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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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Cover by Michael E. Erkel, Afton, Virginia

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Send papers on all subjects to the Editor:
CRSQeditor@creationresearch.org or to
Tim Clarey, 1806 Royal Lane, Dallas, TX 75229.

Send book reviews to the Book Review Editor:
Don B. DeYoung, 200 Seminary Dr.,
Winona Lake, IN 46590, dbdeyoung@grace.edu.

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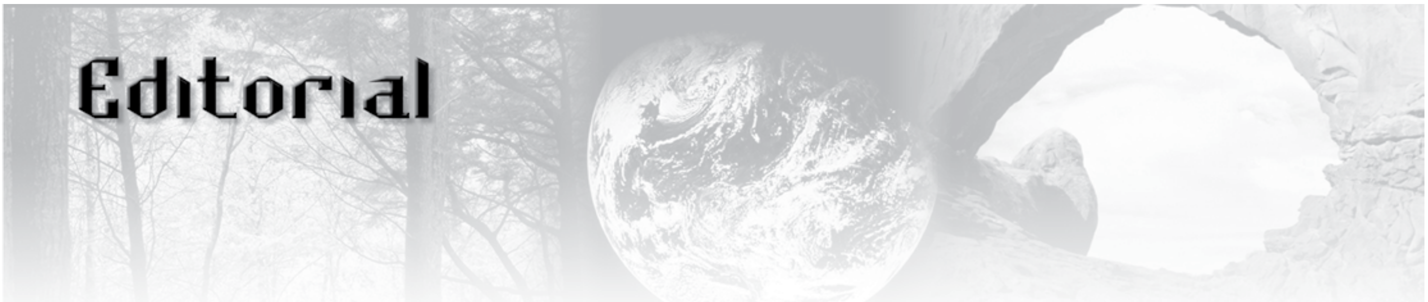

Creation Model-Building and Evolution Bashing: Room for Both?

In the past few issues of the *CRSQ* several Letters to the Editor were published on the Creation Model Controversy, some citing the benefits of model building and others the benefits of so-called 'evolution bashing.' I personally feel there is a need and room for both.

Yes, we do need to try to build better creation models. But, models built on the truth and clarity of scripture and on actual scientific data. And yes, we also need to call out evolutionary scientists for their shoddy pseudo-science (1 Timothy 6:20). This pseudo-science or pseudo-knowledge is nothing more than evolutionism. A little 'evolution bashing' in this regard is necessary.

As Rev. Lemuel Bissell wrote over 100 years ago, "God is a God of peace; he is also a God of war. Christ is the peacemaker; he is also the sword bringer" (Bissell, 1898, p. 6). We need to occasionally swing the sword and fight back against evolutionary dogma and propaganda.

Needless Quarreling

Secondly, do we quarrel just to quarrel, losing sight of our real goal? Let me give an example. A few years ago, I attended the annual CRS meeting in Ann Arbor. An evolutionary geology professor whom I knew also attended. After the meeting was over he told me how surprised he was by the quarrelsome nature at the conference. He thought creation scientists, of all people, should get along better and treat each other with more dignity and respect. Needless to say, I was embarrassed. And I realized I was as guilty as any of the other attendees.

Sadly, this is nothing new for the Christian community. I recently found some still timely wisdom in a 19th-century book of sermons. The introduction was written by Rev. Bissell, who wrote:

> He who is constantly fighting is intolerable; but he who never dares to fight is contemptible…Let love nerve your arm. Strike for a purpose. Let the purpose consecrate the blow. When the purpose is accomplished, declare peace. Don't fire blank cartridges. He who is always quarreling, never fights. He who fights only for God and humanity, never quarrels. (Bissell, 1898, pp. 6–7)

We all need to reflect on the way we treat one another in disagreements, myself included. Sure, we can, and often do have differing opinions. That's always going to be true in science. But we need to get along and love one another as Christian brothers and sisters even when we disagree. Christ commanded us to love one another (John 13:34–35).

Model-Building Takes Perseverance

Finally, I would like to relay my own experience with model building. It has lent both some insights and some precautions. Creation model building is difficult. It takes work. It is time-consuming to do quality research. There are so few of us compared to the evolutionary community. And it is hard to introduce a new model. Paradigms are strong and difficult to change. Preconceptions are even more difficult to overcome.

My friend Kevin Horton retold the story of Hungarian physician Ingaz Semmelweis in a book he wrote (Horton, 2018). In 1846, Dr. Semmelweis began investigating the 13% death rate of women at his hospital following childbirth. His first clue that something was amiss was when he noticed the death rate in the midwife wards was only 2%.

In 1847, he realized that most doctors at his hospital routinely performed autopsies in the mornings and went right into the delivery room, without washing their hands. His colleagues figured that hand washing was a waste of time as they would just soil their hands with blood again during a delivery.

Semmelweis introduced hand washing to his protocol and reduced his childbirth death rate to 2.4%. With this data in hand, he encouraged his colleagues to wash their hands also. But instead, they rejected his findings and ostracized him, laughing "at his foolish time-consuming practice that was based upon the premise that particles were being passed from the blood of the dead and this caused disease" (Horton, 2018, p. 7). Ultimately, Semmelweis was fired and took another job at another hospital where he further lowered his death rate for childbirth to a mere 0.85%. In 1861, he published a book explaining his findings with the data he had collected. Unfortunately, this was ignored and outright rejected by the leading scientists of the day and he was labeled a "radical fool" (Horton, 2018, p. 8).

Dr. Horton went on to explain why the scientific community ignored and marginalized Semmelweis. In the book *The Structure of Scientific Revolutions*, written by Thomas Kuhn in 1962, Horton found the answer. Kuhn explained that scientists see their world through their paradigms. These are a "preconceived set of rules around which the scientist organizes his data" (Horton, 2018, p. 9). Semmelweis was fighting against the paradigms of his day. In the 19th Century, physicians organized their observations "around the concepts of balancing the four humors" (Horton, 2018, p. 9). Everything was filtered through this paradigm. All new ideas that didn't fit this worldview were rejected, regardless of the data behind it. It was simply regarded as unscientific nonsense.

"Today, evolution is the paradigm of science" (Horton, 2018, p. 10). Unfortunately, it is the standard by which all secular science is measured. All new scientific ideas get filtered through the evolutionary dogma. If it is too radical, the idea is rejected. As creationists, we do this too. We filter everything through our own paradigms. Things we believe are true based on what we have already accepted or read or wrote. We develop our own dogmas and tend to reject new ideas. Sometimes pride gets in our way.

The peer-review process is the method used in modern science to filter. Admittedly, the system can be flawed, but it is at least a filter. This filtering is why it is nearly impossible to publish a creation-science paper in a mainstream secular journal, or even a radical new idea that goes against mainstream scientific thought. All new research has to conform to the prevailing paradigm. Again, creation scientists do this too.

Alfred Wegener battled the prevailing paradigms of his day when proposing continental drift. He was ignored and ridiculed by the geologic community for suggesting the continents could move. Of course, 30 years after his passing, the scientific community incorporated Wegener's data into the modern theory of plate tectonics. It was the overwhelming volume of data collected in the world's oceans and across the seafloor that unlocked the story of plate motion. It also took a bunch of open-minded scientists to examine the data with so-called fresh eyes. These pioneering scientists were not as committed to the established ideas (old paradigms) as were the senior scientists. This major shift in geological thinking took place in the 1960s and 1970s. It revolutionized the way geologists examine the Earth. Now, the modern theory of plate tectonics has become one of the major paradigms of geology.

Paradigms are hard to break. And, like the examples of Semmelweis and Wegener above, most new models likely won't become accepted right away. But we must continue to press forward and work on the development of a comprehensive Flood model. We may even have to swing the sword against evolution. At other times we may have to admit we were flat out wrong. But *we must follow the data*.

As creation scientists, we must not readily adopt secular ideas or merely shorten the time to fit the Biblical worldview without assessing the data. Everything must be critically thought through. Adopt what fits the data, like catastrophic plate tectonics, and toss out other evolutionary ideas if they don't fit the data. We must continually ask ourselves if an idea makes sense. Does it fit all available data? Models based on few data are weak. Regardless, if they become ingrained in the mind, they become paradigms.

Read the creation literature and all relevant Bible passages. Don't think we have it all figured out. Don't hold to paradigms that are not based on data. Keep our minds open to new ideas. Only then can we hope to advance a new creation model or build on an existing model. And remember, we should not argue for the sake of arguing.

Differences arise in all sciences. It is how we treat one another that makes us different from secular science. We need to listen carefully to one another. We are followers of Jesus. He showed us love while we were still undeserving sinners (Rom. 5:8). Show that same unconditional love to others in the creation community, regardless of disagreements.

In the meantime, I am working on compiling more stratigraphic data from my sixth continent, doing data-driven science, and adjusting my Flood model as necessary (Clarey, 2020).

Let us all continue to build data-based creation models and attack poor evolutionary 'science' as needed! We can and should do both.

Timothy L. Clarey
Editor
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References

Bissell, L.B. 1898. Introduction. In W. Radcliffe (editor), *The Presbyterian Pulpit, A Volume of Sermons by the Ministers of the Synod of Michigan*. Bissell and Eastman Sermon Printing House, Monroe, MI.

Clarey, T. 2020. Carved in Stone: Geological Evidence of the Worldwide Flood. Institute for Creation Research, Dallas, TX.

Horton, K. 2018. *The Foundation of Everything: Genesis 1–3*. Elm Hill, Nashville, TN.

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Dr. Benjamin Rush:
Christian Patriot, Scientist, and Physician

Kenneth Lawson*

Abstract

Dr. Benjamin Rush (1745–1813) was a leading founding father of the United States of America. He received the best medical education available in his day. Dr. Rush patriotically served his new nation both in peacetime and war. As a pioneer in physical and mental health, he was respected on both sides of the Atlantic. Throughout his long and useful life, Rush was a devout Christian who treasured the Holy Scriptures as God's Word. Much of the foundation for his medical and benevolent activities he learned from the first chapters of the book of Genesis, which he believed were composed of actual, historical people and events. This article examines the scientific and medical genius of Dr. Benjamin Rush and his Christian faith that guided his research and life.

Key Words: Medical science and the Bible, mental health and the Bible, Christianity and science, science and the Bible, Christianity and U.S. history

Introduction

In the history of the United States there were heroic men who helped form their new nation, such as George Washington, Benjamin Franklin, John Adams, and Thomas Jefferson. One man who worked closely with these founding fathers was Dr. Benjamin Rush of Philadelphia. He was a signer of the July 4, 1776, Declaration of Independence, and he advised the founding fathers on numerous cultural and political matters. For many of them he was their personal physician. When the American Colonies fought for their independence against Great Britain, Rush served as a physician for troops in the field. After the war, Dr. Rush was a member of the Pennsylvania State Convention that ratified the Constitution of the United States. As important as Rush was to the founding of the United States, he also made lasting contributions as a scientist and a physician. Guiding his honorable life were his firm Christian convictions. He believed the whole Bible and asserted that all people were made in the image of God. He saw the early chapters of Genesis as factual history.

Early Influences

Benjamin Rush was born in Pennsylvania on December 24, 1745. He was educated by his uncle, Rev. Samuel Finley, an evangelical Presbyterian minister who was a firm advocate of the Great Awakening which was spreading through parts of the American Colonies. As a youth, Rush was a student at Princeton College, graduating in 1760

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* Kenneth E. Lawson, Highland Park, NJ, kvaamm@yahoo.com
Kenneth Lawson earned a Ph.D. in United States History, and serves as the historian for the Associated Gospel Churches, Greenville, SC.

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at age fifteen. He then studied medicine in Philadelphia, then in Scotland at the prestigious University of Edinburgh. He also attended medical lectures in Paris. Rush returned to Philadelphia in 1769, where he developed a reputation as a medical researcher and as the most influential physician and mental health scientist of his generation.

