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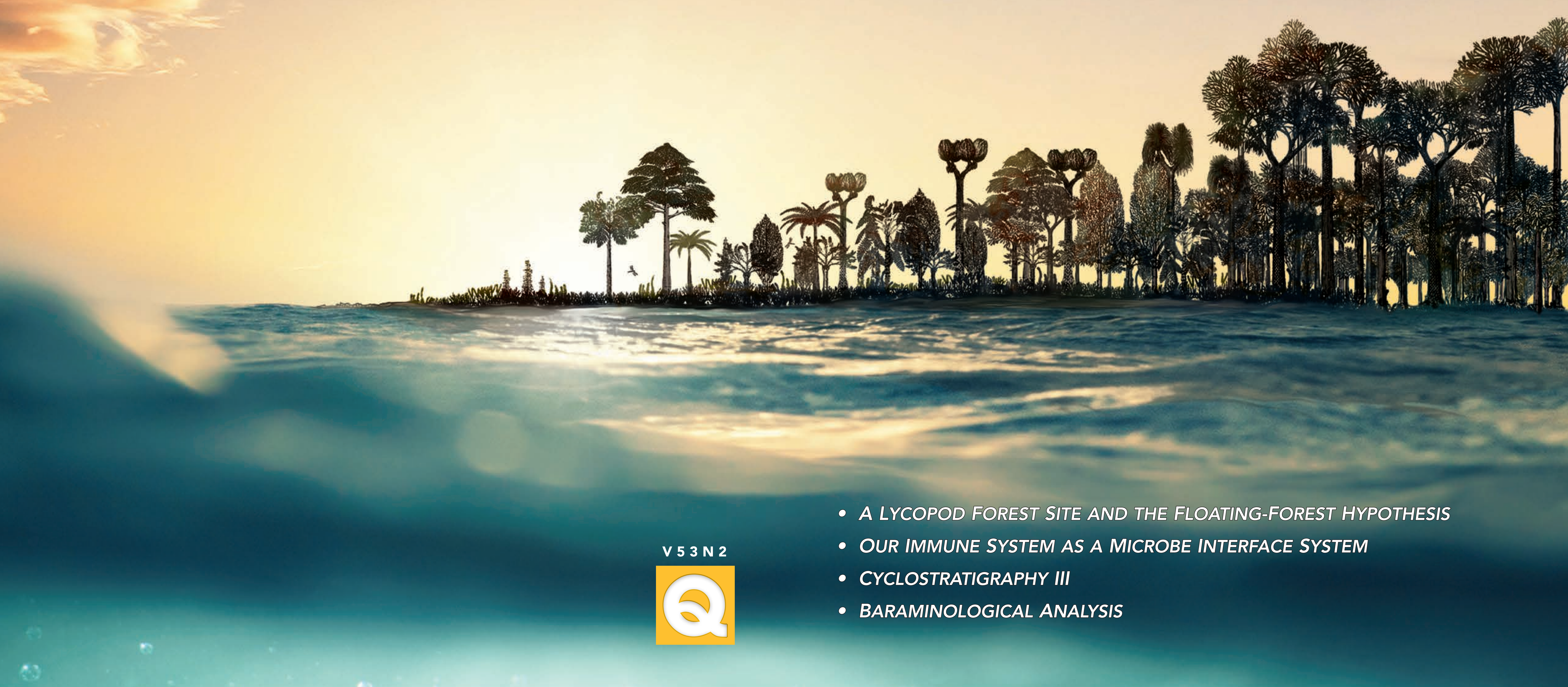

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Haec Credimus

For in six days the Lord made heaven and earth, the sea, and all that in them is, and rested on the seventh.—Exodus 20:11

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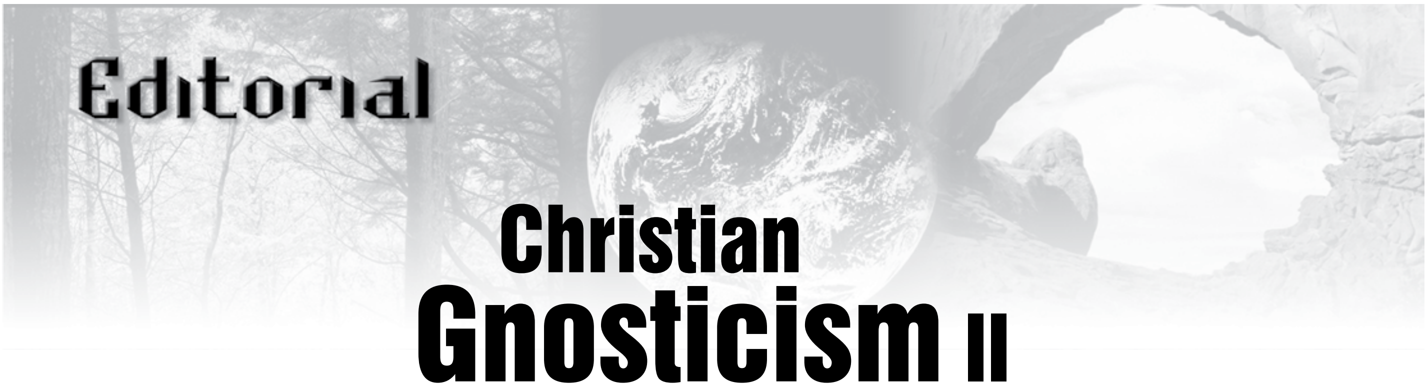

Christian Gnosticism II

In an earlier editorial (Faulkner, 2015), I identified a form of Gnosticism present in Christianity today. This Gnosticism is characterized by a thirst for secret, hidden, or otherwise little-known knowledge. Like the Gnostics of old, the special knowledge allegedly leads one either to greater spiritual maturity or to a deeper understanding of spiritual things. Often, the knowledge amounts to a shortcut to these things without the diligence and hard work that is required to truly achieve them. Part of the motivation for believing secret knowledge may be pride—if one has come to understand something generally not known, then it can lead to self-satisfaction in having grasped it. In my earlier comments on the subject, I discussed the Bible code, numerology, the gospel in the stars, and consumption with Bible prophecy as examples of "Christian Gnosticism." Here I will discuss belief that the earth is flat as an example of a kind of Gnosticism.

Many people probably think that belief in a flat earth is preposterous and may wonder why I am wasting ink discussing it. However, I have noticed a sharp rise in interest in a flat earth over the past year or two, in the form of questions at presentations and through correspondences. The major creation ministries around the world, including the Creation Research Society, have experienced the same thing. In response, several of us have written articles showing why we know the earth is spherical rather than flat (Carter 2016; Carter and Sarfati 2016; Faulkner 2016a, 2016b, 2017). This is to counter what we perceive as a grave threat to Christians but especially to the creation movement.

Proponents of the flat-earth view today believe in what some call the *snow-globe earth*, so called because of its resemblance to a snow globe. In this model, the earth is round and flat, with the North Pole at it center. There is no South Pole. Rather, the round earth is ringed by an ice wall we call Antarctica. There is a dome over the earth on which the stars are located. This dome extends down to and rests upon the earth somewhere beyond the ice wall. Each day the dome spins around an axis perpendicular to the earth's surface and passing through the North Pole. The sun and moon are located below the dome a few thousand miles above the earth's surface. Each day they revolve around the same axis the dome does.

Nearly everyone is familiar with the Flat Earth Society, thinking that its few members are just cranks. In actuality, there have been several flat-earth societies, each with varying degrees of adherence to belief in a flat earth. Some are made up of true believers, though their membership must be meager, because flat-earth organizations frequently fold when their founders die. Other flat-earth organizations have been tongue-in-cheek. While many people think belief in a flat earth extends back to ancient times, the flat-earth movement began in the nineteenth century. After some initial following, the belief in the flat earth gradually waned over the years. It appears the contemporary flat-earth movement began when some individuals discovered the writings of the nineteenth-century flat-earth movement and repackaged them for today. The recent resurgence encompasses an increasing number of people. Consequently, in the West there may be more believers in a flat earth today than in any era since ancient times.

The flat-earth movement perpetuates two commonly held misconceptions. One misconception is that most people thought the earth was flat until the time of Christopher Columbus five centuries ago. In reality, people in the West had known that the earth was spherical since the time of the ancient Greeks. Eratosthenes even measured the earth's circumference around 200 B.C. The other misconception is that *the church taught* the earth was flat until about the time of Columbus. However, the church *never* taught that the earth is flat, as powerfully demonstrated by Russell (1991). Neither misconception has a basis in history. Their roots lie (again) in the nineteenth century. It is no coincidence that the flat-earth movement also arose in the nineteenth century. As it were, there were three major developments in the nineteenth century that paved the way for the flat-earth theory to come about.

The first important development was

the discipline of archaeology as we know it. Early in the nineteenth century, studies of the ancient Near East revealed a cosmology involving a round, flat earth covered by the vault, or dome, of heaven. This model closely resembles the snow-globe earth.

The second development was that Bible scholars, or those who would now be better described as Bible skeptics, developed the documentary hypothesis. The documentary hypothesis, in its classic form, suggested that the Pentateuch was written several centuries after Moses (if the biblical Moses even existed), using four sources. This supposedly happened while the Jews were in exile, and hence they assimilated certain ideas from the ancient Near East. Of course, this assimilation supposedly included the ancient Near Eastern cosmology of a vaulted dome over a flat earth. Correspondingly, the skeptics interpreted biblical passages touching on cosmology, such as Genesis 1:6–8, in terms of this cosmology.

Finally, the nineteenth century saw the development of the *conflict thesis*, the belief that Christianity had held back progress during the Middle Ages and that civilization had just recently thrown off this debilitating restraint. A major part of the conflict thesis was creating the myth that the church had taught that the earth was flat but Columbus had shown otherwise. The Roman Catholic Church *had* endorsed the ancient *Greek* cosmology, including geocentrism and the Ptolemaic model, but in the nineteenth century, this was morphed into the supposed dominant cosmology of the ancient Near East. I say supposed, because later study revealed that there was no single ancient Near Eastern cosmology. Instead, there were many, of which the vaulted heaven over a flat earth was just one. Let me be very clear: the church *never* taught that there was a vaulted dome over a flat earth. Rather, the church embraced the idea of a spherical earth surrounded by a celestial sphere, a theory that came from the ancient Greeks. This is very different from the supposed cosmology of the ancient Near East.

It was out of this nineteenth-century convergence of the mistaken ancient Near Eastern cosmology from archaeology, the documentary hypothesis, and the conflict thesis that the flat-earth movement was born. Two prominent advocates of the flat earth, Samuel Rowbotham and William Carpenter, readily accepted this faux history concocted for the conflict thesis and made it part of their argument. While the flat-earth movement gained a few followers right away, by the early twentieth century interest had waned. Therefore, it is a bit of a surprise to see such a resurgence of adherents to the flat earth now in the twenty-first century. What is responsible for this?

Undoubtedly, the Internet has played a major role. I recently googled "flat earth," and I had 229,000 results. Obviously, I didn't visit all those websites. However, there is a major segment of our population today that gets its news and information solely from the Internet. In the past, we relied upon printed matter for such information. There is considerable financial cost associated with dissemination of printed matter, so the marketplace of ideas tended to weed out poor sources. Cranks could produce their material, but it was difficult and expensive to publish books or articles and distribute them so that a significant number of people could have access to them. But today, with the Internet, it is relatively easy and cheap to disseminate even the craziest ideas. Unfortunately, many people have difficulty distinguishing between what are credible and non-credible sources. Hence, with so many flat-earth resources readily available to everyone with Internet service, it is very easy to dupe gullible people.

Still, the earth being flat is a big pill to swallow, so what is the appeal? It probably is the allure of secret knowledge that Gnosticism holds out, the perverse attraction of saying, "I know something you don't know." But this involves far more than just knowing the true shape of the earth. Within the thinking of flat-earthers, why did people begin believing the earth was spherical a few centuries ago? The answer is simple: it's part of a huge conspiracy. What is the motivation of the conspiracy? Supposedly, it was to remove God from the picture and prepare the way for belief in evolution. If the earth is flat under a dome, there is no way it could have come into existence by itself; but if the earth is a globe orbiting the sun, that could have happened naturally.

Interestingly, a similar argument is made by geocentrists. They argue that the downward road toward evolution didn't start with Darwin or even Lyell or Hutton. It began with abandonment of the geocentric theory in favor of the heliocentric theory five centuries ago. The real culprits were Copernicus, Galileo, and Kepler. This similarity is not coincidental, because if the snow-globe earth model is correct, then the earth cannot orbit the sun. Therefore flat-earthers are geocentrists too, though I expect the geocentrists I have dealt with before (Faulkner 2001) probably want nothing to do with the flat-earthers.

You may protest that photographs from space show that the earth is spherical. Ah, but photographs can be faked, especially with Photoshop, something else that did not exist prior to the Internet. Furthermore, if the snow-globe cosmology is right, space as we know it doesn't exist. We haven't been to the moon. In fact, we haven't even been into space. Everything that NASA has done is fake. What about astronauts, some of whom are Christians, who say they have been in space and even have walked on the moon? They're all liars. They lie, because they're all Freemasons, and thus are part of the conspiracy. Other conspirators include the Illuminati and the Jesuits. (Never mind that the Jesuits are a Roman Catholic order and the Illuminati supposedly are masterminded by Jews, and until recently the Freemasons didn't admit either Jews or Catholics. The people running the conspiracy just want you to think that different branches of the conspiracy don't get along, but at the top they always have.) The number of people who must be in on the conspiracy is staggering. What about me, an astronomer? Shouldn't I be able to know the earth's true shape? As an astronomer, I have very good reasons to know that the earth is spherical. No one yet has accused me of being a Freemason or anything like that, but I expect it is coming.

I suppose some people reading this have lost interest and already stopped reading, thinking this is some weird satire piece. I wish it were, but I could not be more serious. The lengths to which supporters of the flat earth go to prop up their theory are amazing. The things one must disbelieve in order to believe the earth is flat are stunning. In a world where so many TV shows (e.g., *The X-Files*) and movies (e.g., *The Matrix* and its two sequels) spin wild conspiracies, it's no wonder at least some people find grand conspiracies preferable to reality.

But why, of all people, have Christians fallen for this? I suppose the deep desire for secret knowledge, any secret knowledge, no matter how poorly developed, is very powerful for some people. Add to this what perhaps is an overestimate of the power of the deceiver (John 8:44) to develop the alleged vast conspiracy, and belief in such a fantastic tale may not seem so far-fetched to some people. Furthermore, like their nineteenth-century forebears, flat-earthers interpret certain biblical passages in terms of their model, erroneously thinking their interpretation goes all the way back to the writing of the Bible, when in reality, that interpretation is hardly a century and a half old.

Or perhaps some believers just want a silver bullet to destroy evolution. The flat-earthers are right about one thing—if the snow-globe earth is correct, then the world is so contrived that atheism and belief in evolution are not options. Some flat-earthers claim they have found arguments for a flat earth to be an effective evangelistic tool, turning many atheists to Christ, though I am skeptical of that claim. I keep thinking of what the supposed converts will think if and when they come to realize that nearly everything else that flat-earth evangelists told them was wrong. All that we do must be grounded in truth.

This is especially true in discussing creation. Creation evangelism can be an effective tool in winning souls to Christ, which ought to be one of the key motivations of all creationists. However, there are no magic, silver bullets. A silver bullet, if it existed, would allow us a shortcut to our goal. But that would deprive us of the hard work we are called to do.

This is why the work of the Creation Research Society is so important. We are dedicated to building the best creation models. Your continued support is vital to accomplishing our goal. How can you help? We need financial support, so your contributions are much appreciated. Reading and promoting the Society website (creationresearch.org) and our printed material, such as the *Creation Research Society Quarterly*, is important. Continued membership, along with recruitment of new members, is important too. Finally, attendance at Creation Research Society meetings is a boost to the Society as well. Our next meeting is July 27–29, 2017 on the campus of Bob Jones University in Greenville, South Carolina. Please join us.

Danny R. Faulkner
Editor
Creation Research
Society Quarterly

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Cyclostratigraphy

Part II: History of the Method

John K. Reed and Michael J. Oard*

Abstract

Part I of this series described the modern stratigraphic method of cyclostratigraphy, which is linked to astrochronology. The latter uses properties of Earth's orbital mechanics to develop an absolute chronometer back through time. Cyclostratigraphy uses properties of sedimentary rocks as proxies for these orbital cycles to connect the astronomical "clock" to the sedimentary record. In this part of the series, we trace the historical development of these methods, their increasing influence on the geologic timescale, and the implications for a more gradualistic view of uniformitarianism.

Introduction

Creationists must remain current with trends in the earth sciences, especially those that support secular natural history. Stratigraphy is one of these; it is at the center of Earth's history and has evolved over the last half century from a simpler, more empirical discipline to a complex, integrated one, centered on the geological timescale. Changes in stratigraphy are mirrored by those in the timescale. Its current incarnation is of nearly one hundred Phanerozoic stages of a few million years duration, which are defined by the fiat placements of GSSPs (Reed, 2008). Increasing detail requires increasing precision in geochronology, which has spurred a demand for new methods. Cyclostratigraphy has moved rapidly to a place of prominence for Cenozoic rocks because of its alleged precision of 10^4–10^5 years (e.g., 0.02 million years; Hinnov and Ogg, 2007), and geologists are hopeful that it can be extended to older rocks as the method develops.

Cyclostratigraphy uses features of sediments and sedimentary rocks as proxies for changes in climate. These proxies are thought to mirror changes in solar insolation driven by cyclical changes in eccentricity, precession, and obliquity over time (Reed and Oard, 2015). Popular proxies include oxygen and carbon isotope ratios, clay and microfossil assemblages, lithology changes in lithofacies, grain size, and sediment color. Some of these are also used to date ice cores to date glacial and interglacial periods, especially those of the Pleistocene (Hebert, 2014; Oard, 2005).

Many creationists, like many other nonspecialists, are unaware of the dramatic advances in stratigraphy and corresponding changes in the timescale. Since methods in natural history are commonly driven by human factors, it is important to trace these factors, as well as the technology, that have contributed to the development of cyclostratigraphy. In this paper, we will trace these developments, first in the area of astrochronology—an outgrowth of the Milankovitch theory of the ice ages—and then in stratigraphy itself. This bipartite division will pave the way for the final two

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papers in this series, which will critique astrochronology and cyclostratigraphy.

The Astronomical Theory of Ice Ages

Astrochronology grew out of the theory that ice ages occurred due to cyclical changes in orbital mechanics. The early emphasis on ice ages reflected the popularity of that topic in the late nineteenth and early twentieth centuries. Miall agreed with Zeller (1964) and Dott (1992) that geologists had a propensity for cyclic explanation, noting, "Two themes that recur throughout the evolution of geological thought are *pattern recognition* and *cyclicity*" (Miall, 2010, p. 26). There is nothing inherently wrong with these themes, although Zeller's (1964) study demonstrated that geologists often see pattern where none exists.

Cyclostratigraphy, described in Reed and Oard (2015), attributes cyclical changes in glacial and interglacial periods to cycles in: (1) Earth's eccentricity, with strong maximum variations at approximately 100,000 and 400,000 years; (2) the precession of the equinoxes, with a major periodicity of 22,000 years; and (3) the tilt of Earth's rotational axis, with a period of 41,000 years. Other peaks are recognized, but these are considered the primary factors affecting sunlight, or *insolation*, between latitudes and seasons. In theory, changes in summer insolation at high latitudes affect glacial/interglacial oscillations. Less summer sunlight results in glacial episodes, while the opposite brings interglacial periods.

The astronomical theory was originally developed hand in hand with the four-ice-age model. But during the 1960s and 1970s, scientists realized that there had been dozens of these oscillations in the Northern Hemisphere and inferred that there had been dozens of ice ages. Today, based on cycles in deep-sea sediment cores, scientists believe that there were about fifty ice ages during the last 2.6 million years—the Pleistocene or the Quaternary of the geological timescale (Pillans and Gibbard, 2012).

Early Ideas

The idea of cycles in earth processes found its way into geology from its inception (Dott, 1992; Gould, 1987). Cyclothems and other sedimentary indications of depositional cycles were popular throughout the twentieth century; Barrell (1917) spoke of the role of Earth's "rhythms" in geology. The idea of astronomical climate forcing was proposed even earlier, by Herschel (1830), and developed by mathematician Joseph Adhémar (1842) in his book *Revolutions of the Sea*. Newspaper publisher Charles MacLaren linked glaciation to sea-level change in 1842 (Miall, 2010).

Seizing on Kepler's theory of elliptical orbits, Adhémar suggested that the differences in sunlight, caused by the difference between *aphelion*, Earth's greatest distance from the sun (94.5 million miles) on its elliptical path, and *perihelion*, its nearest approach (91.5 million miles), affected climate and contributed to the ice ages. He reasoned that elliptical variations, combined with the precession of the equinoxes caused ice ages to cycle every 22,000 years but alternate between the hemispheres every 11,000 years. He claimed that the Southern Hemisphere was already in an ice age, as evidenced by the Antarctic ice sheet, because the planet was at aphelion during the Southern Hemisphere winter, resulting in seven less days of sunlight.

Adhémar was correct that Earth's eccentricity varies slightly, from near zero (zero being a perfect circle and one a straight line) to 0.06 in a 100,000-year cycle. Thinking that the eccentricity influenced climate, which varied between hemispheres, Adhémar suggested that the most recent ice age in the Northern Hemisphere occurred 11,000 years ago and that another would begin in another 11,000 years. His theory was initially rejected because scientists of his day did not believe that slight changes in sunlight caused by eccentricity were a sufficient cause of the ice ages.

In the 1860s and 1870s, James Croll, a self-taught Scottish scientist, resurrected Adhémar's idea. While affirming the importance of eccentricity, he focused on changes in Earth's tilt, noting that eccentricity modulates the amplitude of the precession cycle. When eccentricity is high, precession is too. When eccentricity is low, precession is low. French mathematician Le Verrier had previously shown that the total amount of sunlight on Earth during an entire year is unaffected by eccentricity, but Croll believed that when the two cycles were high, climate could change enough to start an ice age due to less winter sunlight. But the effect of both cycles was still small, so Croll added a boosting mechanism of positive feedback. Slight decreases in winter temperatures led to more snow cover, which in turn reflected more sunlight, boosting the cooling. Combining these factors, Croll predicted that the most recent glacial epoch had occurred between 80,000 and 250,000 years ago and that ice ages oscillated between the hemispheres, out of phase, every 11,000 years, in tune with the precession cycle.

Croll's ideas generated intense debate. Seeds and plants found between layers of glacial deposits in the Alps reinforced the idea of multiple ice ages. Scientists posited between two and six ice ages but challenged Croll's timing. Instead of 80,000 years ago, they insisted the most recent ice age ended only 10,000 years ago and that glaciation did not cycle between the hemispheres. They cited the ongoing migration of Niagara and St Anthony's falls in the north-central United States as evidence of a recent ice age. Both had been receding, they thought, since the end of the last ice age, and they used the rate of recession to date that event between 6,000 and 32,000 years. The more recent date was based on a more rapid recession of Niagara Falls and was based on careful observations, but the older date was more generally accepted because it was proposed by Lyell.

Croll's theory was first rejected by American scientists and then later in Europe as, once more, meteorologists claimed the orbital effects were too minor to trigger ice ages:

> Moreover, theoretical arguments were advanced against the theory by meteorologists who calculated that the variations in solar heating described by Croll were too small to have any noticeable effect on climate. (Imbrie and Imbrie, 1979, p. 96)

So, the astronomical theory lay dormant—just one more fading theory of the ice ages.

Milankovitch Rescues the Astronomical Theory

Geology entered another cycle of theorizing about astronomically caused climate change when Milutin Milankovitch, an engineer from Serbia, became interested in the ice ages. With help from renowned climatologist, Wladimir Köppen, he proposed that ice ages were triggered by cool summers, not cold winters, as Adhémar and Croll had believed. Hot summers melted snow, he reasoned, even after cold winters. Cooler summers would preserve snow cover, which would then accumulate to form glaciers and ice sheets. In 1924, Köppen and Wegener used the calculations of Milankovitch to correlate alpine ice-age deposits with insolation minima. Others noticed an apparent agreement between Milankovitch's solar radiation curves and the timing of the four ice ages (Penck and Brückner, 1909) on the north slopes of the Alps. This "confirmation" was so close that even the "great interglacial" between the second and third ice ages could be seen on the Milankovitch curves. This "great interglacial" was deduced from the thickness of Swiss lacustrine sediments. It was a striking "verification" that persuaded a majority of scientists that there was an astronomical trigger for the ice ages. Milankovitch (1941) published what most consider the landmark research for the astronomical theory, and scientists began using his curves to "date" surficial glacial debris. Schaefer (1953) had earlier called the Alpine theory into question with the discovery of warm-climate mollusks in terraces supposedly formed during glacial melting, but his results were ignored.

But this simple scheme faced problems. Geologists soon realized that each ice age would erode sediments deposited by previous ice ages and redeposit them. The apparent succession of tills for the four ice ages in the northern Midwest of the United States was discontinuous and jumbled, making it hard to test Milankovitch's theory in the field. A potential solution came when Libby introduced carbon-14 dating. Scientists used it to date ice-age deposits, but the carbon dates did not match Milankovitch's curves. They found an interglacial warm phase during a summer insolation minimum at 65°N, and glaciation during a winter insolation maximum. These contradicted the theory, and during the 1950s and early 1960s, the Milankovitch mechanism appeared dead:

> By 1969 it was embarrassingly clear that the entire climatic scheme developed for the Alpine terraces by Penck and Brückner, expanded by Eberl, and accepted by a generation of geologists was no more than a house built—not on sand—but on shifting gravel. And when the house finally collapsed, the argument used by Köppen and Wegener to confirm the Milankovitch theory collapsed with it. (Imbrie and Imbrie, 1979, p. 156)

Marine Geology Revives the Astronomical Theory

But the theory was revived to explain the explosion of data from the new discipline of marine geology. After World War II, mapping and sampling the ocean floor was pursued with great energy. In 1968, the Deep Sea Drilling Program (DSDP) began under the auspices of JOIDES, with exploration legs aboard the *Glomar Challenger*. In 1975, the International Phase of Ocean Drilling united scientists from the United States, the UK, France, West Germany, Japan, and Russia. In 1985, the DSDP was replaced by the Ocean Drilling Program (ODP) with the new research vessel, *JOIDES Resolution*. In 2003, the ODP was replaced by the International Ocean Discovery Program (IODP). As of 2015, 356 legs had been completed, and the vast data from the world's oceans has revolutionized earth science (IODP, 2015).

One of the primary sources of data from ocean drilling was a set of cores of ocean-floor sediment. Initially, it was hoped that sea-floor sediments would show a pristine record of each ice age. Scientists only needed to identify the proper sedimentary proxy to identify glacial and interglacial periods. Researchers proposed several. One was the percentage of $CaCO_3$ in each layer, based on the assumption that the volume of $CaCO_3$ would be controlled by temperature. As a result, they correlated percent $CaCO_3$ to glacial and interglacial periods, and the numerous cycles suggested numerous ice ages. But other methods were being developed.

Another potential proxy was the abundance of the foraminifera, *Globorotalia medardii*. Foraminifera are microscopic shells built by plankton. Scientists immediately noticed that higher occurrences of these foraminifera corresponded to the long interglacial proposed by Penck and Brückner (1909). Another proxy was being developed by Emiliani (1955, 1966), who proposed the use of oxygen isotope fractions in calcareous foraminifera shells, thinking that changes in oxygen isotope ratios could be correlated to ocean temperature and salinity, which would change slightly during glacial and interglacial periods. The isotope ^{17}O is rare, but the ratio of ^{16}O to ^{18}O offered hope as a reliable proxy. Emiliani (1966) discovered that the pattern of ice ages based on this ratio differed from that using the foraminifera curve, but he was able to convince scientists that the oxygen isotope ratios reflected astronomically driven climate change.

Problems with Emiliani's solution soon appeared; for example, he thought that the glacial/interglacial cycle was on the order of 40,000 to 50,000 years (Emiliani, 1955). But geologists considered the oxygen isotope method superior to that comparing the relative abundances of warm and temperate species of pelagic foraminifera or carbonate percentages. Kemp and Eger (1967) noted that it was already then the preferred method by geologists. Shackleton (1967) proposed that the oxygen isotope ratios could be used if they were seen as reflecting ocean volume, rather than directly showing changes in temperature and salinity. This would indicate changes in sea level that could then be correlated to glacial and interglacial periods. This is due to the smaller mass of the water molecule with ^{16}O than a water molecule made with ^{18}O. The lighter water molecule made with ^{16}O would more likely evaporate and fall as precipitation on the continent. This would tie up water molecules high in ^{16}O in ice sheets. leaving behind in the oceans water molecules high in ^{18}O.

Work continued and in what is considered the definitive beginning of widespread acceptance of the "Milankovitch processes" (Miall, 2010, p. 327), Hays et al. (1976) were able to show a quantitative link between oxygen isotope ratios and Milankovitch cycles. Then Imbrie et al. (1984) showed that the isotope signature could be correlated to the Brunhes magnetic chron in all the oceans, indicating its global value. Imbrie (1985) followed up with an astronomical theory linking orbital mechanics to the Pleistocene ice ages.

Paralleling these advances in isotope profiling of cores was the development and expansion of the magnetostratigraphic timescale, which for several decades was used to identify sea-floor spreading rates (Vine and Matthews, 1963). The two methods began to be used in tandem, and still are (Kodama and Hinnov, 2015), but this has raised several questions. Among them was an indication that ice ages were most strongly influenced by the 100,000-year eccentricity cycle, which has a minimal effect on insolation.

The astronomical theory was originally developed to model the antiquated four-ice-age model. As the number of ice ages grew, the astronomical clock was adjusted to accommodate them. Today, based on cycles in deep-sea sediment cores, scientists believe that there were approximately fifty ice ages during the Pleistocene (Quaternary) (Pillans and Gibbard, 2012).

Pushing Deeper into the Past

If orbital forcing of climatically controlled sedimentation during the Pleistocene ice ages could be seen in marine sediment cores, geologists reasoned that climate forcing might extend to other depositional environments and be a major factor in deposition through time. The basis for the idea was firmly in place, thanks to a body of work on North American cyclothems (Merriam, 1964; Wanless and Weller, 1932) and speculation by G. K. Gilbert (1895) that orbital cycles influenced carbonate content in Cretaceous strata in Colorado. As the theory took hold, climate-based cyclicity was identified at other locations (e.g., Fischer, 1986; Van Houton, 1964). Milankovitch and the DSDP efforts focused attention on the Pleistocene ice ages, as noted above, but the idea of climate forcing in older sediments required merely a shift in focus; the paradigm had already been established. As Miall (2013, p. 176) noted:

> A key question, central to the issue of sedimentation rate and time scales, is the degree to which orbital frequencies could be retrodicted or reconstructed for the distant geological past, given the possibility of changes in the orbital behavior of Earth.

As geologists began seeking examples of climate forcing in older sediments, they faced a problem of circularity: "some astronomers … suggesting that geological data could be used to calibrate the orbital frequencies of the geological past" (Miall, 2013, p. 176), while "geologists experienced in the incompleteness and inconsistencies of field data and knowledgeable about the warnings associated with the use of time series analysis offered by signal theorists" (Miall, 2013, p. 176) understood the necessity of a standard *for* the stratigraphic record, not vice versa. Another problem was the ability to calibrate the relatively precise astronomical curves to accepted dates, since radiometric methods cannot reliably achieve the precision of tens to hundreds of thousands of years.

Another problem—though one not fully appreciated even today—was the completeness of the sedimentary record. After all, if hundreds of thousands of years of section were missing in a given outcrop, each hiatus would have to be identified and dated before the resulting astronomical spectral peaks could be properly interpreted. Practically speaking, the latter two problems required that astrochronology be able to justify its timescale apart from the sedimentary record, if it was to be used as a stratigraphic dating and correlation method. But this has proven difficult because the two are so intertwined. Miall (2013, p. 171) noted that astrochronology was a "logical extension of cyclostratigraphy," acting as "a 'pacemaker' tracing Earth history."

Despite these problems, geologists quickly began to interpret increasingly older sediments as the products of astronomical climate forcing, based on extrapolation of sea-level changes estimated from Pleistocene ice ages. Once Imbrie (1985) had proposed a complete cyclostratigraphic timescale for the Pleistocene, geologists moved to older sediments. Shackleton et al. (1990) began to push the clock back, but it was the landmark work of Hilgen (1991a, 1991b) on pelagic sediments on the coast of Sicily that broke away from the limits of the Pleistocene and showed how to migrate the astronomical clock back into the Cenozoic. Hinnov (2004), in an article supporting the application of cyclostratigraphy to the Geological Time Scale 2004 (GTS2004), extended this timescale back to 23 Ma, in the mid-Tertiary. In conjunction, mathematical development of the Astronomical Time Scale (ATS) improved, indicating that cyclostratigraphic calibration and correlation was possible for older sediments.

