest-king of Salem (i.e. Jerusalem; figure 3). So, we have a 'priest-king of Salem' who is *superior* to this 'new Adam'. This suggests that, while Abraham was a new Adam, a greater Adam than him was still to come.

So, it is fitting that for Abraham most of God's promises remained as promises (an exception is with the birth of Isaac—Genesis 17:19). He did not live to see their fulfilment. The promises were reiterated to Isaac and Jacob, but even they did not see their fruition (Hebrews 11:39–40). And Jacob eventually went down to Egypt.

Israel: A national 'Adam' in a new 'Eden'

In some respects, Israel is not so much a *new* 'Adam' as it is the expansion of God's Adamic commission of Abraham to a whole nation. God continued with Abraham's line because, unlike Adam, Abraham trusted God (Genesis 15:6; though this was not without its issues—e.g. using a concubine to bear Ishmael). Thus, God would fulfil the Adamic commission through Abraham and his descendants, i.e. Isaac, Jacob, and the nation of Israel.

Israel began fulfilling the 'be fruitful and multiply' commission in Egypt: "the Israelites were exceedingly fruitful; they multiplied greatly, increased in numbers and became so numerous that the land was filled with them" (Exodus 1:7).

God saved them from slavery in Egypt and brought them to "the mountain of God" (Exodus 18:3) at Sinai. This is where God would first meet with his people. The first thing God did was declare his Adamic commission to Israel in Exodus 19:3–6:

> "Thus you shall say to the house of Jacob, and tell the people of Israel: 'You yourselves have seen what I did to the Egyptians, and how I bore you on eagles' wings and brought you to myself. Now therefore, if you will indeed obey my voice and keep my covenant, you shall be my treasured possession among all peoples, for all the earth is mine; and you shall be to me a kingdom of priests and a holy nation.' These are the words that you shall speak to the people of Israel."

As Adam was a priest-king, so the Israelites were to be a kingdom of priests. The commission to Israel in Exodus 19:3–6 has a similar combination of royal and priestly overtones for similar ends to the Adamic commission. In His closing words to Israel in Exodus 23:20–33, God promises to bring them to "the place that I have prepared" (v. 20). This parallels the language of how God 'put' Adam in the Garden of Eden (Genesis 2:8, 15). And in this land, if they obey:

> "… he will bless your bread and your water, and I will take sickness away from among you. None shall miscarry or be barren in your land; I will fulfill the number of your days. I will send my terror before you and will throw into confusion all the people against whom you shall come, and I will make all your enemies turn their backs to you" (Exodus 23:25–27).

Thus, God would put his kingdom of priests in the blessed land He had prepared—reminiscent of the Garden of Eden (cf. Isaiah 51:3; Ezekiel 36:35; 47:12; and Joel 2:3 where the Promised Land is likened to the Garden of Eden).

But, like Adam, Israel fell; but not just once. Israel committed idolatry in the Golden Calf incident. The Exodus generation believed the bad report of the spies and did not trust God to go into the Promised Land. They also grumbled all along the way. When they got into the land, Israel made covenants with the Canaanites. And idolatry—so much idolatry! Joshua and especially Judges record the ever-descending spiral of sin in the land. In the end: "Everyone did what was right in his own eyes" (Judges 21:25).

Figure 3. *Meeting of Abraham and Melchizedek,* canvas by Dieric Bouts the Elder, c. 1464–1467. Melchizedek shows that Abraham, though a 'new Adam', was not the *last* Adam.

David: a new Adam for a new line

Israel had lost the plot. They needed direction. They needed a leader to lead them in God's ways. Israel needed a new Adam!

So, God gave them David. He turned Israel's desire for a king 'like the nations' to his own purpose (1 Samuel 8:5–8). First, though, God gave them what they asked for: Saul. That was a disaster. But then God raised up David—a new Adam to lead the corporate Adam.

As the king, David also engaged in activities with clear priestly overtones, forging a link between the priestly and kingly roles. For example, he leads the procession of the Ark of the Covenant into Jerusalem, dancing and celebrating while dressed in a linen ephod, which is priestly garb (2 Samuel 6:14). He offers sacrifices, and then blesses the people with good food and sends 'each to his own house'. The presence of God (in the Ark) has come to the centre of the Promised Land, and God has given His people rest.