Dr. Benjamin Rush held a lifelong belief in the God of the Bible. In his *Autobiography*, he wrote about his admiration for two revival preachers of the Great Awakening who he heard preach frequently, the American Rev. Gilbert Tennent and the Englishman Rev. George Whitefield (Corner, 1948, pp. 55–57, 163). Rush had a personal conversion experience, and developed a lifelong practice of faithful church attendance and of personal devotions in his home. With his wife and children, he met twice daily for scripture reading and the reciting of the *Shorter Catechism of the Church of Scotland* (Corner, 1948, p. 31). One of Rush's biographers wrote that his life was centered on the religion he learned from his parents (Brodsky, 2004, p. 12). Rush himself wrote of his parent's faith, stating, "I have acquired and received nothing from the world which I prize so highly as the religious principles I inherited from them; and I possess nothing that I value so much as the innocence and purity of their characters" (Barton, 1999. p. 15).

First Accomplishments

Dr. Rush was one of the most respected medical professionals in the English-speaking world and beyond. Some of his medical practices are outdated, but in his day, his accomplishments in science and medicine were remarkable and respected by the intelligentsia of his time (*History of Pennsylvania Hospital*, accessed 2021, p. 1).

In the early 1770s, Rush gained a national audience in teaching on the evils of slavery, the folly of alcohol abuse, and the promotion of public health through improved community sanitation and personal hygiene. His teachings were first published in Philadelphia newspapers and then republished throughout the American colonies and Great Britain. During the early years of the Revolutionary War, Rush served as a medical officer for the soldiers, treating the sick and wounded. He observed the soldiers living in filth, experiencing sleep deprivation, wearing poor clothing in cold weather, and suffering with an inconsistent and unhealthy diet. He recognized these factors directly contributed to the poor physical and mental health of the soldiers. Rush eventually resigned his military medical responsibilities in protest of the poor treatment of the troops (*Penn University Archives & Records Center*, accessed 2018, p. 1). The experiences of Dr. Rush with the Continental Army of the colonies would motivate him to research, write, experiment, and teach on medical and scientific issues for the rest of his life.

After leaving the army, Rush soon resumed his medical practice in Philadelphia and his teaching at the City Medical College. He became involved in many scientific activities and associations that propelled him to international significance. He served for twenty-nine years as surgeon at the Pennsylvania Hospital; helped found Dickinson College in Pennsylvania as a science-oriented school in 1783; was a founder of the College of Physicians; and he served as chair of the chemistry department of the Philadelphia Medical College. In 1787 he joined the Pennsylvania Abolitionist Society for the eradication of slavery. All the while he maintained a private medical practice through which he assisted both the wealthy and the poor in Philadelphia.

A Man of Christian Character

The Christian character of Dr. Rush was on full display during the various epidemics that set upon Philadelphia. Numerous diseases swept through the city during the Revolutionary War and afterwards, such as scarlet fever, croup, influenza, measles, typhoid, and smallpox. Rush was relentless not only in skillfully treating patients, but also in displaying compassion, praying for the sick, and conducting experiments as to the nature of the diseases and potential remedies. He read the Bible with his patients and was persistent in seeking their spiritual and physical good. Rush made some enemies from his innovations, as he ignored racial separation practices by treating blacks alongside slave-owning whites, and as he pioneered new treatments for the ill while some older, tradition-bound physicians objected (Brodsky, 2004. p. 89).

Amid the 1793 yellow fever epidemic in Philadelphia, Rush wrote to his wife Julia, who had departed the city with their children. First, he quoted a text spoken by Jesus in John 13:34, A *new commandment I give unto you, that ye love one another, even as I have loved you*. Then Rush stated to his wife, "Had I not believed in the full import of that divine and sublime text of Scripture, I could not have exposed myself with so little concern, nay with so much pleasure, for five weeks past to the contagion of the prevailing fever. I did not dare to desert my post, and I believed even fear for a moment to be an act of disobedience to the gospel of Jesus Christ" (Butterfield, 1951, p. 688).

Rush pioneered the idea that good health, cleanliness, and public hygiene could hinder the spread of diseases. Through numerous experimentations, he believed that stagnant water, public waste, and other filth contributed to the urban health problem. His world class research laboratory in Philadelphia kept meticulous records tracking when certain diseases came, the weather at the time, the prevalence of bugs and mosquitoes, the ships in port and where they came from, the aggressiveness of the disease, how the disease was transmitted, how the disease affected various ages, and the effectiveness of his medicinal experiments at seeking cures. All of this was pioneering science which required great patience and diligence. Rush also developed new treatments related to quarantines, diet, exercise, sanitation, and testing food and water that comforted thousands and saved numerous lives (Brodsky, 2004, pp. 83, 251–255). These approaches were innovative. His attention to detail and his skill in science and medicine provided increased knowledge that gave him and his staff the ability to develop better medical aids and cures. He saw all people as made in the image of God and, therefore, sought to heal both the body and the soul.

While writing about his medical practice and science experiments during an epidemic in Philadelphia, Rush wrote, "Heaven alone bore witness to the anguish of my soul in this awful situation. But I did not abandon a hope that the disease might yet be cured. I had long believed that…there does not exist a disease for which the goodness of Providence has not provided a remedy" (Rush, 1805, p. 226). Considered a worldwide expert on epidemiology, Rush published his medical findings related to the spread and treatments of various diseases. In addition to his many accolades for his scientific research and medical practice, in 1805 the King of Prussia issued Dr. Rush a medal for his expertise in science and medicine.

Guiding Influences

The guideline for Benjamin Rush's life was the Bible. Beginning with Genesis, he believed a literal Garden of Eden existed before sin that had "original equality," and was free from the defects of the "tyranny" of the fall (Brodsky, 2004, p. 255). He believed in the great ages of humans before the Genesis Flood, what he called the "prolonging [of] life to the antediluvian age" (Brodsky, 2004, p. 359). Rush also believed in "the deluge which overwhelmed the world," in the days of Noah (Brodsky, 2004, p. 231). He rejected the extreme rationalism of secular philosophers and agnostic scientists with his personal faith in Jesus Christ. After winning a prolonged legal battle which included a mean-spirited rivalry with a jealous Philadelphia journalist, Rush wrote in 1801, "Thrones and kings and secular priests and usurpers must fall and perish. Their doom is fixed in the scriptures of truth. The Messiah alone will rule as King of Saints and Lord of the whole earth. All will end, not only well, but gloriously for those who believe and trust in his name" (Butterfield, 1951, p. 837).

Christian compassion guided Rush to help the outcasts of society. In addition to his expertise in physical health, Benjamin Rush spent much of his later adult years studying mental health. He believed that Christ came to redeem the soul, but also to heal the body and the mind. Rush observed mental disease with exhausted Revolutionary War soldiers who saw the horror of war and simultaneously fought malnutrition and exhaustion. He also witnessed mental disorders resulting from the anxieties and panics created from various epidemics. Those with mental illness in his day were institutionalized or imprisoned, but Rush created advanced medical treatments for them. He treated hundreds of patients with mental disorders, maintaining detailed clinical records. For his unique research and experiments in mental health he has rightly been labeled, "The founder of American Psychiatry" (Starr, 1982, p. 42; Brodsky, 2004, pp. 5, 291; Rutkow, 2012, p. 33).

Throughout his extraordinarily successful life, Benjamin Rush never lost his personal faith in the God of the Bible. During his lifetime existed the rising influence of deism and humanism, but Rush maintained his Biblio-centric view of the world. In his *Autobiography*, Rush noted he was friends with Thomas Jefferson but critical of his (Jefferson's) deism (Corner, 1948, p. 334). In later life, Rush still supported traditional or orthodox Christianity, although this was not popular with many intellectuals of that time. For example, as an older man he still believed in the Biblical God as creator, and he supported the idea of a literal first human named Adam (Corner, 1948, p. 337). Rush understood the entire human family as descended from a historic Adam and Eve, and supported the historicity of Biblical persons such as the ancient man named Job (Corner, 1948, p. 338). As a scientist, Rush was critical of the natural theology of his day which negated the Biblical account of creation. Rush realized that such teachings led people from God, and he believed in "the truth of the Mosaic account of the creation" (Corner, 1948, p. 339).

Benjamin Rush conversed with the most brilliant minds in America, Great Britain, and elsewhere. His scientific and academic writings were studied in America, Great Britain, and continental Europe (*Encyclopedia Britannica*, accessed 2021; North, 2000, pp. 45–49). He saw no conflict with academic excellence and scientific query with the Bible. Rush did not diminish his confidence in the accuracy and historicity of the Bible for the acceptance or approval of the intelligentsia of his day. While many humanistic scientists believed in the impossibility of bodily resurrection, Rush asserted that Jesus was "raised from the grave by His Father," as the key to "the salvation of human souls" (Corner, 1948, p. 340). Rush accepted the early chapters of Genesis as accurate history. Not only did he accept the idea of a historic Adam, but he also endorsed the idea of a global flood in the days of Noah, writing of that event, "Every living substance [was] destroyed by the flood (Corner, 1948, p. 341)."

Conclusions

Dr. Benjamin Rush was a pioneer and a reformer. He sought diligently to improve the medical, educational, and social practices of his day. As a forward-looking scientist and physician, he was limited by the time in which he lived. Medicine is always developing, and some of Rush's techniques seem crude or simplistic by today's technological standards. But the timeless foundation of his life was his faith. He believed the Bible from cover to cover. Benjamin Rush is an example of a brilliant scientific and analytical mind with a benevolent Christian heart. His life illustrates that a person can be both scientifically distinguished and believe the whole Bible as the Word of God. After decades of prominent medical and scientific labors with international accolades, Rush wrote, "My only hope of salvation is in the infinite transcendent love of God manifested to the world by the death of His Son upon the cross. Nothing but His blood will wash away my sins. I rely exclusively upon it. Come, Lord Jesus! Come quickly!" (Corner, 1948, p. 166).

References

Barton, D. 1999. *Benjamin Rush: Signer of the Declaration of Independence*. WallBuilders Books, Aledo, TX.

"Benjamin Rush," *Encyclopedia Britannica*, https://www.britannica.com/biography/Benjamin-Rush. (accessed May 28, 2021).

"Benjamin Rush," *Penn University Archives & Records Center*, https://archives.upenn.edu/exhibits/penn-people/biography/benjamin-rush. (accessed March 20, 2018.

Brodsky, A. 2004. *Benjamin Rush: Patriot and Physician*. St. Martin's Press, New York, NY.

Butterfield, L. 1951. *Letters of Benjamin Rush: Volume II: 1793–1813*. Princeton University Press, Princeton, NJ.

Corner, G.W., compiler. 1948. *The Autobiography of Benjamin Rush: His Travels Throughout Life Together with His Common-Place Book for 1789–1813*. Westport, CT: Greenwood Press Publishers, Westport, CT.

"Dr. Benjamin Rush," *History of Pennsylvania Hospital*, https://www.uphs.upenn.edu/paharc/timeline/1751/tline7.html. (accessed May 30, 2021).

North, R.L. 2000. "Benjamin Rush, MD: Assassin or Beloved Healer?" *Baylor University Medical Center Proceedings*.

Rush, B. 1805. *Medical Inquiries and Observations*, vol. III. J. Conrad & Company Publishers, Philadelphia, PA.

Rutkow, I. 2012. *Seeking the Cure: A History of Medicine in America*. Scribner Books, New York, NY.

Starr, P. 1982. *The Social Transformation of American Medicine*. Perseus Books, New York, NY.