In addition, Hinnov (2004) and others distinguished between a cyclostratigraphic timescale linked back through time and tied firmly to accepted dates, and less precise "floating timescales" based on the 405-kyr eccentricity signal. These "floating timescales" were an initial step and would become a part of the calibrated record as ties were established to the timescale stages. "Floating scales" are calibrated to specific sections of the stratigraphic record but not fully linked from present to past. Since accepted dates for key boundaries of the timescale are tied to radiometric methods, it is difficult to demonstrate a complete astronomical record. For example, if a radiometric date had an error range of one million years, that would be 2.5 times the length of an eccentricity cycle and 50 times the length of a precession cycle. Interpretation is required; Hinnov and Ogg (2007) claimed that the beginning of the Messinian salinity event corresponded to climate forcing by an eccentricity cycle. They provide a good summary of progress through the early twenty-first century, confidently asserting that the ATS would be soon fully calibrated all the way to the base of the Mesozoic.

Various methods have been developed over recent decades to connect the astronomical and stratigraphic signals. Hinnov and Ogg (2007, p. 242) noted, "Astronomical (orbital) tuning is the mainstay of ATS calibration." Astronomical tuning involves the statistical time-series analysis of spectral peaks that can then be linked to the various astronomical cycles. However, Miall (2015) warns of pitfalls in this method when it is not linked to a careful sedimentological/facies analysis. Nevertheless, extraordinarily rapid progress is being made.

> Cyclostratigraphic studies have been published or are in progress for at least one section spanning each geologic stage throughout the Cenozoic and Mesozoic, and there is a steadily growing literature devoted to Paleozoic cyclostratigraphy. (Hinnov and Ogg, 2007, p. 242)

Furthermore, geologists are using cyclostratigraphy to calibrate a chronology that sheds light on everything from the motions of the planets to evolution. It is clearly a time of great optimism that cyclostratigraphy will unlock many mysteries of the past. Voices of caution exist however. Miall (2015, p. 29) stated:

> It is common practice to show the sections in the time domain, which makes correlation to a calculated

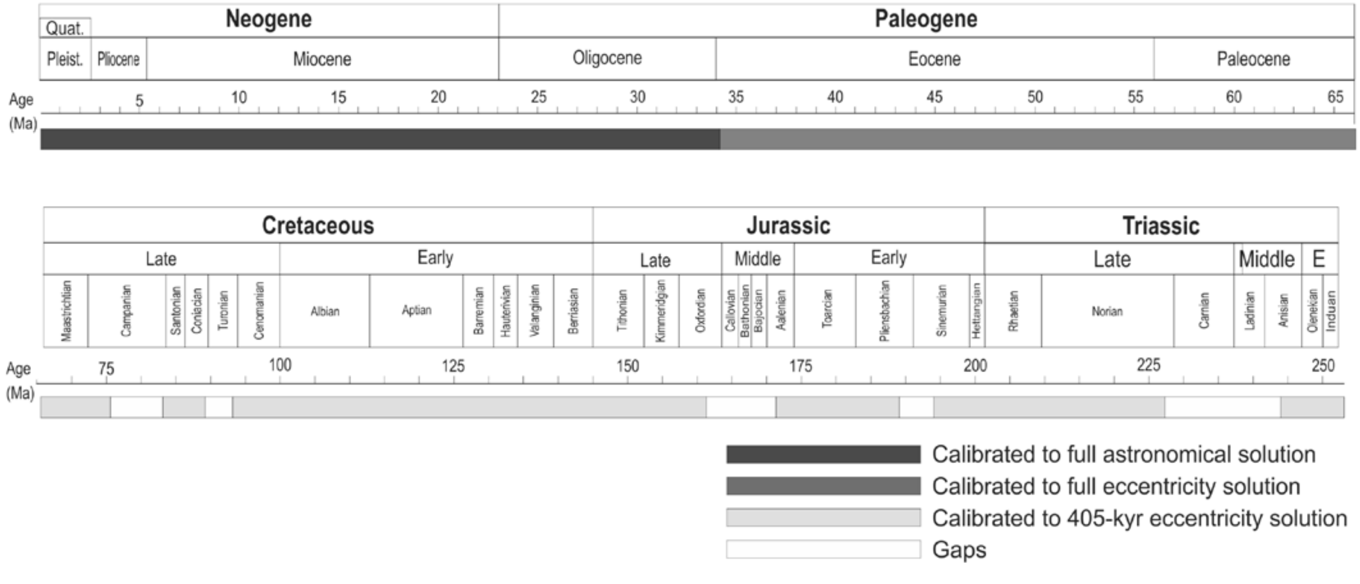

Figure 1. Parts of geological timescale calibrated to astronomical timescale as of 2012. After Hinnov and Hilgen (2012).

> astronchronological scale straightforward. However, caution is to be recommended, because this practice may hide irregularities in the succession caused, for example, by autogenic processes. Time series analysis of sections in the thickness domain cannot be used to explore orbital control where there are significant autogenic effects on lithofacies and unit thickness. … it is incumbent on proponents of cyclostratigraphic control for hanging sections representing the distant geological past to do more than provide statistical "proof" of their reality, such as from amplitude spectra of time series studies.

At present, mathematical models of Earth's orbital dynamics through time have been developed to produce astronomical Milankovitch curves back through the Cenozoic. Significant recent advances in mathematical models of orbital mechanics through time (Laskar et al., 2004; Laskar et al., 2011) extend a full astronomical solution, or a composite continuous cyclostratigraphic correlation, back to 34 Ma (Figure 1). It provides a full eccentricity solution to the base of the Cenozoic (66 Ma) and a partial solution based on the 405-kyr eccentricity cycle to the base of the Mesozoic (250 Ma) (Hinnov and Hilgen, 2012). This has been an amazing progression in less than two decades.

Conclusion

Recent decades have seen explosive activity bent on finding an "astronomical clock" in sediments throughout deep time. Patches of Mesozoic strata from the Triassic, Jurassic, and Cretaceous have all been calibrated to the astronomical clock, although geologists have not yet been able to link these sections to cover the entire Mesozoic (see chapters 25–27 of Gradstein et al., 2012). Other geologists are "seeing" astronchronological cycles in Paleozoic sediments such as the Permian Castile Formation (Anderson, 2011), Pennsylvanian cyclothems (Heckel, 2008), and Mississippian limestones in Ireland (Schwarzacher, 1993). Hinnov and Hilgen (2012) report "astronomical-scale cycles" in Devonian, Silurian, Ordovician, and Cambro-Ordovician sediments. Some work has even been started in Precambrian sediments as old as the Archean (Hofmann et al., 2004).

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An Investigation into an In Situ Lycopod Forest Site and Structural Anatomy Invalidates the Floating-Forest Hypothesis

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Abstract

The hypothesis of an extinct pre-Flood floating-forest ecosystem has been promoted in the creationist literature for several decades and used as an explanation for the massive Carboniferous coal beds. However, it was recently shown that the idea sharply conflicts with both the available geological data and timing of global coal deposits and with the necessary hydrological criteria to sustain a freshwater lens. In this report, we present additional evidence negating the floating-forest hypothesis based on a well-preserved in situ lycopod biome known as the "Fossil Grove" in Glasgow, Scotland. This site reveals relatively equidistant-spaced trees at the same stratigraphic level that would typically occur in a forest ecosystem. The fossilized trees have downward penetrating roots within a lithified clay-rich soil in the same ecological schema as modern-day lowland/swamp trees. In addition, we present evidence that conflicts with the speculation by some creationists that both the aerial trunks and stigmarian roots of lycopods were hollow, a feature required to reduce weight and make the floating forest tenable. Based on data presented in this paper, combined with that given in a previous report, we strongly recommend that the floating-forest hypothesis be abandoned by the creationist community.

Introduction

The idea of a floating forest has its original ideological roots in the ideas of nineteenth-century writings of Kuntze, a German author who could not envision a land-based source of origin for the transportation of plant debris to form the vast global coal deposits (Kuntze, 1895). This led Kuntze to the hypothesis that these plants must have been aquatic floaters. The work of Kuntze was published in German and not readily accessible to English-speaking researchers. Woolley (2010) recently published an account of Kuntze's ideas and the development of his silvomarine floating-forest idea.

Within the creationist community, Scheven (1981, 1996), was the first major proponent of the floating-forest

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hypothesis, which relied upon the early work of Kuntze. Building upon Scheven's reworking of the Kuntze hypothesis, other creationist authors such as Wise (2003, 2008), Woolley (2010, 2011a, 2011b), and Wieland (1995) have further elaborated upon the floating-forest idea and promoted the hypothesis within the creationist community.

The floating-forest hypothesis in its current form, postulates that an arboreal lycopod-dominated biome with trees up to 100 feet or more (30.5 m) in height existed on floating forests of continent-scale extent. In this scenario, the supposed hollow nature of lycopod trunks and stigmarian roots are thought to have made the floating forest possible. These floating forests were believed to have become so structurally and ecologically advanced that even freshwater pools and springs capable of supporting animal life were possible (Wise 2003, 2008).

The floating-forest hypothesis was developed by some creationists to explain extensive coal beds found in Carboniferous rocks. However, this paleontology-based hypothesis was never adequately tested against geological data. Clarey (2015) recently published a paper that presented three geological challenges to the floating-forest hypothesis. First, floating forests are incapable of maintaining a freshwater lens sufficient to support plant life, pools, and springs as suggested. Second, tsunami-like waves triggered by plate movements (Baumgardner, 2016) and other causes would have broken up the floating-forest biome earlier in the Flood than suggested, depositing coal beds throughout much of the stratigraphic column, contradicting the rock record. Third, relatively few coal beds developed as a result of the closure of the Iapetus Ocean ("proto-Atlantic") early in the Flood as Rodinia began to fragment. It is not until after this pre-Flood ocean was completely consumed that extensive coal beds deposited on the adjacent continents are found. When examined against available geological data, the floating-forest hypothesis lacks explanatory ability.

In addition to the coal-deposition argument, creationists have also used the claim that the dominant plant species of the carboniferous coals, arborescent lycopods, which can achieve heights of 111 feet (34 m) (Thomas and Watson, 2007), were the dominant plants of floating forests. It is believed that they formed floating mats with their stigmarian root systems, growing more densely than do trees in modern forests. But most importantly, it is believed that they contained hollow trunks and stigmarian roots that provided sufficient buoyancy to enable floating. These claims of alleged hollow trunk and roots lack significant support from available paleontological and geological data.

Allochthonous vs. Autochthonous Upright Fossil Trees

One of the issues creationists must deal with is the claim by secular science that many upright fossil trees are found in growth position, commonly referred to as in situ trees. Secular paleontologists have used this claim as evidence against the Flood, even arguing that fossil-erect, in situ trees demonstrate an autochthonous origin for coal (Gastaldo, 1984, 1999). Creation scientists have countered this argument with evidence supporting the allochthonous origin of coal, showing many claimed in situ trees are better explained by active transport of trees and other vegetation during the global Flood.

The beginning of the allochthonous interpretation for coal goes back to the work of Kuntze (1895), Lemiére (1905), Nelson (1927), Price (1943), and Whitcomb and Morris (1961). These authors argued that pre-Flood trees were swept from the land during the Flood event, transported and subsequently buried as coal deposits. Upright trees or stumps were explained as trees that sank upright and were buried erect by additional Flood sediment (Nelson, 1927), resulting in polystrate fossils.

More recently, Austin (1979) and Scheven (1981, 1996) and Wise (2003, 2008) have concluded, albeit somewhat differently, that vast mats of floating vegetation existed in the pre-Flood world, either along the continental margins and/or across the open ocean. These proposed massive mats are envisioned to have later broken up during the Flood event, becoming deposited as represented by the globally extensive Carboniferous coal beds.

Though Clarey (2015) presented three geologic arguments against any pre-Flood floating-forest biome, he supports an allochthonous origin of coal. Clarey envisioned forests of lycopod trees fringing coastal and lowland areas of the pre-Flood continents that were similar to the cedar swamps and mangrove forests today. He postulated that as the height of the Flood waters increased, tsunami-like waves tore the lycopod forests free and deposited them *en masse* as coal seams within the sedimentary strata.

Over the course of this debate, many sites containing upright trees and stumps have been identified. There is no disagreement that upright trees and stumps exist in the rock record, but a central question remains: are these upright trees allochthonous or autochthonous? The answer to this question has tremendous implications for the extent of the Flood and the development of any global Flood model.

Empirical support for the allochthonous origin for upright fossil trees was found soon after the 1980 eruption of Mt. St. Helens. Austin (1986) estimated that more than 19,000 upright and randomly spaced trees had accumulated in the sediment beneath Spirit Lake in just a few years. These trees became waterlogged and sank upright because of their heavier bases and roots. Austin postulated that if these trees were buried by additional sediment, they would give the appearance of an in situ forest.

But does this explain all claims of in situ trees by secular science? In other words, are there any claimed in situ sites where the trees are in original growth position, or are they all products of transport during the Flood? The answer to this question also tests the validity of the floating-forest hypothesis. If a true in situ site is identified, showing no evidence of transport and with complete root systems embedded in a pre-Flood soil horizon (as opposed to having the roots torn off close to the trunk), it would strike a major blow to the floating-forest model. More importantly, it would demonstrate that lycopod forests existed rooted in soil, not floating as mats in water as proposed. However, the identification of an in situ site would not necessarily invalidate the allochthonous origin of coal beds. An in situ site could merely represent a location where the tops of the trees were sheared off, leaving the trunks and stumps buried in place.

This paper presents geologic criteria to assess whether or not an upright tree (or trees) is (are) in situ or not. And it identifies a site near Glasgow, Scotland, that appears to meet the vast majority of these proposed criteria and is possibly the first identified truly in situ lycopod forest.

Geologic Criteria to Determine In Situ Trees

There are many claims of in situ tree sites in the secular literature, sometimes preserved as either Lagerstätten, or mass burials of entire ecological communities (Locatelli, 2014), or upright trees in claimed growth position, called T^0 assemblages (DiMichele and Falcon-Lang, 2011). Proposed in situ trees are most commonly found in Pennsylvanian system rocks (DiMichele and Falcon-Lang, 2011), the upper part of the Carboniferous. And all claimed Carboniferous in situ trees are from the Lower-Middle Pennsylvanian only (DiMichele and Falcon-Lang, 2011), corresponding to the onset of the Absaroka megasequence, the fourth of six recognized marine transgressions of the continents (Blakey, 2010; Morris, 2012).

Finally, the majority of the fossil Pennsylvanian system upright trees are arborescent lycopsids, or the rush, *Calamites*, preserved as mud- or sandcast plant stems, with only the basal 1–2 m of the fossil foliage commonly preserved in the rock record (DiMichele and Falcon-Lang, 2011). Secular paleontologists also believe that Pennsylvanian lycopsid forests were most likely preserved in wetlands, or wetter parts of dry environments that were buried and preserved due to a rapid rise in sea level (DiMichele and Falcon-Lang, 2011), coinciding with the advance of the Absaroka megasequence.

Interestingly, DiMichele et al. (2009) found that most of the stumps within claimed in situ assemblages, even as many as 800 trees at a single site, are randomly distributed spatially, not equidistantly spaced, and not interacting with one another in terms of the expected biological spacing for trees. The trees at these sites were undoubtedly transported and deposited by Flood waters and were not buried in their actual growth position. Tree spacing in such cases of transport would be expected to be random, showing no semblance of nearly equidistant spacing as observed in extant forests, as DiMichele et al. (2009) observed. Sites with claimed in situ and upright solitary trees also seem to be placed haphazardly and randomly and are often found above extensive deposits of coal and other sediments (DiMichele and Falcon-Lang, 2011). These individual stumps must also have dropped in place after a significant amount of Flood sediment was already deposited.

As creationists, how do we ascertain which trees are truly in situ, if any, and which ones are not? Criteria need to be developed in order to discern which fossil assemblages were buried in growth position and which were transported. The following are suggested criteria for the determination of an in situ assemblage. Some of these are from the secular literature, and others are tied directly to a global Flood perspective. Fossil trees that fulfill all, or at least most, of these criteria likely represent in situ assemblages.

1. Finding multiple, single-species trees spaced in growth position in the same horizontal plane, nearly equidistantly spaced in all directions from the trunks, tree to tree, and not merely randomly spaced (DiMichele and Falcon-Lang, 2011; DiMichele et al., 2009; DiMichele and DeMaris, 1982; Gastaldo, 1984).
2. Finding multiple trees in the same rock layer or along a common surface and/or stigmarian (root) axes interlacing with other trees over a common, three-dimensional, single rock layer (Gastaldo, 1984).
3. Finding trees with root systems (stigmarian axes) that crosscut bedding layers up to and even exceeding 30 degrees and possessing perpendicularly inserted radiating appendages (rootlets) (Gastaldo, 1984).
4. Evidence of rapid burial by thick sediment and water, which is common for most standing lycopsids (DiMichele and Falcon-Lang, 2011; DiMichele et al., 2009), and multiple trees at a single site that were distorted by water flow in the same direction during burial (Gastaldo, 1986).
5. Finding a lack of sedimentary rock layers underneath the trees. The presence of Flood-related layers underneath the trees would eliminate the possibility of in situ growth. In contrast, a lack of sedimentary layers under the trees, other than the fossil soil (paleosol) layer that contains the trees, would support the interpretation of an original pre-Flood setting.

In other words, in situ trees should have no substantial sedimentary layers beneath or fossils beneath or coal layers beneath.

6. Likewise, finding no bowing or distortion of any sedimentary layers beneath the tree stumps, which would indicate the tree was transported and emplaced from above during burial, distorting the underlying sediments (Oard and Giesecke, 2007).
7. Finding accompanying vegetation like *Calamites*, although rare, that crosscut the same layers as the lycopod tree stumps (Gastaldo, 1984).

Geologic Setting of the Glasgow "Fossil Grove" Site

We have identified one particular site, in Glasgow, Scotland, that seems to meet nearly all these criteria. It is our contention that this site represents the remnants of a pre-Flood forest, with the fossil trees still rooted in a pre-Flood soil horizon (paleosol), now lithified to rock. If so, it is possibly the best preserved example of an in situ lycopod forest in the world (Gastaldo, 1986), and possibly the first identified in a Flood context. "Fossil Grove," as it is called, is located in Victoria Park in Glasgow, Scotland (Figure 1).

The Victoria Park "Fossil Grove" was discovered in 1887 as a path was being cut across an abandoned quarry outside of Glasgow (Owen et al., 2007). After excavation down to the common "soil" horizon containing the tree stumps and roots, a building was constructed to protect the site and allow public viewing. The site (Figure 2) consists of a monotypic assemblage of eleven lycopod tree stump casts with attached axial root systems (Gastaldo, 1986). However, only ten stumps are presently preserved and on view; one stump was significantly damaged in World War II (Owen, et al., 2007). The lycopod tree fossils at Victoria Park are found in rocks of the Clackmannan Group (Mississippian-Pennsylvanian systems), in a rock unit called the Limestone Coal Formation (Figure 3).

The 10 remaining stumps vary in height from 15–68 cm, and the tree spacing suggests a density of 4,500 trees per square kilometer (Owen et al., 2007). Each tree has preserved branching roots anchoring them in an irregularly laminated silty or sandy mudstone with

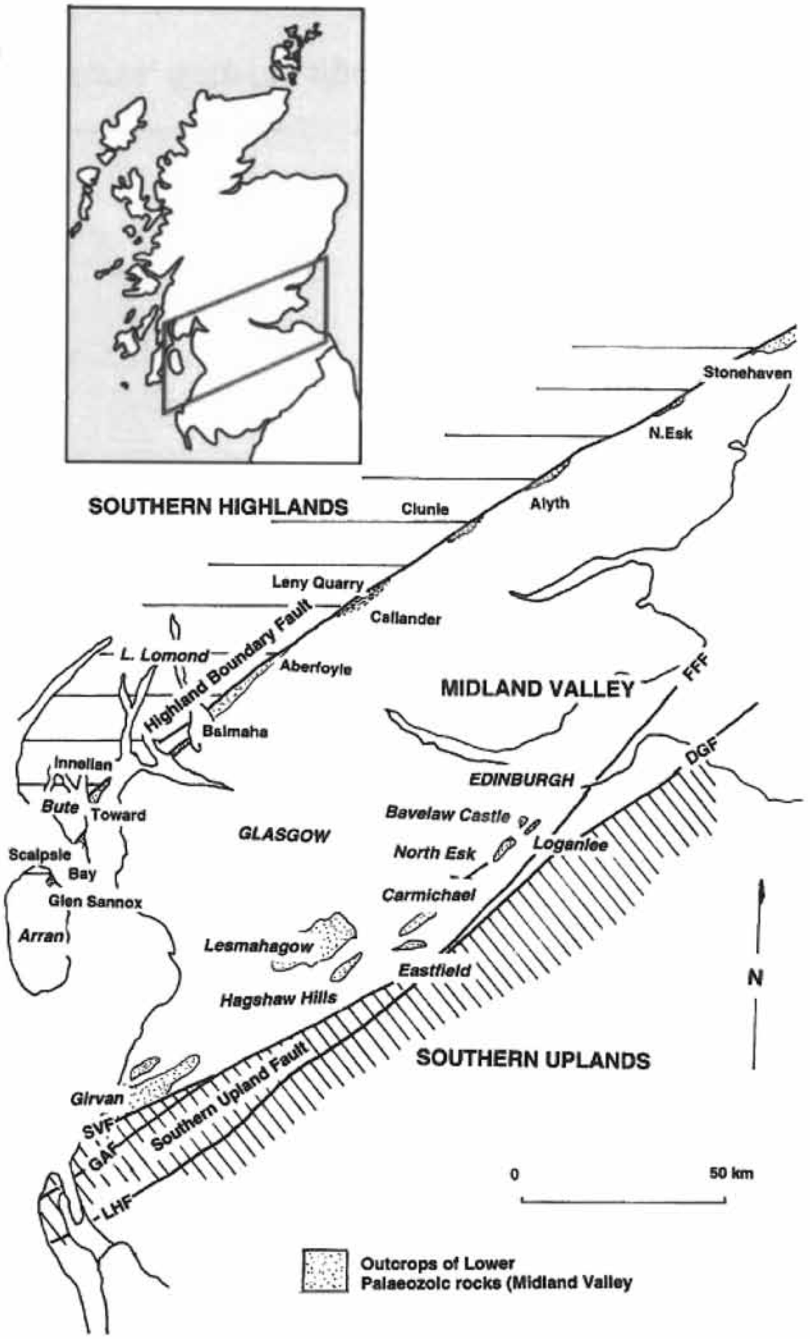


Figure 1. Location map for Fossil Grove, Victoria Park, Glasgow, Scotland. Map shows the Midland Valley terrane bounded to the north and south by major fault systems. Map also shows the Lower Paleozoic outcrops clustered along the southern and northern boundaries of the terrane (modified from Bluck, 2002).

Figure 2. Late 1880s photograph of the lycopod tree stumps at Victoria Park, Fossil Grove. Note the intact roots penetrating the common subsurface horizon and the nonrandom (growth position), equidistant-spaced trees. Reproduced courtesy of Glasgow Museums and the Glasgow City Council.

stigmarian (subterranean stem) "rootlets" penetrating the "paleosol" horizon (Gastaldo, 1986). This layer may have been a clay loam or a silty clay soil, according to the USDA classification system, and prior to burial, compaction, and lithification. The top of the mudstone is exposed as the surface layer of the exhibit (Figure 2).

Criteria to conclusively determine a preserved paleosol often involves a three-dimensional exposure and can be ambiguous (Klevberg et al., 2009). Unfortunately, the Fossil Grove site is exposed only down to the silty mudstone surface containing the tree stumps, making identification of soil structure impossible. Any sort of true, organic-rich A or O horizon may have been removed during deposition of the high-energy, overlying sandstone (see below). However, assuming the trees grew in a swampy, wetland-type environment; it is likely the trees would have been rooted in a clay-rich soil as observed (Mitsch and Gosselink, 1993).

The sandstone that had previously encased the stumps (before removal during excavation of the site) is a fine- to medium-grained, massively bedded sandstone (beds thicker than 20 cm) with asymmetrical ripples (Gastaldo, 1986). All of the tree stumps terminated upwards into this encasing sandstone layer. The sandstone also contains fossil casts of sand-filled *Stigmaria* and compressed *Cyperites* and prostrate broken trunk fragments, oriented in a dominant NE-SW direction (Gastaldo, 1986). Ripples in the encasing sandstone indicate water flow to the southwest during deposition, matching the long-axis orientation of the trunk fragments. The ten upright tree stumps also show marked distortion in the NE-SW direction, matching the flow orientation.

However, the tree roots (stigmarian axes) of the stumps imbedded in the mudstone paleosol below the encasing sandstone are not distorted in a NE-SW direction, and only show distortion vertically from burial (Gastaldo, 1986). This indicates that the tree roots were embedded in the underlying soil layer prior to burial by the encasing sandstone, strongly supporting an in situ interpretation. This sandstone also served as the casting lithology for the lycopod stumps and axial root systems (Gastaldo, 1986). Gastaldo (1986) also suggested that the "streamlining" of the stumps and loose trunk fossils in a NE-SW direction, the asymmetrical ripples, and the massively bedded character of the sandstone, indicate a high (mid-upper) flow regime during burial of the stumps.

Above the encasing sandstone is another thinly laminated, rippled, and cross-bedded coarse siltstone and interbedded sandstone. A disordered and transported coalified megaflora is found in this rock layer (Gastaldo, 1986). Both the encasing sandstone and the sandstone layer above indicate rapid deposition, contributing to the burial and preservation of the tree stumps.

In summary, the Glasgow site fulfills geologic criteria #1, #2, #3, and #4 for an in situ assemblage. The 11 single-species stumps were found in growth-position spacing as opposed to random spacing (Figure 2). The trees are all found in one common rock layer, likely representing a pre-Flood soil horizon. The root systems penetrate the paleosol horizon, similar to modern root systems. The encasing sandstone layer contains ripples and oriented, broken trunk fragments indicative of a high-energy flow system directed toward the southwest. The ten tree stumps are also consistently distorted in a southwesterly direction, matching the paleo-flow direction. This indicates all of the trees were likely in place prior to burial by the encasing sand.

Likewise, it is significant that the roots of the tree stumps are not distorted in a southwesterly direction like the tree stumps. If the tree stumps, roots and all,

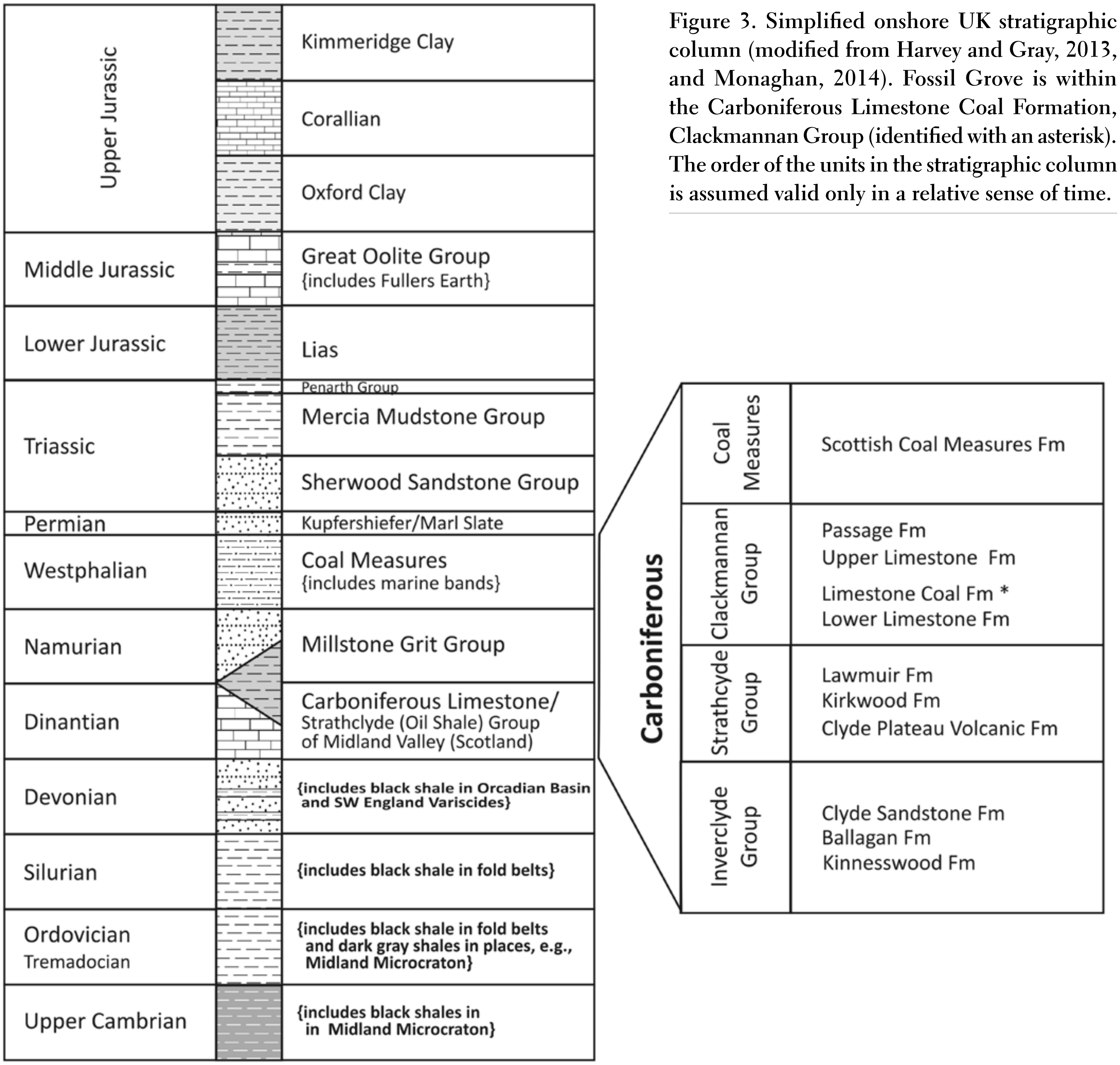


Figure 3. Simplified onshore UK stratigraphic column (modified from Harvey and Gray, 2013, and Monaghan, 2014). Fossil Grove is within the Carboniferous Limestone Coal Formation, Clackmannan Group (identified with an asterisk). The order of the units in the stratigraphic column is assumed valid only in a relative sense of time.

were transported in and deposited, there should be a consistent southwest distortion to the trunks and also to the roots. However, the lack of directional distortion in the roots (Gastaldo, 1986) suggests that the trees were rooted in the substrate prior to burial by the encasing sandstone. The only distortion of the roots is in a vertical direction, likely from compaction.

The consistent distortion of the trunks, the lack of similar distortion of the roots, and the nearly equidistant spacing of the tree trunks within a single horizon, collectively provide strong support for an in situ interpretation.

Regional Geology of the Fossil Grove Site

The Fossil Grove site is in the center of the Midland Valley terrane of southern Scotland (Figure 1). This terrane is bounded to the north by the Highland Boundary Fault and to the south by the Southern Upland Fault. These two steeply dipping fault systems divide the Midland Valley terrane from the Southern Highlands to the north and from the Southern Uplands to the south (Figure 1). Lower Paleozoic sediment outcrops are found along and near both boundaries. Any potential Lower Paleozoic exposures between the two fault systems, including near Glasgow, are covered by Upper Paleozoic strata (Bluck, 2002). The lack of observed Lower Paleozoic rock exposures across the Midland Valley has left room for much speculation about its stratigraphic history (Bluck, 2002). As Bluck cautioned, "Flanking rocks may record a history that is not directly related to the Midland Valley itself but possibly to some extension of it along strike" (Bluck, 2002, p. 149). In other words, Lower Paleozoic sediments may not exist beneath Glasgow at all.

If the Glasgow fossil forest is truly an in situ site, Lower Paleozoic sediments within the Midland Valley terrane should gradually thin and become nonexistent in the Glasgow area. There should not be Flood-derived sediment underneath the fossil forest, according to criteria #5 and #6 above. The Glasgow area would have been high ground in the pre-Flood world so that the earliest Flood sediments (assumed to be Lower Paleozoic) failed to cover it until the water level became high enough to inundate the forest itself, encasing the tree trunks in sediment.