And in response to David's priest-king portrayal God gives him the grand promises of 2 Samuel 7. As Beale notes:

> "Second Samuel 7 (= 1 Chr. 17) closely links the need to build a temple (7:2–13) with the following

> aspects of Genesis 1:28: (1) ruling and subduing (7:9–16), and (2) a blessing on God's kingly vice-regent (7:29). It may also not be unexpected, therefore, that 2 Samuel 7:9, 'I will make you a great name', would allude to Genesis 12:2, 'I will . . . make your name great.' Accordingly, it is natural that the overall purpose is linked to God giving 'rest' to Israel's king from his enemies (7:1, 11)."[16]

In response, David goes out 'subduing and ruling' in 2 Samuel 8–10. He extends his Adamic dominion over all the land God promised for Israel. But then Chapter 11 happens.

> "In the spring of the year, the time when kings go out to battle, David sent Joab, and his servants with him, and all Israel. And they ravaged the Ammonites and besieged Rabbah. But David remained at Jerusalem.
>
> "It happened, late one afternoon, when David arose from his couch and was walking on the roof of the king's house, that he saw from the roof a woman bathing; and the woman was very beautiful. And David sent and inquired about the woman. And one said, 'Is not this Bathsheba, the daughter of Eliam, the wife of Uriah the Hittite?' So David sent messengers and took her, and she came to him, and he lay with her. (Now she had been purifying herself from her uncleanness.) Then she returned to her house. And the woman conceived, and she sent and told David, 'I am pregnant'" (2 Samuel 11:1–5).

It's Genesis 3 all over again! David has his own fall. From there things just get worse. David has family troubles and dies, a shadow of his former glorious self. He does hand things off to Solomon, who completes the temple. But like David, Solomon starts well … and then messes it all up (1 Kings 11:1–8). And this pattern continues with the kings of Israel and Judah until God has had enough of their sin and exiles Israel from the Promised Land.

The Exile is another 'removal from Eden'. The garden is gone. The nations curse Abraham's line. David's crown is in the dust.

Jesus: the Adam to end all Adams

At Noah's birth, his father Lamech prophesied that Noah would bring rest and relief from the painful toil associated with the Curse (Genesis 5:29). However, though Noah filled a role as a second Adam, he was not sinless. As such, he failed to bring true and lasting rest. And the Flood, as destructive as it was, did not cleanse the hearts of mankind (Genesis 6:5, 8:21). Likewise, Abraham, the nation of Israel, and David were far from perfect and thus unable to provide the solution.

The true rest Lamech prophesied was to be found in the Last Adam, who is Jesus Christ (1 Corinthians 15:45). He was like us in every way, yet *without sin* (Hebrews 2:17, 4:15). As such, He succeeded where all the other Adams failed, and thus ended the need for any more Adams.[17] He:

- is more than a 'living creature' from the dust (Genesis 2:7) because He is a 'life giving spirit' (1 Corinthians 15:45–47)
- is the spiritual father of all who believe (1 John 3:1–2)
- tends His garden to produce righteous fruit (Isaiah 5:1–7; Galatians 5:22–24)
- does not just name or protect animals, but names (Revelation 2.17; 3.12) and protects (John 10:28) every one of His people
- had to toil under the consequences of the Curse by humbling Himself (Isaiah 53:3; Philippians 2:7–8; Hebrews 12:2) so that He could abolish the Curse of toil for us (Romans 8:22–23; Revelation 22:3) and fulfill Lamech's prophecy
- is the mediator of the better New Covenant in His blood (Luke 22:19–20; Hebrews 7:22)
- has been given ultimate authority over all creation (Matthew 28:18; John 17:2)
- will fill an empty new paradise with His people—the ones whom He came to the earth to die for and to save (Luke 23:43; Revelation 2:7; 7:9)
- resisted the temptation of wine, unlike Noah, when it was offered to dull His pain (Mark 15:23), and to taste forbidden 'fruit' (Matthew 4:1–11), unlike Adam
- became associated with the shame of sinful human nakedness when His tormentors stripped Him and cast lots for His clothing (Mark 15:24)
- had His nakedness covered by others, before being laid in a tomb (Matthew 27:59)
- as God, has sons who are also His holy brothers and sisters (Hebrews 2:10)
- brings about family reconciliation among the saved, rather than discord (Colossians 1:20)
- gives His sons blessings, not curses (Psalm 2:12; Matthew 5:3–12; Luke 24:50)
- does not live for a little short of a millennium, but forever (Revelation 1:8), and gives His people eternal life (John 3:15–16)
- died voluntarily (John 15:13; Hebrews 2:9), so that He could conquer death through His Resurrection (Psalm 110:1; Romans 1:4; 1 Corinthians 15:26; Revelation 1:18)
- walked with God in full obedience (Psalm 40:8) and fellowship (John 17:21)
- gave His own blood as the final perfect sacrificial lamb (John 1:29; Hebrews 7:27; 9:12)
- is blessed by God (Matthew 3:17; Luke 1:42)
- saves His family from everlasting fire (1 Peter 3:20–22), not just from the waters of a cataclysm
- is the true seed of Abraham (Galatians 3:16)
- is the faithful Israelite called out of Egypt (Matthew 2:15, Hosea 11:1)
- is a high priest (Hebrews 4:14) after the order of Melchizedek (Hebrews 5:10)
- He is the true son of David (Matthew 1:1).

But with every ending comes a new beginning. In His Resurrection, the Last Adam became the 'second man' (1 Corinthians 15:47). In 1 Corinthians 15:44, Paul says that the body is sown a *sōma psychikon* (perhaps best rendered 'soulish body') and raised a 'spiritual body' (*sōma pneumatikon*). In v. 45, Paul quotes Genesis 2:7 to justify the sown body as *psychikos* ('soulish') since Adam was made a *psychēn zōsan* ('living soul'). He then contrasts Jesus to Adam by saying that Jesus "became a *life-giving spirit*" (*pneuma zōopoioun*). Verse 46 then says that the 'soulish' (*psychikos*) must come first, *and then* the 'spiritual' (*pneumatikos*). So, Adam was the 'first man' because he was the first with a 'soulish body', and Jesus was the 'second man' because He was the first with a 'spiritual body', with which He was raised with. Thus, Jesus became the 'second man' *at His Resurrection*.

Jesus is thus the beginning of a new mankind. He is the founder of a new everlasting spiritual race of mankind that is greater than the first natural race, which, through disobedience, would be subjected to death. This new race of mankind (Revelation 14:4) will live with Jesus forever in everlasting righteousness with spiritual bodies (1 Corinthians 15:44) designed to exist in the new heavens and earth.

However, there is a *twofold* contrast in 1 Corinthians 15:45. First, Adam became a 'soul' (*psychē*) at his creation and Jesus became a 'spirit' (*pneuma*) at His Resurrection (neither lacked a body, but had bodies governed by different life-principles).[18] Second, Adam became 'living' whereas Jesus became 'life-giving'. Through His Resurrection, Jesus is not just the first with a 'spiritual body'; He actually *gives* life! But who is the one who gives life to the dead? Only God (Romans 4:17). Nonetheless, it is something He does through His Spirit (Romans 8:11), and the Son also gives life to whomever He wants (John 5:21). In other words, only God can give life to the dead, but Jesus participates in it. As with creation (Colossians 1:16–17; Hebrews 1:3), so with resurrection. After all, it is *new creation* (Galatians 6:15, 2 Corinthians 5:17). The second man is more than a mere man—He is the God-man.[19] No wonder He can change the hearts of His people (John 3:7–8) and thus provide the true rest (Matthew 11:28–30) Lamech prophesied.

Conclusion

Jesus is the *last* Adam, not the second Adam. Moreover, this only makes sense if there *really were* other 'Adams'—other people who were given the priest-king vocation of the first Adam to subdue and rule, and through whom the world would be blessed with God's presence, such as Noah, Abraham, the nation of Israel, and David. Jesus was not just the fulfilment of myths; He was the fulfilment of what God made man to be, and always wanted him to be. Jesus is the climax of salvation *history*; a history that began with the creation of the first Adam.

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