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Inflation, the Multiverse, and the Creator

Andrew Repp*

Abstract

The physical constants of the Universe are fine-tuned to support life, and a design inference logically follows. One can avoid this inference under the assumption that cosmic inflation has produced an inflationary multiverse comprising many universes, a few of which possess the conditions requisite for life. Thus this article first reviews the presuppositional bankruptcy of naturalism and then examines the scientific merits of both inflation and its consequent multiverse, as well as of the hypothesis that a quantum fluctuation produced the Universe. We find that, besides the *a priori* failure of naturalism in general, the hypothesized scenario is in tension with fundamental principles of science and functions rather as a modern origins myth.

Key Words: Fine-tuning, inflation, multiverse, Anthropic Principle

Introduction

The fine-tuning of the Universe for life has provoked significant discussion (e.g., Leslie, 1989; Barrow, 2002; Barnes, 2012). Fine-tuning is unsurprising given a Creator, but those who reject Him must seek alternatives. For this purpose, the theory of inflation is attractive: besides solving the flatness and horizon problems (see below), it is theoretically difficult for inflation to occur only once. Hence, our Universe could be but one of many inflation-generated universes (the entire collection being the "multiverse"), and each of these "pocket universes" could have different values for physical constants. Thus, it is argued, a more scientific alternative to design is to posit *many* universes, one of which (ours) by pure chance possesses the conditions required for life.

This article examines, from a Biblical perspective, the argument above. Since multiple authors have advanced this line of reasoning (in various forms), we focus on the presentation by Lawrence Krauss (2012) in *A Universe from Nothing*. Krauss is by no means the first to present such arguments; for broadly similar proposals, see, e.g., Vilenkin (1982); Tegmark (2003a); Lapiedra and Morales-Lladosa (2015). However, Krauss's book seems to have communicated to a broad audience, reaching the *New York Times* best-seller list ("Nonfiction," 2012).

Thus, we here first review the general relationship between science and revelation, which Krauss consistently pits against each other. We next consider the hypotheses of inflation and of an inflationary multiverse. (Note that a variety of multiverse theories exist; the Appendix briefly surveys four categories of these theories, including the inflationary type.) Thereafter we proceed to examine the proposal that the Universe/multiverse originated as a quantum fluctuation. We conclude by remarking on the similarity of these proposals to ancient origins myths.

Science and Revelation

In his first sentence, Krauss acknowledges that he is "not sympathetic" toward divine creation (p. xi), and the rest of the

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* Andrew Repp, Ph.D. mathematics; Ph.D. astronomy

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book fairly drips with scorn regarding it. He concludes, "If we are to be intellectually honest, we must make an informed choice, informed by fact, not by revelation" (p. 183), and this dichotomy appears to motivate much of his thinking. Here the word "fact" has become a proxy for "naturalistic"—because an infinity of unobservable universes qualifies as a potential fact, but a Resurrection with 500 eyewitnesses apparently does not. The Resurrection is (presumably) untenable because it requires supernatural intervention, whereas the multiverse qualifies as a scientific theory, as long as any discussion of it remains on strictly naturalistic grounds. This reasoning hence implicitly incorporates methodological naturalism into the definition of science: one might grant the bare possibility that "something" is out there—but science, one would say, must limit itself to naturalistic explanations.[1]

Other works (e.g., Meyer and Nelson, 2017; Dilley, 2017) provide cogent responses to the assertion that methodological naturalism is definitional to science. We here restrict ourselves to brief consideration of naturalism as a worldview, noting that only a theistic worldview provides grounds to trust the power of science—so that science logically depends on revelation for confidence in its own effectiveness. (For more analysis see, e.g., Lewis, 1947; Bahnsen and Booth, 1996; Reed and Williams, 2011.)

First, science (like any field) assumes that rational thought is superior to irrational. The intrinsic superiority of rational thought is in fact inescapable—any attempt to prove the opposite defeats itself by giving *reasons* to distrust reason. But for a naturalistic worldview there is no essential difference between rational and irrational thought: both a physicist's conclusions and a lunatic's ravings reflect (chance) interactions between the particles in their brains. Even a deep conviction of the superiority of scientific thought is the product of electrochemical reactions and thus no more rational (or irrational) than a forest fire or tornado. Since naturalism thus renders rationality meaningless, a rational argument for naturalism can succeed only in establishing its own meaninglessness—and thus defeating itself.[2]

Second, science implicitly assumes the Universe follows rational laws discernable through careful investigation. But what foundation can naturalism give for this assumption? One may not appeal to experience, because such appeals implicitly expect the future to be like the past—thus assuming lawlike temporal uniformity and begging the question. The laws of nature, for naturalism, can only be brute facts, with no reason to expect their existence now or their continuation in the future. Thus, in their work (which assumes these laws) naturalistic scientists implicitly deny naturalism—and they *must* do so, for naturalism cannot provide a presuppositional basis for science itself.

The Christian worldview, on the other hand, provides just such a foundation. The God who establishes His faithfulness in heaven itself (Psalm 89:2) upholds the Universe by His powerful Word (Hebrews 1:3), and the One in whom all things hold together (Colossians 1:17) is named the Logos (John 1:1)—i.e., rationality itself. It is the Christian worldview and (arguably) only the Christian worldview which can make sense of rationality and the laws of science. It is therefore fundamentally incoherent to presuppose naturalism while lauding science or to argue that "scientific" explanations must exclude revealed truth.

Since, then, naturalism is flawed at the presuppositional level, we could legitimately end our analysis at this point and refrain from further discussion. However, the Word of God reminds us that "the things that have been made" reveal God sufficiently well to leave men "without excuse" (Romans 1:20). Therefore, no matter how deeply we probe the created order, we can be confident that testimony to God's eternal power and divine nature will stubbornly persist.[3] Therefore it is instructive to consider the theories reared on this (faulty) foundation of naturalism in order to demonstrate their own difficulties. We thus proceed to address the scientific arguments for an inflationary multiverse.

Inflation

We begin by considering the theory of *inflation*, which provides the initial conditions for the subsequent expansion of the Universe. Inflation, originally proposed by Alan Guth (1981), proposes that the Universe, when only about 10^{-36} seconds old, expanded by a factor of 10^{26} or more. This exponential expansion[4] was extremely rapid, occupying less than 10^{-30} seconds. (It is difficult to express how fast this is: inflationary theory postulates that a patch of the Universe the size of a proton expanded to the size of the orbit of Venus, and it did so

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[1] This position is not uncommon; e.g., a college-level text (Bennett et al., 2012) asserts that "modern science seeks explanations for observed phenomena that rely solely on natural causes" (p. 72).

[2] Since truth inheres in the nature of God (John 14:6), denial of God's existence forfeits the ultimate ground for distinguishing truth from falsehood.

[3] It follows that believers should probe creation as deeply as possible (Prov. 2:3–5; 25:2), both to see God's glory for themselves (Ps. 19:1; Rom. 1:20) and to expose His glory to those who would hide from it (Jn. 8:12; Matt. 5:14–16).

[4] Governed by $a \propto \exp Ht$, where a is the expansion factor and H is a constant.

in less time than it takes light to cross a proton today.)

At the end of inflation, the expansion began to decelerate, eventually slowing to its current rate.[5] Some regard inflation as the instigation of the big bang itself, while others seem to assume pre-inflationary expansion (see, e.g., Siegel, 2019). In any case, the dominant model understands inflation to have provided the initial conditions for both the expansion of the Universe and the subsequent formation of structure.[6]

The rationale for inflation

Inflation provides an elegant solution to several puzzles, two of which are the horizon and flatness problems.

The *horizon problem* arises from the fact that the Universe is thermally smooth, exhibiting the same temperature (to one part in 100,000) in every direction—and that it seems to have achieved this near-equilibrium state without causal contact between its widely separated parts. Inflation solves this problem by allowing pre-inflationary contact between different regions which inflation has since driven apart.

The *flatness problem* refers to the fact that the large-scale spatial geometry of the Universe is nearly Euclidean, and that certain *a priori* considerations make it very difficult to achieve a flat Universe by chance. Inflation solves this puzzle by noting that such expansion would flatten pre-existing curvature (just as the Earth's curvature is less noticeable than that of a marble).

Inflation has the additional advantage of providing the type of statistical fluctuations we see in the cosmic microwave background (CMB), which gravity could then amplify to produce the large-scale structure we observe today. Furthermore, the concept of inflation is not as outlandish as it might seem: certain types of scalar fields would be capable of driving it—if those fields exist; however, no such *inflaton* field has yet been observed.[7]

Difficulties with inflation

Because inflation tidily accounts for a variety of observations, it is the default explanation for the initial conditions of cosmic expansion. Nevertheless, inflation is not without its own difficulties, some of which we here note.

One difficulty is the lack of observational evidence for the putative inflaton field. This paucity of observational data has allowed a proliferation of inflationary models, although increasingly accurate measurements of the CMB have provided a few constraints (Planck Collaboration et al., 2020).

One prominent cosmologist who harbors significant doubts about inflation is Paul Steinhardt—ironically so, given his role in developing the theory (e.g., Guth and Steinhardt, 1992). He points out (e.g., Ijjas et al., 2014) that the "classical" inflationary theory—which most naturally solves the horizon and flatness problems—is disfavored by the observational data noted above. In order to repair the classical theory, one requires a high degree of fine-tuning combined with unlikely initial conditions. Furthermore, even with these repairs there is as yet no way to show that a universe like ours is a probable outcome. As Leslie (1989, p. 3) observes, "*Inflation could itself seem to have required fine tuning* for it to occur at all and for it to yield irregularities neither too small nor too great for galaxies to form" (emphasis in original).[8]

Another prominent dissenter is Roger Penrose, who appeals to entropy and the second law of thermodynamics; he points out that the smoothness cited above (as part of the horizon problem) represents a very low-entropy state.[9] According to the second law, inflation cannot decrease entropy, so it follows that any pre-inflationary state could have possessed no more entropy than the current Universe. Hence, inflation could result in a smooth universe (solving the horizon problem) only if it began with a smooth universe in the first place. Penrose estimates the probability of this state of affairs to be $1/10^{10^{124}}$, an incomprehensibly tiny number (Penrose, 2010, p. 127).

Falsifiability is another issue. In March 2014, researchers with the BICEP2 (Background Imaging of Cosmic Extragalactic Polarization) telescope in Antarctica announced the detection of *B*-modes from gravitational waves in the polarization of the CMB. Since inflation predicts such waves, this detection was hailed as "direct proof" of inflation (e.g., Moskowitz, 2014). However, the peer-reviewed paper reporting these observations (BICEP2 Collaboration et al., 2014) backed away from the claimed discovery, noting that some or all of the signal might be due to dust in our galaxy. The next year, a joint analysis by the BICEP2 and *Planck* teams concluded that *all* of the *B*-mode signal was attributable to Milky Way dust (BICEP2/Keck Collaboration et al., 2015) so that

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[5] Today it appears to be accelerating again under the influence of dark energy.

[6] Note that inflation is not identical to the Big Bang framework itself; one can reject inflation while accepting the Big Bang, just as (say) one can reject Hydroplate Theory while accepting the overall Flood model.

[7] The Higgs boson is a scalar field, but identifying the Higgs with the inflaton is problematic; see Steinwachs (2019) and Horn (2020) for discussion.

[8] One might rephrase these objections to say that—for inflation to occur and to produce our Universe—it would need to be designed and guided, which of course is not an option for naturalists.

[9] Since gravity tends to pull material into clumps, a smooth distribution of matter is unlikely and corresponds to low entropy.

no primordial gravitational waves had been found.

As a result, one astrophysicist privately remarked to the author, "If detection of *B*-modes proves inflation, doesn't non-detection falsify it?" In fairness, one might more accurately say that their detection would have confirmed the "classical" type of inflation theories, which the lack of detection has thus ruled out. However, the comment highlights the difficulty of disproving inflation in general, to the point that Ijjas et al. (2017) claim it has become "so flexible that no experiment can ever disprove it." If inflation is thus virtually unfalsifiable, its status as a scientific theory is doubtful.[10]

Hence, while most cosmologists accept inflation (at least as a working assumption), there is a non-fringe minority which continues—with good reason—to be skeptical.