The Case for a Pre-Flood High at Victoria Park, Glasgow

The oldest likely Flood-related rocks in the Midland Valley are Cambrian system limestones found along the northern edge of the terrane (near the Highland Boundary fault) (Bluck, 2002). Although creationists do not universally agree (Snelling, 2014), it is assumed that the Lower Paleozoic layers represent the earliest, globally extensive Flood deposits. Below these rocks lies a metamorphic complex composed primarily of amphibolite (Bluck, 2002). The Cambrian system rocks are overlain stratigraphically by limited amounts of Ordovician system black shale and more limestone on the southern margin of the terrane (Bluck, 2002) (Figure 3). Silurian system deposition was a bit more extensive in the Midland Valley; these black shales blanket the Ordovician system rocks along the southern margin of Midland Valley, just north of the Southern Uplands fault (Figure 1). Some of these Silurian system rocks may even be part of the lowermost Old Red Sandstone sequence (Bluck, 2002).

However, throughout this Early Paleozoic depositional cycle, the Glasgow area seems to have been a topographic high, receiving little, if any deposition. Bluck (2002) showed a topographic high, termed the Midland Valley Arc, likely existed during deposition of the Ordovician and Silurian system sediments in the center of the Midland Valley terrane, including the Glasgow area, sloping downward on both the north and south flanks. The Midland Valley in general is not a simple graben, or downthrown block, between major fault systems (Figure 1); "it is composed of a series of inter-related depocentres and intra-basinal highs" (Monaghan, 2014, p. 26).

The lack of sediment accumulation in the Glasgow area apparently continued during deposition of the Lower Old Red Sandstone (Silurian?), where outcrops are visible only along the northern and southern margins of the Midland Valley terrane and seem to match the extent of other Lower Paleozoic sediments (Trewin and Thirlwall, 2002). The Middle and Upper Old Red Sandstone (Devonian) sequence also thickens on the margins of the Midland Valley terrane with some deposits of over 1,000 meters along the northern margin and several hundred meters along the southern margin (Trewin and Thirlwall, 2002). Neither of these rock units can be observed in the vicinity of Glasgow, which may indicate that a sizable pre-Flood high prevailed in the Glasgow area with deposition only on the adjacent flanks (Figure 4). Bluck (2002, p. 166) said, "The difficulty [of these geologic interpretations] lies not only in the paucity of evidence but also in the ambivalence of the evidence available."

Analysis of the Lower Carboniferous strata (below the level of the Fossil Grove strata) (Figure 3) also indicates thinning near Glasgow (Read et al., 2002), indicative of a paleo-high. Rocks of the Mississippian system Inverclyde and Strathclyde Groups are either nonexistent or are observed to thin dramatically near Glasgow (Read et al., 2002) (Figure 5). Although Read et al. (2002) interpreted some deposition of

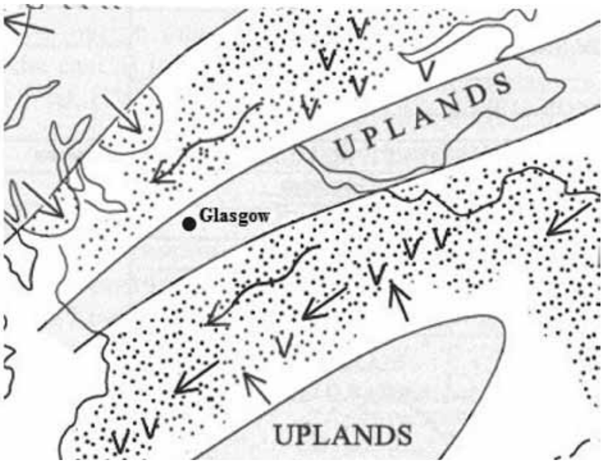


Figure 4. Paleogeographic map of the Lower Old Red Sandstone (Silurian system?) (modified from Trewin and Thirlwall, 2002). Note the interpreted uplands across the Glasgow area where no deposition is observed.

the Strathclyde Group near Glasgow, the thickness is only postulated and not based on empirical borehole data.

One oil well was drilled about 10 km east of Glasgow in 1989, the Marinex Bargeddie 1, that encountered rocks of the Strathclyde Group (West Lothian Oil-Shale Formation), finding some minor natural gas (Monaghan, 2014). However, there are no available deep well data beneath the city of Glasgow and Victoria Park. Monaghan (2014) reported that 98 oil wells were drilled in the Midland Valley between 1919 and 2008, and only 15 of these wells went deep enough to penetrate the Mississippian (Lower Carboniferous) Strathclyde Group. This lack of empirical information has added to the difficulty in the subsurface interpretation. All existing data indicate that a high existed during the deposition of the Mississippian system (Lower Carboniferous) units near Glasgow.

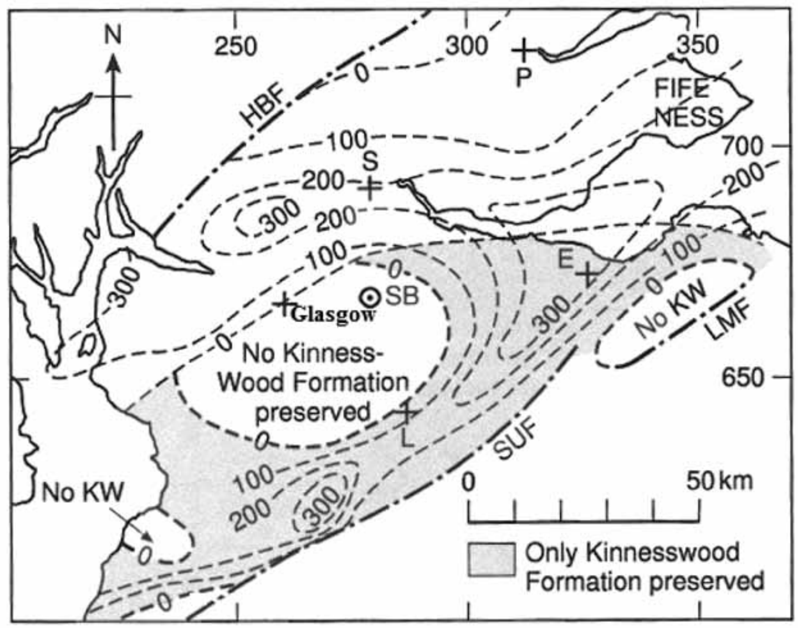
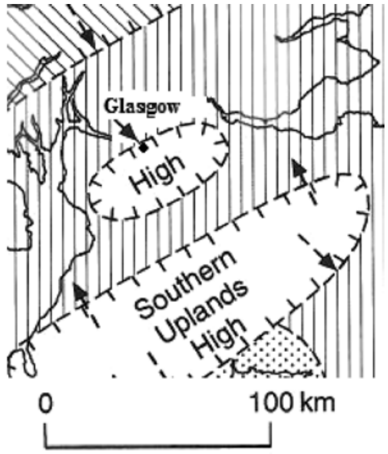


Figure 5. (5A, above) Isopach map (m) of the Kinnesswood Formation, Inverclyde Group in central Scotland, showing little to no deposition near the city of Glasgow. The Inverclyde is the unit below the formation containing Fossil Grove (Figure 3). SB = Salsburgh Borehole; HBF = Highlands Boundary Fault; SUF = Southern Upland Fault (modified from Read et al., 2002).



(5B, left) Paleogeographic map of the Ballagan Formation, Inverclyde Group, showing a well-developed high interpreted across the Glasgow area during deposition of this unit (Figure 3), resulting in no deposition. Vertical lines = marine sediments, Dotted areas = siliciclastics (Modified from Read et al., 2002).

The next unit deposited in the Midland Valley was the Clackmannan Group (Mississippian-Pennsylvanian). The lowermost unit in the group is called the Lower Limestone Formation (Figure 3). The next younger unit above is the Limestone Coal Formation, which contains the lycopod tree fossils at Victoria Park. The Lower Limestone Formation, the unit just below the fossil forest layer, has been interpreted to have attained a thickness of about 150 meters near Victoria Park, Glasgow (Read et al., 2002). However, Read et al. (2002, p. 276) pointed out:

> Because the Lower Limestone Formation lies below most of the economically workable Carboniferous coals, borehole information is sparse and our knowledge is more dependent on scattered outcrops. Thus the isopach map [showing 150 m of sediment] and the map summarizing palaeogeography, active structures and volcanicity are more conjectural than the corresponding maps for higher formations [including the layer containing the lycopod trees].

As for the layer that contains the fossil forest, Read et al. (2002) mapped a thickness of about 300 m for the Limestone Coal Formation across the Glasgow area. It is well exposed over a large portion of the central Midland Valley and has been extensively studied from outcrop and shallow borehole data in the search for coal (Read et al., 2002).

Possibly the strongest argument for a pre-Flood high persisting until the Carboniferous at Fossil Grove, Glasgow, comes from a recent three-dimensional seismic model done by the British Geological Survey (Monaghan, 2014). The model utilized 1,325 km of onshore seismic data, 478 km of offshore seismic data, 37 of the deepest oil wells from the 98 total boreholes, and all available coal mine data in the Midland Valley. Unfortunately, the seismic data did not extend across the city of Glasgow but was limited to about 3 km to the east, and the nearest oil well was also about 6 km east of the city of Glasgow (Monaghan, 2014). Results of the three-dimensional study showed a dramatic thinning of all Carboniferous units from the east, near Edinburgh, to the west, near the city of Glasgow (Monaghan, 2014, Section B-B' their Figure 66). Their model confirms the interpretation of a preexisting high found early in the Flood, preserving the Fossil Grove in Victoria Park from flooding until encased by the sandstone of the Limestone Coal Formation.

Were the Trunks and Roots of Arborescent Lycopods Hollow?

Another line of reasoning put forth in support of the floating-forest hypothesis is that the arborescent lycopod trees were allegedly hollow in both their main aerial trunks and in their stigmarian roots—a contention based primarily on superficial speculation and not soundly supported by the scientific literature. The postulated hollowness of these large trees by floating-forest proponents would be required to reduce weight, provide buoyancy, and keep the whole floating forest from sinking into the primeval ocean.

The idea that the stems and roots were actually hollow rather than filled with easily degraded parenchymous tissues seems to be the track favored and promulgated among creationists, first by Scheven (1981, 1996) and then later by Wise and Woolley (Wise 2003, 2008; Woolley 1999, 2010, 2011a, 2011b). Unfortunately, the majority of these studies do not take into account a number of key reports describing the non-hollow internal structure of lycopods that will be briefly recounted here. For all practical purposes, creationist authors such as J. F. Woolley and Wise have taken Scheven's assertions regarding the alleged hollow nature of lycopods without serious critical analysis of the existing literature on the topic.

Prior to the creationist promotion of the hollow-lycopod hypothesis, the idea that they were hollow or contained possible air cavities within the parenchymatous tissue (known as *aerenchyma*) was first promoted by Kuntze (1895). However, there is a significant difference between empty space inside the trunks and roots of a large tree-like plant as opposed to the presence of supporting structural tissue. The concept that the internal cortex tissue may have in fact been parenchymatous with small air spaces is a viable idea since the woody stele containing the central vascular system of the stem and roots would have required an extensive network of support tissue to keep it situated in place in addition to the lateral vascular rays emanating from the stele and connecting with the outer periderm. This is even more true regarding the large stigmarian roots that are horizontal to the gravitational field of the earth. To assume that there was not parenchymatous cortex support tissue inside them to keep the central woody stele and vascular rays in place defies the laws of physics and common sense.

In fact, this basic non-hollow anatomy is well established in arboreal lycopod stem tissue, which is typically well preserved (DiMichele 1981). The problem lies in the fact that very little of this internal cortex tissue is well preserved in the large trunks and stigmarian roots. Based on evidence of the preserved trunks at the Fossil Grove site mentioned above, which contains much better-preserved specimens than are typically found, Gastaldo (1986) was able to re-create the internal anatomy of lycopod trunks as shown in Figure 6. From these fossilized tree tissues, Gastaldo was able to show that three layers of internal parenchymatous cortex tissue existed that became preferentially degraded over the other intervening layers and central vascular stele.

The idea that easily degraded aerenchymatous tissue is the best explanation for the apparent hollowness of lycopod casts contains significant support from porous parenchyma found in the root cortices of many wetland plants alive today (Green 2010). In addition, in many other non-wetland plants, aerenchymatous tissue can develop in response to oxygen-depleted soils in a process called "induced" or "facultative" aerenchyma, while in other species it is formed irregardless of the growth conditions (Green 2010). In fact, the spongy mesophyll tissue in dicot plant leaves is also known as aerenchyma. Given that it is widely acknowledged that arboreal lycopods inhabited tropical lowland and/or wetland areas based on the types of sediments in which they are found (DiMichele and Philips 1994), it is not surprising that they would exhibit a tissue structure similar to modern plants inhabiting the same environs.

It is believed that root respiration in lycopods would not have been possible without the ability of the aerenchyma system to facilitate the supply of oxygen downward to the stigmarian roots (Green 2010). Based on the apparent rapid accumulation of biomass in lycopod forests, the amount of carbon acquired from leaf stomata would have been limiting. Therefore, it is highly probable that carbon was obtained from the clay-rich soils in which they grew. This rapid biomass accumulation scenario further limits the viability of a floating mat but is best explained by a lowland clay-rich soil.

Our knowledge of the stigmarian root structure of arborescent lycopods is chiefly based on the tree-sized lycopod species *Stigmaria ficoides*. The three most complete studies of this structure come from Williamson (1887), Frankenberg and Eggert (1969), and Eg-

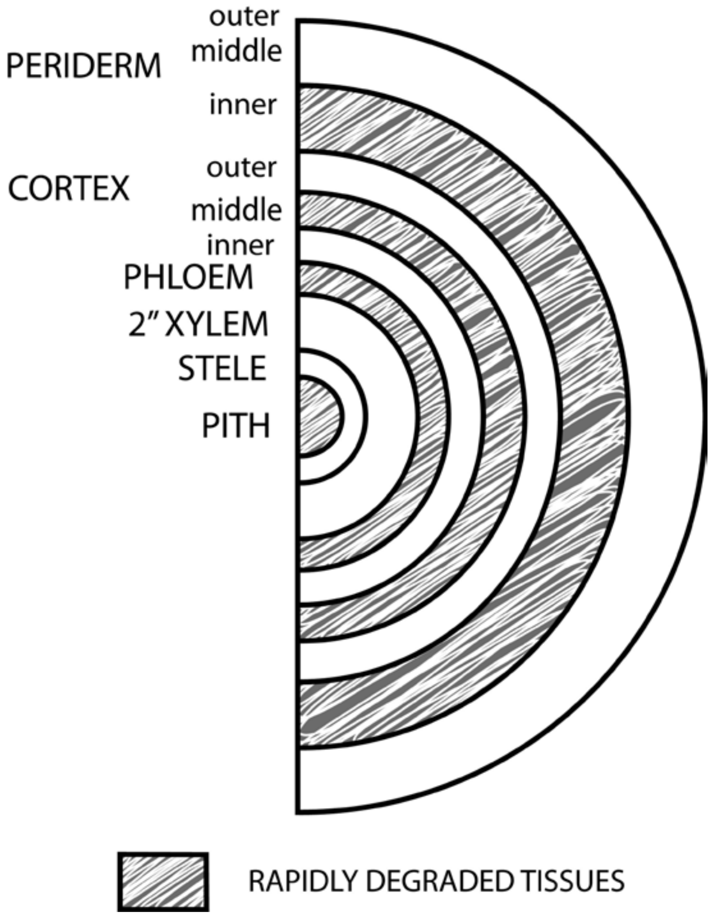


Figure 6. Diagram of the anatomy of lycopod trunks at the Fossil Grove site in Glasgow, Scotland, showing tissues predisposed to early degradation prior to being encased in sediments. This feature provided the mechanism for introducing sediments into the trunk for casting. Figure adapted from Gastaldo (1986).

gert (1972). The stigmarian roots are composed of a central woody stele that contains the vascular tissue surrounded by pithy tissue. Then surrounding the central stele is a three-zoned cortex similar to that of trunks but on a smaller scale. The inner cortex composed of parenchyma surrounding the stele is typically poorly preserved. However, a specimen in the curation of the Institute for Creation Research (ICR) clearly shows a contiguous region of well-preserved aerenchymatous tissue between the central stele and outer periderm (Figure 7). This specimen has yet to be sectioned for further study but adds additional strong evidence of internal supporting tissue, negating the alleged hollowness of stigmarian roots.

Discussion and Conclusions

Local geologic studies, based on extensive seismic, well, and outcrop data, support the interpretation that early Flood sedimentation did not occur at the Fossil Grove site in Glasgow. In addition, the site satisfies six of the seven proposed criteria for an in situ site. The only criterion it does not meet is the expectation of accompanying vegetation crosscutting the same horizon as the trunks (#7), likely because the evidence for other plant fossils was destroyed during the removal of the encasing sandstone to expose the trees. Nonetheless, because this site meets the vast majority of the criteria, the Fossil Grove site is interpreted as a true remnant of a pre-Flood forest that was not inundated and buried until deposition of the latest Mississippian/earliest Pennsylvanian (Carboniferous) system rocks, approximately midway through the rising portion of the Flood. Allochthonous layers of coal were further deposited on top of the trees as part of the Scottish Coal Measure Group (Figure 3).

This interpretation supports the suggestion by Clarey (2015) that as the Flood waters increased, tsunami-like waves tore the bulk of the lycopod forests free and deposited them elsewhere as coal beds (allochthonously). As is the case with the Fossil Grove, the lycopod trees were likely already dead and their trunks already broken off, allowing substantial decay of the stumps to have occurred prior to burial in the encasing sand (Gastaldo, 1986).

If this interpretation is correct, Fossil Grove would be the first documented in situ preservation of antediluvian soil and plants. However, it does not support the floating-forest hypothesis as the tree roots of the eleven stumps are found embedded throughout a common paleosol horizon. All geological findings indicate that these tree stumps are in growth position and were inundated, buried, and fossilized in situ by rising Floodwaters. The trees are nearly equidistantly spaced, their roots penetrate downward into the soil horizon, and there is no indication of earlier Flood sedimentation beneath the soil layer. Even if the argument is made that the Glasgow site represents a landslide that transported the eleven intact tree stumps during the Flood, along with the surrounding soil, it still demonstrates that the trees were rooted

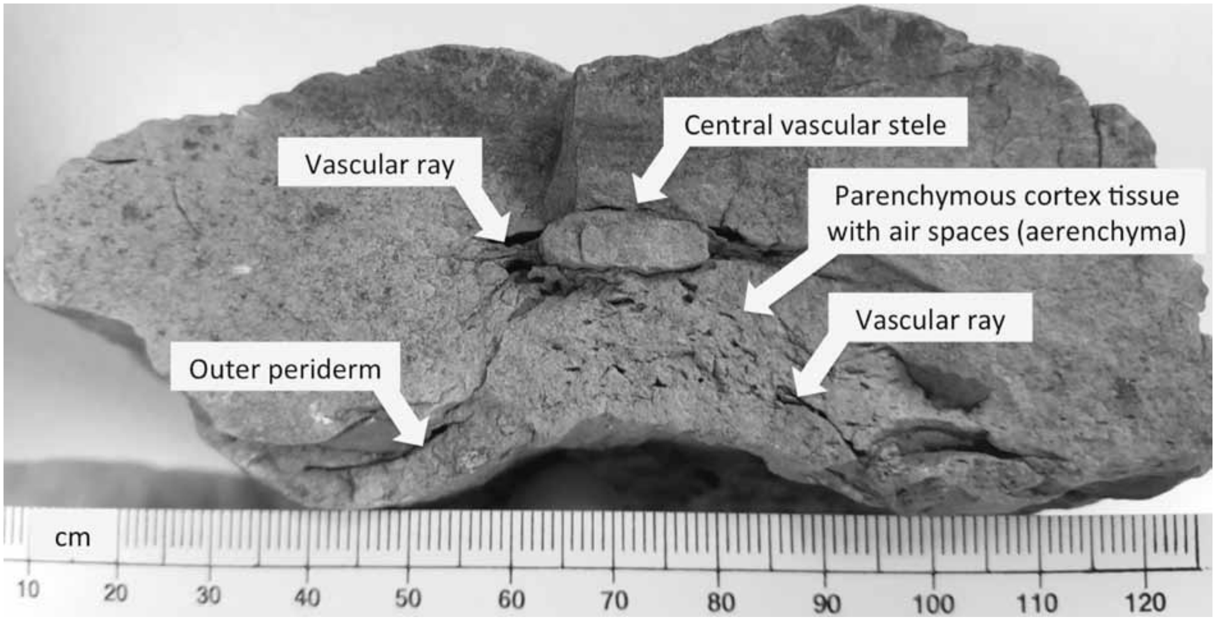


Figure 7. Cross section of a stigmarian lycopod root recovered in northeast Texas near the Oklahoma border.

and not part of a floating-forest biome. The floating-forest hypothesis clearly fails the test based on this site.

The aerial parts of arborescent lycopods were structurally composed of a limited amount of secondary xylem tissue in proportion to a large quantity of periderm (DiMichele, 1981). Figure 6 depicts the anatomy of lycopod trunks as determined by a study done at the fossil grove in Scotland discussed above. The trees in the fossil grove had achieved significant levels of decay prior to being buried in sediments, given that they were easily sheared off at different heights (Gastaldo, 1986). Because the outer bark is quite woody and durable, this clearly shows that a significant level of tissue decay had taken place before the trees were sheared and inundated with sediments.

In fact, it is now becoming apparent that the global Flood occurred in successive waves of inundation (Snelling, 2014) and that initial stages would have caused a great deal of plant death followed by decomposition of easily destroyed parenchyma tissue in the internal cortex region of lycopod trunks and roots. The aerial structures and stigmarian root systems would have undergone selective decay of tissues in the central cortex while retaining overall morphological shape during the hollowing process in which sediments were introduced into the cavity, creating casts. In addition, intact non-decayed aerial stems of arborescent lycopods clearly indicate a contiguous tissue structure across the breadth of the stem with the same general schema found in trunks and roots, although the trunks tend to rarely have the inner cortex tissues preserved.

The idea that the more resilient central stele tissues inside the stems and particularly within roots somehow stayed situated in the center of these structures in defiance of gravity during normal growth, and without the aid of any supportive tissue besides the vascular rays, is patently absurd and not observed in any known plant species today. Furthermore, a well-preserved stigmarian root in the curation of ICR clearly shows that the parenchymatous cortex forms a contiguous progression from the stele to the outer periderm (Figure 7), adding further fossil evidence negating the alleged hollowness of these structures required for reducing weight in a floating mat.

All available geologic and fossilized anatomical data support the existence of pre-Flood lycopod forests rooted in soil. These forests were likely located in wetlands and/or coastal lowland areas as suggested by Clarey (2015). Detailed analysis further demonstrates the trunks and the roots were not hollow as previously claimed. Based on these data, and that of Clarey (2015), we strongly recommend abandoning the floating-forest model.

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Design Analysis Suggests That Our "Immune" System Is Better Understood as a Microbe Interface System

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Abstract

The immune system is often regarded only as a defense, keeping us free from harmful microbes. What if our immune system today is functioning not very differently than it did in the pre-Fall world? A better understanding of its purpose may emerge if we reframe it (1) via design-based system analysis, and (2) in light of contemporary microbiome research findings. Microbiome research reveals far more harmony than antagonism in organism-microbiome relationships. Systems analysis indicates one design certainty: an interface system must coordinate independent entities to harmonize together. Therefore, design-based creationist research would look for, and find, human-designed interface systems possessing nearly indistinguishable counterpart elements as found in immune systems. When dynamic host system-to-microbe relationships are understood in light of design analysis, the clear properties of a rich, multifunctional "microbe interface system" (MIS) are evident—which is the key link associating us to trillions of microbes in a mutually beneficial symbiotic relationship. Concentrating on the presence of interface-distinctive elements could better characterize what may misleadingly be labeled an "immune" system.

Introduction

Microbial colonization of hosts is increasingly recognized as a mutually beneficial relationship that is critical for life in humans and many animals. Colonization on and within hosts is extensive, but the gut is a primary target of research. For instance, gut luminal cells help regulate the composition of microbiota (Salzman, 2010). In turn, gut microbiota can be vital in host metabolism, development, immunity, socialization, and well-being; imbalance may be associated with infections, and may also be associated with other diseases like obesity (Breton et al., 2016; Belkaid and Naik, 2013; Hooper et al., 2012; McFall-Ngai, 2012; Koren et al., 2011; An et al. 2014; Smith et al., 2013; Tremaroli and Backhed, 2012; Yong, 2015; Turnbaugh et al., 2009).

We began by questioning the whole notion of seeing immune systems as as-

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semblies for "defensive" purposes. This introduction details some reasons and assumptions prompting the reconsideration of something so firmly believed. First, voluminous new findings of extreme host-microbe mutualism need to be addressed. New discoveries of mutual microbe-host control (Maron, 2016) only make sense if Adam *had to* relate to his microbiota since his creation. Joseph Francis was an early creationist advocate of the nonadversarial host-microbe relationship, and has recently expanded his views (Francis, 2003, 2013). His pioneering approach applied Scripture to microbiology. His concepts have been overwhelmingly confirmed by research institutions worldwide. Other creationists have advocated for some nondefensive pre-Fall immunological functions. For example, Gillen and Conrad (2014) state: "Although no one knows for sure, it seems the immune system would be useful to the body even in a perfect world, because without an immune system and its components such as macrophages, the body would not be able to cleanse itself of worn-out blood cells."

Should deep-rooted thinking about the "immune" (meaning "to be free" or "exempt") system change? The whole idea of defensive immunity harkens back to conflict, as one researcher summarized: "For some, learning about our gut microbiomes brings back childhood memories … we saw our relationship with microbes portrayed in warlike, rather than in mutually beneficial, terms" (Gordon, 2012, p. 1251). Thus, a better explanation for host-microbe relationships could start with the "very good" creation perspective.

Since the origin and purpose of a system seem to be logically intertwined, we not only wanted to wholly reject the view that current host-microbe relations were produced through a death-driven, survival-of-the-fittest process, but we wanted to replace that approach with the Romans 1 alternative: intelligent design. This starts by asking a question: How would a human engineer *de-novo* solve problems to facilitate host-microbe interrelationships?

Creationist biologists, and not exclusively engineers, should ask this question. This assumes that if God's designs are "clearly seen" to humans regardless of culture or era, then His design characteristics must be analogous to the design characteristics of things humans have built or could build. We should be able to make a reasonable inference that living things are designed since their underlying principles and elements match so well with human-designed things. Thus, per Romans 1, people need neither a special "key" to understand God's designs, nor are they beyond the capability for humans to decipher them—though some deciphering comes only after considerable effort. Not speaking of life itself, but strictly in terms of function, we cannot think of any areas where the potential for human-contrived elements analogous to God's are not theoretically possible. It is likely that God is pleased when humans copy His designs into useful human technologies; and He is honored—provided that He is credited. It is also likely that God is glorified, not by "stumping" human researchers, but, rather, by the fact that they can discover *ad infinitum* elements of systems that display His great engineering genius.

We see entities work together all the time and rarely consider a profound design reality: that two autonomous entities will never spontaneously work together. Some bridging mechanism is a design absolute. Human engineers get distinct human and microbe systems to interact effectively by connecting them via an interface system. We are not referring to either what happens at the host-microbe contact surface, i.e., *an* interface (Shanahan, 2002), or a "social" interface (Muraille, 2013), but to something analogous to what human engineers would devise: a vital- regulatory-communication system pervasive to the organism, functioning to facilitate harmonious "requestor-provider" exchanges of information and products between entities. Could God have used something similar to facilitate harmonious host-microbe relationships?

If God did design interface systems into hosts and microbes, then it is reasonable that their harmonious operation would greatly exceed anything humans have devised. The host-microbe relationship could be so tight—so "seamless"—that it could be easily overlooked by researchers (as discussed below) that there remain two autonomous, barrier-bounded, distinct entities.

By way of overview, we will first briefly explain (1) how humans are extensively colonized with microbes and (2) what evolutionists believe for why host-microbe mutualism exists. We will then identify the interface-distinguishing elements within human-engineered interface systems. Then we will determine if immune systems have those distinguishing elements and if they function in a manner like human interfaces. We will conclude with several implications for the creationist model if the hypothesis of microbe interface systems in organisms is true.

Colonization with Microbiota in Humans

Today we know that humans cannot live without microbes. It seems likely, then, that Adam's system was *vitally* important—even at a time when he was not subject to disease and death. Some background on the microbiota explains why a human-microbe interface system is an organism-wide necessity.

Humans are primarily colonized with microbes from their mother at birth and with continued skin-to-skin contact. When comparing formula-fed and breast-fed neonates, there is a marked difference in the composition of gut microbiota, and "the nutritional composition of breast-milk as compared to formula milk is believed to be a key determinant to this end" (Martin et al., 2009, p. 2090). Crucial gut microbiota become established within 2–3 years (Ray, 2012).

It was thought that the placenta, uterus, and gastrointestinal tract of a normal fetus was sterile *in utero* followed by rapid colonization with microbes after birth (Martin et al., 2009). Colonization from external sources may be the predominant mechanism, but studies have shown that the womb is in fact not sterile. The placenta harbors a distinct microbiome and appears to be seeding the fetal gut while in the womb (Collins, 2014).

The composition of placental microbes is neither static throughout pregnancy nor identical from mother to mother. Neonates weighing less than 1200 grams, or babies born less than 37 weeks gestation, are usually dominated by both *Firmicutes* and *Tenericutes* phyla, with fewer numbers of *Actinobacteria*. The full-term neonatal is "largely colonized by the phyla *Actinobacteria* (including *Bifidobacterium*), *Proteobacteria*, *Bacteroides*, and, much less, *Firmicutes* (including the *Lactobacillus* spp.), which dominate the vaginal flora" (Aagaard et al., 2014, p. 1).

By any estimate, the number of microbes cohabitating with humans is enormous. The commensal intestinal bacteria alone attain densities of 10^{12} organisms per ml of luminal contents (Mackie et al., 1999). "There are about 1000 species present, mostly anaerobes, but less than half of these species can be successfully cultured *ex vivo*. This immense load of commensal bacteria means that the number of bacterial cells being carried in the intestine is greater than the number of eukaryotic cells of the host's own body" (Macpherson et al., 2005, p. 153). That assessment appears to be in line with the most recent estimates.

The ratio of microbe-to-human cells has been revised downward. "Human bodies don't contain 10 times as many bacteria as human cells, new calculations suggest. A 'standard man' weighing 70 kilograms has roughly the same number of bacteria and human cells in his body.… This average guy would be composed of about 40 trillion bacteria and 30 trillion human cells, calculate researchers at the Weizmann Institute of Science in Rehovot, Israel.… Scientists who study the microbiome … have peppered research papers with an estimate that bacteria outnumber human cells 10-to-1 or even 100-to-1.… Judah Rosner, a molecular biologist … called the 10-to-1 ratio a 'fake fact' in a 2014 issue of *Microbe*. It probably wormed its way into scientific literature because it sounds good, Rosner says" (Saey, 2016).

The sheer numbers and types of microbes anticipates an immense impact of mutual host-microbe relationships. They affect the host at the most basic levels right from birth. For instance, in animals removed by c-section and maintained in a germ-free environment, immunological development in the gut mucosa is hypoplastic. But after commensal bacteria are introduced, the majority of the all the body's leucocytes are in the intestine (Macpherson et al., 2005). McFall-Ngai's research indicates that maintenance by vertebrates of gut microbiota, both throughout life and across generations, aids in a more efficient digestion not obtainable by invertebrates (McFall-Ngai, 2012).

What about Adam's microbiota? It is reasonable that Adam was created with a fully functional microbe interface system enabling him to relate to communities of microbes. God ensured that the necessary collection of gut microbes were in him at his creation. Eve possibly obtained her microbiome from Adam. It is probable that Adam's flora was more diverse than most urbanized people today. Samples of oral, skin, and fecal flora from Yanonami villagers of isolated Amazon tribes and rural people groups in Papua New Guinea demonstrate the most diverse gut bacteria yet documented in humans. Compared to US populations, most bacterial species are identified in both groups, but abundance profiles differ vastly, and tribespeople harbored numerous strains undetectable in US populations. The ratios of different species in US populations were more individualized (Martinez et al., 2015). The genetic diversity in fecal and oral bacteria in isolated populations compared to US residents was nearly double. Remarkably, gut bacteria carried genes conferring antibiotic resistance for drugs to which these tribespeople had no known exposures (Clemente et al., 2015).