Inflation and Genesis

The most objectionable aspect of inflation is its naturalism: whatever the original intentions might have been, for Krauss (2012) it becomes a crucial part of unbelief's attempt to explain all things apart from a Creator. As believers, we utterly reject such an antitheistic motivation.

On the other hand, there is nothing inherently unbiblical in postulating rapid expansion during creation. Sudden expansion plays a key role in some creationist cosmologies; for instance, Humphreys' white hole cosmology (1994) postulates expansion by a factor of at least 10^{10} in a few days of Earth time. Though this rate is far from that assumed by inflation, it is nevertheless conceptually similar.

Furthermore, a creationary treatment of the horizon problem would be welcome—why *do* distant regions of the Universe have essentially the same temperature? Appeals to inscrutable divine fiat are unhelpful given the lack of apparent reason for God to have done so: large-scale thermal smoothness seems utterly unconnected to the habitability of Earth. Might thermalization of the "deep" have occurred on Day 1, before rapid (God-driven and God-directed) expansion on Day 2 produced the "expanse"? As noted above, naturalistic inflation suffers from significant difficulties; however, if future observations unambiguously detect primordial gravitational waves, then it might be worthwhile to investigate whether a divinely driven/directed Creation-Week inflation might explain the data.

However, that day has not yet—and may never—come. Hence, even though rapid "inflationesque" expansion might be compatible with Scripture, it is mandated neither by Scripture nor (at this point, it seems) by observations.

An inflationary multiverse

As inflation proceeded, any original matter and energy would have been diluted to almost nothing by the tremendous expansion; when inflation finally ended,[11] the vast potential energy of the inflaton field would have decayed into other particles. This decay process would have dumped a large amount of new matter and radiation into the Universe, and thus the end of inflation is denoted as "reheating." Furthermore, quantum fluctuations in the inflaton field would result in slight over- and under-densities in this new matter/energy, and these fluctuations could function as "seeds" for the formation of large-scale structure (see, e.g., Peacock, 1999; Dodelson, 2003).

However, these same quantum fluctuations can have another result: if the density variations are too large, inflation will end significantly earlier in some regions than in others. Consequently, volumes of space where inflation has ceased will be carried away from each other by the ongoing inflation in surrounding regions—a scenario denoted "eternal inflation." The result is a virtually infinite collection of "pocket universes" (Guth, 1997, pp. 246–250), each one disconnected from the others—i.e., an *(inflationary) multiverse*.[12]

For Krauss (2012), the inflationary multiverse provides an explanation for the fine tuning of the Universe. For, if the different universes each have different values of the physical constants, some of them will (purely by chance) happen to have the right values to support life—and we, being alive, of necessity find ourselves in such a universe. How, then should we evaluate this multiverse theory?

We first note that these other universes are not directly detectable, being in fact causally disconnected from ours. At the very least, this fact should warrant caution in appealing to them to solve observational problems—or to explain away design.

Second, we note that the original rationale for inflation has now reversed. Theorists first posited inflation to explain observations. But if inflation in fact produces every conceivable type of universe, how could one possibly infer inflation from any given feature of *our* Universe? How could it *explain* anything? If on the other hand some

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[10] See also Penrose (2004), who recounts that proponents of inflation originally predicted a flat universe, then modified their models to allow for an open universe, and now "appear to have reverted to $K = 0$ as being a prediction of inflationary cosmology" (p. 1023).

[11] Or, more precisely, when the exponential (vacuum-dominated) expansion gave way to power-law (radiation-dominated) expansion.

[12] Other multiverse scenarios arise in the literature, but Krauss (2012) largely confines his attention to the inflationary variety. See the Appendix for a brief consideration of other multiverse scenarios.

universes are more probable than others, then we might be able to examine the set of life-sustaining universes to see if ours is typical. But there is no agreement on how to determine such probabilities (the "*measure problem*"): the most natural way of assigning probabilities yields a value of less than $10^{-10^{55}}$ for the type of universe we observe (Ijjas et al., 2014).

Third, multiverse explanations of fine-tuning rely on the fact that, given an infinite number of trials, any result with non-zero probability will eventually occur. In other words, anything that can happen will happen. This reasoning, however, cuts both ways: the "anything that can happen" seems per force to include *Boltzmann brain* scenarios, in which spontaneous vacuum fluctuations produce a functioning brain (with a coherent but fictitious string of memories); this brain exists long enough to have a moment of consciousness before fluctuating back into the vacuum.[13] Given a universe effectively bounded in space and time, the probability of such an event is so small as to be utterly negligible; but given an infinite multiverse, it is—by the same reasoning which explains fine-tuning—bound to happen.

Even worse, the accelerating expansion of our universe seems destined to dilute matter and energy into a permanent vacuum state. This state would have an eternity to produce (eventually) an unbounded number of Boltzmann brains—far more than the number of conscious observers that have existed until now. Thus, by this reasoning, it is far more probable that we are Boltzmann brains rather than true observers of a real external universe. This conclusion strikes at the validity of science itself, yet given a multiverse it seems difficult to avoid. As Brian Greene states (in Sample, 2020),

> I am confident that I am not a Boltzmann brain. However, we want our theories to similarly concur that we are not Boltzmann brains, but so far it has proved surprisingly difficult for them to do so;

he writes elsewhere,

> The deep skepticism that emerges from the possibility of spontaneous brain formation forces us to be skeptical of the very reasoning that led us to entertain the possibility in the first place (2020, p. 301).

Hence, multiverse reasoning seems dangerously prone to solipsism, destroying its own foundation.[14]

Fourth, even if one dismisses as absurd the possibility that *we* are Boltzmann brains, one must confront the fact that multiverse theories typically predict Boltzmann brains to be the most common observers.[15] In other words, if a multiverse generator produces too narrow a variety of universes, it is likely to produce no life-permitting universes at all; but if it produces too many, than it produces a multiverse filled with Boltzmann brains, so that most "observers" (being Boltzmann brains) never truly see a life-sustaining universe. Thus, it seems difficult to explain our situation (presumably genuine observers of a life-supporting universe) without somehow fine-tuning the multiverse creation mechanism. Indeed, Penrose (2004, pp. 764–765) estimates that it is $10^{10^{123}}$ times more likely for an observer to see a universe similar to ours but only one tenth the diameter. (Note that this number has more *digits* than there are particles in the observable Universe.) Thus, unless we fine-tune the multiverse itself, we are immensely more likely to produce only small pockets of low entropy than the Universe we see today. As Lewis and Barnes (2016, p. 319) state,

> If Penrose's argument is correct then—as before—most observers in the inflationary multiverse will be Boltzmann Brains, small islands of order in a sea of chaos. And so the theory seems headed for the dustbin.

It thus seems that multiverse proponents have not evaded fine-tuning at all, instead having only pushed it back into more poorly-understood territory. Other considerations lead to similar conclusions. For instance, an ensemble of two-dimensional universes would probably not support life (Tegmark, 1997), nor, presumably, would one containing only the gravitational force with no electroweak analogue. In short, the multiverse might need its own fine-tuning. And if the fine-tuning of the Universe demands explanation, surely a more comprehensive tuning of the multiverse would also. As Leslie notes,

> It can often seem that some fundamental constant needs tuning for several different reasons, all of which very fortunately demand that it be tuned in the same way. A slightly different Fundamental Theory might have made it impossible for there to be even a single life-permitting combination of constants (1989, p. 57).

Finally, we note that resort to the multiverse hypothesis effective excludes, from the outset, an entire category of explanation—namely, anything involving design.[16] As Gonzalez and Richards (2004) explain,

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[13] The name seems to originate with Albrecht and Sorbo (2004) and involves a *reductio* on Ludwig Boltzmann's proposal (Boltzmann, 1895, 1897) that "the observed universe should be regarded as a rare fluctuation out of some equilibrium state."

[14] As does naturalism in general; absolutization of spacetime seems in several ways to undercut the validity of scientific knowledge itself.

[15] Lewis and Barnes (2016) refer to these problems as the "Boltzmann Me" and "Boltzmann Observer" problems, respectively.

[16] Regarding the claim that fine-tuning itself constitutes evidence for a multiverse (e.g., Leslie, 1989; Tegmark, 2003a), see the conclusive refutation by White (2000), who demonstrates that any such reasoning

> [Given a multiverse hypothesis,] *no amount of evidence for apparent design could ever count as evidence of actual design.* But if science is a search for the best explanation, based on the actual evidence from the physical world, …how responsible is it to adopt a principle that makes one incapable of seeing an entire class of evidence? (p. 270, emphasis in original)

In summary, let us explicitly list the ingredients necessary to escape fine-tuning through an inflationary multiverse. First, inflation itself depends on speculative physics: no inflaton has ever been observed in a particle accelerator, nor is it likely to be, given the enormous energy scale at which inflation would operate. Second, we have seen prominent (secular) scientists who provide cogent reasons for skepticism about inflation in general. Third, there is no agreement on the details of inflation, to the point that its very falsifiability is questionable. Fourth, even if one could show that inflation would lead to a multiverse, the hypothesis that different pocket universes would have different values for the physical constants has not yet been established.[17] Fifth, even with all of the preceding assumptions, there is as yet no way to show that this scenario is likely to produce the type of universe we observe (the measure problem). Sixth, it appears that a multiverse is more likely to support Boltzmann brains than genuine observers—so that even if one rejects as absurd a "Boltzmann Me" scenario, one must explain the fact that we (presumably non-Boltzmann brains) are observing the Universe we do. Seventh, it seems that to escape fine-tuning, one must assume the existence of a multiverse-creation mechanism which can produce life-supporting universes without *itself* being fine-tuned. Finally, appeals to a multiverse appear to beg the question by assuming from the outset that design explanations are untenable.

Far too many would rather swallow all of these assumptions than seriously consider the Biblical testimony to special creation—preferring to accept an infinitude of unobservable universes than to bow to the Creator who has revealed Himself. Occam's Razor cuts far too close for their comfort.

Quantum Fluctuations

Finally, let us examine the ultimate claim underlying Krauss's presentation, namely that the Universe (and multiverse) originated as a vacuum quantum fluctuation.[18] This idea dates at least to Tryon (1973), who argues, "our Universe is simply one of those things which happen from time to time." Because any vacuum hosts continual, tiny fluctuations of energy, it is claimed (e.g., Krauss, 2012, p. 168) that the inflaton field could have taken one of these fluctuations and inflated it into our Universe (or a multiverse). Furthermore, the process would require no source of energy because the loss of gravitational potential energy would always balance the increasing matter/radiation energy of the Universe (Tryon, 1973; Krauss, 2012, p. 167). As Leslie (1989, p. 79) summarizes, "Inflation might quickly generate 10^{50} tons of universe from something weighing under 10^{-5} grams and measuring 10^{-33} cm or less." Hence the Universe is, according to Alan Guth, "the ultimate free lunch" (Guth and Steinhardt, 1992, p. 54).

At the outset, we should note that this scheme is by no means *creatio ex nihilo*,[19] for it assumes a pre-existing framework (whether spacetime, or something more fundamental) endowed with the elaborate laws of quantum field theory (plus speculative extensions like the inflaton field). The Bible, on the other hand, teaches that everything which exists and is not God was created by God—all spacetime, all matter and energy (including vacuum energy), all fields (classical or quantum), all laws of nature, etc. To call the quantum-fluctuation hypothesis "a universe from nothing" (the title of Krauss's book) is mere wordplay. As Carroll (2012) writes concerning that book,

> But it doesn't, and doesn't even really try to, explain why there is something rather than nothing—why this particular evolution of the wave function, or why even the apparatus of "wave functions" and "Hamiltonians" is the right way to think about the universe at all. And maybe you don't care about those questions, and nobody would question your right not to care; but if the subtitle of your book is "Why There Is Something Rather Than Nothing," you pretty much forfeit the right to claim you don't care.