Evolutionary Origination of Host-Microbe Symbiosis

Evolutionary biologists believe that the very tight symbiotic relationships between autonomous organisms emerged through coevolution (see Box 1). Even vital host-microbe symbiosis arose through an iterative fortuitous selection for ever more specific mechanisms. "Humans and their microbiomes have coevolved as a physiologic community composed of distinct body site niches with metabolic and antigenic diversity," which Aagaard claims happened over untold generations: "Over the past 4 million or so years, hominids have coevolved with their microbiomes as physiologic communities composed of distinct body site niches" (Aagaard et al., 2014, p. 1). Coevolution extends beyond the individual as gut microbiota of infants are "ecologically engineered" by mother's breast milk: "An opportunity to gain insights into how natural selection has shaped the coevolution of hosts and microbes can be found in mammalian mother-infant dyads, as our microbiota are ecologically engineered by mothers and breastmilk" (Hinde and Lewis, 2015, p. 1427).

"Coevolution" as a scientific explanation satisfies no more observational

Box 1: "Coevolved" Is Code for an Interface

Secular scientists maintain the complex microbiome and immune system evolved through vast eons of evolutionary time.

> We also need to think deeply about the evolutionary significance of our gut communities, for example, in the context of the origins and functions of our innate and adaptive immune systems. (Gordon, 2012)
>
> Shaped by millennia of evolution, some host–bacterial associations have developed into beneficial relationships, creating an environment for mutualism. (Round and Mazmanian, 2009, p. 313)
>
> In this Review, we discuss recent evidence suggesting that a beneficial partnership has evolved between symbiotic bacteria and the immune system. (Round and Mazmanian, 2009, p. 313)

In addition, evolution is animated to the point that it can create both molecules and unique mechanisms, establish relationships, and forge alliances.

> Nevertheless, current evidence supports that idea that certain beneficial bacteria have evolved molecules (known as symbiosis factors) that induce protective intestinal immune responses. (Round and Mazmanian, 2009, p. 320)
>
> An evolutionary alliance has been forged between mammals and beneficial bacteria that is crucial for maintaining the long-term survival of both. (Round and Mazmanian, 2009, p. 315)
>
> Bacterial pathogens have evolved a number of unique mechanisms to target and manipulate host cell signaling. (Sreelatha et al., 2013, p. 11563)
>
> The existence of this mutualism, established by evolution on both sides, has been long appreciated, but we are only beginning to understand the complex ways in which host and bacteria each adapt to the other's presence. (Macpherson et al., 2005, p. 153)

In their attempt to explain the origin of the human-microbe relationship a substantial ad hoc appeal is made to co-evolution—the supposed complementary evolution of two or more species and the sophisticated mechanisms they contain.

> Our microbial partners have coevolved with us to forge mutually beneficial (symbiotic) relationships. (Backhed et al., 2004, p. 15723)
>
> All coelomate vertebrates and invertebrates have coevolved with symbiotic gut microbes that perform multiple digestive and metabolic functions for the host.... The nature of the gut microbiome-host interactions seems such that the host controls the microbiome community structure, a process that has evolved to attain specific benefits ranging from protection to nutrition to physiology. (Martin et al., 2009, p. 2090)
>
> An animal's normal microbiota suggest that the presence of complex communities of coevolved bacteria is a shared feature among vertebrates. In general, the coevolved partnerships of invertebrates seem to be much less diverse. ... These coevolved, resident communities are often in direct contact with our tissues, are relatively resistant to perturbations, such as starvation, and provide us with the metabolic benefit of millions of additional genes and activities. ... Careful characterization of the gut microbiota of various vertebrates and invertebrates could address the basic premise that all vertebrates have a coevolved microbiota, whereas invertebrates rarely do. Similarly, comparative physiology could test the prediction that maintenance by vertebrates of coevolved microbial consortia, both throughout life and across generations, provides advantages, such as more efficient digestion, that are not available to invertebrates. (McFall-Ngai, 2012, p. 153)
>
> Millions of years of coevolution have molded this human-microbe interaction into a symbiotic relationship in which gut bacteria make essential contributions to human nutrient metabolism and in return occupy a nutrient-rich environment. (Vaishnava et al., 2008, p. 20858)
>
> Although this mutualism can break down in individuals with inflammatory bowel disease, coevolution of commensals and their hosts has ensured that inflammatory intestinal immunopathology is relatively rare. … it is likely that the commensals have coevolved with their hosts not to do this [subvert host control systems]. (Macpherson and Uhr, 2004, p. 1665)

Coevolution is *not* a scientific explanation and does nothing to elucidate sophisticated mutual or symbiotic relationships. Furthermore, appealing to ethereal "selective pressures" and peppering explanations with "just-so" descriptions reveals the naive nature of evolution.

> Our findings that the human gut microbiome can rapidly switch between herbivorous and carnivorous functional profiles may reflect past selective pressures during human evolution. Consumption of animal foods by our ancestors was probably volatile, depending on season and stochastic foraging success, with readily available plant foods offering a fallback source of calories and nutrients. Microbial communities that could quickly, and appropriately, shift their functional repertoire in response to diet change would have subsequently enhanced human dietary flexibility. Examples of this flexibility may persist today in the form of the wide diversity of modern human diets. (David et al., 2014, p. 561)

criteria than, for example, claiming that similar traits exist in two diverse creatures as being due to "convergent evolution." Coevolution is an *ad hoc*, after-the-fact explanation of present processes or conditions observed in nature.

There clearly seems to be some type of overriding logical information controlling the interrelationships of these different creatures. It may turn out that it is not located in either host or microbe DNA. But that would not rule out that it does not exist. The conundrum for explaining the origin of this information becomes even sharper below.

Microbe Interface System: A Design-based Explanation of Host-Microbe Associations

Research programs begin with identifying a phenomenon that needs to be explained such as the behaviors in symbiotic relationships between different organisms. However, recognizing a relationship happens is far from explaining the mechanisms enabling that relationship to happen. *This is a fundamental question at the foundations of biology: How do two autonomous entities with distinct boundaries work together?*

Methodology

We propose design analysis (DA) as a useful investigative approach to biological systems. Current biological research is reverse engineering, which methodically disassembles systems. DA, however, begins with researchers forward engineering systems by thinking through how they would select and organize major elements and assembly sequences to achieve outcomes (e.g., vision) *before* reverse engineering commenced. Reference to similar human-made systems is valuable. This endeavor aids predicting findings before reverse engineering, assists correlating functions of discoveries, and helps rank their significance (i.e., from indispensable to merely aesthetic.)

A fundamental axiom of DA is that for human-designed entities, 100% of functional causality originates from within the object designed. To construct objects that successfully interact in their environments, designers must craft appropriate object-environment interfacing. Assuming a creation perspective, could God have done something similar in organisms? DA methodology describes all, but only tangible, system elements. It scrutinizes these elements in order to neither omit nor concoct anything that might confuse accurately discerning if the true cause for success/failure at solving environmental challenges is derived from the interplay of elements found in the organism. If it is found to be in fact an organism's traits that are operative, then DA rules help prevent biological explanations from attributing engineering causality to mystical expressions of environmental agency.

Would our understanding of immune systems be different with a fresh look by DA coupled with Francis's nonwarlike conception of our microbiota?

DA Implies that Interface Systems Are a Fundamental Principle of Design

Understanding symbiosis based on design analysis starts by looking for an analogous human-designed relationship, whose mechanisms for operation are already understood, and see if there is a true correspondence between its constituent elements and those elements found within symbiotic biological relationships. One clear possibility, which contrasts sharply with warlike scenarios, is a mutually beneficial *business* relationship. Controlled communications enable transactions of information and resources. One party is a "requester," and the other is a "provider." Procedures may govern a ready reversal of "requester-provider" roles (which is likely the case in host-microbe relationships). Other analogous interface-regulated relationships also abound between distinct computing systems and even between humans and machines.

Biochemist Michael Behe popularized a biological principle known as "irreducible complexity." Irreducible complexity is even more fundamentally a basic principle of design. A*n irreducibly complex system is "a single system composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning.*" (Behe, 1996, p. 39)

Our research below indicates that relationships between entities cannot arise naturalistically merely guided by natural laws. This means that distinct entities will interoperate in a useful manner only if organized to do so and cannot be forced to work together. Even if humans met a sentient "space alien," the two could not relate without some type of interface—notwithstanding how strongly each desired to do so. All relationships between biological entities is likely rooted in a basic design principle that something must *enable* them to work together.

We would propose another principle equally as fundamental as irreducible complexity: *In order for two autonomous, automated entities with distinct boundaries to work together, they must be connected by an interface with three distinctive elements: authentication mechanisms, standardized protocols, and a mutually accessible medium to both entities.*

Our method yields an explanation contrasting sharply with "coevolution." That oft-repeated coevolution claim, it should be remembered, is not an observation; it is solely a declaration. Coevolution is an assertion unhelpful for explaining the *origins* of elaborate, vital mechanisms that must link two distinct organisms. In reality, interface systems are the specific category of mechanism enabling these relationships. We will identify the interface-distinguishing elements within human-engineered interface systems.

Interfaces Are Design Essentials for Two Interrelated Entities

"Interface" itself refers only to the relationship of two distinct entities. Therefore, an interface may range from a contact between two rock formations to elaborate programmed *systems* depicted as "icons" on computers that connect software programs to a human user. A placenta is a biological interface comprised of multiple systems from two distinct entities transiently connecting parent to offspring. Epithelial cells also display traits that, as will be shown, have the features of designed interface systems. Computer interface systems or placentas possess objectively identifiable interface-distinctive elements, mechanisms, interrelated steps, and functions.

Prominent interface designers, Kim Clark and Brian Petrini underscore the necessity of interfaces for cooperation, pointing out that "understanding interface characteristics is fundamental to understanding how systems interact with one another" and the uniqueness of their central elements, since "whilst some integration specifics [listed] come and go over time, the characteristics of integration between systems have remained largely the same" (Clark and Petrini, 2012).

Extreme Information Demands: Interface Designers Must Understand Elements of *Both* Entities' Systems

Interface design is challenging. It is an information-intensive task to devise physical or logical mechanisms to harmonize independent, often dissimilar, entities. A mind is the only known origin of interface systems.

Clark and Petrini underscore the importance of an interface designer's *thorough knowledge* of *both* systems' operational details to be integrated "that there are really two sets of interface characteristics to be captured: … the capabilities of the provider, but you also need to know the requirements of the requester. As you compare the characteristics of requestor and provider, you can then establish the integration patterns that will be required to resolve the differences." And if that were not enough, they add, "To expose services effectively, you need to collate interface characteristics from the anticipated requesters for your system and also estimate the potential future requesters" (Clark and Petrini, 2011).

In fact, it is best to have a mind highly experienced with interface design since "nothing can replace the eye of an experienced integration specialist, who will be able to infer from the early characteristics captured that deeper investigation into some interfaces will be needed" and since "many projects fail to assess integration effectively. It is no doubt also clear that it would take significant experience to capture and assess such a large amount of information at one time" (Clark and Petrini, 2011).

Distinctive Elements Characterize Interface Systems

Interfaces are regulatory-communication systems facilitating harmonious information/product exchanges (Clark and Petrini, 2012). Designers use in-depth operational knowledge of both unrelated entities to integrate their functions into three indispensable interface elements:

1. **Authentication** mechanisms differentiating self and non-self entities;
2. **Protocols** standardizing rules/processes governing exchanges; functioning through a
3. **Medium** of conditions mutually accessible to both entities.

These three well-matched elements constitute the minimal interacting parts needed to attain the basic function of an interface. *Removal of any one of the parts causes an interface system to effectively cease functioning*.

The following condenses Clark and Petrini's extensive discussion and integrates their material into a design analysis framework.

Authentication. To design an interface between two entities, the first task is to establish a mechanism called "authentication" to recognize "self" from "non-self." When you log into Amazon Corporation's website, you, along with your personal computer, will undergo authentication which is composed of several substeps. You will be *authenticated* as a non-Amazon entity while the interface system *verifies* your identity. Likely you will be *authorized* to begin transactions with Amazon. Some people's system will fail authorization and the encounter is ended. If you desire to purchase, additional authentication happens as you will be required to *disclose* specified information to Amazon, which the company's interface system will *validate*. Software on your computer may require Amazon to do similar actions.

Authentication is a special category of protocol. It accomplishes such a singularly important task that it is identified as a separate characteristic of interfaces. Rules and physical elements are both used to establish the identity and authenticity of other entities. Authentication protocols and internal programming may need to be sophisticated since a non-self entity could, for nefarious reasons, try to look like "self" or possibly the "non-self" of a completely different entity. Thus, interface designers usually devise authentication control logic for how the identity of an entity is to be authenticated. Then after an entity is accurately identified, other elaborate mechanisms will establish appropriate authorization for access.

Authorization encompasses rules governing more than recognition. It includes the concept of "validating" non-self. Since interfaces control the exchange of information and materials within "requestor" and "provider" relationships, providers expose their time and resources to requestors. Validation is critical for ensuring that only "authorized" or prearranged systems are able to make requests (or exchange products if desired). Without proper validation, a malicious requestor could try to monopolize a provider's computational resources by making endless requests.

When associations with multiple non-self entities is anticipated, a provider may have established procedures to either have a common response to all non-self entities regardless of differences or be able to differentiate between types and formulate customized responses. Data exchanges during validation usually occur at the request-response step. The extent of *exposure* and *disclosure* of one entity to another may be strictly unilateral, tightly regulated, or fully bilateral. This means that either entity may have procedures *not* to reveal the presence of "self" to the other entity.

Our body relates to hundreds of different kinds of microbes simultaneously. Examples below will show how certain cells in our own interface system mandate disclosure, validate information, authenticate identities, and authorize exchanges with only certain microbes.

Protocols. These are uniform or "standardized" rules, processes, or mechanisms established by the interface designer that work between requestor and provider in order to *regulate* the relationship. They control how, when, why, where, with what transactions are made. They specify acceptable shared data volumes, formats, codes, and interpretation rules to control the message conversation. For data to be intelligible, both systems must understand the format (e.g., order and punctuation) of the data. Protocols may enable a system to utilize multiple data formats and message mediums to interface with different entities simultaneously.

Physical attachment often precedes control. If actual physical contact will be an element of control, protocols specify the physical conditions (i.e., for living things protocols specify the trait(s) that enables physical attachment), which facilitate regulation through physical contact. Therefore, it is common that a *uniting element* fits together material elements at the boundaries of both entities like the Apollo-Soyuz docking station. In cases where physical contact is the sole means of control wherein a uniting element is used, the uniting element *is* the common access medium as discussed below. By physically attaching to a non-self entity, control over it to produce the desired outcome(s) is facilitated.

Many fascinating mechanisms for physical control exist. However, non-physical control mechanisms can be even more spectacular—and are harder to design and understand. One obvious example of where "noncontact" control is a highly desired outcome are "collision avoidance" systems. These systems are actually interface systems operating between aircraft, trains, and increasingly on automobiles. They rapidly gather, and may even exchange, information to control responses between potentially antagonistic objects. In this case, designers understandably do *not* want direct physical contact.

Nonengineering communities may not know how this control is achieved. The control of self is *always* through its *own* innate systems. The result is self-adjustments upon detection of changed conditions (either internal or external). Therefore, control of a non-self entity is predominantly *not* by violating distinct boundaries and directly manipulating non-self systems.

One aspect of design analysis directs researchers to think through the parts and steps of a system that a human engineer would need to specify in order to obtain the desired outcome. This helps to show that engineers must know the basic function of each system *up front*. Some of the information always remains external to both entities. Some of it may be utilized to preprogram each entity's system. The result is that *one system* will execute its own self-adjustments per its own innate systems in response to traits or conditions detected from the *other system*.

This is analogous to one factory producing products, say electric motors and switches, and moving them out of their factory to a transfer dock, where a second factory picks them up, uses them in its own process to produce a product, say a drill press, then moves that to the transfer dock, where the first factory picks it up and uses in its processes. Each factory has the capability to detect when the other's products are at the transfer dock, identify them, and then convey them into their factory. When one factory's product is at the transfer dock, it is a stimulus for the other factory.

Thus, for entities to harmonize, the interface designer foresees the outcome desired for each entity that will result from the relationship. These outcomes are actually the *consequential* end product of its own internal processes, which start after it detects specific conditions (i.e., stimuli) by another non-self system. It takes an elaborate design for one entity to *present specific external conditions* to an environment, that when those conditions are detected by a second entity, it self-initiates production of a product that results as a *particular* and *necessary consequence* of its own systems that it will put back into the environment, and the product is useful to the first entity—and then vice-versa (see Figure 1).

To the casual observer, it looks like one entity is directly controlling the other, but they are not. Each entity is actually controlling itself. But this relationship is tricky to understand because the interface designer and the logic he

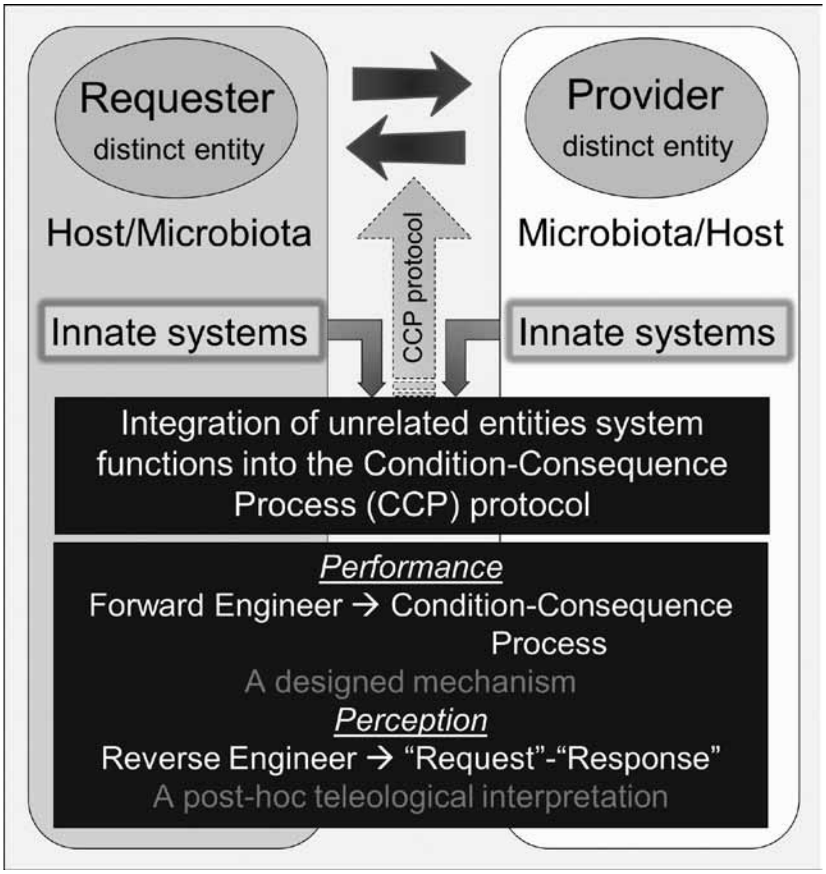

Figure 1. Protocols are engineered interface mechanisms establishing reciprocal control in symbiotic relationships.

Symbiosis is a relationship between autonomous entities characterized by mutually beneficial product/information transactions between requesters and providers. To develop protocols for symbiosis, designers must have in-depth knowledge of (1) unrelated entities innate system functions, and (2) system integration capability. The condition-consequence process is a principle control protocol developed when designers foresee eliciting a desired consequence caused by one entity's systems when presented with a specific environmental condition, particularly ones produced by the other entity's system. Reverse engineering correctly perceives the purpose but often mis-ascribes sufficient causality of outcome to the condition.

employed that enables the harmonization are not seen. The interface system's logic is "controlling" both through the outworking of actual physical elements within each individual entity. People are comfortable thinking about an immaterial thing like information controlling physical operations within the same entity. In this case, it is immaterial information controlling physical operations within *two* or more distinct, autonomous entities, but the logic information is not found within either.

What, then, is the design basis for a "stimulus?" A stimulus is an important element in the condition-consequence process. What makes any condition a stimulus for an entity? For human-made entities, the designer specifies a particular condition *to be* a stimulus—usually for specific purposes. The designer must also equip the entity with a detector sensitive to that condition and insensitive to other conditions. Then mechanisms to transmit data from detectors to logic centers, and so on, will be designed into the entity as well. Therefore, interface designers accomplish the stimulus-designation step by specifying in advance within one entity's systems very particular traits or products of the *other* entity to be "stimuli." Then designers program logic decisions controlling variable response actions. The same steps are followed for the other entity's systems. This prior programming serves as a common code of outcomes that facilitates very precise control (see Figure 2).

Designers must also formulate the interface's logic. When looking at any relationship (e.g., host-microbe, entity-environment, self and non-self) from the "detecting entity's" perspective, designated external conditions are either present (e.g., "on," "+," 1) or they are absent (e.g., "off," "-," "0"). When present and detected, then those conditions specified to be stimuli are "stimulating." In addition, the detecting entity's detectors and logic center may be designed to afford a "graded," not a strictly discreet, "on-off" response to varying quantities of the condition. The bottom line is that in precise engineering terms, conditions just exist; they are not active. Therefore, since the requester and provider each is controlling its own processes, specifying the exact external conditions to be stimuli for itself, supplying its own detectors, etc., then we may rightly call an external condition a "stimulus" or a "cue," but not accurately call it an "inducer" or a "trigger."

To the reverse engineer, the condition-consequence process between entities looks like an interchange of a "request" and a "response," which, if the interface designer did a thorough job, in a way it should. The interface de-

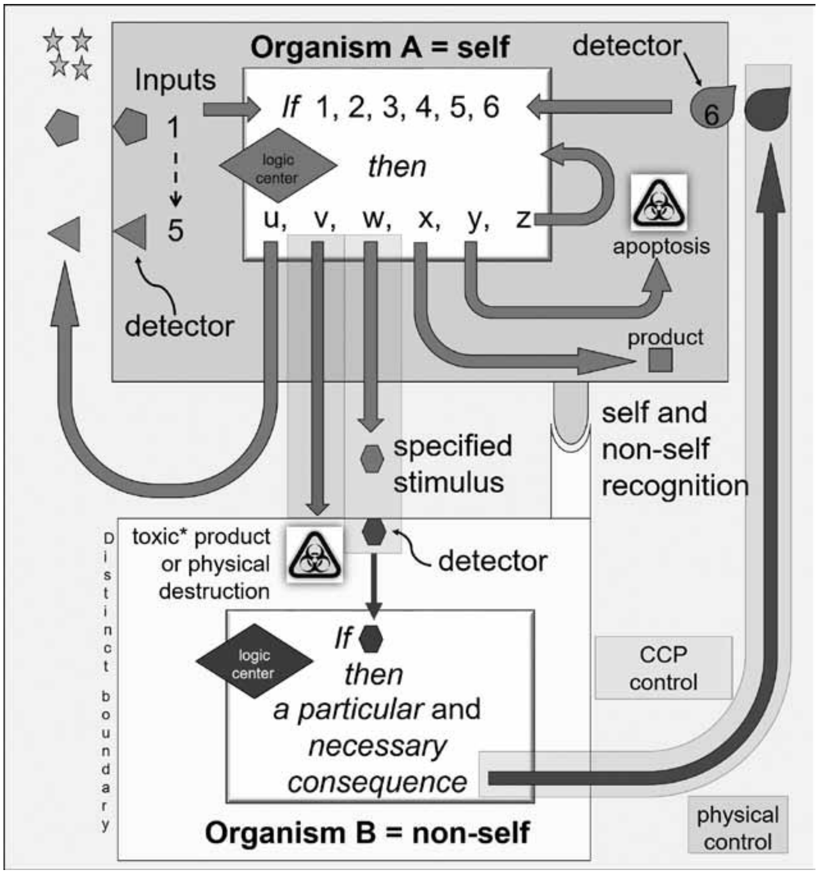

Figure 2. How an interface utilizes the condition-consequence process.

For autonomous and automated entities to harmonize, an elaborate interface design sets each up so that as organism A presents specific external conditions to organism B, B will elicit a particular and necessary consequence due to the outworking of its systems. Control of non-self is predominantly not by physically violating distinct boundaries and never bypasses non-self systems (Cabej, 2013). Each entity's systems specify in advance for themselves which trait of the other entity to be a stimulus. Therefore, it is crucial to know that this interface control is perceived only by outside observers since the true cause of control for both entities remains with innate self-adjustments via internal programming and detectors upon detection of either internal or external changed conditions.* Toxicity of products to organism B are determined by traits of B.

signer set the relationship up to look like one entity "requests" something from the other, which "responds" with a product (see Figure 1). However, what it appears like is not strictly congruent with reality. It is likely that in the majority of cases that happen at the subconscious level, each entity is operating totally "blind" to the larger picture. It does not understand that it is making a request or a response. It is itself simply functioning according to its own systems, but it is *also* functioning as a cog in a bigger system. The bigger system is really a type of protocol—just on a larger scale—for controlling outcomes through the presentation of conditions or data from one system that will produce an expected and necessary response from another system.

Since reverse-engineer biologists are "third-party" viewers, they *could* see the whole system operate exactly like the interface designer envisions it operating. But they must be trained to see things from a design perspective where cells, cellular components, and processes, for instance, are seen as elements in systems, and these elements are understood in their proper design role (i.e., detectors, logic centers, effectors, etc.).

Common Medium. Per Clark and Petrini, "You cannot even make two systems connect unless you can find a common transport" (Clark and Petrini, 2012), which means that a common medium is essential for any interface. This medium is a condition external to two or more entities that each must have at least one trait capable of being able to associate with. When one person speaks and another hears, they utilize the common medium of air, where one's vocal cords compress air, and the other's eardrums vibrate when energized by the compressed air.

In sum, with interfaces there are two major levels of intelligent design. The lower level is all of the information and materials to construct an entity and enable its autonomous operation. For man-made things, this information is stored on drawings and in computers. In living things, construction and operational information is contained *within* the organism. The higher level of design is information for how two or more entities are to work together. This information is not contained within the entities—it exists outside of them. Think of it like a radio transmitter that will transmit normally whether a radio is present or not, and a radio that will operate normally whether or not there is a signal from the transmitter. There are separate fabrication plans for the individual radio and individual transmitter. But the radio transmitter and the radio were designed to interface together as part of a larger communications system. The information for that system starts in the mind of the interface designer, and it is then developed into yet another set of overarching plans for that entire communications system. Thus, there are two levels of information.

The interface design argument is powerful. Evolutionists struggle to explain the origin of information for even an individual organism. But when it comes to highly interfaced relationships such as host-microbe, bee-flower, or male-female, evolutionary naturalists must claim that these relationships were never elements of any overarching plans, and then must appeal to everything coevolving together. When one reads "coevolution" in evolutionary literature, he or she should interpret that as evolution speak for two interfaced organisms. But, if "coevolution" amounts to no more than a declaration, then we must ask, where are the plans located to interface all the diverse organisms within ecosystems?

Findings Illustrative of a Microbe Interface System in Humans

Given their intricate and vital relationships, it looks as though microbes were meant to work together with various hosts, including humans. And given that no known autonomous entities can even get sufficiently close (or even touching) one another that they start working together—but that some interface is still a necessity—then it would be tempting to simply declare that the immune system should be understood as an interface system. However, those observations would be meaningless if the characteristic of our immune system looked nothing like any interface systems that had ever been devised. We must determine if our immune system does, in fact, demonstrate essential characteristics identifiable as the three distinguishing elements of an interface.

Authentication

If two factories are working very closely in support of each other, observers still recognize two distinct factories. We see, however, within the host and microbe incredibly tight integration of systems through bewilderingly complex mechanisms that masterfully resolve the problems arising from fundamental differences in form and function. Such thorough integration interventions, coupled to the observation that microbes live so intimately around, and sometime inside, the cells of the host, makes it powerfully tempting to assert that two autonomous entities have indeed become one. Do capabilities to achieve what engineers refer to as "seamless" operations forego the need to distinguish self and non-self—or is there still a host-microbe "seam"?

As pointed out by Kim, "Self versus non-self discrimination is a central theme in biology from plants to vertebrates, and is particularly relevant for lymphocytes that express receptors capable of recognizing self tissues and foreign invaders" (Kim et al., 2005, p. 709). But microorganisms must also make self versus non-self distinctions as evidenced by "clustered, regularly interspaced, short palindromic repeat (CRISPR) loci [to] protect bacteria and archaea from invasion by phage and plasmid DNA through a genetic interference pathway," which "evolve rapidly, acquiring new spacer sequences to adapt to highly dynamic viral populations" (Marraffini and Sontheimer, 2010, p. 568).

Authentication of self is an interface-distinguishing characteristic. One wide-ranging authentication mechanism in microbe interface systems is to employ the major histocompatibility complex I (MHCI) surface molecule possessing a unique "self" pattern. They are found on all nucleated cells in the body. To interface, both systems must recognize these patterns and, just like human-designed interfaces, become a common code (Janeway et al., 2001).

The toll-like receptors (TLRs) subgroup of sensors exemplify entity-to-entity bridging characteristics. TLRs consist of an extracellular ligand-binding domain, a transmembrane domain, and a cytosolic signaling domain. There are six major families of vertebrate TLRs that are distinct from that of invertebrates. The critical need for "recognition of and response to pathogen-associated molecular patterns has maintained a largely unchanging TLR recognition in all vertebrates" (Roach et al., 2005, p. 9577).

In many organisms, membrane-bound and cytosolic detectors called "pattern recognition receptors" recognize molecular arrangements on microbes. These sensors function very similarly to TLRs. Detectors fit and bind multiple microbial products (pathogen-associated molecular patterns) including lipopolysaccharides, lipopetides, flagellin, and DNA or RNA motifs. They are found in plants, yeast, invertebrates, and vertebrates (Boller and Felix, 2009). Lightner emphasizes this authentication features even in plants, stating that "ironically, in plants, the same group of compounds that is used to identify symbiotic microbes so healthy relationships can be established is also used to identify pathogens so the plant can defend itself. These compounds, lectins, are proteins that are able to bind to carbohydrates. The portion of the molecule involved in binding is highly variable, much like immunoglobins in our immune system" (Lightner, 2010).

Interfaces elements utilize downstream systems to convey data from external boundaries inward to control centers. Microbial interface systems employ ligand-gated, G-protein coupled, and a plethora of molecules to transfer data from cell-surface detectors inward. Authentication coupled with this other information in the pathway enables the human side of the interface to influence the composition of the gut microbiota that enables "mucosal immune responses to indigenous flora [which] require precise control and an immunosensory capacity for distinguishing commensals from pathogens" (Shanahan, 2002, p. 915).

Protocols

Is there evidence that microbes and their host, specifically the host's epithelial cells that contact microbes, actually demonstrate a type of reciprocal control indicative of underlying protocols? Recent research has identified "the maintenance of physiological equilibrium at the mucosal interface, on which both host and gut microbiota exert reciprocal control" (Martin et al., 2009, p. 2090). Reciprocity, especially in symbiotic relationships, is highly indicative of the outworking of underlying protocols. Findings of *reciprocal* control means that "this raises the possibility that the mammalian immune system, which seems to be designed to control microorganisms, is in fact controlled by microorganisms" (Round and Mazmanian, 2009, p. 313).

A classic example of direct physical control is the complement cascade system. This multistep, complicated system consists of circulating pro-proteins that can be activated directly by certain membrane markers on bacteria or by the binding of antibody to a bacterium. After activation, the end result of either path is the assembly of the membrane-attack complex. This complex generates a pore in a bacterium's lipid bilayer membrane, which leads to its destruction (Janeway et al., 2001).

In some cases, analogous to how the uniting element fits together the boundaries of both entities (e.g., the Apollo-Soyuz docking station), protein structures in humans may physically match external characteristics of different microbes that literally enable a cell or molecule to dock with them. Specificity ranges from low to high fidelity. For instance, α-defensins can attach to a large range of microbes, while some microbial elements can be bound only by specific antigen-binding regions of immunoglobulins (Dietrich et al., 2008). Physical attachment to a non-self entity facilitates control of it by stimulating consequence-eliciting outcomes.

A couple of fascinating examples illustrate what looks like one entity directly controlling the other but is actually the interface system "controlling" both as a whole. They illustrate the condition-consequence process, where one entity presents specific external conditions to the other one that will elicit a particular and necessary consequence in another system.

Hosts "shape" the composition of the microbiota by several mechanisms. For example, microRNAs (miRNAs) were found to be normal constituents within feces of mice and humans, produced by gut epithelial and other specialized cells. The research on mice showed that these epithelial produced murine miRNAs are one link in *interspecies* gene regulation to enable host control of gut microbiota. Host-produced miRNAs are transported out of epithelial cells into the gut lumen. A yet unidentified transporter in the cell wall of bacterial species such as *F. nucleatum* and *E. coli*, import the murine miRNAs, where they are processed by intrabacterial cellular machinery. The result is a specific regulation of bacterial gene transcripts that affect bacterial growth. Mice genetically modified to not produce miRNAs were found to have uncontrolled growth and composition of microbiota and inflammation of the intestinal lining. However, fecal transplants from normal mice to miRNA-deficient mice restored control over the microbiota (Liu et al., 2016).

After someone eats a meal, what causes satiety, or that feeling of being full? Current explanations of appetite control reference mechanisms of gut-derived exocrine satiety hormonal signals to anorexigenic and orexigenic pathways in the hypothalamus (Berthoud, 2011). The satietogenic hormones, glucagon-like peptide-1 (GLP-1) and peptide YY (PYY), are produced and released by enteroendocrine cells in the gut. However, new findings demonstrate that gut microbiota also play an important role via the condition-consequence process. Within 20 minutes of eating, gut bacterial growth, particularly *E. coli*, increases exponentially, and they exhibit a remarkable change in proteome. *E. coli* proteins are released into the gut lumen. One protein, caseinolytic protease (Clp) B, is an antigen-mimetic of a satiety hormone produced within the host. Clp-B is transported by human gut cells into circulation. In addition, when other *E. coli* proteins are detected by the host enteroendocrine cells, they release into circulation their satietogenic hormones, which travel to the hypothalamus (Breton et al., 2016). It is currently unclear, but *E. coli*-derived proteins may be essential for enteroendocrine cells to release their hormones.

In like manner, body cells and microbes exchange many products that are controlled by diverse nonattachment interface mechanisms. Additional protocols seem to regulate requester-provider processes to control microbiota composition and microbiota regulation of lymphoid structure development and epithelial function via MyD88-dependent RegIIIγ signaling pathways (Hooper, 2012). Intestinal paneth cell defensins regulate the composition of small intestinal bacterial microbiota by shifting dominant bacterial species without changing total bacterial numbers, which shows "a novel role … in intestinal homeostasis, by regulation of the small intestinal microbiome" (Salzman, 2010, p. 401).

For instance, certain cells in your body's interface system may authenticate three different types of bacteria in your gut; say, *Escherichia*, *Bifidobacterium*, and *Staphylococcus*. Your interface cells may physically attach to these bacteria (or other proteins may directly attach to them as noted above) for the purpose of regulating their activity and population sizes in the gut. Some examples of "desired" outcomes of this host-microbe relationship include self-setting specific conditions so that the bacterium produces a product, initiating a bacterium's preprogrammed self-destruction, or by directly destroying the bacterium.

Microbiome research provides fresh insights into the effectiveness of these interface controls. Early research on the gut showed that certain gut microbes are regulated by intestinal homeobox genes. Reciprocally, commensal-gut microbiota could elicit host gut responses, such that, "taken together, these results reveal that *Cad* [a homeobox gene] acts as a critical host factor that maintains the immune homeostasis responsible for preservation of the normal commensal community structure" (Ryu et al., 2008, p. 781).

Common Medium

Biochemical physical conditions are mutually accessible to host and microbe. Biochemical conditions are the common medium that facilitates essentially all transactions between host and microbe via the interface characteristic. One example of how these biochemical reactions work is defensin-bacterial interactions. Defensins work by interacting with the *charge* of the bacterial cell envelope through covalent modification of anionic molecules or altering membrane fluidity (Peschel, 2002).

Design Analysis Enables Predictions

We know that some human-designed interfaces operate by a logic to place requests and responses in a queue. Is there any type of queue or queueing effect at the microbe-host interface? We are unaware of any type of effect yet documented in literature on immune systems. Given the numbers and different types of microbes in the gut, we can only imagine the number of transactions processed by each host MIS cell. Without some kind of processing control, they could produce chaos. We suspect that future research will find mechanisms in our MIS to logically arrange transactions into a queue (or parallel queues) for subsequent processing. These could be identified as multiple systems management procedures for working with more than one discreet process at a time. They will display protocols to map and regulate sharing real-time information from associations with one or more non-self/requestor system.

Since *timing* is always important to either cell cycles or circadian rhythms, for instance, we anticipate that protocols for synchronization will be found.

Tolerance to different dynamic conditions will display design strategies for self-adjusting to changed, exceptional, or unexpected conditions. This means that there will also need to be rules for error handling and management rules for how and by which system exceptions are handled. By basic principles of design for dynamic systems, the MIS must demonstrate *resilience*, meaning it must be robust enough to maintain its central function but also plastic to flex with unforeseen conditions—some of which may not have shown up on earth yet.

Changing Views: Name Changes Often Reflect a Better Understanding

Is a proposal to adopt a new perception of host-microbe interface systems for regulatory purposes and drop perceptions of "immune" systems for defensive purposes a radical idea or simply an effort to keep up with the latest data? Host-microbe mutualism has been understood for decades, but not everyone tracks with the latest data or concepts.

For instance, consider conflicting comments from three texts all published in 2012. "Every second of every day, an army of hostile bacteria, viruses and fungi swarms on our skin and invades our inner passageways—yet we stay amazingly healthy most of the time. The body seems to have developed a single-minded approach toward such foes—if you're not with us, then you're against us!" (Marieb, 2012, p. 403). But, as Gordon (2012, p. 1251) noted above, this harkens childhood memories of how "we saw our relationship with microbes portrayed in warlike, rather than in mutually beneficial, terms." Others have recently compared the vital, life-sustaining commensal benefits of microorganisms to our health to being "married" to them since "they have a fundamental role in synthesizing vitamins and in helping to breakdown nondigestible products that provide energy to the human body" (Ray, 2012, p. 555).

Careful microbiota researchers like McFall-Ngai have progressed to a current, if not more correct, view of seeing at least adaptive "immunity" in a regulatory function. Though she eschews design in favor of evolution, she says, "I propose a different explanation: that adaptive immunity has evolved in part to *recognize and manage* complex communities of beneficial microbes living on or in vertebrates" (McFall-Ngai, 2012, p. 153, emphasis added). Molecules on the cell wall of bacteria are collectively called "pathogen-associated molecular patterns" or PAMPs. But, a recent article in *Nature* notes a call to replace the misleading word "pathogen" with a more neutral "microbe" or MAMPs (Yong, 2015).

One Belgian researcher has also recommended a complete redefinition the immune system based on a cooperative and non-warlike understanding in his 2013 paper, *Redefining the Immune System as a Social Interface for Cooperative Processes* (Muraille, 2013). Though the "social interface" he suggests is very different from the functional interface we propose, central to his concept was the basic purpose of regulating relationships. Creationist microbiologist Joseph

Francis was a decade ahead of the evolutionary biologists.

Implications for the Creationist Model

The power of a theory rests in its ability to offer a plausible causal mechanism to an observation that needs explaining. Its power is enhanced if it can also account for multiple phenomena related to the observation.

In this case, the observation raises this question: How do two automated, autonomous entities with distinct boundaries work together? This question is answered with a principle of design indispensable to engineering practice: They must be connected by an interface with three distinctive elements: authentication mechanisms, standardized protocols, and a mutually accessible medium to both entities. The following implications are based on this principle being true.

First, looking only at the microbe interface system itself, we see several important implications.

- An engineered-based explanation offers a better way for creationists to answer the question, "If God originally created the world without death and disease, where did our bodies get their disease-fighting capabilities?" The reality of a MIS makes creationist explanations totally different than widely held ones. Pre-Fall disease fighting systems are somewhat of an enigma to explain when seen in death-survival naturalistic paradigms, but there is no enigma when this is not a defensive system but is as interface that is an absolutely necessary design requirement to harmonize autonomous entities. The MIS steers clear of postulating that since God foreknew the Fall, He hid in Adam a latent immune system whose activation was mediated by post-Fall conditions. The MIS is preferable because explanations that work only by invoking God's omnipotence/omniscience do not truly explain anything since, obviously, they can explain everything. In addition, no known scientific tests unambiguously detect mediating interventions by either God or environmental conditions.
- Since humans have likely associated with microbes since creation, which means that an MIS was a design certainty, then design-oriented researchers should have been looking to find—and describe—the interface system for decades. Given the wisdom of God, the fact that an MIS and microbiomes function together in what human engineers would call a "seamless operation" is not surprising. Interface design shows multiple levels of system knowledge and irreducible complexity, which makes the standard evolutionary explanation, "the gut epithelia of virtually all organisms have evolved to form a mutually beneficial strategic alliance with microorganisms" (Ryu et al., 2008, p. 782), implausible.
- The MIS has likely *not* changed much from its original—and continuing—main *regulatory* purpose.
- Cell-destructive capacity of the interface system for regulatory purposes (and some recycling purposes, e.g., antiquated red blood cell destruction in the spleen) was always an MIS design feature. Post-Fall destruction for subsequent "defensive" purposes is still clearly a manifestation of regulation. What has changed post-Fall are (a) the potential for breakdown and loss of regulation; (b) potential to be overwhelmed; (c) displacement of microbes into "abnormal" environments; (d) destruction of mutant and cancer cells; and (e) very dire consequences of the loss of control.
- In this view, parasitism is the *violation* of distinct boundaries of one entity upon another. This is in contrast to mutualism which does not violate boundaries between entities.
- The MIS is dynamic and augments a creature's ability to rapidly "fit and fill" new niches without necessarily involving genetic changes in themselves. Research on humans "demonstrate[s] that the gut microbiome can rapidly respond to altered diet, potentially facilitating the diversity of human dietary lifestyles." Microbiota composition may rapidly adjust since "work in inbred mice shows that shifting dietary macronutrients can broadly and consistently alter the gut microbiome within a single day" (David et al., 2014, p. 559). The remarkable result is that "symbiotic gut microbes ... perform multiple digestive and metabolic functions for the host, and this has resulted in the ability of organisms to engage in enhanced adaptive radiation to exploit new dietary resources" (Martin et al., 2009, p. 2090). This apparently seamless operation between two independent systems is wonderfully illustrated in a study showing how desert wood rats could rapidly fill a new niche by consuming normally toxic creosote plants and access nutrients. The change was a different composition of gut microflora that could detoxify creosote (Kohl, 2014).

Second, there are several important implications for utilizing design analysis in biological research.

- Design analysis identifies innate condition-consequence mechanisms as the true engineering cause for creatures driving themselves through space-time. An innate interface system enables a certain flexibility in an organism to perform well in a world that isn't precisely modeled ahead of time. Organisms that use their preexisting innate systems to either successfully solve environmental challenges or not oppose the accepted notion that as organisms they *are being* driven or "pressured" by environmental challenges. Evolutionists claim that organisms are slowly being crafted by nature over time—which is purported to be the true cause of their apparent design.

- Design analysis identifies multiple, definitely bounded individual kinds of self-regulated entities—a host and a microbe—with no loss of distinctiveness or identity. Some researchers may believe that hosts and microbes engage in seamless "interactions," but DA shows that there really is a seam. To not recognize the seam may advance misleading conclusions about autonomy-blurring amalgamations such as human-microbe mosaics, supra-organisms, or trans-human collectives. Whole understanding of distinct "kinds" of organisms, including humanity, may become fuzzy. For instance, consider this perception: "However, if the view of what constitutes a human is extended … if humans are thought of as a composite of microbial and human cells, the human genetic landscape as an aggregate of the genes in the human genome and the microbiome, and human metabolic features as a blend of human and microbial traits, then the picture that emerges is one of a human 'supraorganism'" (Turnbaugh et al.,

Box 2: Evolutionary Assertions of Loss of Autonomy

The Bible is clear that man was created in God's image. Conversely, secularists maintain that further research of the microbiome suggests humans and microbes may not be autonomous entities. They suggest humans and microbes are now a "superorganism," or a "splendid amalgamation" of trillions of prokaryotic and eukaryotic cells.

> I'm fascinated by the fact that we are a multispecies self. That sounds kind of highfalutin, but what it means is that we as humans need to have a larger view of ourselves as a life-form. We have our human self. We also have a microbial self. (Garrett, 2014, p. 7)
>
> Integrating microbes into our concept of 'self' contextualizes our views of human development, our sense of individuality, and our connections to family and environment in new and different ways.… We are prompted to consider that there is another dimension to our human evolution and human condition.… Even though we now know that we are a splendid amalgamation of microbial and human cellular and genetic parts—more microbial than human in many ways. (Gordon, 2012, p. 1251)
>
> We may think of ourselves as just human, but we're really a mass of microorganisms housed in a human shell. (Brody, 2014)
>
> Outnumbered (on a cellular level alone) by our microbial 'mates' by 10 to 1, a question arises: are we more microbe than man? Increasingly, it seems that the gut microbiota can be considered as a human microbial 'organ'. From an ecological point of view, it could be argued that humans are a superorganism, a communal collective of human and microbial cells working as one. (Brody, 2014)
>
> What is self is a fundamental question in biology.… Based on the unique ability to discriminate between cooperative and cheater partners of an SI [social interface], the self becomes the sum of cooperative and interdependent partners. (Muraille, 2013)

As much as secular biologists would want to see us as just a blend of human and microorganisms, the reality is that creatures reproduce after their kinds. When human egg and sperm fuse are fertilization, there is *no* genetic material from the microbiome transmitted, only human.

Another secular assertion is viewing the microbiome as another human "organ" functioning like an "ancillary," "supplementary," or even a "virtual" organ.

> Collectively, the resident flora represent a virtual organ with a metabolic activity in excess of the liver and a microbiome in excess of the human genome. An improved understanding of this hidden organ holds secrets relevant to several infectious, inflammatory and neoplastic disease mechanisms. (Shanahan, 2002, p. 915)
>
> The microbiota can be viewed as a metabolic "organ" exquisitely tuned to our physiology that performs functions that we have not had to evolve on our own. (Backhed et al., 2004, p. 15718)
>
> The consortium of symbiotic gut microorganisms (the microbiome) can be viewed as a metabolically adaptable, rapidly renewable and metabolically flexible virtual "organ." (Martin et al., 2009, p. 2090)

2009, p. 804). Multiple scientific papers affirm the amalgamation of humans and microbiome into some type of mosaic (see Box 2). When researchers conclude that "our data also suggest that major mammalian metabolic processes are under gut symbiont homeostatic control" (Martin et al., 2009, p. 2102), they express a concept arising from the notion of coevolution, where one entity is molded by external pressures to service the other entity. Design analysis objectively identifies multiple interface systems and highlights independent condition-consequence mechanisms so clearly that each *never could* co-regulate or engage in symbiotic homeostatic control.

- DA eliminates mystical steps in biological descriptions and identifies true engineering causality in condition-consequence processes. DA identifies extensive integration of distinct innate systems, which makes the explanation for the vital, incredibly tight fit as being coevolution far less plausible.

Summary

Adam was likely created with a fully functional microbe interface system enabling him to relate to communities of microbes on his body. The necessary collection of gut microbes was placed in him by God at his creation. Even those who embrace the origin of a defensive system through a struggle for survival occasionally marvel at the overwhelming host-microbe peaceful coexistence: "Although the immune system is classically thought to have evolved to protect from infection by microbial pathogens, animals peacefully coexist with a vast and complex microbiota, which extensively interacts with the immune system" (Round and Mazmanian, 2009, p. 313). Noting the same widespread incongruity, could the application of design analysis offer a more precise explanation for the function of the "immune" system as that of a necessary interface system if any mutually beneficial microbe-host relationship could exist?

The interface designer's *thorough knowledge* of *all* the systems to be integrated is essential. Creationists and ID advocates should begin to accentuate this point when making the case for ID. This greatly compounds the "what-is-the-source-of-information" question. It is difficult enough to come up with a plausible evolutionary explanation for the information carried by DNA. Now, a natural explanation would have to be offered to explain the source of information controlling two or more entities—all linked together in massive ecological webs—and the complete set of logic involved remains to a major part to be elucidated (unlike, for example, the information for genetic logic switches *is* in DNA). Evolutionists simply appeal to explanations that it evolved and coevolved.

So, why should microbes relate to inanimate or animate entities at all? Well, one function may be that microbes themselves act as a collective interface to sources of raw materials. Any individual microbe is an impressive biochemical cycler and the prodigious outcome of their cumulative action is vital for life's functions on earth. Though nearly ubiquitous within habitable zones, they are, appropriately, found "in the highest concentration at interfaces between major parts of the biosphere, that is, the interface between the lithosphere and hydrosphere, or the hydrosphere and atmosphere (Curtis, Sloan, and Scannell 2002)" (Francis and Purdom, 2009, p. 86). Another reason is that they confer benefits that last a lifetime and cross multiple generations. But most importantly, since building an interface demonstrates the ability to know both functions and the capabilities and needs of both, they display the incredible design genius of our Creator.

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Baraminological Analysis of a Set of Archaea Species Based on Genomic Data

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Abstract

Archaea have not yet been classified in detail by creationist taxonomy. Also, the Bible does not mention archaea or any other kinds of microbes specifically by name. However, clusters of orthologous genes have been determined for a set of 168 archaeal species. In this study an all-versus-all comparison of whole-gene content was performed on these 168 species, and eight groups, or tentative holobaramins, were determined based on their whole-gene content by using a new baraminology method that measures the Jaccard coefficient value. The member species of these holobaramins had a high mean Jaccard coefficient value compared to one another and a low value compared to other species from different archaeal baramins and bacterial taxa. This paper presents a holistic way of measuring species distance as compared to phylogenetic trees based on evolutionary methods. Open reading frames also were predicted for three ancient halophile archaea species (*H. hubeiense*, *H. salifodinae*, and *H. carlsbadense*) and compared to these 168 species. These three species may closely represent the archebaramin, or originally created ancestors, of one of the predicted archaeal holobaramins, which consist of extreme halophilic species. On average, baraminic boundaries could be set at the level of order or class for Archaea. Archaeal baramins can also be characterized by the ecological niche that they exist in, due to special sets of genes that are necessary to help these archaeal species to adapt to these sometimes extreme environmental conditions.

Introduction

Until now, very few creationist studies have been undertaken to analyze boundaries of different kinds of microbial holobaramins, such as archaea, bacteria, and protozoa. This is all the more difficult, as the Bible does not specifically mention microorganisms anywhere. According to some views, microbes were created after the Fall, due to the pathogenic characteristics of many bacteria. However, only about 5–10% of bacteria are pathogenic, and many viruses act as harmless passengers within their hosts. In fact, pathogens have not yet been discovered among archaea (Pace, 1997), yet some think they have the potential to become pathogenic (Cavicchioli et al., 2003). It has become increasingly

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evident that microbes aid in digestion and produce vitamins and minerals as part of a symbiotic relationship with their hosts. According to the biomatrix or organosubstrate theory (Francis, 2003; Linares, Ross, and Stanton, 2016), microbes were created as a link between multicellular organisms and the physical world to extract inorganic materials and to participate in the geochemical cycling of elements and compounds. Therefore, according to this view, microbes would have been created on Days 3, 5, and 6, along with their plant and animal hosts (Gillen, 2008).

So far, around 11,000 prokaryotic species have been discovered and given a Latin name (Kyrpides et al., 2014). Similar to bacteria, archaea form a separate domain of life; both are separate from eukaryotes. Both bacteria and archaea are prokaryotes, meaning that they lack a cell nucleus and membrane-bound organelles. Archaea share genetic properties with both eukaryotes and bacteria but also have unique cellular characteristics. They have isoprenoid ether lipids in their unique plasma membranes and are the sole group of organisms capable of methanogenesis (Gribaldo and Brochier-Armanet, 2006). According to secular taxonomy, the Archaea are divided into two phyla, the Crenarchaeota, which consist mainly of thermophiles and thermoacidophiles, and the Euryarchaeota, which are made up of halophiles, methanogens, thermophiles and thermoacidophiles (Woese, Kandler, and Wheelis, 1990). They also use a wide range of energy sources, such as ammonia, metals, and hydrogen. Archaea exist in extreme environmental niches, such as hydrothermal vents, or hypersaline environments, but also in non-extreme environments as well. Their cellular structures allow them to exist in such extreme conditions.

Due to their cellular structure, microbes such as bacteria and archaea are discontinuous (forming an apobaramin) from multicellular organisms and even protists. Elder (2015) describes both archaea and bacteria each as a specific cognitum, which is a grouping of creatures that seem to naturally go together by use of the senses. Because both bacteria and archaea are single-celled organisms, different biochemical and genetic characteristics are taken into account in order to classify them.

Genome decay, gene loss, and pseudogene accumulation have been observed in a number of bacterial genera (O'Micks, 2015), meaning that all species that are members of these genera share a common ancestral genome. In archaea, less than 10% of the genome resides within pseudogenes, compared to up to 50% in bacteria. The insertion-to-deletion ratio is also lower in archaea, as well as strand slippage due to mononucleotide repeats. Compared to bacteria, the number of inactivating mutations per gene as well as the proportion of truncated pseudogenes is greater in archaea (O'Micks, 2016). On the other hand, the average pseudogene-to-total-gene ratio is about the same (3.5–4.5%) between archaea and bacteria, as is their organization of genes into operons (Tenori-Salgado et al., 2011). Archaeal transcription factors (TFs) also make up a smaller proportion of the genome, and are also shorter, 43.5% of them between only 100 and 200 amino acids long.

Materials and Methods

A list of 412,531 archaea genes from 13,444 archaeal cluster of orthologous genes (arCOGs) belonging to 168 archaea species in 77 genera was downloaded from the NCBI COG database (ftp://ftp.ncbi.nih.gov/pub/wolf/COGs/arCOG/ar14.arCOG.csv). A cluster of orthologous genes, or a COG, is a specified gene with a copy in at least three lineages, which are paralogous or homologous to each other (thus an arCOG is an archaeal COG). Data for comparison with bacteria was taken from ftp://ftp.ncbi.nih.gov/pub/wolf/COGs/Prok1402/Prok1402.tar.gz. This data set was chosen because it involved refined algorithms for orthology identification and was combined with manual curation. The arCOG annotations were based on comparisons with pfam, Conserved Domain Database, tigrfams, and comparisons with COGS database (Makarova, Wolf, and Koonin, 2015).

An R script (JaccardClusters.R) was written that calculates the Jaccard coefficient value (JCV) for each of the 14,028 possible species pairs and depicts the JCV heat map for all species. It also creates a .noa and a .sif file for visualization in Cytoscape. The R script is available at https://github.com/jeanomicks/JCV. The JCV is calculated in the following way: $JCV = |A \cap B|/(|A|+|B|-|A \cap B|)$; that is, the intersection of common genes divided by the union of all genes for species A and B, where $0 \leq JCV \leq 1$. R version 3.1.3 was used. In the JCV heat map, lighter colors mean higher JCVs, closer to 1.0, whereas darker colors correspond to lower JCVs, closer to 0.0.

The genomes of the three ancient halophile species were downloaded from NCBI (*Halobacterium hubeiense*: NZ_LN831302.1; *Halococcus salifodinae*: AOME00000000.1; *Halosimplex carlsbadense*: AOIU00000000.1). CLC Genomics version 8.0 was used to find open reading frames (ORFs) in the genomes of these species. The ORFs found in these genomes were BLASTED (a sequence comparison algorithm) against the 168 archaeal proteomes using blastx without gap extensions (all six translated frames of a DNA sequence compared to a protein sequence) to find matching homologs for JCV calculation. An e-score cutoff of 1^{-10} was used.

Results

Principle of Investigation

Until now, baraminology studies have avoided using systematic data derived from DNA sequence comparisons, because such comparisons are done on genes that are similar between species. Thus, if gene sequences were used in these studies, they would be biased toward similarity between species, which may not show up in the phenotype (Wood, 2002). Nevertheless, some baraminology studies have been carried out using molecular data. Wood (2013) compared alignments of a certain region of the mitochondrial DNA within species of the cat, dog, and horse kinds compared to outliers pertinent to these three kinds. Wood found that based on the number of transversions to transitions, species from these three kinds could be separated from their outliers.

When analyzing microbial baramins, we have to take into account that they lack macromorphological characteristics, such as length of limbs or cranial capacity. Thus, we are forced to take genetic characteristics, such as gene content, into consideration. On the molecular and cellular level, genes code for proteins, which are responsible for different functions in the cell, such as structural proteins, enzymes, or transcription factors. Thus, a haploid single-celled organism's cellular phenotype is directly determined by its gene content.

Whereas the baraminic distance correlation (BDC) method measures the percentage of characters in which the two species differ in their character states (Wood, 2002), the JCV measures the percentage of common genes to all genes in both species. BDC measures distance and dissimilarity, whereas the JCV measures similarity. Since this method holistically takes the whole-gene content of a species into account, this should alleviate objections by previous workers as to the usefulness of genetic data in baraminology studies. As opposed to BDC, which captures the state of a given character, JCV captures binary information about whether a certain gene is absent or present in a given species. However, compared to BDC, the JCV does not suffer from information loss by losing characters between pairs of species. With the JCV, a higher number of orthologous genes between two single-species signifies continuity, whereas a smaller number of common genes corresponds to discontinuity. Species within a holobaramin would have high JCVs when compared to one another but low JCVs when compared to members of another holobaramin.

The JCV method can be used to detect discontinuity via additive evidence. If we start out with a small number of seed species that all belong to the same holobaramin, we can calculate the average JCV between all members of the holobaramin. Here we would expect this value to be relatively high. Afterwards, we could keep adding newer and newer members of the holobaramin and expect the average JCVs between all species pairs to remain relatively high. This would remain so until an outlier species is added, which statistically would have a significantly lower average JCV compared to the members of the existing holobaramin. This could be determined by using the Student's t-test. For example, the average JCV between seven nitrous archaea is 0.69, whereas the average JCV between these species drops to a value of 0.18 (p-value = 6.1x10-17) when the outlier species *Nanoarchaeum equitans* is added..

Archaeal Holobaramins

It is not clear from the Bible on which day microbes, such as archaea, were created. Neither do we know to what extent they exhibited genetic continuity when they were created. The latter is an important factor, as horizontal gene transfer (HGT) is widespread among archaea.

We can use data from NCBI's COG database delineating in which species which genes correspond to which orthologous group (archaeal COG, or arCOG). In archaea, Makarova, Wolf, and Koonin (2015) carried out a comparison listing which gene corresponds to which arCOG in 168 species. A list of these species and the number of proteins per species is given in Supplemental Table 1.

JCVs were calculated for all possible species pairs of the 168 archaea species that had information in the arCOG data set. These values were put into a matrix and then visualized in a heat map, which can be seen in Figure 1. Lighter colors correspond to higher JCVs close to 1, whereas darker colors correspond to lower JCVs, closer to 0. As we can see, a number of archaeal groups are visible that have high JCVs among their individual species members. In Figure 1 there are eight of these groups that have at least seven members. These groups of species that have high common gene content can be inferred to correspond to created archaeal holobaramins. As we can see, compared to all other species, these archaeal holobaramins have low JCVs, which are denoted with darker squares in Figure 1. Since this is the first gene-based baraminology study of its kind, and the first one to study Archaea, the holobaramins identified here should be considered tentative.

These archaeal holobaramins are listed in Table 1 along with their mean JCV±standard deviation and the number of member species within them. What is also interesting is that these archaeal holobaramins are comprised of species that generally belong to the same ecological niche (sulfur reducing, salt-rich environment, extreme heat, or methanogens). This could be due to the core genes belonging to most or all of these species enabling them to survive in extreme conditions, or code for enzymes that are capable of utilizing alternative energy sources.

Thermoacidophiles: *Sulfolobales*

The first predicted archaeal baramin is that of the genus *Sulfolobus*, along with two *Metallosphaera* species and one *Acidianus* species. *Sulfolobales* is an order of the Crenarcheota, which live in extreme thermal and acidic environments and lack a cell envelope. According to Gao and Gupta (2007), 264 proteins were identified that are characteristic only of *Sulfolobales*, suggesting that these genes may be considered markers of this holobaramin.

Halophiles

Halophilic archaea are species that require 5–10 times the salinity of seawater. This holobaramin contains 27 species in 18 genera, meaning that these species are quite diverse. Characteristic of these species is a high GC content in their genomes, the presence of chloride pumps, and also the capability to use solar energy to synthesize ATP. Gao and Gupta (2007) found 127 proteins that are characteristic of almost all the species in this holobaramin.

Methanogens 1 and 2

Methanogens have been divided into two main groups according to the secular literature: Class I includes the orders *Methanobacteriales*, *Methanococcales*, and *Methanopyrales*; Class II consists of the orders *Methanomicrobiales* and *Methanosarcinales* (Bapteste, Brochier, and Boucher, 2005). These microbes are capable of producing methane from simple carbon compounds such as CO_2, formate, or acetate (Thauer et al., 2008). Anderson et al. (2009) state that methanogenic archaea can be divided into three groups, but this is only based on phylogenetic trees based on seven core proteins found in all methanogens. Phylogenetic methods for the most part give contradictory trees and thus do not present as holistic a picture of species relationships as the present method does. The present analysis shows two clusters of methanogenic archaea, covering the same groups as those outlined by Bapteste, Brochier, and Boucher. According to Gao and Gupta (2007), 31 proteins are exclusively characteristic of methanogenic archaea and have functions in the production of methane. Of these, 11 have been selectively lost from the methanogenic baranome in *Methanosphaerea stadtmanae*.

Nitrous archaea

Seven species from four genera (*Nitrosoarchaeum*, *Nitrosopumilus*, *Nitrososphaera*, and *Cenarcheaum*) grouped together based on their ability to oxidize ammonia to nitrite (Hallam et al., 2006; Bartossek et al., 2010). These species had an average JCV of 0.69, which is relatively high and had 844 genes in common. Each of these species also had two subunits of the nitrite reductase NirD in common (arCOG02852 and arCOG02854).

Thermophiles 1: *Thermoproteales*

The first group of thermophiles consists of twelve species from the genera *Pyrobaculum*, *Thermoproteus*, *Vulcanisaeta*, and *Caldivirga*. These are species that belong to the order *Thermoproteales*. These species share different combinations of introns at twelve specific loci (374, 548, 722, 781, 901, 907, 908, 919, 1093, 1205, 1213, and 1391) within the 16S rRNA gene, with *Pyrobaculum* and *Thermoproteus* sharing the most of them. What is surprising, however, is that these introns also occur at most of the same positions in *Desulfurococcales* (Jay and Inskeep, 2015). It might be suggested, therefore, that *Thermoproteales* and *Desulfococcales* should be classified as a single holobaramin. However, this is the only gene out of hundreds of genes that are common to both of these two groups (the median JCV between these two holobaramins is only 0.26). Species from the order *Thermoproteales* lack an intron at loci 802 that is present in *Desulfurococcales*, which would reflect differential intron loss if indeed the two groups in fact had a common ancestor—this as opposed to the evolutionary idea that this gene was newly gained. However, multiple copies of the 16S rRNA gene can be found in different groups of bacteria and archaea, such as *Aigarcheota* (Roux et al., 2011; Jay and Inskeep, 2015); therefore, it is possible that the intron-carrying variant was transferred between these two holobaramins via HGT, meaning no common ancestor.

Thermophiles 2: *Desulfurococacceae*

Seven species from four genera (*Desulfurococcus*, *Staphylothermus*, *Thermospharea*, and *Thermogladius*) make up a second group of thermophiles that belong to the family *Desulfurococacceae*. These species are anaerobic hyperthermophiles, which reduce organic sulfur to hydrogen sulfide (Kochetkova et al., 2016). Several archaeal potential holobaramins metabolize sulfur; however, this can be done seemingly in different manners between holobaramins, which is reflected in the difference in their gene content. Such species are *Hyperthermus butylicus*, and *Thermofilum pendens*, which also appear on the heat map, but it is not clear which holobaramin they belong to. These species differ in the way they process nutrients. This is reflected in their differing sets of transporters and other enzymes; for example, ABC transporters, glycosidases, sulfur reductases and other oxireductases (Anderson et al., 2009). The differences are so large that the JCV between *S. marinus* and *H. butylicus* and between *S. marinus* and *T. pendens* are only 0.31 and 0.24, respectively, while the mean JCV for this holobaramin is 0.69. These two JCVs fall outside of the range of intrabaraminic JCVs (see Tables 1 and 2).