David Albert, professor of philosophy at Columbia University, elaborates, noting that today we recognize the fundamental "physical stuff" to be fields, not particles. He then explains,

> Relativistic-quantum-field-theoretical vacuum states—no less than giraffes or refrigerators or solar systems—are particular arrangements of elementary physical stuff. The true relativistic-quantum-field-

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requires a prior preference for a multiverse over against design. He summarizes, "Our good fortune to exist in a life-permitting universe gives us no reason to suppose that there are many universes" (p. 274).

[17] The argumentation here typically depends on string theory, which is not yet a secure framework for fundamental physics.

[18] Thus, quantum fluctuations would be the multiverse-creation "mechanism" of the previous section.

[19] Despite the fact that some (e.g., Barrow and Tipler, 1986, pp. 442–443) refer to it as such.

> theoretical equivalent to there not being any physical stuff at all isn't this or that particular arrangement of the fields—what it is (obviously, and ineluctably, and on the contrary) is the simple absence of the fields! … The fact that some arrangements of fields happen to correspond to the existence of particles and some don't is not a whit more mysterious than the fact that some of the possible arrangements of my fingers happen to correspond to the existence of a fist and some don't. And the fact that particles can pop in and out of existence, over time, as those fields rearrange themselves, is not a whit more mysterious than the fact that fists can pop in and out of existence, over time, as my fingers rearrange themselves. And none of these poppings—if you look at them aright—amount to anything even remotely in the neighborhood of a creation from nothing (2012).

Ikjyot Singh Kohli (2014, pp. 1–2) evaluates the approach of Krauss (2012) and others as follows:

> The issue with all of these works is that on one hand, the authors claim that these proposals are universes *from nothing*, while on the other hand [they] assume at a minimum all of the complex machinery of variational principles, differential and pseudo-Riemannian geometry, topology, quantum field theory, and general relativity, while *never* addressing the deeper issue of where the latter come from. The other issue is that if all of this machinery is supposed to create universes from nothing, which is clearly not nothing in any sense of the word, then why do the authors go to such lengths to describe this machinery as nothing? (emphasis in original)

Why indeed, if not to provide a substitute for special creation? For though the quantum-fluctuation hypothesis does not give us *creatio ex nihilo*, it does do away with an absolute beginning, obviating the need for a Beginner.[20]

We have already noted that testimony to the Creator will stubbornly persist even under the closest investigation of creation. In this case, testimony to the bankruptcy of the quantum-fluctuation creation hypothesis comes from the twin ideas of energy and entropy, long familiar to creationists in the form of the first two laws of thermodynamics.[21] We examine each in turn.

Energy

First consider the energetics of quantum fluctuations. The Heisenberg Uncertainty Principle prescribes the length of time a fluctuation can last; specifically,

$$\Delta E \cdot \Delta t \sim \hbar \,, \tag{1}$$

where ΔE is the uncertainty in energy measured over a time interval Δt, and is the reduced Planck's constant.[22] The value of is extremely small, around 10^{-34} Joule-seconds. For reference, a tank of gasoline contains about 10^{8} Joules of energy, so a fluctuation with a gas tank's worth of energy would last less than 10^{-42} seconds. So how (one might ask) could a fluctuation produce not just a tank of gas but an entire Universe, which (according to Krauss) has lasted for billions of years?

The answer Krauss gives is that the total energy of the Universe might in fact be zero, because gravitational potential energy (which drives inflation) is negative. So, as the Universe inflates, it essentially "rolls downhill"; the gravitational potential energy becomes more negative, and the inflaton energy becomes more positive—while the total remains zero. Thus, if the net energy of the fluctuation/Universe is zero, there is no limit to how long it could last. He states,

> Including the effects of gravity in thinking about the universe allows objects to have—amazingly—"negative" as well as "positive" energy. This facet of gravity allows for the possibility that positive energy stuff, like matter and radiation, can be complemented by negative energy configurations that just balance the energy of the created positive energy stuff. In so doing, gravity can start out with an empty universe—and end up with a filled one (p. 99).

However, this response suffers from multiple difficulties. First, it is not clear how one could show that the gravitational energy of the Universe *exactly* balances out its positive energy; remember that even a mismatch the size of a tank of gas presents an impossibly high barrier.

Second, even if the energy does balance, the question remains of how this state of affairs arose in the first place. If a powder keg explodes under my house, neither I nor the police will be satisfied with an explanation that says, "The loss of chemical energy in the powder balances out the kinetic energy gained by the fragments of the house, so there's nothing to explain—things like this just happen." After all, if there is truly no energy cost to creating a universe, why do we not see new universes popping into

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[20] Even a universe with no beginning would require a Cause logically (if not temporally) prior to it, unless one argues that the Universe is its own ground of existence. Some such postulate (identifying a changing, contingent universe as the ultimate ground of reality) is necessary to evade the cosmological argument for God's existence.

[21] …and corresponding roughly to the cosmological and teleological arguments for the existence of God.

[22] Contrary to some popular accounts, the system never violates energy conservation, although the mass of a virtual particle need not match its "normal" mass on short timescales.

existence daily?[23] Or if the pre-inflation state were somehow different—so that it was capable of producing universes while today's vacuum is not—then how did the pre-inflation state come to be so precariously balanced?

Third, it is not obvious that one can assign a definite value to gravitational potential energy—which one must do to claim that the total energy vanishes. In classical mechanics of course, the zero point of the gravitational potential is arbitrary. In general relativity, while the notion itself can be ill-defined,[24] it *is* possible to define the total energy of an isolated system (Misner et al., 1973, pp. 451–459). However, it is not always possible to do so for the Universe as a whole; whereas Krauss claims, "There is one universe in which the total energy is definitely and precisely zero…. It is a closed universe" (p. 166), Misner et al. (1973) argue that such a statement is meaningless:

> There is no such thing as "the energy (or angular momentum, or charge) of a closed universe," according to general relativity, and this for a simple reason. To weigh something one needs a platform on which to stand to do the weighing…. These terms are undefined and undefinable. Words, yes; meaning, no" (pp. 457–458).

But what about quantum field theory? This brings us to a fourth problem with the zero-energy explanation, namely, that the proper way to incorporate gravity into quantum field theory remains unknown. Any rigorous demonstration that a universe could spontaneously pop into being by conversion of gravitational potential energy to matter requires a self-consistent theory that handles gravity and quantum fluctuations together. As yet there is no such theory, and it follows that the zero-energy explanation is still speculation, not science.[25]

In summary, to circumvent energy conservation, Krauss proposes that the Universe has zero total energy. But first, it is difficult to see how one could ascertain that the total energy vanishes exactly, which it must in order for this proposal to work; second, it does not explain the apparent instability of the pre-inflationary state; third, it is unclear that the notion of total energy is well-defined in this case; and fourth, there is no actual theory within which one can rigorously assess these claims. All experience to date—including the formalized experience known as science—assures us that (as much as we might wish otherwise) gas tanks do not spontaneously fill with gas. Much less do vacua give birth to universes.

Entropy

Entropy provides a second barrier to the production of the Universe from a quantum fluctuation. In discussions of life on Earth, evolutionists attempt to circumvent the second law of thermodynamics by appealing to the fact that the Earth is an open system. That appeal is not available for the Universe as a whole, and as a matter of fact cosmologists routinely appeal to entropy considerations when studying the expanding universe (e.g., Dodelson, 2003, p. 45).

Therefore, the problem cannot be avoided: how did the Universe come to have such low entropy when all natural processes *increase* net entropy? Recall Penrose's calculation of one chance in $1/10^{10^{124}}$— and recall that inflation only exacerbates low-entropy difficulties. A quantum fluctuation is, after all, the very definition of a probabilistic process—and if odds this low do not rule out a hypothesis, is it truly falsifiable?

One possible response is anthropic, namely, that a low-entropy universe is necessary for life: if the Universe were high-entropy, then we would not be around to observe it, and since we *are* around to observe it, it is no surprise that we observe low entropy. But, first, this argument implicitly assumes a multiverse; as Krauss notes, "This argument, however, makes mathematical sense only if there is a possibility that many different universes have arisen" (p. 125). More seriously, this response fails to deal with how *very* low the entropy is. Even if we ignore Boltzmann brain scenarios, a low-entropy pocket of (say) 1 Gpc^3 should easily allow life to exist, and it would be vastly more probable than what we *do* observe. So the question remains: how could this extremely complex and yet low-entropy Universe have come into being by chance?

We conclude that both energetic and entropic considerations mitigate against the formation of the Universe from a quantum fluctuation in a vacuum. Why is there something—and, in particular, *this* something—rather than nothing? When all is said and done, there will never be a better answer than Genesis 1:1.

Conclusion

It is likely that everyone has at some point stood in awe of the ineluctable factuality and beauty of the Universe. It might seem incredible that anyone should believe it an overgrown vacuum glitch. And yet very intelligent men—who surely have admired their share of starry nights and sunsets—compose eloquent presentations of precisely that theory.

They are not the first to do so. Rodríguez (2015) provides a fascinating

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[23] Or if a large activation energy is involved, why not at least around supernovae, active galactic nuclei, etc.?

[24] In general relativity, gravitational potential energy is not part of the energy-momentum tensor, having been absorbed into the geometry of spacetime.

[25] Ikjyot Singh Kohli (2014) provides a technical explanation of the problems with one such scheme.

review of ancient near-eastern origins myths, which frequently begin with a "nothingness" that is not quite *nothing* ("darkness and a limitless ocean or primeval waters …[yet] a lifeless, motionless state of absolute inertness and nonexistence," p. 295). From the potential within this not-quite-nothingness, everything spontaneously arises—first the forces of nature (personified as gods) and then, out of these forces, everything else. Today's origins myths are much more sophisticated, adorned with brilliant mathematics, yet in the end they are strikingly similar to what pagans have believed for millennia.

We have here noted the presuppositional failures of the naturalistic foundation for one such modern myth. We have seen that inflation, to which it appeals, is more problematic now than when first proposed forty years ago. We have noted the difficulties of the inflationary multiverse hypothesis.

And in the end, this myth falls afoul of fundamental physical principles which dictate that one cannot get something—much less the extremely ordered something in which we live—out of true nothingness.

Why would sober scientists—well-versed in the concepts of energy and entropy—prefer an origins account that derives the Universe from a neo-paganesque fluctuation in a sea of not-quite-nothingness?

Surely, in at least some cases, it is because the alternative—a transcendent, personal Creator and Judge—is to them abhorrent: "we will not have this Man to rule over us." And thus their very wisdom leads them to folly, for the foolishness of God is wiser than men. Let us, then, who have seen the glory of God in the face of Christ be faithful to declare His glory, even among the sophisticated pagans of the twenty-first century.

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Appendix: Various Multiverse Theories

Max Tegmark (2003a) provides a useful taxonomy of multiverse theories, discussing the following four (nested) levels:

- Type I: multiple horizons within an infinite ΛCDM (Lambda-CDM or Lambda cold dark matter) universe.
- Type II: multiple "pocket universes" caused by chaotic inflation. (The main body of this paper deals with such a multiverse theory.)
- Type III: the "many worlds" postulated by the eponymous interpretation of quantum mechanics.
- Type IV: the grand collection of all self-consistent mathematical structures, each assumed to be a description of some reality.

We note that all of these scenarios are difficult to falsify given our current state of knowledge; therefore, presuppositional argumentation (see the second section of this paper) is supremely relevant in dealing with them.

Type I Multiverse Theories

Type I-multiverse theories start from the assumption of an infinite expanding universe with essentially random initial conditions. We, from our vantage point, are unable to observe outside our Hubble volume (beyond which the expansion of the Universe prevents light from reaching us). But if the Universe is infinite, there must also exist an infinity of such vantage points, situated within an infinity of disjoint Hubble volumes. This collection of volumes is a Type I multiverse.

It is crucial for these theories to assume spatial infinity and some degree of homogeneity, and these assumptions are extrapolations (rather than deductions) from our observations.[26] Tegmark deals with objections to infinite space by reviewing evidence for flatness as well as CMB (Cosmic Microwave Background) tests of topology; he deals with objections to homogeneity by reviewing evidence for large-scale uniformity: "assuming this pattern continues, space beyond our observable universe teems with galaxies, stars and planets" (2003a, p. 42). But he then extrapolates to $10^{10^{118}}$ m away—an extrapolation much more audacious than that of an ant who concludes that the Earth is flat. As Carroll notes, "Our observable patch of space is pretty uniform on large scales, it's true. But to simply extrapolate that smoothness infinitely far beyond what we can observe is completely unwarranted by the data. It *might* be true, but it might equally well be hopelessly parochial" (2007, emphasis in original). These theories also typically make the philosophically-loaded assumption of stochastic initial conditions, so that the multiverse contents realize all possible configurations.

However, since each of the universes in a Type I collection obeys the same physical laws, such collections are not directly relevant to the issue of fine-tuning.

Type II Multiverse Theories

Type II-multiverse theories postulate an ensemble of post-inflation pocket universes, possibly governed by different physical constants. (Note that each pocket universe could potentially be an entire Type I multiverse.) The main body of the paper deals with this type of multiverse.

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[26] Even a spatially flat homogeneous universe could be finite if endowed with a nontrivial topology (e.g., that of a 3-torus or an orbifold).

Type III Multiverse Theories

Type III-multiverse theories rely on the Many Worlds Interpretation (MWI) of quantum mechanics (QM), first advocated by Hugh Everett (Everett, 1956). According to MWI, observation of (say), Schrödinger's cat does not stochastically collapse the wavefunction into one of two eigenstates (alive or dead); instead, the wavefunction branches into two separate universes, the cat being alive in one and dead in the other. This continual bifurcation of reality produces an ensemble of parallel universes which collectively realize all possible outcomes.[27]

We note first that there is no general consensus in favor of MWI or, for that matter, of any particular interpretation of QM:

> Quantum theory provides a framework for modern theoretical physics that enjoys enormous predictive and explanatory success. Yet, in view of the so-called "measurement problem," there is no consensus on how physical reality can possibly be such that this framework has this success. The theory is thus an extremely well-functioning algorithm to predict and explain the results of observations, but no consensus on which kind of objective reality might plausibly underlie these observations (Friederich and Evans, 2019).

Thus, neither theory nor evidence requires MWI (reminding us again of the importance of presuppositions).[28]

Second, even proponents of MWI disagree on the "reality" of these alternate universes. As Martin Gardner writes,

> If all these countless billions of parallel universes are taken as no more than abstract mathematical entities—worlds that could have formed but didn't—then the only "real" world is the one we are in. In this interpretation of the MWI the theory becomes little more than a new and whimsical language for talking about QM. It has the same mathematical formalism, makes the same predictions. This is how Hawking and many others who favor the MWI interpret it. They prefer it because they believe it is a language that simplifies QM talk, and also sidesteps many of its paradoxes (2001, p.14).

Thus, to escape fine-tuning via MWI requires a double extrapolation from experimental science: only a realistic interpretation of MWI (which is itself an interpretation of QM) will yield an actual multiverse.

In addition, MWI seems to suffer from the same problems as radical skepticism—namely, that its advocates do not (cannot?) live according to it. For instance, Phillip Ball argues that proponents of MWI should have no reservations about a game of "quantum Russian roulette," in which there is a 10^{-9} chance that they wake up with $1 billion (and otherwise die)—because "you can be certain, in this view, that you'll wake up to be presented with the cash. Of course, only one of 'you' wakes up at all; the others have been killed. But those other yous knew nothing of their demise" (Ball, 2018). Yet presumably even the most ardent supporter of MWI would decline such a wager.

Finally, returning to the issue of presuppositions, note that Everett's argumentation (1956) for MWI assumes that the wave function—evolving in a deterministic fashion—is a complete description of reality (e.g., "the wave function itself is held to be the fundamental entity, obeying at all times a deterministic wave equation," p. 115). Neither chance nor human observers (nor divine sovereignty) collapses the wavefunction, since the wavefunction never collapses. As a result (at least in a realistic interpretation of MWI) there seems to be no room for providence or, for that matter, any expression of divine righteousness or goodness in the natural world—since all possible events occur. Few other interpretations of QM integrate naturalism so thoroughly.[29]

Thus, ultimately there appears to be no reason (beyond philosophical and/or presuppositional ones) to prefer MWI to other interpretations, much less the realistic variant required for a Type III multiverse.

Type IV Multiverse Theories

Type IV is the most comprehensive—and speculative—level of multiverse, postulating the existence of universes collectively realizing every conceivable (non-contradictory) mathematical structure. These mathematical structures could describe not only systems of physical laws but also specific contents of a universe.[30] In essence, Type IV proposes that every conceivable state of affairs occurs—physical laws, physical constants, material contents, etc.—as long as that state is not actually self-contradictory. Tegmark employs phrases such as "complete mathematical symmetry" and

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[27] For this reason, Tegmark (2003a) comments that Type III-multiverse theories actually add nothing to Types I and II, since those types already span all possible outcomes.

[28] See Duwell (2007) regarding the claim of David Deutsch (e.g., 1997) that quantum computing depends on MWI; Duwell argues "that this view is not tenable" (p. 1007).

[29] For an overview of various interpretations (compared to the Relational Quantum Mechanics interpretation), see Laudisa and Rovelli (2021).

[30] For instance, my location on the couch typing on my laptop could in principle be expressed as a string of 1s and 0s, and thus part of a mathematical structure. One could also subsume quantum indeterminacy by rephrasing to state that all non-contradictory structures are realized in some Type III multiverse.

"radical Platonism" to describe such a state of affairs.

This multiverse concept is so far removed from observational support that one can reasonably invoke the adage that "he who asserts must prove," reminding us that the burden of proof rests on those who propose Type IV, not on those who question it. Even Tegmark (2003a) provides in support only (1) the fact that mathematics is "unreasonably effective" (Wigner, 1960) in describing our universe, and (2) the generality and objectivity of abstract mathematics, which seems capable of describing any conceivable universe. He elsewhere adds (3) the claim that mathematical democracy "provides the only answer so far" to the question (attributed to Wheeler) "Why these particular equations, not others?"—and thus it "resolves the fine-tuning problem …once for all" (Tegmark, 2003b).

The first two of these arguments (i.e., the effectiveness and generality of mathematics) are unsurprising in a specially created universe. The third argument requires a prior commitment to naturalism, dismissing out of hand any teleological answer to Wheeler's question. In essence, Type IV takes an observed feature of our universe—namely, that not every abstract mathematical form corresponds to reality—and postulates (without evidence) that each of these forms *is* a reality in another universe (indeed, that they actually *constitute* those other universes). Rephrasing in theological terms, one can observe the freedom of the Creator (to create or not to create) in the existence of this particular "something" (rather than nothing, or a different "something"); Type IV denies this freedom by postulating that all self-consistent "somethings" exist. Stephen Hawking famously asked what breathes "fire into the equations and makes a universe for them to describe" (Hawking, 1988); Type IV, rather than admit a free Creator, supposes that equations generate their own fire.

The question also arises as to why these structures must be internally consistent—for if the laws of logic govern which structures can exist, then whence do these laws arise? It seems that mathematics here replaces God as the ultimate, self-existent reality[31]—but, unlike the Biblical God who wills, chooses, and creates, this god is pantheistic (or at least panentheistic—"all *in* God") in that it simply constitutes all things. Once again we see the influence of presuppositions, which in this case dictate a preference for untethered speculation rather than acceptance of God's revelation through Christ in Scripture.

Concluding Thoughts

We should also note that the *measure problem* (described in the body of the paper) bedevils all multiverse levels save the first. We note in addition that the most obvious objection to multiverse theories (of any type, but especially of Types II–IV) is their violation of the principle of parsimony (Occam's Razor), which states that one should not postulate more entities than necessary to explain the phenomena.[32]

Tegmark attempts to answer this objection—Lewis and Barnes (2016) provide a similar response—by noting that "an entire ensemble is often much simpler than one of its members"; for instance, an extremely simple algorithm can generate all positive integers, including arbitrarily large ones. Thus, he argues, "In this sense, the higher-level multiverses are simpler" (Tegmark, 2003a, p. 51). But—while granting the principle—surely this application of it is specious. Is it more parsimonious to explain the existence of a red book on my desk by postulating an infinitude of universes containing a variety of books (of various colors, quantities, etc.) positioned on (under, beside, etc.) various pieces of furniture—or by concluding that someone put it there? Leslie concurs:

> [P]hilosophy as such supplies no really good grounds for accepting many and varied universes. Indeed, it might actually supply grounds for rejecting them even after all due attention had been paid to the arguments of physicists and cosmologists. Simplicity is fairly powerfully advanced the fewer universes we believe in and the more we insist that any other universes must resemble ours (1989, p. 98).

Martin Gardner was no biblicist, yet his words provide an apt rejoinder to multiverse speculation:

> The stark truth is that there is not the slightest shred of reliable evidence that there is any universe other than the one we are in.… Surely the conjecture that there is just one universe and its Creator is infinitely simpler and easier to believe than that there are countless billions upon billions of worlds, constantly increasing in number and created by nobody. I can only marvel at the low state to which today's philosophy of science has fallen (2001, p. 16).

References

Albert, D. 2012. On the origin of everything. *New York Times*. March 23. https://www.nytimes.com/2012/03/25/books/review/a-universe-from-nothing-by-lawrencem-krauss.html (accessed April 13, 2021).

Albrecht, A., and L. Sorbo. 2004. Can the universe afford inflation? *Physical Review D* 70(6):063528 [10 pages].

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[31] Tegmark himself certainly seems to regard mathematics as the ultimate reality, entitling his 2014 book, *Our Mathematical Universe: My Quest for the Ultimate Nature of Reality*.

[32] While Occam's Razor is neither mathematical axiom nor physical law, it helps regulate speculative attempts to "save" a favorite theory through increasingly complex elaborations.

Bahnsen, G.L., and R.T. Booth. 1996. *Always Ready: Directions for Defending the Faith*. Covenant Media, Nacogdoches, TX.

Ball, P. 2018. Why the many-worlds interpretation has many problems. *Quanta Magazine*, October 18. https://www.quantamagazine.org/why-the-many-worlds-interpretation-of-quantum-mechanics-has-many-problems-20181018 (accessed March 27, 2021).

Barnes, L.A. 2012. The fine-tuning of the Universe for intelligent life. *Publications of the Astronomical Society of Australia* 29(4):529–564.

Barrow, J.D. 2002. *The Constants of Nature: From Alpha to Omega*. Pantheon, New York, NY.

Barrow, J.D., and F.J. Tipler. 1986. *The Anthropic Cosmological Principle*. Clarendon Press, Oxford, UK.

Bennett, J., M. Donahue, N. Schneider, and M. Voit. 2012. *The Essential Cosmic Perspective*, 6th edition. Pearson Addison-Wesley, San Francisco, CA.

BICEP2 Collaboration: P.A.R. Ade, R.W. Aikin, D. Barkats, S.J. Benton, C.A. Bischoff, J.J. Bock, et al. 2014. Detection of B-mode polarization at degree angular scales by BICEP2. *Physical Review Letters* 112(24):241101 [25 pages].

BICEP2/Keck Collaboration, Planck Collaboration: P.A.R. Ade, N. Aghanim, Z. Ahmed, R.W. Aikin, K.D. Alexander, et al. 2015. Joint analysis of BICEP2/Keck array and Planck data. *Physical Review Letters* 114(10):101301 [17 pages].