Thermophiles 3: *Thermococcus* and *Pyrococcus*

The last large holobaramin is one that consists of nine *Thermococcus* and seven *Pyrococcus* species. These belong to the family *Thermococcaceae*, which is the sole family of the class Thermococci. These species differ in their temperature range, growth rate, and toxicity tolerance; they all transform sulfur into hydrogen sulfide. Both of these genera form monophyletic groups and form

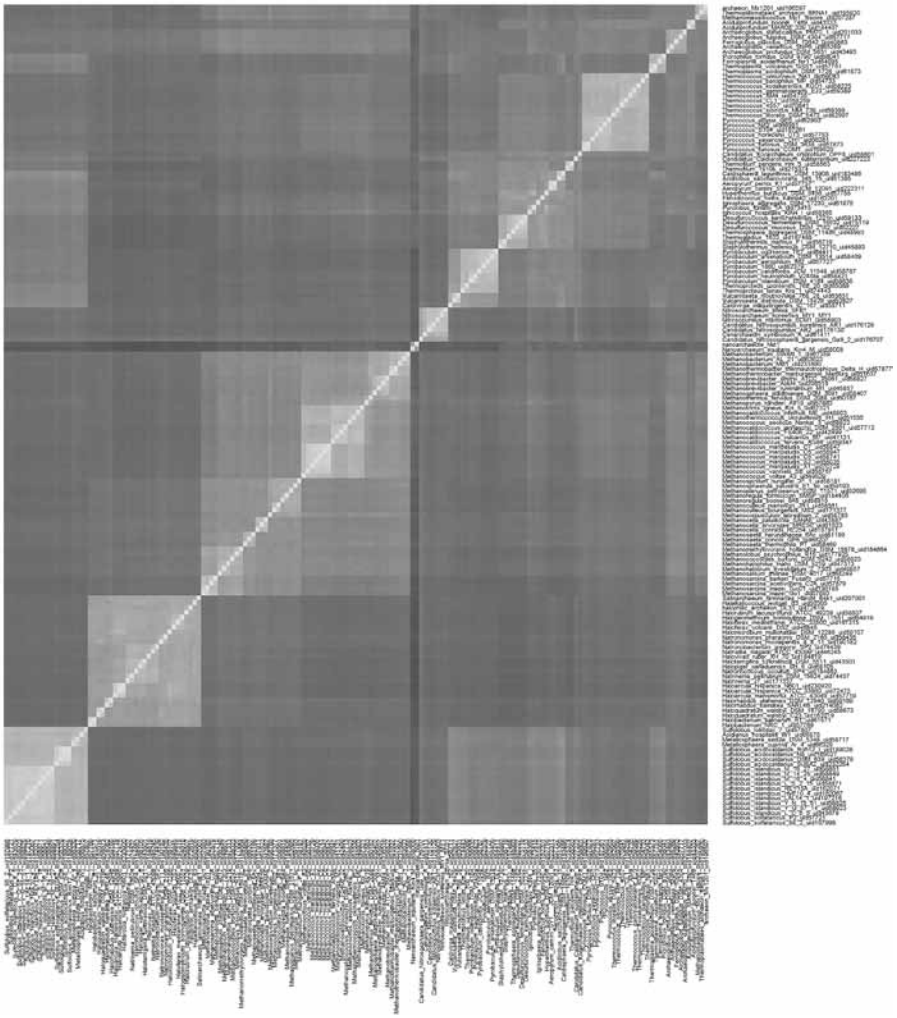

Figure 1. Heat map of Jaccard Coefficient Values for all pairs of 168 archaeal species with COG data from NCBI. Lighter colors correspond to higher JCVs, and darker ones correspond to lower values. Groups of archaeal species can be seen clustered together. Eight clusters of archaea with at least seven members were chosen for further analysis, as described in the text.

different clades based on differences in the DGGE fragment of their 16S rRNA gene (Teske et al., 2009). Interestingly, here the genus *Pyrococcus* intermingles between two different clades of *Thermococcus* species. According to Gao and Gupta (2007), 141 proteins are common to the four *Pyrococcus* species. However, according to Cohen et al. (2003), much HGT has occurred between these species and those of the genus *Thermococcus*, which warrants putting them in the same holobaramin..

Other groups

While the previous eight putative holobaramins have been delineated, there are other archaeal species in this analysis that merit further notice. For example, there are two nanoarchaeal species (*Nanoarchaeum equitans* and nanoarchaeote Nst1) that differ very much from all the other 168 species in this analysis. The JCV between them is 0.51. The median JCV between these two species and all other archaea in this study is 0.16, which is even lower than the median JCV between holobaramins in general (0.28). *N. equitans*, an obligate symbiote hyperthermophile, has the smallest cellular genome (490 Mbp) and is lacking one-third of all the genes in other archaeal species, yet about 15% of its genes are unique (Waters et al., 2003; Gribaldo and Brochier-Armanet, 2006) and has a volume 1/100th that of *E. coli*.

Interbaraminic and Intrabaraminic JCV Comparisons

Each of these eight archaeal holobaramins is made up of several genera, which would correspond to different monobaramins within these holobaramins. The mean and median JCV (±SD) was calculated for four taxonomical categories: (A) species belonging to the same genus, (B) species belonging to the same holobaramin, (C) species belonging to the different holobaramins, and (D) Archaea and Bacteria. Species from five bacterial genera were used as an outgroup in comparison D to see if we get the same kind of JCVs as between archaeal holobaramins. These bacterial species came from those genera that had the most species and had annotated COGs in the COG database.

These JCVs were visualized in the boxplot depicted in Figure 2. This was done in order to better characterize distance relationships within holobaramins and between holobaramins. What we can see in Figure 2 is that the range of JCVs is about the same for genera and within holobaramins (categories A and B). However, there is a large drop in the median JCV when comparing species from the same holobaramin (category B) to different holobaramins (category C) (0.64 to 0.26). This is a clear signal of discontinuity between archaeal holobaramins as characterized

Main baraminic property	Number of species	Number of genera	Species to genus ratio	Mean JCV±stdev	Number of core genes
Thermoacidophiles	20	3	6.67	0.74±0.08	1071
Halophiles	27	18	1.5	0.57±0.06	799
Methanogens	50	25	2	0.45±0.12	420
Methanogens 1	26	10	2.6	0.56±0.12	670
Methanogens 2	24	15	1.6	0.49±0.09	33
Nitrous archaea	7	4	1.75	0.69±0.1	844
Thermophiles 1	12	4	3	0.63±0.13	821
Thermophiles 2	7	4	1.75	0.69±0.09	782
Thermophiles 3	16	2	8	0.68±0.05	865

Table 1. List of archaeal holobaramins and the number of member species and genera predicted by JCV analysis.

by their common gene content. The median JCV (0.18) between archaeal species and bacterial species (category D) is comparable to that of category C, though slightly lower. This illustrates additive evidence when adding species to a given holobaramin in that the JCVs between members of different holobaramins should be statistically significantly lower than JCVs between members of an individual holobaramin.

Genomic Comparisons of Ancient Halophile Species to Other Species

Jaakkola et al. (2016a) have sequenced the whole genome sequences of three extreme halophilic archaeal species, *Halobacterium hubeiense* (Jaakkola et al., 2016b), *Halococcus salifodinae*, and *Halosimplex carlsbadense*. Characteristics of these species are listed in Table 3. These three species were discovered in evaporate basins and are capable of existing in extremely high ion concentrations and anoxic conditions. These are also allegedly the oldest known organisms to live on Earth. Therefore, it would be extremely interesting to measure their common gene content with that of other archaeal species. These species could more closely represent the archebaramin of the halophilic archaeal holobaramins.

The whole genome sequence for these three species was available either as contigs or a full genome. If contigs, they were first assembled into whole-genome sequences. ORFs of at least 300 bp were determined using CLC Genomics software version 8.0. The six-frame translation products (frames 1, 2, and 3 in the forward and reverse direction of the DNA) of these ORFs were matched (blastx) against protein sequences for the examined 168 archaeal species. JCVs were then calculated between each of the three ancient halophiles and all of the 168 archaeal species. These JCVs are depicted in Figure 3 for all three species compared to the 168 archaeal species that have data from the COG database. The JCVs for all three species comparisons are available in Supplemental Table 2.

What we can see in Figure 3 for all three archaic species is that their JCV distribution resembles a hockey stick graph in that a smaller group of these archaeal species have a larger than average JCV compared to the rest of the species. This smaller group of species is made up of extreme halophiles from the second discovered holobaramin (all

	Within genus	Within baramin	Between baramins	Between archaea and bacteria
Mean	0.75±0.08	0.64±0.13	0.28±0.06	0.18±0.06
Median	0.74	0.64	0.26	0.18
Range	0.53–0.98	0.37–0.98	0.11–0.56	0.01–0.37

Table 2. Statistical characteristics of JCVs according to three taxonomic categories with three separate methanogen holobaramins.

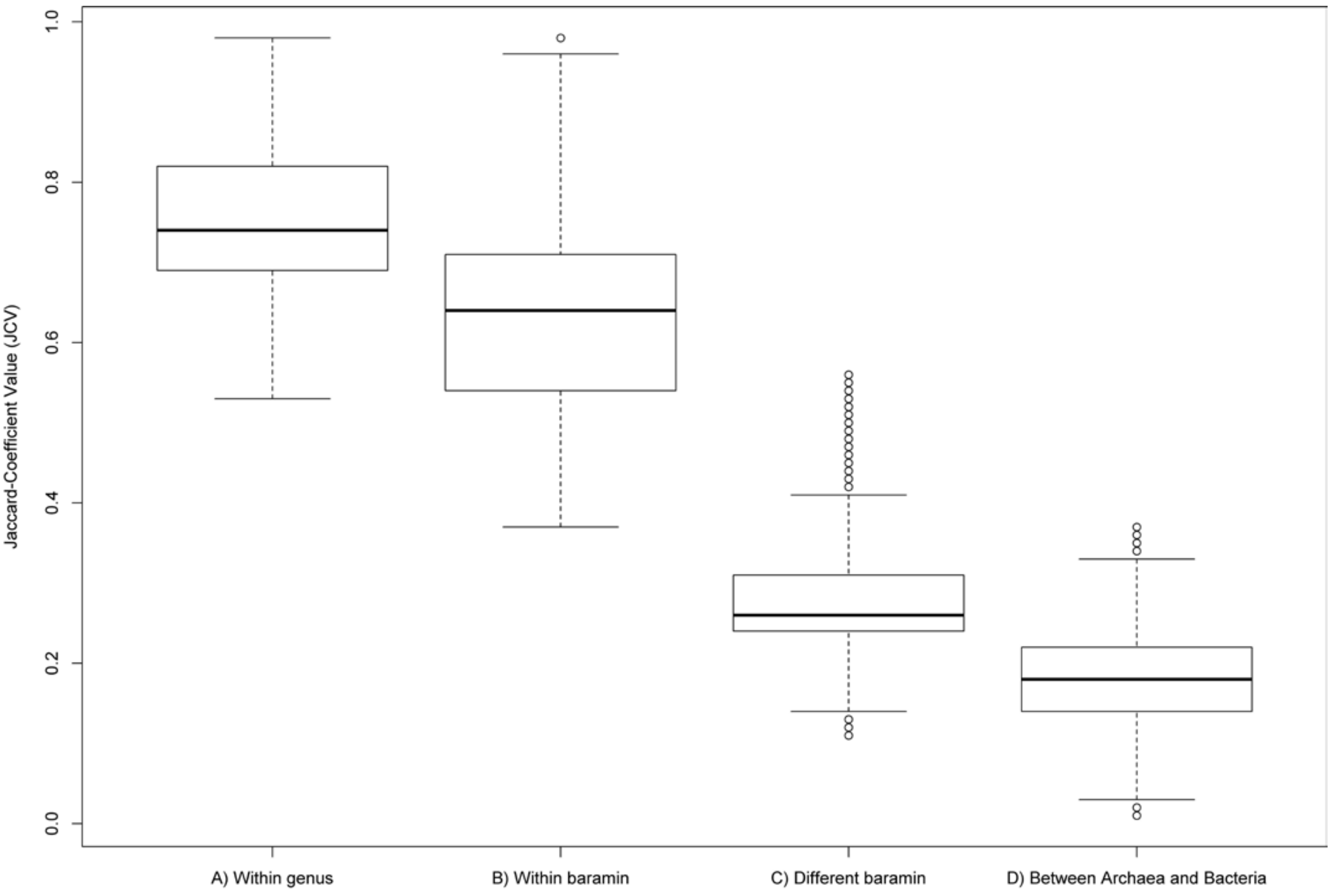

Figure 2. Boxplot diagram of JCVs for four different taxonomic categories: (A) within archaeal genera, (B) within the eight archaeal holobaramins studied in detail, (C) between different archaeal holobaramins, and (D) between archaea and five bacterial genera with the most species with data from the COG database. The four categories depict the range, the 50% percentile, and the median for the JCVs.

27 species). The mean and median JCV, as well as their value range, can be seen in Table 3 for all three archaic species. Their intrabaraminic and interbaraminic JCVs also overlap with those calculated in Table 2. The JCVs that correspond to halophiles differ very significantly from the rest of the 168 species (p-values: *H. hubeiense*: 2.4e-99; *H. salifodinae*: 1.9e-126; *H. carlsbadense*: 9e-115) and is another illustration of additive evidence of adding species to an existing holobaramin until a statistically significant difference in gene content is encountered.

Discussion

Evolutionary explanations of the origin of Archaea are fraught with difficulties. Archaea were assigned to a third domain of life beside Bacteria and Eukarya based on protein trees based on universal small subunit ribosomal RNA (SSU rRNA) (Woese, Kandler, and Wheelis, 1990). However, Gribaldo and Brochier-Armanet (2006) bemoan that it is possible that there will be a demoralizing lack of resolution in the evolutionary history of Archaea based on molecular data similar to bacterial and eukaryotic phylogenies. What is interesting is that Archaea seemingly use eukaryotic proteins but in a bacteria-like context.

Two views of the origin of Archaea exist, and they are contradictory. According to the first view, Archaea are derived from Bacteria. However, this does not explain how and why the bacterial replication apparatus, an irreducibly complex information-integration system, was replaced by an unrelated archaeal one, or how the glycerol backbone of bacterial lipids in their plasma membrane was changed. This would

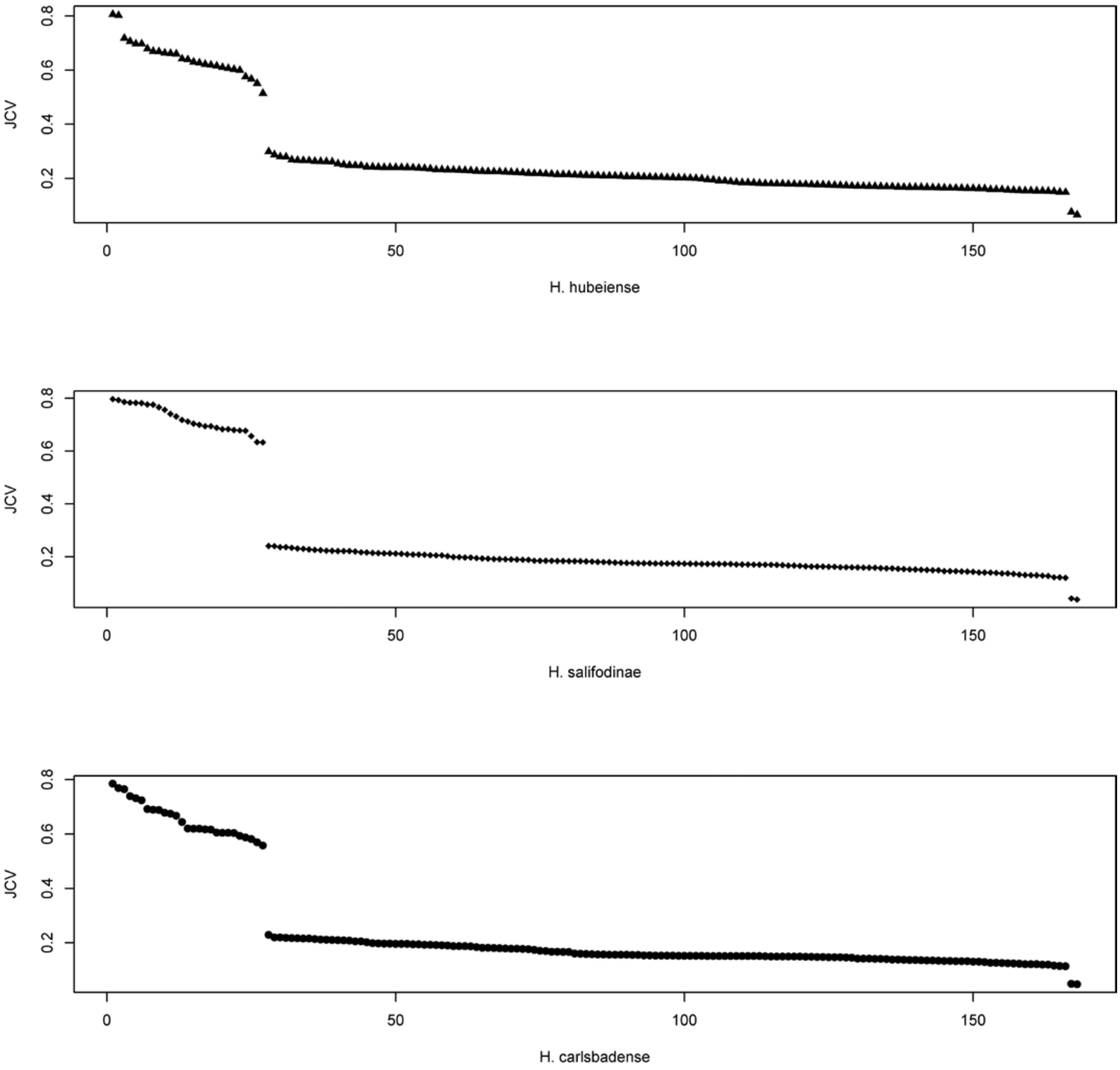

Figure 3. JCV distribution for three ancient halophile species, *Halobacterium hubeiense*, *Halococcus salifodinae*, *Halosimplex carlsbadense*, compared to the 168 archaeal species with data from the COG database. For all three species, distinctly high JCVs were calculated between each ancient halophile species as well as the 27 halophiles from the COG database. P-values for differences in JCVs between the halophiles and all other archaea were statistically significant: *H. hubeiense*: 2.4e-99; *H. salifodinae*: 1.9e-126; *H. carlsbadense*: 9e-115.

require unobservable, highly accelerated molecular evolution leading from Bacteria to Archaea (Gupta, 1998). In this view, methanogenic Archaea must have suddenly acquired the complete set of enzymes for methanogenesis (Gribaldo and Brochier-Armanet, 2006). According to the second view, Archaea are more ancient than both Bacteria and Eukarya (their name, ἀρχαῖα meaning "ancient things"), of which Eukarya retained ancestral traits resembling those of Archaea

	Halobacterium hubeiense	*Halococcus salifodinae*	*Halosimplex carlsbadense*
GenBank id	NZ_LN831302.1	AOME00000000.1	AOIU00000000.1
Estimated evolutionary age	123 Mya	225–280 Mya	250 Mya
Genome size	2.51 Mbp	4.27 Mbp	4.77 Mbp
No. of ORFs	4,074	7,968	7,540
Mean intrabaramin JCV	0.65	0.72	0.65
Median intrabaramin JCV	0.64	0.71	0.62
Range	0.51–0.81	0.63–0.8	0.56–0.78
Mean interbaramin JCV	0.2	0.18	0.16
Median interbaramin JCV	0.2	0.17	0.15
Range	0.07–0.3	0.05–0.24	0.05–0.23

Table 3. Biological characteristics of the three ancient halophile species whose whole genome sequence was studied in Jaakkola et al. (2016a).

(Gribaldo and Brochier-Armanet, 2006). This view fits better with evolutionary conceptions of the early stages of life on Earth, since Earth's putative early atmosphere reflected the metabolism of Archaea such as methanogens. There is no sound explanation as to why one group of organisms would retain ancestral genes yet another group would undergo major genetic derivation.

In a common ancestry scenario, the ancestral single cell could have been a combination of all three cell types, but this would entail early complexity followed by simplification across the board. Otherwise, the ancestral cell could have been extremely simplistic with few specific features of the three cell types, which would not be biologically feasible either, in order to evolve and replace underlying genetic structures as we observe in the three basic cell types. Alternatively, according to Woese (1998), early life existed not as a single cell but rather as a set of diverse cell types, but this still leaves the sudden origin of diversity unexplained.

It is precisely because of these difficulties in evolutionary models of Archaea that the creation model is more consistent with the data. Treating Archaea, Bacteria, and Eukarya as separately created, discontinuous holobaramins and calculating species similarities based on whole-gene content makes much more sense in light of the data than the idea that they all have a common evolutionary origin.

In this paper the tentative boundaries of eight putative archaeal baramins were on the level of order and even class. For the most part, especially in eukaryotic organisms, the boundary line is usually on the level of genus, family, or order. This might be reflective of the ever-changing status of microorganismal taxonomy. For example, the taxon Nanoarcheota was proposed as a new kingdom by Huber et al. (2002), but by now is reclassified as a member of the phylum Euryarchaeota. We will have to wait until further archaeal species are classified and described in more detail.

With more species to examine, current clusters of archaeal species might become more finely tuned. What we can see clearly is that archaea tend to form groups based on the specific ecological niche that they inhabit. In the case of specific archaeal groups that inhabit niches under extreme conditions (excessive heat, anaerobic atmosphere), this means that different types of basic genetic apparatuses would be necessary to process different basic metabolites.

Studying the three ancient halophiles, we can see that these three species are very similar to other halophilic archaea. The average JCV within the extreme halophile baramin is 0.57, yet the average JCV between these three species and the 27 members of the halophile baramin are all at least 0.65. Even if they do not represent members of the halophilic archebaramin, these species show that not too many genes have changed during their existence here on Earth. These three archaic archaeal halophile species can be viewed as microbial living fossils.

This study is the first attempt to use genomic data to determine continuity and discontinuities among putative microbial holobaramins. Therefore, further analyses should be done to corroborate the conclusions of this paper. The JCV method could be used to complement existing baraminology studies—for example, those for which holobaraminic status has been proposed based on the BDC. If the results agree, then this novel technique has been corroborated, but if not, then either the JCV method should be refined, or problems should be found with the BDC. The JCV method could also be applied on bacteria or eukaryotes to see if we get meaningful results.

With this analysis we can be hopeful that with more data and more species examined, we will be able to study archaeal species in more depth in order to help classify them into possible holobaramins. This would help microbial baraminology, an area of creation science that has not yet been developed much recently.

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Supplemental Table 1.

Species	Number of Proteins
Acidianus hospitalis W1	2329
Acidilobus saccharovorans 345-15	1499
Aciduliprofundum boonei T469	1544
Aciduliprofundum sp. MAR08-339	1525
Aeropyrum camini SY1 = JCM 12091	1645
Aeropyrum pernix K1	1700
Archaeoglobus fulgidus DSM 4304	2420
Archaeoglobus profundus DSM 5631	1823
Archaeoglobus sulfaticallidus PM70-1	2216
Archaeoglobus veneficus SNP6	2090
Caldisphaera lagunensis DSM 15908	1478
Caldivirga maquilingensis IC-167	1963
Candidatus Caldiarchaeum subterraneum	1730
Candidatus Korarchaeum cryptofilum OPF8	1603
Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1	1820
Candidatus Methanomethylophilus alvus Mx1201	1651
Candidatus Nitrosoarchaeum koreensis MY1	1945
Candidatus Nitrosoarchaeum limnia SFB1	2038
Candidatus Nitrosopumilus koreensis AR1	1890
Candidatus Nitrosopumilus sp. AR2	1974
Candidatus Nitrososphaera gargensis Ga9.2	3565
Cenarchaeum symbiosum A	2014
Desulfurococcus fermentans DSM 16532	1421
Desulfurococcus kamchatkensis 1221n	1471
Desulfurococcus mucosus DSM 2162	1345
Ferroglobus placidus DSM 10642	2480
Ferroplasma acidarmanus fer1	1951
Fervidicoccus fontis Kam940	1385
Halalkalicoccus jeotgali B3	3873
Haloarcula hispanica ATCC 33960	3859
Haloarcula hispanica N601	3918
Haloarcula marismortui ATCC 43049	4243
Halobacterium salinarum R1	2749
Halobacterium sp. NRC-1	2622
Haloferax mediterranei ATCC 33500	3863
Haloferax volcanii DS2	4015
Halogeometricum borinquense DSM 11551	3898
Halomicrobium mukohataei DSM 12286	3349
Halopiger xanaduensis SH-6	4221
Haloquadratum walsbyi	1
Haloquadratum walsbyi C23	2652
Haloquadratum walsbyi DSM 16790	2643
Halorhabdus tiamatea SARL4B	3023
Halorhabdus utahensis DSM 12940	2998
Halorubrum lacusprofundi ATCC 49239	3560
Haloterrigena turkmenica DSM 5511	5113
Halovivax ruber XH-70	3099
Hyperthermus butylicus DSM 5456	1603
Ignicoccus hospitalis KIN4/I	1434
Ignisphaera aggregans DSM 17230	1930
Metallosphaera cuprina Ar-4	2029
Metallosphaera sedula DSM 5348	2256

Supplemental Table 1 (continued).

Species	Number of Proteins
Methanobacterium sp. AL-21	2493
Methanobacterium sp. MB1	2021
Methanobacterium sp. SWAN-1	2397
Methanobrevibacter ruminantium M1	2217
Methanobrevibacter smithii ATCC 35061	1793
Methanobrevibacter sp. AbM4	1671
Methanocaldococcus fervens AG86	1581
Methanocaldococcus infernus ME	2
Methanocaldococcus jannaschii DSM 2661	1771
Methanocaldococcus sp. FS406-22	1816
Methanocaldococcus vulcanius M7	1742
Methanocella arvoryzae MRE50	3089
Methanocella conradii HZ254	2455
Methanocella paludicola SANAE	3004
Methanococcoides burtonii DSM 6242	2273
Methanococcus aeolicus Nankai-3	1490
Methanococcus maripaludis C5	1822
Methanococcus maripaludis C6	1826
Methanococcus maripaludis C7	1788
Methanococcus maripaludis S2	1722
Methanococcus maripaludis X1	1848
Methanococcus vannielii SB	1678
Methanococcus voltae A3	1717
Methanocorpusculum labreanum Z	1741
Methanoculleus bourgensis MS2	2618
Methanoculleus marisnigri JR1	2490
Methanohalobium evestigatum Z-7303	2254
Methanohalophilus mahii DSM 5219	1987
Methanolobus psychrophilus R15	3167
Methanomethylovorans hollandica DSM 15978	2556
Methanoplanus petrolearius DSM 11571	2785
Methanopyrus kandleri AV19	1687
Methanoregula boonei 6A8	2452
Methanoregula formicica SMSP	2816
Methanosaeta concilii GP6	2850
Methanosaeta harundinacea 6Ac	2371
Methanosaeta thermophila PT	1696
Methanosalsum zhilinae DSM 4017	1976

Species	Number of Proteins
Methanosarcina acetivorans C2A	4540
Methanosarcina barkeri str. Fusaro	3625
Methanosarcina mazei Go1	3368
Methanosarcina mazei Tuc01	3252
Methanosphaera stadtmanae DSM 3091	1535
Methanosphaerula palustris E1-9c	2655
Methanospirillum hungatei JF-1	3131
Methanothermobacter marburgensis str. Marburg	1757
Methanothermobacter thermautotrophicus str. Delta H	1873
Methanothermococcus okinawensis IH1	1595
Methanothermus fervidus DSM 2088	1283
Methanotorris igneus Kol 5	1772
Nanoarchaeum equitans Kin4-M	540
Natrialba magadii ATCC 43099	4212
Natrinema pellirubrum DSM 15624	4199
Natrinema sp. J7-2	4302
Natronobacterium gregoryi SP2	3656
Natronococcus occultus SP4	4154
Natronomonas moolapensis 8.8.11	2749
Natronomonas pharaonis DSM 2160	2820
Nitrosopumilus maritimus SCM1	1796
Picrophilus torridus DSM 9790	1537
Pyrobaculum aerophilum str. IM2	2602
Pyrobaculum arsenaticum DSM 13514	2299
Pyrobaculum calidifontis JCM 11548	2149
Pyrobaculum islandicum DSM 4184	1978
Pyrobaculum neutrophilum V24Sta	1966
Pyrobaculum oguniense TE7	2835
Pyrobaculum sp. 1860	2824
Pyrococcus abyssi GE5	1783
Pyrococcus furiosus COM1	2064
Pyrococcus furiosus DSM 3638	2122
Pyrococcus horikoshii OT3	1950
Pyrococcus sp. NA2	1979
Pyrococcus sp. ST04	1748
Pyrococcus yayanosii CH1	1865

Supplemental Table 1 (continued).

Species	Number of Proteins
Pyrolobus fumarii 1A	1967
Salinarchaeum sp. Harcht-Bsk1	3013
Staphylothermus hellenicus DSM 12710	1599
Staphylothermus marinus F1	1573
Sulfolobus acidocaldarius DSM 639	2224
Sulfolobus acidocaldarius N8	2275
Sulfolobus acidocaldarius Ron12/I	2317
Sulfolobus acidocaldarius SUSAZ	2146
Sulfolobus islandicus HVE10/4	2720
Sulfolobus islandicus L.D.8.5	2948
Sulfolobus islandicus L.S.2.15	2737
Sulfolobus islandicus LAL14/1	2601
Sulfolobus islandicus M.14.25	2608
Sulfolobus islandicus M.16.27	2657
Sulfolobus islandicus M.16.4	2735
Sulfolobus islandicus REY15A	2644
Sulfolobus islandicus Y.G.57.14	2902
Sulfolobus islandicus Y.N.15.51	2900
Sulfolobus solfataricus 98/2	2679
Sulfolobus solfataricus P2	2978
Sulfolobus tokodaii str. 7	2826
Thermococcus barophilus MP	2265
Thermococcus gammatolerans EJ3	2156
Thermococcus kodakarensis KOD1	2306
Thermococcus litoralis DSM 5473	2516
Thermococcus onnurineus NA1	1975
Thermococcus sibiricus MM 739	2035
Thermococcus sp. 4557	2133
Thermococcus sp. AM4	2222
Thermococcus sp. CL1	2017
Thermofilum pendens Hrk 5	1878
Thermofilum sp. 1910b	1896
Thermogladius cellulolyticus 1633	1413
Thermoplasma acidophilum DSM 1728	1484
Thermoplasma volcanium GSS1	1501
Thermoplasmatales archaeon BRNA1	1523
Thermoproteus tenax Kra 1	2049
Thermoproteus uzoniensis 768-20	2186
Thermosphaera aggregans DSM 11486	1387
Vulcanisaeta distributa DSM 14429	2493
Vulcanisaeta moutnovskia 768-28	2320
halophilic archaeon DL31	3476
methanocaldococcus infernus ME	1439
nanoarchaeote Nst1	647

Supplemental Table 2.

Species	JCV
Halobacterium salinarum R1	0.805982
Halobacterium sp. NRC-1	0.801938
Halorubrum lacusprofundi ATCC 49239	0.717917
Halogeometricum borinquense DSM 11551	0.706177
Halomicrobium mukohataei DSM 12286	0.697199
Haloferax volcanii DS2	0.697074
Haloarcula hispanica ATCC 33960	0.678588
Haloferax mediterranei ATCC 33500	0.669529
Haloarcula hispanica N601	0.667998
Natronomonas pharaonis DSM 2160	0.662895
Natronomonas moolapensis 8.8.11	0.661668
Haloarcula marismortui ATCC 43049	0.659813
Salinarchaeum sp. Harcht-Bsk1	0.641794
Halopiger xanaduensis SH-6	0.639166
Natrinema pellirubrum DSM 15624	0.630244
halophilic archaeon DL31	0.626956
Halovivax ruber XH-70	0.62168
Halalkalicoccus jeotgali B3	0.618537
Natronobacterium gregoryi SP2	0.615274
Natrinema sp. J7-2	0.61016

Supplemental Table 2 (continued).