Boltzmann, L. 1895. On certain questions of the theory of gases. *Nature* 51:413–415.

Boltzmann, L. 1897. Zu Hrn. Zermelo's Abhandlung "Ueber die mechanische Erklärung irreversibler Vorgänge." *Annalen der Physik* 296(2):392–398.

Carroll, S. 2007. How did the universe start? *Discover*, April 27. https://www.discovermagazine.com/the-sciences/how-did-the-universe-start (accessed April 12, 2021).

Carroll, S. 2012. A universe from nothing? *Discover*, April 28. https://www.discovermagazine.com/the-sciences/a-universe-from-nothing (accessed June 2, 2021).

Deutsch, D. 1997. *The Fabric of Reality*. Allen Lane, New York, NY.

Dilley, S. 2017. How to lose a battleship: Why methodological naturalism sinks theistic evolution. In Moreland, J., S.C. Meyer, C. Shaw, A.K. Gauger, and W. Grudem (editors), *Theistic Evolution: A Scientific, Philosophical, and Theological Critique*, Chapter 20, pp. 593–632. Crossway, Wheaton, IL.

Dodelson, S. 2003. *Modern Cosmology*. Academic Press, Amsterdam, Netherlands.

Duwell, A. 2007. The many-worlds interpretation and quantum computation. *Philosophy of Science* 74(5):1007–1018.

Everett, H. 1956. *The Theory of the Universal Wave Function*. Ph.D. thesis, Princeton University, Princeton, NJ.

Friederich, S., and P.W. Evans. 2019. Retrocausality in quantum mechanics. In Zalta, E.N. (editor), *The Stanford Encyclopedia of Philosophy*. Metaphysics Research Lab, Stanford University, Summer 2019 edition. https://plato.stanford.edu/archives/sum2019/entries/qm-retrocausality (accessed March 25, 2021).

Gardner, M. 2001. Multiverses and blackberries. *Skeptical Inquirer* 25(5):14–16.

Gonzalez, G., and J.W. Richards. 2004. *The Privileged Planet: How Our Place in the Cosmos is Designed for Discovery*. Regnery Publishing, Washington, DC.

Greene, B. 2020. *Until the End of Time: Mind, Matter, and Our Search for Meaning in an Evolving Universe*. Alfred A. Knopf, New York, NY.

Guth, A. 1997. *The Inflationary Universe: The Quest for a New Theory of Cosmic Origins*. Addison-Wesley, Reading, MA.

Guth, A.H. 1981. Inflationary universe: A possible solution to the horizon and flatness problems. *Physical Review D* 23(2):347–356.

Guth, A.H., and P.J. Steinhardt. 1992. The inflationary universe. In Davies, P. (editor), *The New Physics*, pp. 34–60. Cambridge University Press, Cambridge, UK.

Hawking, S.W. 1988. *A Brief History of Time. From the Big Bang to Black Holes*. Bantam, New York, NY.

Horn, B. 2020. The Higgs field and early universe cosmology: A (brief) review. *arXiv e-prints*, art. arXiv:2007.10377.

Humphreys, D.R. 1994. *Starlight and Time: Solving the Puzzle of Distant Starlight in a Young Universe*. Master Books, Green Forest, AR.

Ijjas, A., P.J. Steinhardt, and A. Loeb. 2014. Inflationary schism. *Physics Letters B* 736(C):142–146.

Ijjas, A., P.J. Steinhardt, and A. Loeb. 2017. Pop goes the Universe. *Scientific American* 316(2):32–39.

Krauss, L.M. 2012. *A Universe from Nothing: Why There is Something Rather than Nothing*. Free Press, New York, NY.

Lapiedra, R., and J.A. Morales-Lladosa. 2015. On cosmic quantum tunneling from "nothing." *Journal of Physics Conference Series* 600(1):012020 [4 pages].

Laudisa, F., and C. Rovelli. 2021. Relational quantum mechanics. In Zalta, E.N. (editor), *The Stanford Encyclopedia of Philosophy*. Metaphysics Research Lab, Stanford University, Spring 2021 edition. https://plato.stanford.edu/archives/spr2021/entries/qm-relational (accessed March 25, 2021).

Leslie, J. 1989. *Universes*. Routledge, London, UK.

Lewis, C. 1947. *Miracles: A Preliminary Study*. Macmillan, New York, NY.

Lewis, G.F., and L.A. Barnes. 2016. *A Fortunate Universe*. Cambridge University Press, Cambridge, UK.

Meyer, S.C., and P.A. Nelson. 2017. Should theistic evolution depend on methodological naturalism? In Moreland, J., S.C. Meyer, C. Shaw, A.K. Gauger, and W. Grudem (editors), *Theistic Evolution: A Scientific, Philosophical, and Theological Critique*, Chapter 19, pp. 561–592. Crossway, Wheaton, IL.

Misner, C.W., K.S. Thorne, and J.A. Wheeler. 1973. *Gravitation*. W.H. Freeman, New York, NY.

Moskowitz, C. 2014. Gravity waves from big bang detected. *Scientific American*, March 17. https://www.scientificamerican.com/article/gravity-waves-cmb-b-mode-polarization (accessed April 26, 2021).

"Nonfiction." 2012. Hardcover nonfiction. *The New York Times*, January 29. https://www.nytimes.com/books/best-sellers/2012/01/29/hardcover-nonfiction (accessed July 13, 2021).

Peacock, J.A. 1999. *Cosmological Physics*. Cambridge University Press, Cambridge, UK.

Penrose, R. 2004. *The Road to Reality: A Complete Guide to the Laws of the Universe*. A.A. Knopf, New York, NY.

Penrose, R. 2010. *Cycles of Time: An Extraordinary New View of the Universe*. A.A. Knopf, New York, NY.

Planck Collaboration: Y. Akrami, F. Arroja, M. Ashdown, J. Aumont, C. Baccigalupi, M. Ballardini, A.J. Banday, et al. 2020. Planck 2018 results: X. Constraints on inflation. *Astronomy & Astrophysics* 641:A10.

Reed, J.K., and E.L. Williams. 2011. Battlegrounds of natural history: Naturalism. *Creation Research Society Quarterly* 48(2):147–167.

Rodríguez, A.M. 2015. Biblical creationism and ancient near eastern evolutionary ideas. In Klingbeil, G.A. (editor), *The Genesis Creation Account and Its Reverberations in the Old Testament*, pp. 293–328. Andrews University Press, Berrien Springs, MI.

Sample, I. 2020. Physicist Brian Greene: "Factual information is not the right yardstick for religion." *The Guardian*, February 8. https://www.theguardian.com/science/2020/feb/06/briangreene-theoretical-physicist-interview-until-the-end-of-time (accessed February 24, 2021).

Siegel, E. 2019. What came first: *Inflation* or the Big Bang? *Forbes*, October 22. https://www.forbes.com/sites/startswithabang/2019/10/22/what-came-first-inflation-or-the-big-bang (accessed April 26, 2021).

Singh Kohli, I. 2014. Comments on: a universe from nothing. *arXiv e-prints*, art. arXiv:1405.6091.

Steinwachs, C.F. 2019. Higgs field in cosmology. *arXiv e-prints*, art. arXiv:1909.10528.

Tegmark, M. 1997. Letter to the editor: On the dimensionality of spacetime. *Classical and Quantum Gravity* 14:L69–L75.

Tegmark, M. 2003a. Parallel universes. *Scientific American* 288(5):40–51.

Tegmark, M. 2003b. Parallel universes. *arXiv e-prints*, art. astro-ph/0302131.

Tegmark, M. 2014. *Our Mathematical Universe: My Quest for the Ultimate Nature of Reality*. A.A. Knopf, New York, NY.

Tryon, E.P. 1973. Is the universe a vacuum fluctuation? *Nature* 246(5433):396–397.

Vilenkin, A. 1982. Creation of universes from nothing. *Physics Letters B* 117(1-2):25–28.

White, R. 2000. Fine-tuning and multiple universes. *Noûs* 34(2):260–276.

Wigner, E.P. 1960. The unreasonable effectiveness of mathematics in the natural sciences. *Communications in Pure Applied Mathematics* 13(1):1–14.

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Statistics, Baraminology, and Interpretations: A Critical Evaluation of Current Morphology-Based Baraminology Methods

Harry Sanders and Matthew Cserhati*

Abstract

Baraminology has been a hotbed of creationist research for the last two decades. Dozens of studies have been published, most using a single methodology, called BDIST. However, there has yet to be a thorough evaluation of the methodology, though a few have raised concerns about its results. This paper reviews the body of work for the most popular statistical baraminology method and finds that it depends on numerous false assumptions and is prone to deliver false results. The method is characterized by evolutionary assumptions and a lack of critical evaluation of the secular literature. Creation science needs to pursue a more accurate method of determining baraminic relationship. Several ideas are suggested, as well as potential revisions to the dominant methodology that might help it return more accurate results.

Key Words: Baraminology, baramins, BDIST, characters, discontinuity

Introduction

Biological diversity has long been a subject of much speculation. It was this diversity that Darwin attempted to explain without a Creator in his *Origin of Species*, first published in 1859 (Darwin, 1872). However, Darwin wrote in absence of any understanding of heredity which Mendel had yet to publish (Mendel, 1866). It was easy for Darwin to conceive of one basic type of animal changing into another over long periods of time. Such is no longer the case with our modern knowledge of genetics (Watson and Crick, 1949), information theory (Gitt, 2005) and genetic entropy (Sanford, 2014). However, creation science still must undertake the task of explaining and understanding both the Biblical kinds, and the diversification that has happened within them since they were created. To do this, a field of creation science has been created called baraminology. The name for this field of study comes from two Hebrew words and one Greek word. The word בָרָא (barah) means 'he created', and the word מִינ (min) means 'kind', or 'type.' The Greek word λογος means 'science.' Therefore, 'baraminology' is the scientific study of the created kinds.

A Brief History of Baraminology

Baraminology has long been a focus of creation science efforts. One of the founders of the Creation Research Society was Dr. Frank Marsh who coined the term 'baramin' to describe created

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* Harry F. Sanders, III, Moore's Hill, IN, hsanders@answersingenesis.org
Dr. Matthew F. Cserhati, Rosemead, CA, csmatyi@protonmail.com

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kinds in 1941 (Marsh, 1941). Marsh also published works numerous times on the topic of the baramin, from 1964 to 1992. Marsh's ideas served as the foundation for discontinuity systematics (ReMine, 1990) and modern baraminology (Wise, 1990).

Wise built his baraminology on the discontinuity systematics of ReMine, who coined the major terms used in baraminology today such as 'apobaramin,' 'holobaramin,' and 'monobaramin.' According to ReMine, the holobaramin was the created unit of reproduction, described in Genesis 7:2–3, 19–20, and Genesis 1:11, 21–22, and 24, though ReMine deliberately built his system to avoid any reference to the Bible (ReMine, 1990). The apobaramin is a group containing multiple holobaramins, and a monobaramin was a group containing taxa united by ancestry, but which also potentially shared ancestry with other taxa within a holobaramin.

Wise built on this and coined the term "neo-creationist orchard" to explain the discontinuity of baramins as well as premiering the term "baraminology" to name the study of created kinds (Wise, 1990). Wise greatly expanded ReMine's criteria for identifying baramins. For example, he incorporated cladistic methodology to determine baramins, and visualized them using "baraminograms." He further recommended the use of cladistics and the construction of the most parsimonious tree to identify homoplasies, traits which were shared across groups but are not ancestral. He argued that the greater the homoplasies between two groups, the more likely they belonged to different holobaramins (Wise, 1992).