Species	JCV
Halorhabdus utahensis DSM 12940	0.606383
Natronococcus occultus SP4	0.602737
Halorhabdus tiamatea SARL4B	0.599638
Haloquadratum walsbyi DSM 16790	0.575917
Natrialba magadii ATCC 43099	0.567238
Haloquadratum walsbyi C23	0.551104
Haloterrigena turkmenica DSM 5511	0.514257
Methanosalsum zhilinae DSM 4017	0.29912
Methanohalophilus mahii DSM 5219	0.28793
Methanohalobium evestigatum Z-7303	0.280453
Archaeoglobus veneficus SNP6	0.279635
Methanocella conradii HZ254	0.268999
Methanoculleus marisnigri JR1	0.267426
Ferroglobus placidus DSM 10642	0.266229
Methanomethylovorans hollandica DSM 15978	0.265848
Archaeoglobus fulgidus DSM 4304	0.263587
Archaeoglobus sulfaticallidus PM70-1	0.263135
Methanococcoides burtonii DSM 6242	0.262196
Methanocella paludicola SANAE	0.261176
Methanoculleus bourgensis MS2	0.254358
Methanosarcina mazei Go1	0.25097
Methanolobus psychrophilus R15	0.248545
Methanocella arvoryzae MRE50	0.248017
Methanosarcina barkeri str. Fusaro	0.24725
Methanosaeta harundinacea 6Ac	0.242733
Methanosaeta thermophila PT	0.242659
Methanosphaerula palustris E1-9c	0.241725
Methanoplanus petrolearius DSM 11571	0.240747
Methanoregula boonei 6A8	0.24055
Methanosarcina mazei Tuc01	0.24054
Archaeoglobus profundus DSM 5631	0.240346
Methanoregula formicica SMSP	0.239977
Pyrococcus sp. ST04	0.239583
Methanosarcina acetivorans C2A	0.238499
Pyrococcus furiosus COM1	0.237579
Pyrococcus abyssi GE5	0.23574
Pyrococcus furiosus DSM 3638	0.232478
Pyrococcus sp. NA2	0.232234

Species	JCV
Methanocorpusculum labreanum Z	0.231562
Thermococcus barophilus MP	0.231113
Methanospirillum hungatei JF-1	0.230499
Methanosaeta concilii GP6	0.229698
Methanothermobacter marburgensis str. Marburg	0.228814
Thermococcus kodakarensis KOD1	0.226953
Thermococcus litoralis DSM 5473	0.226053
Thermococcus onnurineus NA1	0.225493
Methanobacterium sp. MB1	0.22506
Methanothermobacter thermautotrophicus str. Delta H	0.224931
Thermococcus gammatolerans EJ3	0.223997
Thermococcus sibiricus MM 739	0.223054
Thermococcus sp. 4557	0.22181
Thermococcus sp. CL1	0.221164
Pyrococcus yayanosii CH1	0.21956
Pyrococcus horikoshii OT3	0.218608
Thermococcus sp. AM4	0.21809
Methanobacterium sp. SWAN-1	0.216914
Methanobacterium sp. AL-21	0.215924
Aciduliprofundum sp. MAR08-339	0.214506
Methanotorris igneus Kol 5	0.21444
Methanocaldococcus fervens AG86	0.214375
Methanococcus maripaludis S2	0.21306
Methanococcus maripaludis C5	0.212729
Methanococcus maripaludis C7	0.211571
Aciduliprofundum boonei T469	0.210907
methanocaldococcus infernus ME	0.210429
Methanothermus fervidus DSM 2088	0.209474
Methanocaldococcus sp. FS406-22	0.20917
Methanocaldococcus vulcanius M7	0.209148
Methanococcus maripaludis X1	0.208453
Methanobrevibacter sp. AbM4	0.206629
Methanococcus aeolicus Nankai-3	0.206612
Methanococcus maripaludis C6	0.206601
Methanobrevibacter smithii ATCC 35061	0.205713
Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1	0.205558

Supplemental Table 2 (continued).

Species	JCV
Methanococcus vannielii SB	0.204824
Methanocaldococcus jannaschii DSM 2661	0.204632
Methanothermococcus okinawensis IH1	0.203844
Candidatus Caldiarchaeum subterraneum	0.203291
Aeropyrum pernix K1	0.202427
Thermoplasma volcanium GSS1	0.202154
Thermoplasma acidophilum DSM 1728	0.201165
Methanobrevibacter ruminantium M1	0.200214
Aeropyrum camini SY1 = JCM 12091	0.199203
Picrophilus torridus DSM 9790	0.195476
Methanopyrus kandleri AV19	0.19493
Methanosphaera stadtmanae DSM 3091	0.191252
Ferroplasma acidarmanus fer1	0.191074
Methanococcus voltae A3	0.188363
Sulfolobus acidocaldarius SUSAZ	0.186037
Pyrobaculum calidifontis JCM 11548	0.184536
Vulcanisaeta distributa DSM 14429	0.1843
Metallosphaera sedula DSM 5348	0.183755
Sulfolobus acidocaldarius N8	0.182216
Sulfolobus acidocaldarius DSM 639	0.18097
Sulfolobus islandicus M.14.25	0.180849
Sulfolobus islandicus HVE10/4	0.18055
Sulfolobus acidocaldarius Ron12/I	0.180506
Sulfolobus islandicus LAL14/1	0.179206
Sulfolobus islandicus M.16.27	0.178934
Sulfolobus islandicus M.16.4	0.178181
Candidatus Methanomethylophilus alvus Mx1201	0.17802
Pyrobaculum arsenaticum DSM 13514	0.177958
Thermoproteus uzoniensis 768-20	0.176821
Sulfolobus solfataricus 98/2	0.176699
Sulfolobus islandicus REY15A	0.175787
Sulfolobus islandicus L.S.2.15	0.174969
Metallosphaera cuprina Ar-4	0.174417
Nitrosopumilus maritimus SCM1	0.17367
Caldivirga maquilingensis IC-167	0.172348
Thermoproteus tenax Kra 1	0.171506
Thermoplasmatales archaeon BRNA1	0.171491
Pyrobaculum aerophilum str. IM2	0.171199
Candidatus Korarchaeum cryptofilum OPF8	0.170973
Sulfolobus solfataricus P2	0.169996
Sulfolobus islandicus Y.N.15.51	0.169672
Vulcanisaeta moutnovskia 768-28	0.169581
Sulfolobus islandicus L.D.8.5	0.168642
Sulfolobus islandicus Y.G.57.14	0.167831
Pyrobaculum sp. 1860	0.167609
Pyrobaculum oguniense TE7	0.167601
Pyrobaculum islandicum DSM 4184	0.167343
Candidatus Nitrosoarchaeum limnia SFB1	0.166667
Sulfolobus tokodaii str. 7	0.166217
Candidatus Nitrososphaera gargensis Ga9.2	0.165636
Pyrobaculum neutrophilum V24Sta	0.165042
Candidatus Nitrosoarchaeum koreensis MY1	0.164613
Pyrolobus fumarii 1A	0.164511
Acidianus hospitalis W1	0.164219
Candidatus Nitrosopumilus sp. AR2	0.163523
Cenarchaeum symbiosum A	0.163027
Caldisphaera lagunensis DSM 15908	0.162498
Candidatus Nitrosopumilus koreensis AR1	0.16228
Hyperthermus butylicus DSM 5456	0.159038
Acidilobus saccharovorans 345-15	0.158885
Thermofilum pendens Hrk 5	0.158879
Thermofilum sp. 1910b	0.157409
Staphylothermus marinus F1	0.156657
Desulfurococcus fermentans DSM 16532	0.155684
Staphylothermus hellenicus DSM 12710	0.154927
Ignicoccus hospitalis KIN4/I	0.154739
Ignisphaera aggregans DSM 17230	0.153766
Desulfurococcus mucosus DSM 2162	0.153701
Desulfurococcus kamchatkensis 1221n	0.152839
Thermogladius cellulolyticus 1633	0.152361
Thermosphaera aggregans DSM 11486	0.149747
Fervidicoccus fontis Kam940	0.149091
Nanoarchaeum equitans Kin4-M	0.076277
nanoarchaeote Nst1	0.065929

Author and Title INDEX for Volume 52, 2015–2016

Robert Mullin*

This title/author index covers articles, panorama notes, and other features. For items with two or more pages, the reference is to the first page only. After the page number, a letter indicates which type of entry is involved: article (A), panorama note (P), letter to the editor (L), book or video review (R), cover photo (CP) or other departments (such as editorials, editor's forum, laboratory director's comments, president's remarks, photo essays, etc.) (D).

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*Robert Mullin, Colorado Springs, CO

Letters to the Editor

An Open Letter to *Scientific American*

Editor's note: The following is an open letter to *Scientific American*, written by a member of the Creation Research Society. Since *Scientific American* declined to publish the letter or publicly acknowledge it, the *CRSQ* publishes it here as a service to our members.

Dear Editor(s),

I would like to respond to an article by Blancke and Kjaergaad (2016) published in the Evolution section on the Scientific American website on October 1, 2016, titled "Creationism Invades Europe."

I am a founding member of the Hungarian Protestant Creation Research Group, established in December, 2001. I have a PhD in biology and a BSc in computer science and have published a number of papers in secular and creationist journals.

I have found a number of inaccuracies and biases in the article, and I would like to take the time in this article to respond to them.

First of all, the title is highly misleading. Creationism never "invaded" Europe, as the literal six-day view of creation had always been the orthodox view of creation, at least in the churches. For example, Hungarian believers have translated books such as *In the Beginning was Information* by Dr. Werner Gitt (2005), head of the Department of Information Technology at the German Federal Institute of Physics and Technology. I also find it quite odd that not a single European creationist organization is mentioned by name, therefore making it hard to double-check the statements made by the authors.

I also take issue with the statement that creationism is, as the authors call it, "antiscience." Anybody who is slightly familiar with the history and methodology of science knows that science itself didn't begin with Darwin, but in fact was born within the Christian culture. Many great scientists were Christians, and it was an Austrian monk by the name of Gregor Mendel who founded the science of genetics. It would be very unfair to caricaturize anything other than evolutionary ideology as "antiscience," especially when even secularists at American universities state that in principle, researchers and instructors are free to teach anything they want.

As pointed out by the renowned philosopher of science Karl Popper (1963), evolution does not meet the demands of true science. Regarding the concept of natural selection, Popper made the following observations: "There is a difficulty with Darwinism: it is far from clear what we should consider a possible refutation of the theory of natural selection. If, more especially, we accept that statistical definition of fitness which defines fitness by actual survival, then the survival of the fittest becomes tautological and irrefutable."

Furthermore, since the origin of life and the universe are unrepeatable events, we do not have direct access to study these events. Therefore, evolutionary theory itself cannot objectively be called science. Rather, it rests upon the subjective worldview of naturalism, which assumes there is no Designer. The authors have no scientific basis whatsoever in saying that nature is everything that was, is, and shall be. Evolutionary models merely discuss how certain evolutionary events could possibly have happened, but they never demonstrate that they *did* indeed happen that way. There is a fine line between the two. The second is science; the first is not.

Painting the picture of creationism as antiscience is just simply creating a totally false dichotomy. The reader might find it a revelation that the Bible actually mandates scientific inquiry in the very first chapter of the book of Genesis: "Then God blessed them, and God said to them, 'Be fruitful and multiply; fill the earth and **subdue it; have dominion** over the fish of the sea, over the birds of the air, and over every living thing that moves on the earth'" (Genesis 1:28 NKJV).

Here, since God commands Adam and Eve to have dominion over the earth and subdue it, this means they cannot do it in a haphazard manner, but rather only if they understand how nature works. This is how science operates. In fact, we read about the first taxonomist in history, Adam, who gave names to the animals in Genesis 2:19: "Out of the ground the Lord God formed every beast of the field and every bird of the air, and brought them to Adam to see what he would call them. And whatever Adam called each living creature, that was its name" (NKJV).

Modern open-minded progressivists should be the very people to lead the charge to have all kinds of scientific epistemologies fairly represented in society, regardless of whether they are theistic or not (especially if, for example, they are so keen on having same-sex marriage accepted, even though only 1–2% of the

American population is gay). Let us remember that it was none other than the ACLU that advocated for equal time for teaching evolution in the public schools in 1925 during the famous Scopes trial (Bergmann, 2016).

I also take issue with the authors' claims that creationism is supposedly having a bad effect on education. This I can say after having reviewed a German high school biology textbook, about 350 pages long, which teaches biology and uses scientific facts to support the Bible (Junker and. Scherer, 2013). American public schools, which teach evolution, are faring rather abysmally in international school competitions, whereas homeschool students, who are to a large extent raised in the church and thus learn creationism at home, regularly outperform public school students in exams by up to 30% (Shortt, 2004).

As to some creationist organizations being well funded, I do have to wonder which organizations are getting so much money. Our own creation group pays all of its expenses entirely out of pocket, compared to millions and billions of dollars that are lavished on organizations that perform evolution-based research.

Members of our group have also been interviewed on the radio, and an associate of ours has also debated a science philosophy professor from the famous Eötvös Loránd University. Furthermore, mtv2, a Hungarian television channel even asked us to do a short series on faith and science. This is part of the democratic process, and nobody can restrict or punish open-mindedness on the part of the media.

Since the article describes creationism as a "threat," I would like to remind the readers that it is the Declaration of Independence of the United States that begins with the very creationist idea that all men are created equal. On the other hand, evolutionism spawned ideologies such as racism, Lebensraum (put into direct practice on a large scale by Adolph Hitler during World War II), and Communism (Hitler, 1981; Metaxas, 2010). Thus, since at least two of these extremely destructive ideologies (causing the deaths of over 100–150 million victims) (Courtois, 1997; Bergman, 2014) originated from within Europe, it is high time that they be counterbalanced within Europe by the creationist teaching that we are all made in the image of a loving God and therefore have intrinsic value and equal rights, instead of being an accidental product of random chance.

Matthew Cserhati
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Acknowledgment

I would hereby like to thank Jean K. Lightner and Paul Gosselin for their critical review of my letter.

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Creationist Models—Solidly Grounded in Scripture?

Inarguably the greatest hallmark of the modern creationist movement is its commitment to the authority of Scripture in the area where Scripture—in our present time, at least—is most brutally attacked. It almost goes without saying that the notion of the special creation of the universe by a God who presents Himself in the way that Scripture does (that is, as a supremely authoritative Being who exercises His sovereign prerogative to determine right and wrong for all men, of all time, in every place) is bound to be unpopular. Adding to this concept of creation—as a literal reading of the Genesis text indicates—a timeframe for earth's history that is on the order of thousands, and not billions, of years results in a worldview commitment that is singularly unpopular as judged by the secular scientific community. Nevertheless, modern creationists have staunchly held to the biblical position, endeavoring to defend it exegetically, theologically, and scientifically *simply because such is what the Bible plainly teaches*. For this, creationists are to be commended.

I fear, however, that since its founding the modern creationist movement has drifted from its commitment to the authority of Scripture—arguably not in principle, but certainly in practice. Particular models (and sometimes not even models but mere "interpretive perspectives") that achieved popularity due to the writings of some of the more prominent leaders in the creationist community have been elevated to the point where *they* are regarded as authoritative—despite the fact that they are demonstrably at odds with what the Scriptures actually teach. These models, or interpretive perspectives, are to be regarded as *sacred cows* in the classic sense of the term—that is (as the *Oxford English Dictionary* defines it) "an idea, custom, or institution held, especially unreasonably, to be above criticism." These models and interpretive perspectives are commonly elevated so high by creationists that they dictatorially determine the reading of Scripture and are themselves not subjected to the Scripture rightly exegeted according to a grammatical-historical hermeneutic. This ultimately undermines creationism's commitment to biblical authority.

What precisely are these sacred cows? Three are especially worthy of note—though there are others, to be sure. One of these I mentioned in a letter featured in the previous edition of the *Creation Research Society Quarterly* (Mann, 2016). Modern young-earth creationism in its writings has increasingly conflated the Fall of man and the Curse, frequently maintaining that the Lord, in Genesis 3, cursed man, woman, and the process of childbearing. However, Scripture itself actually *avoids* asserting that mankind—or childbearing—was cursed. There exists in Genesis 3 no exegetical basis for such an idea. God pronounces a curse on the serpent, as well as on the ground for man's sake, but never applies the curse to mankind. Man suffers the ill effects of the Fall as a consequence for sin (and these ill effects do extend to the process of childbearing), but never is he *cursed*, which is, in the context, a direct, punitive determination of the Lord God that anticipates (particularly in the case of the serpent) certain doom. Contextually, the notion of mankind being cursed makes no sense, for in chapter 4 God decrees a curse on Cain. Had Cain already been subject to God's curse due to the actions of Adam and Eve, the pronouncement of the curse in Genesis 4 would be meaningless, for it would be a mere declaration of a state already realized. Cain could have logically retorted to his Creator, "So what?" But the problem is far worse than this logical inconsistency.

Theologically speaking, the notion of a *cursed* humanity (not just one that suffers the ill effects of the Fall) bears enormous consequences. Such a view inevitably demands that Christ Himself was under God's curse (and moreover that He entered into the creation by a process that God had cursed). How then could He be the spotless Lamb of God, qualified to be an atoning sacrifice for the sins of humanity? Henry Morris (1993) recognized this problem, but rather than challenging the sacred cow that modern creationism had enshrined, he altered the orthodox doctrine of Christ's humanity, denying that Christ inherited any human substance from Mary. This undermines the uniform testimony of the Scriptures that Christ is truly human, the bloodline heir of the Davidic throne and the true descendent of Jesse, Judah, Jacob, Isaac, Abraham, and Adam. Unfortunately, modern creationism's unjustified conflation of the Fall and the Curse sets it at odds with the mainline conservative evangelical position and thus needlessly invites criticism.

A second sacred cow of the modern creationist movement is seen in widespread adherence to the chronological scheme proposed by James Ussher. Granted, there are a number of notable modern creationists who do not accept Ussher's chronology, but there are many who *do* accept it, and at least one of the major creationist ministries in the United States frequently promotes Ussher's chronology as that which most accurately reflects the biblical timeline. However, does Ussher's chronology stand up to the scrutiny of the biblical text carefully interpreted? There are several reasons to believe not. First, as the eminent Old Testament scholar James Barr (1985) rightly observed, Ussher did not construct his chronology from the biblical text itself but began with the *a priori* assumption that the Solomonic temple was completed exactly 3000 years from the date of creation and that Christ's birth took place exactly 4000 years subsequent to creation. (It is also worth noting that the corollary to this position was that Christ's second advent would come exactly 2000 years after the first, for a total of 6000 years of history prior to the eschaton. Most creationists today would eschew this belief.) In order to accommodate this idealized scheme, Ussher proved rather careless in his handling of the biblical data. Of principal consideration is his acceptance of the short Egyptian sojourn—though he had to emend the text of Exodus 12:40 and adopt a highly strained interpretation of Genesis 15:13 in order to justify his position.

Compounding this were other mistakes, such as misdating the beginning of the Babylonian captivity (which skewed the dates for all biblical events preceding the sixth century BC), and failing to account for coregencies among Israel and Judah's monarchies. Usher might be excused of blame for these latter issues because he was without many critical resources in his day; but the fact remains that for modern creationists to continue to hold onto the sacred cow of Ussher's chronology is to needlessly bring reproach on the creationist movement on account of blindly (and wrongly) defending—in the name of "biblical authority"—a model that is in fact in some points *opposed* to Scripture. This naturally detracts from the credibility of modern creationism's overall case. Why continue to hold a position that actually hurts the creationist cause?

The third sacred cow deserving mention is the tablet model, a theory of Genesis's composition that maintains that in writing Genesis Moses relied upon preexistent source material, namely a collection of clay tablets authored by the individuals whose respective lives they recount. Such a view, commendably, stands opposed to the documentary hypothesis, in that it at least asserts Moses' involvement; but it is nevertheless at odds with *what the biblical text itself indicates*. In the interest of space, the evidence to follow is but a sampling. First, in making Moses out to be merely the compiler of Genesis, this model overlooks the uniform testimony of Scripture, which strongly suggests otherwise (cf. Exod. 17:14; 24:4, 7; 34:27; Num. 33:1–2; Deut. 31:9, 11; Josh. 1:7–8; 8:31–32; 1 Kings 2:3; 2 Kings 14:6; 21:8; Ezra 6:18; Neh. 13:1; Dan. 9:11–13; Mal. 4:4; Matt. 19:8; Mark 10:4; 12:26; John 5:46–47; 7:19; Acts 3:22; Rom. 10:5; Heb. 10:28). The Bible does not expressly state that Genesis was written by Moses, but as Kidner (1967) observes, the Bible "seems to imply for Genesis a similar relation between substance and final shape as it implies for the rest of the books: that is, that the material is from Moses." Kidner further maintains, "It seems artificial, for instance, to exclude Genesis from our Lord's dictum, 'Moses . . . wrote of me' (Jn. 5:46) and from His Emmaus exposition 'beginning from Moses' (Lk. 24:27; *cf.* 44). Such a distinction would have occurred to none of the original readers of the Gospels" (p. 15).

Beyond this, the tablet model overlooks the internal evidence of the book of Genesis, which attests to its writing in the time of Moses. Details in the text display a familiarity with the land of Egypt and not so with the land of Canaan (the reverse would be expected if the accounts were authored by the patriarchs who preceded Moses). In particular, geographical details in the text describing Canaan betray the fact that the author of Genesis was probably not a resident of the Promised Land. Similarly, noted acquaintance with Egyptian practices (even outside the Joseph narrative) evidence Mosaic authorship. Additionally, Genesis displays an inimitable doctrinal consistency and uniform theological message, which points to a single author who carefully engineered the whole work, rather than many contributors who wrote independently of one another. Themes such as "seed" and "blessing" unite the whole work into a grand theological narrative. The consistency of theme extends beyond what could ever be expected of even the most masterful editor. Finally, the tablet model necessarily reads the *tôlēdôt* markers of Genesis (i.e., "these are the generations of") as colophons rather than transitional headings, but this position is rejected by Old Testament scholars on the grounds that *tôlēdôt* outside of Genesis is consistently used as a heading (e.g., Num. 1; Ruth 4:18). Nowhere in the Bible does *tôlēdôt* clearly refer to what precedes, and often it *must* refer to what follows (such is further commended by the fact that *tôlēdôt* derives from the verbal root *yld*, "to bear," "to beget," "to bring forth"—thus making it more fitting that Genesis's *tôlēdôt* markers relate to the *descendants* of the person noted rather than to the person himself).

Why is the tablet model so hazardous to creationism? Since it fails to square with the biblical text, an outsider could well reason if some creationists hold on to *this* exploded theory, what other antiquated and refuted ideas do they grasp with equal tenacity? In the end, this sacred cow does great damage to creationists' theological, scientific, and intellectual credibility.

In the end, the point that must be made, and the stance on which we must settle, is that we must allow the beliefs of the creationist movement to be determined, ultimately, *by Scripture*. Models, even long-standing models, that override the natural reading of Scripture or violate the preponderance of the scriptural data ought to be discarded. At the very least, we must allow for them to be scrutinized in the light of Scripture rather than letting them stand—as sacred cows—seemingly above all possible criticism. Only in so doing will the modern creationist movement be able to progress and have a positive impact in the church and in the world as a whole.

B. T. Mann

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Your Citation of my Work in *CRSQ* Spring 2016

I wish to respond to "The Challenge of Mount Improbable: A Special Issue of *CRSQ*" by Kevin Anderson and Jean Lightner.

The article says:

> However, Marshall still seeks to incorporate the unnecessary and genetically untenable baggage of universal common descent. He envisions that the action of multiple combinations of these modular systems will move an organism "from any one spot on the tree of life to any other" (Marshall, 2015, p. 144). Yet he is unable to support this claim with natural-occurring examples. No combination has ever been shown to move an organism from any one location on the tree of life to any other given location. This is strictly conjecture and very poor conjecture at that.

One wonders whether the authors of this statement actually read *Evolution 2.0* (or James Shapiro's book *Evolution, A View from the 21st Century* for that matter, which treats the subject with considerably more academic rigor than I do).

There is a large but ignored body of literature reporting real-time, documented macroevolutionary events. Old-school neo-Darwinists don't talk about it because they are intellectually blind to the possibility that major evolutionary events can happen in months, weeks, days, or even hours. Creationists don't talk about it because they insist it's impossible. The media doesn't talk about it because it's too nuanced to fit into easy journalistic sound bites.

Symbiogenesis: The starting point for this is numerous books by Lynn Margulis and an amazing 2012 translation of Kozo-Polyanski's 1924 book originally written in Russian. There is a tremendous amount of evidence supporting the hypothesis that nearly all forms of life incorporate past symbiotic merger-acquisitions. A chloroplast, for example, is a cyanobacterium living inside a eukaryotic cell.

This is not merely conjecture. Dr. Kwang Jeon, a professor at the University of Tennessee, did an experiment where tens of thousands of bacteria took up residence inside Amoeba proteus organisms. A fierce parasitic attack ensued, killing almost all the amoebas.

But in the space of a year, amoeba and bacteria entered into symbiosis. Both modified expression of their genes as necessary to support the mutual dependence.

Jeon learned how to reliably trigger symbiotic cell mergers between amoebas and bacteria. It took 200 generations, about 18 months, for the cells to become fully interdependent. After that, removal of either symbiotic partner proved fatal to both.

We have excellent reasons to believe a symbiotic merger was responsible for plant cells (eukaryote + blue-green algae = plant cell with chloroplast). Likewise, mitochondria are symbiotic bacteria living inside animal cells. Both mitochondria and chloroplasts have their own DNA.

In other words every green leaf and blade of grass you've ever seen is green because blue-green algae lives symbiotically inside plants. Your ability to use oxygen comes from symbiotic bacteria.

The whole neo-Darwinian good ol' boys club thought Lynn Margulis was crazy when she introduced this idea to the West in the 1960s. Her seminal paper on this was rejected by 15 journals.

Not only that, but the Russians had already figured it out 50 years before. But it was totally ignored because it didn't fit the neo-Darwinian dogma. They resisted this with ferocity, but a growing body of evidence from molecular biology was too persuasive to ignore. The profession has now accepted symbiogenesis as a major evolutionary mechanism.

Because Margulis pushed her ideas through with considerable force, in time I think she'll come to be regarded as one of the greatest biologists of our time.

Now add…

- Horizontal Gene Transfer, cells exchanging DNA (see James Shapiro's *Evolution: A View from the 21st Century)*
- Transposition: re-arrangements of DNA in response to changes in the environment (see Shapiro)
- Epigenetics, heritable switching of genes on and off in response to environment (see Eva Jablonka, *Evolution in Four Dimensions)*. Epigenetics means that real-time adaptations are constantly being transferred to offspring, customizing flora and fauna to their environment 24/7/365.
- Retroviruses, which play a major role in transferring genetic material from anywhere to almost anywhere else (see *Virolution* by Frank Ryan)
- Protozoans can splice their DNA into 100,00 pieces and rearrange them in real time in response to threats. This is almost unfathomably sophisticated, but it's a fact (experiment by David Prescott, reported by Shapiro and others)

… and collectively you get a "Swiss Army Knife" of genetic tools that are, at least in principle, capable of getting you anywhere on the tree of life to anywhere else.

By that I mean that the relationship between an organism and its ancestors can be explained genetically as a combination of transposition, horizontal transfer, epigenetic, retroviral, symbiotic or hybridization events. The DNA sequence difference between any organism and any other is a series of modular steps. Some of those steps are quite large and quite sudden.

Cells are demonstrably capable of making such leaps. The David Prescott protozoan experiment mentioned above is enough to confirm this all by itself.

I need to also mention Hybridization (genome duplication) aka Ohno's 2R Hypothesis. This is an empirical, well-known way of producing new species in real time. It works very readily in plants and occasionally in animals. It has been known for centuries. Most of the time in animals it produces sterility but not always.

This fascinating article details many new kinds of plants and animals that have been bred through hybridization: http://messybeast.com/genetics/new-species.htm

Genome data strongly suggest that a hybridization event got us from invertebrates to vertebrates, when two tunicates merged to create a hagfish. Then a second merger got us from vertebrates to jawed vertebrates. This is called "Ohno's 2R hypothesis," where the "2R" stands for "2 Rounds of doubling" of chromosomes.

We are not able to go back and observe tunicate 1 + tunicate 2 = hagfish, of course. But the genetic data is greatly consistent with such a hypothesis.

We know from plant and animal breeding that in a small minority of cases, a hybrid merger produces a very successful new species (like wheat). The new species may have significantly different features than its ancestors.

I freely acknowledge that universal common descent is still far from proven. But again we have an empirical genetic toolbox that demonstrably produces such steps. In principle it appears possible. And considering the extent to which the above information has been ignored by neo-Darwinists, creationists, ID people, and the media, I really don't think it's been examined enough to warrant rejection at this time.

Please notice that if this is possible, what it means ultimately is that God endowed living things with a spectacular capacity for adaptation. Creationists tend to initially bristle at this, but I do not see how this view is dishonoring to God. If anything it shows God to be capable of more than most people ever gave Him credit for.

Furthermore, traditional young-earth creationism *demands* such mechanisms, because belief in a universal worldwide flood demands that all current species descend from a small enough population that would fit on the ark. This means perhaps an expansion from a thousand species to millions.

For this reason, I can't fathom why creationists are so vigorously opposed to macroevolution. Yes, neo-Darwinism itself is dreadful. But post-Darwinian, third way and extended synthesis models are all *necessary* to make a biblical worldview compatible with observable science.

So unless we assume that observable symbiotic and hybrid mergers somehow prove the Bible wrong—and I seriously doubt "kind" was ever meant to exclude such things—then there is no conflict between the Bible and an evolutionary view.

Does not Scripture say God commanded *the earth* to produce animals? And plants?

What I would like to suggest is that if you incorporate this information, we have excellent reasons to infer either total common descent from one cell, or at minimum a dramatic range of speciation from a small number of original created life-forms, and that evolution is all-pervasive and operates in real time.

And again, at the very least, an honest literal biblical interpretation of Genesis and the Flood demands macroevolution. I do not understand why *CRSQ* is arguing against macroevolution when the biblical account requires it.

Sincerely,
Perry Marshall
Chicago, Illinois USA
Author, *Evolution 2.0: Breaking the Deadlock Between Darwin and Design*

Response to Perry Marshall

We thank Perry Marshall for his comments and for participating in this important discussion. In his letter, Mr. Marshall challenges some of our interpretations of his book. Indeed, we think he makes several valid points in *Evolution 2.0* and look forward to some of these points being more fully incorporated into a creation model. Instead, our disagreement with Mr. Marshall hinges deeply upon his total acceptance of universal common descent of all life. By embracing this paradigm, Mr. Marshall then assumes that combinations of specific genetic processes (e.g., directed mutations, recombination, and epigenetic changes) can achieve all the necessary genetic transformations needed for this common descent to occur.

However, we challenge that he fails to distinguish between genetic evidence for universal common descent and the historical reconstructions used to justify claims of universal common descent.

We see this distinction as significant. We do not accept that flowers, sponges, and eagles all evolved from a common biological ancestor sometime in Earth's past. In his letter, Mr. Marshall readily acknowledges that "universal common descent is still far from proven," so why should we feel compelled to accept it? Indeed, we argue that the evidence for universal common descent is far from compelling and is certainly not "demanded" by biblical teachings (rather, it is inconsistent with such teachings; e.g., Genesis 1:24–27; Matthew 19:4).

Mr. Marshall refers to a paragraph of our editorial that highlights part of our disagreements with his conclusions. First, he can be assured that we, as "young-earth" creationists, have *not* ignored the genetic processes that he mentions, but we view them as examples more appropriately understood within a creation model. In fact, in the prior paragraph of our editorial, we wrote that "these modular systems are not unlike systems a biblical creation model also employs." Not only have creationists incorporated some of the examples cited by James Shapiro, Lynn Margulis, and others into our model, but we have also addressed the naturalistic assumptions and unrealistic conclusions that they have carried into their interpretations of the data (e.g., see Bell, 2004; Lightner, 2006, 2009, 2016; Truman and Terborg, 2007; Terborg, 2009; Liu and Soper, 2009; Liu, 2016).

In the same *CRSQ* issue as our editorial, there is a detailed discussion of the long-term evolution experiments conducted by Richard Lenski and his collaborators (Anderson, 2016). This discussion explains why the study does not provide experimental documentation of a genetic mechanism that can drive universal common descent. The ability of these organisms to adapt to their environment is fascinating (and speaks to God's engineering design), and many of the mutations detected could certainly be classified as "beneficial" to the organism. However, none of these mutations involve the type of genetic events needed to account for the *origin* of genes or regulatory systems.

Other articles in the same *CRSQ* issue further support our assertion that universal common descent is genetically untenable. Tomkins (2016) illustrates the genetic uniqueness of humans, indicating that humans have a distinct genetic lineage that is not tied to primates. Carter and Lightner (2016) show that human genetic data is fully consistent with the conclusion that all of humanity descended from a single couple (Adam and Eve), within a biblical time frame of about 6,000 years.

Also, in the same *CRSQ* issue are several media reviews that discuss documented rapid physical changes in animals. These reviews explain the underlying molecular evidence demonstrating how the observed changes require *preexisting* biological complexity. In other words, using the analogy we illustrated in our editorial, these documented changes require the organism to have already ascended most of Mt. Improbable. However, such changes provide no mechanism for the origin of this biological complexity (i.e., how these organisms originally ascended the mountain). Instead, they all require preexistence of the complexity, which is far more consistent with a creation model than any evolution model.

Thus, creation geneticists do not disavow evidence for certain rapid and dramatic changes (perhaps even changes that may fit within some definitions of "macroevolution"). But, such changes are still limited in their extent. Our editorial directly challenged Mr. Marshall's claim that a combination of his proposed "Swiss Army Knife" of genetic tools can move an organism from any one location on the tree of life to any other location. Again, we insist this is strictly conjecture—the examples offered by Mr. Marshall notwithstanding. No amount of naturally occurring recombination, gene transfer, and hybridization has ever been shown to move an oak tree to a chimpanzee.

In response to his comments on symbiosis, we certainly recognize the importance of this subject and the capability of this interaction to transform certain organisms (e.g., see Hennigan and Lightner, 2013). Symbiosis is found throughout creation, and some symbiotic relationships are far more complex than others. This phenomenon is fully consistent with the Trinitarian Christian worldview, since we expect that God's creation will mirror aspects of the Creator (i.e., communication and relationships). Therefore, the ability to induce a symbiotic relationship between bacteria and an amoeba, for example, is not a surprise for a creationist.

On the other hand, evolutionists attempt to exploit symbiotic processes well beyond what has ever been observed. In doing so, they consistently offer historical reconstructions as a means of explaining how certain consortiums and symbiotic interactions led to development of many contemporary biological systems. For example, Margulis and Sagan (2002) propose an endosymbiotic theory for the origin of the eukaryotic world. They speculate that the earliest stage of this endosymbiosis was a consortium of H_2S-producing and H_2S-utilizing cells. Somehow this cell consortium transformed, becoming increasingly interdependent until it became a chimera and then eventually a single organism.

This theory, however, is strictly conjecture—a very creative way of attempting to salvage universal common descent in the absence of other genetic mechanisms. Such a just-so story goes well beyond the observed evidence and is not consistent with much of what we do know. For example, very few mitochondrial proteins have a bacterial homolog (Gray, 2015), mitochondrial ribosomes differ dramatically from both eukaryotic and prokaryotic ribosomes, and eukaryotic processes of replication, transcription, and translation are fundamentally different from the prokaryotic world (e.g., see Manuell et al., 2007; Criswell, 2009; Tan and Tomkins, 2015). All of this is highly inconsistent with Margulis's endosymbiotic theory.

Nor does any endosymbiosis account for the origin of the genetic systems involved in the original symbiotic relationship. Where did the H_2S-producing and H_2S-utilizing organisms acquire these very specific metabolic capabilities? Mr. Marshall's genetic "Swiss Army Knife" does not account for the origination of such features. What is more, the presence of a specific bacterial plasmid is necessary to achieve the amoeba/bacteria symbiosis (Jeon, 2004) mentioned in Mr. Marshall's letter. What was the genetic mechanism that originated this plasmid?

Similar comments could be made about Ohno's 2R hypothesis—it is strictly conjecture. Speciation via genome duplication is not a problem for creationists. In fact, a young-earth model for creation needs to account for rapid speciation within the created kinds. The Creation Research Society is even focusing upon this subject as part of its eKINDS research initiative. However, the 2R hypothesis lacks convincing evidence because it proposes events that go far beyond genome duplication and other observable types of changes (e.g., dramatic changes in body plan and the formation of numerous new genes that must somehow integrate into gene networks with appropriate feedback control).

In summary, imagination can allow envisioning a series of insertions, deletions, and duplications that could transform the genome of any organism into any other organism. However, that does not make the proposed changes realistic; all the changes must be biologically possible and naturally occurring. The organism must also be able to survive such transformations (not a trivial accomplishment). The examples of genomic changes Mr. Marshall cites require incredible design to be already present within each organism (i.e., to have already ascended vast portions of Mt. Improbable). Where did this initial design originate? There are no examples of observed changes that build this kind of complexity or can shift an organism from one branch of the tree of life to any other branch.

When explanations no longer hold to the assumptions of universal common descent, it is far easier to interpret genetic data within the context provided by Genesis 1. Plants and animals were created separately, according to their kinds, over a period of several days. Humans were created separately from plants and animals.

We have no problem with the idea of a genetic "toolkit." Certainly God, as a master engineer, would equip biological systems with the genetic capacity for adapting to a wide array of environmental conditions over the course of earth history. Thus, we readily agree that God created different kinds of creatures with the amazing ability to adapt. This enabled them to fill the earth as God intended (Genesis 1:22; 8:17; Isaiah 45:18).

We recognize that some creationists have likely not understood the works of Shapiro or dismissed the potential impact of hybridization, recombination, etc. This can give rise to stereotypical misconceptions as to what a creation model actually predicts (e.g., fixity of species, no beneficial mutations, only minor transformations, and other erroneous concepts). We encourage Mr. Marshall to spend time more fully studying the information contained in the special *CRSQ* issue on genetics, as well as other articles written by creation geneticists. These articles fully support our comments in the paragraph he cites, and should help to clarify the misconceptions he expressed in his letter.

By not clinging to assumptions of universal common descent, an entirely different perspective of the genetic data comes alive. It is a perspective we challenge is more consistent with both the genetic data and biblical teachings. We also propose that a more complete grasp of what creation geneticists are actually teaching opens the door to some very fruitful dialog.

Kevin Anderson, Ph.D.
Jean Lightner, D.V.M.

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Media Reviews

Amazon Expedition

by Vance Nelson

Untold Secrets of Planet Earth Publishing Co, Inc., Red Deer, Alberta, Canada, 2015,
43 pages, $14.00

This is the third book in the series *Untold Secrets of Planet Earth*. The two earlier volumes concern dragons and fossils respectively, as reviewed in Summer 2012 and 2015 issues of the *CRS Quarterly*. Each book displays attractive glossy pages and abundant color photographs.

Author Nelson holds B.S. degrees in theology and biology. A creation-science writer, speaker, and researcher, his website is www.creationtruthministries.org. In this book, Nelson chronicles an expedition to the Amazon rainforest of Peru, South America. The goal was to study a pictograph that closely resembles a long-neck, long-tail dinosaur surrounded by nine hunters. The overall size of the pictograph is about 1½ feet.

The book shows eleven photos and illustrations of the dinosaur pictograph. Local experts have suggested that the drawn animal may be a camel, llama, or what is called a camelid. Nelson spoke with several South American archeologists who verified the authenticity of the pictograph. With permission, a sample of the red-brown pigment was taken and analyzed by Accelerator Mass Spectrometry (AMS) carbon-14 dating. The age result was 3,290 +/- 110 radiocarbon years.

The South American pictograph is one more evidence that the dinosaur world was not a “land before time.” Instead, post-Flood dinosaurs were hunted by historical Peruvian people and apparently were commemorated in the fascinating pictograph.

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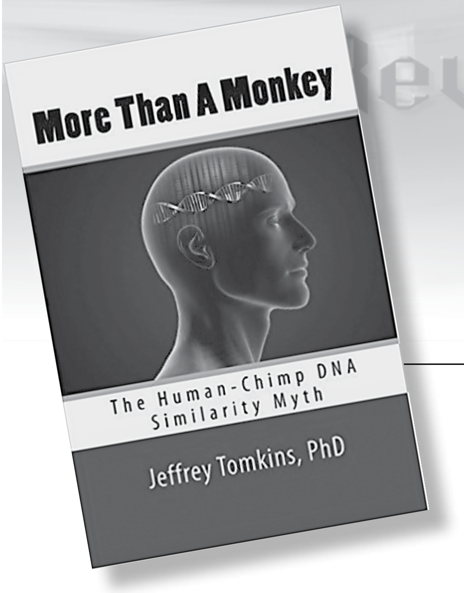

More Than a Monkey: The Human-Chimp DNA Similarity Myth

by Jeffrey Tomkins

Createspace.com, 2014,
108 pages, $12.95.

Author Jeffrey Tomkins was formerly head of the Clemson University genetics lab. He has published widely, including in *Nature* and *Science*. Tomkins explains in the first chapter why he left the prestigious position after 13 years to work for the Institute for Creation Research (ICR).

In this book Tomkins covers the major genetic claims that purport to show humans and apes have a recent common ancestor, documenting the fact that scientific literature clearly supports an unbridgeable genetic chasm that exists between humans and our supposed closest primate cousins, the chimpanzees, as well as other primates. Genetically, the gap is around 0.9 billion base pairs, and it is widest when the human and chimp Y chromosomes are compared. Specifically, the Y chromosome similarity is only 43.2 percent (p. 28). This is significant because the Y chromosome does not normally recombine during zygote formation as do those that exist in pairs, including all of the human and chimp somatic chromosomes.

Tomkins discusses in detail the difficulty in comparing two sets of data that are as different as the human and chimp sets of chromosomes. He also includes a history of the 99%-similarity myth, how it got started, how it has influenced much research today, why it is erroneous, and why it still persists.

Tomkins evaluates the chromosome fusion theory that is often used in an attempt to explain why humans have 46 chromosomes and most apes, including chimps, have 48. He finds by examining numerous lines of evidence that the genetic evidence does not support the claim that two chimp chromosomes fused to produce human chromosome number 2. The allegation that the fusion point was telomere to telomere has little evidence. Telomere-to-telomere fusions are unknown in mammals partly because all known mammal telomeres have highly specialized end caps designed to prevent fusion. Another problem is that a highly expressed gene is located at the putative fusion site, negating the argument that this site is the remnant of two telomeres. The human telomere code, TTAGGG, usually repeated 3,000 to 20,000 times in adults, is strikingly different from all known functional genes (p. 36). In newborns, the sequence is repeated 8,000 times or more, and as the person ages telomeres are lost.

Tomkins covers the evolutionary problem of orphan genes. Orphan genes are those that are so unique to a specific species that descent with modification cannot explain their existence. They appear in the genome fully formed with little or no evidence of a less evolved precursor. The pseudogene claim also is largely overturned by new research (p. 53) as has also the GULO gene, a gene with the so-called shared mistake between humans and primates. The claim was that a genetic mutation common to two animals that are hypothesized to have descended from a common ancestor supports evolution, just as a spelling mistake originating in one book that also appears in a different book, published later, indicates plagiarism in the second book. This a technique actually used to catch plagiarism. Tomkins provides alternative explanations for the similar mutations.

One of the largest chimp-human protein comparison studies was published in 2006. It identified 1,480 human protein-coding genes that had no orthologues (similar proteins) in chimps. This difference is very significant, given that an estimated 27,000 protein-coding genes exist in the human genome. The fewer the number of protein-coding genes there are in the human genome, the more significant is the value of 1,480 genes that differed from chimps. Due to the alternative splicing of the coding segments called exons, the number of possible protein variants in humans is close to a million (p. 70).

One study found orangutans, viewed as the least evolved by evolutionists among the higher apes compared to humans, had more DNA methylation patterns that *were similar* to humans than either chimps or gorillas. Gorillas were the next closest in similarity to humans, and chimps were the least similar. According to standard evolutionary theory, chimps should have been *most* similar to humans, next gorillas, and last orangutans (p. 82).

In conclusion, the total genetic difference is close to, not 1 or 2%, but 30%, and even in homologous regions the difference is 14% (p. 99). The implications of this fact are clear: humans are genetically set apart from the animal world. Governments dominated by "Darwinian evolutionary philosophy that humans are nothing more than animals to be herded and culled in wars, death camps, abortions, food shortage contrived mass starvation and outright slaughter … has claimed over 260 million lives" (pp. 100–101).

Tomkins' excellent review of current scientific literature explains in a clear, reader-friendly fashion that humans are much more than an ape. A chasm exists between humans and chimps, genetically, behaviorally, as well as morphologically. In short, this well-documented book effectively demolishes the genetic evidence for human-chimp evolution from a recent common ancestor. Many major differences exist between human and chimp genomes, including chromosome numbers, orphan genes, Y chromosome DNA, epigenetics, overall genome similarity, and differences in how genes are utilized or expressed.

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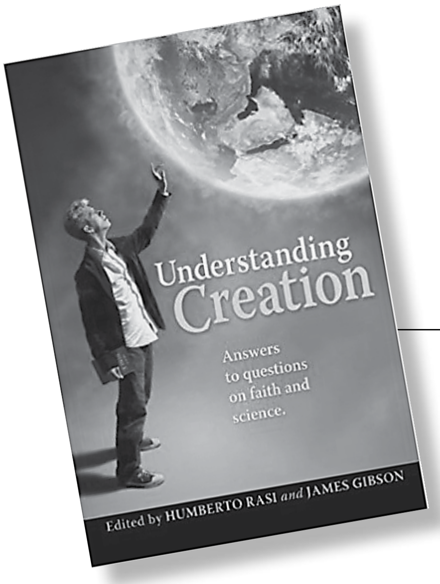

Understanding Creation: Answers to Questions on Faith and Science

Edited by L. James Gibson and Humberto Rasi

Pacific Press Publishing
Association, Nampa, ID, 2011,
223 pages, $20.00

Twenty authors answer basic questions concerning the biblical worldview of origins. Their questions include these: When did Creation occur? What does the fossil record tell us? Can a Christian be a good scientist? Some of the more familiar names include Paul Giem, Ariel Roth, and John Ashton. Most of the writers have present or past affiliations with Loma Linda University, California. This Seventh-day Adventist school has 4500 students and incudes a large medical center.

Also associated with the Loma Linda school is the Geoscience Research Institute (GRI). The current director is editor Gibson. Since 1974, GRI has published the technical journal called *Origins*. There is a rich history of Adventist contributions to the modern creation movement.

In the chapter on radioisotope dating, there is mention of RATE studies, especially the finding of carbon-14 in various samples thought to be ancient (p. 98). There is no book mention of the RATE suggestion of accelerated nuclear decay in the past. A form of the gap theory is discussed on page 94 under the name "Old demonic creation." There are also presented some "out-of-the-box" ideas: "The book of Job hints that God may have fashioned other worlds before he made this one" (p. 30); "The idea that dinosaurs disappeared during the worldwide catastrophe we call the Flood is a hypothesis we should seriously consider" (p. 164).

This hardback book offers clear writing, generous white space, and a few black-and-white figures. No index is provided.

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Instructions to Authors

Submission

Electronic submissions of all manuscripts and graphics are preferred and should be sent to the editor of the *Creation Research Society Quarterly* in Word, WordPerfect, or Star-Office/Open Office (see the inside front cover for address). Printed copies also are accepted. If submitting a printed copy, an original plus two copies of each manuscript should be sent to the editor. The manuscript and copies will not be returned to authors unless a stamped, self-addressed envelope accompanies submission. If submitting a manuscript electronically, a printed copy is not necessary unless specifically requested by the *Quarterly* editor. Manuscripts containing more than 35 pages (double-spaced and including references, tables, and figure legends) are discouraged. An author who determines that the topic cannot be adequately covered within this number of pages is encouraged to submit separate papers that can be serialized.

All submitted manuscripts will be reviewed by two or more technical referees. However, each section editor of the *Quarterly* has final authority regarding the acceptance of a manuscript for publication. While some manuscripts may be accepted with little or no modification, typically editors will seek specific revisions of the manuscript before acceptance. Authors will then be asked to submit revisions based upon comments made by the referees. In these instances, authors are encouraged to submit a detailed letter explaining changes made in the revision, and, if necessary, give reasons for not incorporating specific changes suggested by the editor or reviewer. If an author believes the rejection of a manuscript was not justified, an appeal may be made to the *Quarterly* editor (details of appeal process at the Society's web site, www.creationresearch.org).

Authors who are unsure of proper English usage should have their manuscripts checked by someone proficient in the English language. Also, authors should endeavor to make certain the manuscript (particularly the references) conforms to the style and format of the *Quarterly*. Manuscripts may be rejected on the basis of poor English or lack of conformity to the proper format.

The *Quarterly* is a journal of original writings, and only under unusual circumstances will previously published material be reprinted. Questions regarding this should be submitted to the Editor (CRSQeditor@creationresearch.org) prior to submitting any previously published material. In addition, manuscripts submitted to the *Quarterly* should not be concurrently submitted to another journal. Violation of this will result in immediate rejection of the submitted manuscript. Also, if an author uses copyrighted photographs or other material, a release from the copyright holder should be submitted.

Appearance

Manuscripts shall be computer-printed or neatly typed. Lines should be double-spaced, including figure legends, table footnotes, and references. All pages should be sequentially numbered. Upon acceptance of the manuscript for publication, an electronic version is requested (Word, WordPerfect, or Star-Office/Open Office), with the graphics in separate electronic files. However, if submission of an electronic final version is not possible for the author, then a cleanly printed or typed copy is acceptable.

Submitted manuscripts should have the following organizational format:

1. Title page. This page should contain the title of the manuscript, the author's name, and all relevant contact information (including mailing address, telephone number, fax number, and e-mail address). If the manuscript is submitted by multiple authors, one author should serve as the corresponding author, and this should be noted on the title page.

2. Abstract page. This is page 1 of the manuscript, and should contain the article title at the top, followed by the abstract for the article. Abstracts should be between 100 and 250 words in length and present an overview of the material discussed in the article, including all major conclusions. Use of abbreviations and references in the abstract should be avoided. This page should also contain at least five key words appropriate for identifying this article via a computer search.

3. Introduction. The introduction should provide sufficient background information to allow the reader to understand the relevance and significance of the article for creation science.

4. Body of the text. Two types of headings are typically used by the *CRSQ*. A major heading consists of a large font bold print that is centered in column, and is used for each major change of focus or topic. A minor heading consists of a regular font bold print that is flush to the left margin, and is used following a major heading and helps to organize points within each major topic. Do not split words with hyphens, or use all capital letters for any words. Also, do not use bold type, except for headings (italics can be occasionally used to draw distinction to specific words). Italics should not be used for foreign words in common usage, e.g., "et al.", "ibid.", "ca." and "ad infinitum." Previously published literature should be cited using the author's last name(s) and the year of publication (ex. Smith, 2003; Smith and Jones, 2003). If the citation has more than two authors, only the first author's name should appear (ex. Smith et al., 2003). Contributing authors should examine this issue of the *CRSQ* or consult the Society's web site for specific examples as well as a more detailed explanation of manuscript preparation. Frequently-used terms can be abbreviated by placing abbreviations in parentheses following the first usage of the term in the text, for example, polyacrylamide gel electrophoresis (PAGE) or catastrophic plate tectonics (CPT). Only the abbreviation need be used afterward. If numerous abbreviations are used, authors should consider providing a list of abbreviations. Also, because of the variable usage of the terms "microevolution" and "macroevolution," authors should clearly define how they are specifically using these terms. Use of the term "creationism" should be avoided. All figures and tables should be cited in the body of the text, and be numbered in the sequential order that they appear in the text (figures and tables are numbered separately with Arabic and Roman numerals, respectively).

5. Summary. A summary paragraph(s) is often useful for readers. The summary should provide the reader an overview of the material just presented, and often helps the reader to summarize the salient points and conclusions the author has made throughout the text.

6. References. Authors should take extra measures to be certain that all references cited within the text are documented in the reference section. These references should be formatted in the current *CRSQ* style. (When the *Quarterly* appears in the references multiple times, then an abbreviation to *CRSQ* is acceptable.) The examples below cover the most common types of references:

Robinson, D.A., and D.P. Cavanaugh. 1998. A quantitative approach to baraminology with examples from the catarrhine primates. *CRSQ* 34:196–208.

Lipman, E.A., B. Schuler, O. Bakajin, and W.A. Eaton. 2003. Single-molecule measurement of protein folding kinetics. *Science* 301:1233–1235.

Margulis, L. 1971a. The origin of plant and animal cells. *American Scientific* 59:230–235.

Margulis, L. 1971b. *Origin of Eukaryotic Cells*. Yale University Press, New Haven, CT.

Hitchcock, A.S. 1971. *Manual of Grasses of the United States*. Dover Publications, New York, NY.

Walker, T.B. 1994. A biblical geologic model. In Walsh, R.E. (editor), *Proceedings of the Third International Conference on Creationism* (technical symposium sessions), pp. 581–592. Creation Science Fellowship, Pittsburgh, PA.

7. Tables. All tables cited in the text should be individually placed in numerical order following the reference section, and not embedded in the text. Each table should have a header statement that serves as a title for that table (see a current issue of the *Quarterly* for specific examples). Use tabs, rather than multiple spaces, in aligning columns within a table. Tables should be composed with *14-point type* to insure proper appearance in the columns of the *CRSQ*.

8. Figures. All figures cited in the text should be individually placed in numerical order, and placed after the tables. Do not embed figures in the text. Each figure should contain a legend that provides sufficient description to enable the reader to understand the basic concepts of the figure without needing to refer to the text. Legends should be on a separate page from the figure. All figures and drawings should be of high quality (hand-drawn illustrations and lettering should be professionally done). Images are to be a minimum resolution of 300 dpi at 100% size. Patterns, not shading, should be used to distinguish areas within graphs or other figures. Unacceptable illustrations will result in rejection of the manuscript. Authors are also strongly encouraged to submit an electronic version (.cdr, .cpt, .gif, .jpg, and .tif formats) of all figures in individual files that are separate from the electronic file containing the text and tables.

Special Sections

Letters to the Editor:

Submission of letters regarding topics relevant to the Society or creation science is encouraged. Submission of letters commenting upon articles published in the *Quarterly* will be published two issues after the article's original publication date. Authors will be given an opportunity for a concurrent response. No further letters referring to a specific *Quarterly* article will be published. Following this period, individuals who desire to write additional responses/comments (particularly critical comments) regarding a specific *Quarterly* article are encouraged to submit their own articles to the *Quarterly* for review and publication.

Editor's Forum:

Occasionally, the editor will invite individuals to submit differing opinions on specific topics relevant to the *Quarterly*. Each author will have opportunity to present a position paper (2000 words), and one response (1000 words) to the differing position paper. In all matters, the editor will have final and complete editorial control. Topics for these forums will be solely at the editor's discretion, but suggestions of topics are welcome.

Book Reviews:

All book reviews should be submitted to the book review editor, who will determine the acceptability of each submitted review. Book reviews should be limited to 1000 words. Following the style of reviews printed in this issue, all book reviews should contain the following information: book title, author, publisher, publication date, number of pages, and retail cost. Reviews should endeavor to present the salient points of the book that are relevant to the issues of creation/evolution. Typically, such points are accompanied by the reviewer's analysis of the book's content, clarity, and relevance to the creation issue.

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Conference

July 28–29, 2017

Bob Jones University in Greenville, SC

Abstract Submission Deadline:
April 15, 2017
(see submission instructions at www.CreationResearch.org)

CRS Conference presented in conjunction with the
Henry M. Morris Memorial Lecture
Dr. Kenneth Cumming
Friday (July 28) at 8 pm on the campus of Bob Jones University

Registration:

CRS Members: $50 ($90 after May 31, 2017)
Non-members: $90 ($120 after May 31, 2017)

Register online at www.CreationResearch.org
or mail to Creation Research Society, 6801 N Hwy 89, Chino Valley, AZ 86323

Creation Research Society
Membership/Subscription Application and Renewal Form

The membership/subscription categories are defined below:

1. **Voting Member** ....Those having at least an earned master's degree in a recognized area of science.
2. **Sustaining Member** ....Those without an advanced degree in science, but who are interested in and support the work of the Society.
3. **Student Member** ....Those who are enrolled full time in high schools, undergraduate colleges, or postgraduate science programs (e.g., MS, PhD, MD, and DVM). Those holding post-doctoral positions are not eligible. A graduate student with a MS degree may request voting member status while enrolled as a student member.
4. **Senior Member** ....Voting or sustaining members who are age 65 or older.
5. **Life Member** ....A special category for voting and sustaining members, entitling them to a lifetime membership in the Society.
6. **Subscriber** ....Libraries, churches, schools, etc., and individuals who do not subscribe to the Statement of Belief.

All members (categories 1–5 above) must subscribe to the Statement of Belief as defined on the next page.

Please complete the lower portion of this form and mail it with payment to CRS Membership Secretary, 6801 N. Highway 89, Chino Valley, AZ 86323, or fax for credit card payment to (928) 636-1153. Applications may also be completed online at creationresearch.org.

This is a ☐ new ☐ renewal application for the subscription year beginning Summer ☐ 2016 ☐ __________. *(Please type or print legibly.)*

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Degree ______________________ Field ______________________

Year granted ______________ Institution ______________________

Presently associated with ______________________________

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Indicate applicable category ⬇	*Indicate payment* ⬇			
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☐ Senior [per year]	☐ $33	☐ $53	☐ $70	☐ $26
☐ Life member	☐ $500	☐ $500	☐ $500	☐ $500
☐ Student* [per year]	☐ $33	☐ $53	☐ $70	☐ $26
☐ Subscriber [per year]	☐ $41	☐ $61	☐ $78	☐ $34

* Student members are required to complete the bottom portion of this form.
NOTE: Student members may qualify for the *Future Leaders Sponsorship* program. See the CRS website at www.creationresearch.org for details.
** Rates for the paper option include postage for First Class Mail International

‡ **PAPERLESS option:** You may opt out of receiving paper copies of the CRS periodicals (*CRS Quarterly* and *Creation Matters*). By choosing this option you may register for access to the Premium Area of the website, where you may view or download electronic (PDF) versions of these publications. Of course, regular members and subscribers may also have access to the Premium Area. Only members, however, will have access to the Members Exclusive Area of the website.

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Life membership	+ $__________
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School or institution now attending ______________________
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Your current student status: ☐ high school; ☐ undergraduate;
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Year you expect to graduate or complete your degree ______________

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27	☐	☐	☐	☐	43	☐	☐	☐	☐
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29	☐	☐	☐	☐	45	☐	☐	☐	☐
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35	☐	☐	☐	☐	51	☐	☐	☐	☐
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Expiration date (mo/yr) ______________ Signature______________________________________

Mail to: Creation Research Society, 6801 N. Highway 89, Chino Valley, AZ 86323, USA

Creation Research Society

History—The Creation Research Society was organized in 1963, with Dr. Walter E. Lammerts as first president and editor of a quarterly publication. Initially started as an informal committee of 10 scientists, it has grown rapidly, evidently filling a need for an association devoted to research and publication in the field of scientific creation, with a current membership of over 600 voting members (graduate degrees in science) and about 1000 non-voting members. The *Creation Research Society Quarterly* is a peer-reviewed technical journal. It has been gradually enlarged and modified, and is currently recognized as one of the outstanding publications in the field. In 1996 the *CRSQ* was joined by the newsletter *Creation Matters* as a source of information of interest to creationists.

Activities—The Society is a research and publication society, and also engages in various meetings and promotional activities. There is no affiliation with any other scientific or religious organizations. Its members conduct research on problems related to its purposes, and a research fund and research center are maintained to assist in such projects. Contributions to the research fund for these purposes are tax deductible. As part of its vigorous research and field study programs, the Society operates The Van Andel Creation Research Center in Chino Valley, Arizona.

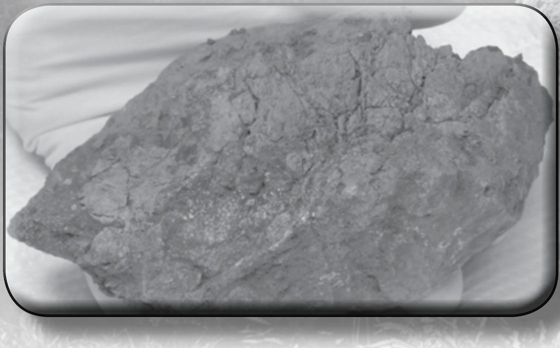
Membership—Voting membership is limited to scientists who have at least an earned graduate degree in a natural or applied science and subscribe to the Statement of Belief. Sustaining membership is available for those who do not meet the academic criterion for voting membership, but do subscribe to the Statement of Belief.

Statement of Belief—Members of the Creation Research Society, which include research scientists representing various fields of scientific inquiry, are committed to full belief in the biblical record of creation and early history, and thus to a concept of dynamic special creation (as opposed to evolution) both of the universe and the earth with its complexity of living forms. We propose to re-evaluate science from this viewpoint, and since 1964 have published a quarterly of research articles in this field. *All members of the Society subscribe to the following statement of belief:*

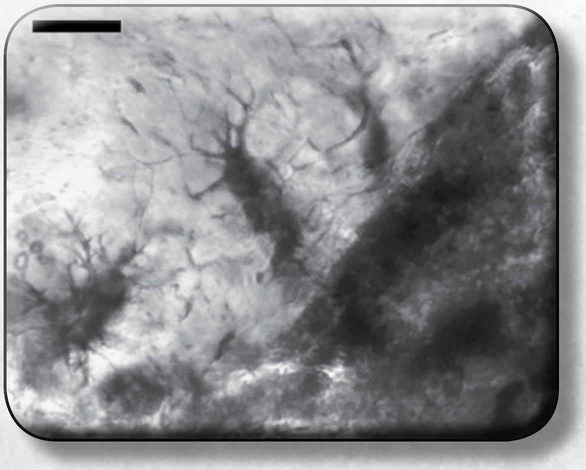
1. The Bible is the written Word of God, and because it is inspired throughout, all its assertions are historically and scientifically true in all the original autographs. To the student of nature this means that the account of origins in Genesis is a factual presentation of simple historical truths.
2. All basic types of living things, including humans, were made by direct creative acts of God during the Creation Week described in Genesis. Whatever biological changes have occurred since Creation Week have accomplished only changes within the original created kinds.
3. The Great Flood described in Genesis, commonly referred to as the Noachian Flood, was a historical event worldwide in its extent and effect.
4. We are an organization of Christian men and women of science who accept Jesus Christ as our Lord and Savior. The act of the special creation of Adam and Eve as one man and woman and their subsequent fall into sin is the basis for our belief in the necessity of a Savior for all people. Therefore, salvation can come only through accepting Jesus Christ as our Savior.

iDINO II

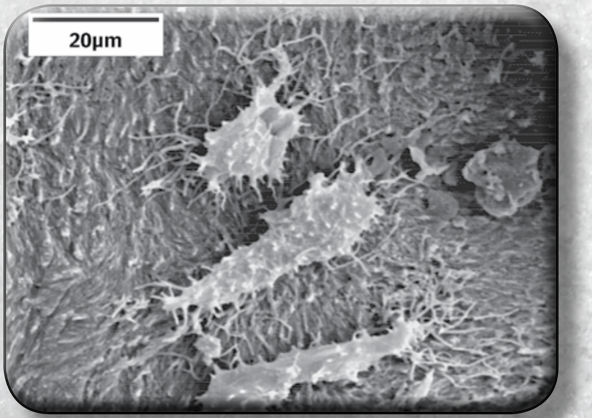
Investigation of Dinosaur Intact Natural Osteo-tissue



A fragment of the *Triceratops* brow horn. Fragments, such as this one, still contain tissue and cells.



Microscopic examination of tissue extracted from a *Triceratops* horn reveals bone cells still present.



Electron microscope picture of intact bone cells still in tissue extracted from a *Triceratops* horn.

How can pliable, stretchable tissue survive inside dinosaur fossils for over 65 million years?

How can this tissue still contain intact cells and even dinosaur proteins?

How can this fragile biological material survive for so long?

The answer to these questions directly challenges the current, evolutionary-biased, geologic timescale.

The Creation Research Society began its iDINO research initiative for the purpose of studying soft tissue in dinosaur fossils. The first phase of the project detected pliable, unfossilized tissue in a brow horn of a *Triceratops*. Within this tissue were intact osteocytes (bone cells). Some results from the iDINO project have been published in a technical microscopy journal and presented at an international microscopy conference. The Spring 2015 issue of the *Creation Research Society Quarterly* also features a special report of the iDINO project. Plus, to further spread the important information about soft tissue, the Society is developing a video (Echoes of the Jurassic).

The **second phase** of the project (iDINO II) will look more extensively at the process of tissue preservation. Evolutionists have offered various theories of how this tissue could survive for millions of years. iDINO II will methodically investigate these preservation claims, assessing their plausibility.

The iDINO results have already provided a strong challenge to the evolutionary worldview. More extensive and detailed examination may provide even stronger evidence that the age of dinosaur fossils is far less than 65 million years. To this end, the Society continues to seek those willing to fund this project with either one-time gifts or monthly donations.

For more information contact us at (928) 636-1153 or crsvarc@crsvarc.com.

Also visit http://tinyurl.com/nphm2c4 for project updates and details.