Prior to Wise, statistics had never been formally proposed as a method of baraminology, though the cladistics methods Wise advocated were hardly new. Most baraminologists had been content with Marsh's hybridization criteria (Marsh, 1964; Siegler, 1974) though a few had proposed using DNA in the future when such data became more available (Frair, 1967). However, Wise's statements about using cladistics opened the door for more statistics-based baraminology methods which have come to dominate the field today. A glossary of terms used in this paper are available in Supplementary Glossary 1 at https://github.com/csmatyi/bdist_review.

Methodology

The BDC

The original baraminic distance correlation (BDC) of Robinson and Cavanaugh (1998a) has developed into the baraminic distance and multidimensional scaling (BDIST) of Wood (2008a). For sake of simplicity, BDIST will be used to refer to the suite of statistical baraminology methods that have been curated by Wood on the Core Academy of Science website.

While methods have changed over time, the core idea of measuring baraminic distance has remained central to the methodology. The statistical calculation that measures the number of mismatched characters between taxon pairs is $d_{ij}=m_{ij}/n_{ij}$ where m is the number of characters that do not match between taxa i and j, and n is the number of comparable characters between the taxa. This coefficient produces a fraction which is said to represent the baraminic distance d (Robinson and Cavanaugh, 1998a). The implied assumption is that the more characters in common a taxon pair share, the more closely related they are.

Assuming that all similarity reveals relationship is problematic. It is an explicitly evolutionary assumption, often phrased as 'common design is equivalent to common ancestry.' When evolutionists look at traits that are similar, they assume that the traits are descended from a common ancestor unless there is reason not to (Brooks and McLennan, 1991). This assumption is not always true. Homologous characters can appear in unrelated organisms, which the evolutionists recognize, and account for by appealing to convergent evolution. However, the first assumption when presented with a similar set of characters is that they are the result of ancestry, not convergence.

It is worth pointing out at this stage that statistical baraminologists assume that all similarities are created equal. As one reviewer helpfully pointed out, all creationist statistical baraminology models assume that most shared features will be a result of design in the original baramins, not common ancestry. While this is correct, the equations and algorithms they use do not know this. The equations and algorithms assume all similarity is the same. Therefore, the results of the equations will reflect this assumption.

Wise (1990) points out that phylogenetics, cladistics, and phenetics (aka taximetrics, i.e., observable traits) all cannot see discontinuity, a key element of modern baraminology, and lists several reasons why these methods are not helpful. Yet Robinson and Cavanaugh (1998a) freely admit to using phenetics derived from others as the basis of their classification. Since phenetics is classification based on similarity, by default the BDC, which Robinson and Cavanaugh introduced, assumes that all similarities are the same.

At its core, the BDC and phylogenetics make similar assumptions. While in some cases homologies are ancestral, in others they are artifacts of design. Fully retractable claws, which are among the diagnostic traits of felids (except cheetahs) are a result of common ancestry. Common forelimb structure such as found in humans, apes, whales, and bats is an artifact of design. Assuming that *all* homologous characters are a result of ancestry rather than design as the BDC model does, is predicated on the evolutionary story being true. It also assumes what it is trying to prove, a logi-

It would be valid to argue as follows:

If organisms are the same kind, then we would expect to see continuity.

We see discontinuity, therefore they are not the same kind.

It is however, not logically valid to argue as follows:

If organisms are not the same kind, then we expect to see discontinuity

We see discontuinity, therefore they are not the same kind.

This is affirming the consequent and can be demonstrated in simple terms this way:

If it is raining, the streets are wet.

The streets are wet, therefore it is raining.

Obviously this is not necessarily true. There are a myriad of reasons the streets could be wet, from a broken water main to a child with a garden hose. The same is true of discontinuity and continuity. There are multiple explanations for the existence of both from similar habitats to selective breeding. The discontinuity argument logically cannot demonstrate baraminic relationship because it is based on a fallacy.

Box 1

cal fallacy known as "circular reasoning" or "begging the question" (See Box 1). While Robinson and Cavanaugh (1998a) were explicit in pointing out that discontinuity needed to be looked for, the BDC equation itself assumes that all similarities are created equal. Discontinuity must be determined after the BDC equation is performed. The BDC does not take into account homoplasy.

Even leaving aside the evolutionary assumption of ancestry, the BDC unaided cannot determine discontinuity in 45% of all cases (Wood, 2012). Obviously, since character choice is a major factor, the BDC cannot be expected to determine discontinuity every time, but 55% success rate is hardly reliable. Other tools have been introduced into the BDC, beginning with ANOPA (Cavanaugh and Wood, 2002) and culminating with bootstrapping (Wood, 2008a). More recently, Wood (2020), has debuted an updated version of statistical baraminology, termed BARCLAY that still relies on the BDC model, but updated from one statistical coefficient to another. However, the fact that the basic method fails to determine discontinuity in nearly half of its applications does not inspire confidence in its ability to accurately define baramins.

Critical evaluation of datasets

The BDIST method is statistically driven using mainly morphological characters to determine baramins. Because statistical applications are only as good as the information they are provided, proper data selection is crucial to ensure that correct baramins are produced. It has been suggested that creationists collect their own data rather than simply using the method to reinterpret the data of others (Wood, 2002). While this has been done at least once (Sanders, 2016) for all practical purposes, every study published using the BDIST method has relied almost exclusively on data collected and interpreted by evolutionists. As noted below, these datasets are not unbiased. It would be very easy, for example for an evolutionist to assemble a dataset containing characters we share with chimps, (large brain size, body hair, opposable thumbs, etc.) to demonstrate we are related to chimps, while ignoring the differences (chromosome number, presence/absence of a tail, etc.).

While this reliance on evolutionists to obtain data is somewhat inevitable, given the budget and access constraints faced by many creation scientists, it is important to critically review the data for bias, and filter out improperly defined characters. Unfortunately this is not done and some authors even argue that a particular bias must be demonstrated before considering the possibility of a general bias (Wood, 2011a). Unfortunately, this is an inaccurate view of the evolutionary community, as even members of the community itself have admitted (Winsor, 1994; Todd, 1999). Because evolutionists are not unbiased, as they themselves admit and demonstrate, it seems reasonable that their bias will affect their datasets. Wood (2011a) even provides an example of this bias from the dataset he used in his paper. Most of the time, however, there is no attempt to determine bias in the data set and it is simply treated as an unbiased set of facts. All this does not mean these data sets cannot be used, but it does mean critical examination is required. The BDIST method does filter out unknown characters if enough taxa in question are missing the character, but this is not critical evaluation of the dataset. It is an evaluation of the completeness, not the accuracy of the data.

Relevance of characters

Proponents of the method might argue that the relevance statistic determines which characters are used is a critical examination of the data. This fails for two reasons. It was not the original purpose of the relevance measurement. The original purpose of the relevance statistic was to measure the completeness of the dataset (Robinson and Cavanaugh, 1998a). The equation is ($a_i=x/n$) where a_i stands for the relevance of the character in question, x represents the number of organisms in the dataset where such a character exists, and n equals the total number of organisms in the dataset. The equation has since been used to exclude characters that did not hit a movable, arbitrary relevance cut-off (Wood, 2002). This movable arbitrariness is the second failure of the statistic. Because the relevance statistic does not examine the characters themselves, but merely determines how complete the data set is with respect to the members of the dataset, it cannot be used as a critical evaluation tool. In other words, the relevance statistic does not determine whether the character states in the data set were measured correctly, or in an unbiased fashion. It merely determines what percentage of the characters are present in all taxa contained in the dataset.

There appears to be some confusion on what the relevance statistic does. Because it is calculated using an algorithm, it is blind to the types of data it is presented. All it sees is a sequence of numbers and symbols. If enough taxa have a number instead of a symbol, that character is retained for analysis. Relevance is not impacted by the desire for holism. If it is given a dataset where certain dental characteristics are present for all or most taxa under analysis, but skeletal or morphological characteristics are only rarely found, it will retain the dental characters, but remove the skeletal or morphological ones. In effect, relevance can have the effect of *reducing* holism.

The relevance cut-off originally proposed was 95% (Robinson and Cavanaugh, 1998a), but Wood lowered this to 90% so that some datasets would give better results (Wood, 2008b) and further to 75% in his examination of human fossils (Wood, 2010). Further fossil studies have also used this 75% cutoff (see Aaron, 2014; Garner and Asher, 2018, for examples). A philosophical justification for this drop has not been presented. Fossils are much more difficult to obtain data from than live organisms as they are often disarticulated and lack soft morphological traits. While it is important to increase sample size, lowering the relevance cut-off does not just increase the number of useable characters. It also increases the potential for statistical noise and increases the potential for inaccuracy. By dropping the relevance cut-off twenty percent to increase the number of characters available for fossils, BIDST creates the possibility of an artificially enlarged baramin. The inverse is also true. If the relevance cut-off is too high, the result could be too many baramins. There needs to be a consistent relevance cut-off, preferably one determined through an appeal to an absolute standard, not an arbitrary one. If an arbitrary cut-off must be used, then let it be immovable for all types of data. As the cut-off is currently used, it gives the appearance that researchers are picking a relevance that suits their preferred outcome.

While rejecting characters which are not present in a high enough percentage of the taxa is useful, it does not constitute a critical examination of the dataset as a critic might object. This requires examining multiple datasets collected by different research teams to determine either a consensus or average value of the characters in question. In effect, the creation scientist is taking all the information available in the literature and synthesizing it into one dataset. Obviously no perfect dataset can be obtained in this way. The researcher would need to know all the characters of a given set of organisms to craft a perfect dataset. However, by synthesizing data, the likelihood of errors or biases changing the results is decreased.

Critical evaluation does not mean taking existing data sets and compiling them into a matrix. A matrix will still contain any errors or biases committed by the original authors. Nor does it mean taking multiple individual datasets and comparing their results. One of the reviewers of this paper has objected that Wood (2010) satisfied the criteria for critical evaluation of the data set because he used multiple data sets. In that instance, the results are being critically evaluated, but the data itself is not. In other words, the data was accepted as accurate, run through BDIST, then the results were evaluated. This adds a layer of error potential between the data and the evaluation. This is also true of Wood's work with turtles (2005) and with Felidae (2008b). In fact, the datasets on Felidae were nearly identical as the latter one was copied from the earlier one, with a few additional characters. Neither contained any attempt to average multiple authors' characters, nor synthesize a mean dataset. Therefore, they do not meet the requirements for critical evaluation of the data. A mean value for common characters will reduce any potential bias, though it may not completely eliminate it.

It is important to realize that the datasets being used in baraminology studies are created by people with biases. As one reviewer was kind enough to point out, this has been demonstrated. McConnachie and Brophy (2008) examined a dataset of Galliformes characters with 102 characters and sixty taxa. Careful work with the BDC and MDS suggested four baramins. Hybridization data linked three of the four groups. This study is very illustrative of the power of bad or biased data. Had McConnachie and Brophy stopped with the BDIST, they would have published results that created Biblically incorrect baramins. Because they did not, their paper demonstrates that the data cannot be implicitly relied upon or considered unbiased.

Alternatively, the baraminologist could take measurements of the characters themselves. While performing the measurements may be impossible due to any number of circumstances, crosschecking is much easier for most organisms, with perhaps the exception of some more obscure groups and fossils. If it is impossible to critically examine the dataset, it is better to admit lack of knowledge than make incorrect pronouncements based on potentially flawed data.

Bootstrapping

Undoubtedly practitioners of the BDIST system will appeal to bootstrapping to justify the data selection. However, bootstrapping, by Wood's own admission merely points to how sensitive the dataset is to random changes in it (Wood, 2008a). By convention, 90% or higher is considered significant. While it is difficult to philosophically justify a particular number as a cutoff for data strength, leaving it open to interpretation does not solve the issue either, as two individuals could look at the same data and come to different conclusions depending on what number they chose to use to represent strong or weak data. As stated with the relevance cut-off, if an arbitrary cut-off must be used, let it be consistent. In this instance, it is consistent, but with relevance it is not and there is no attempt to justify why one is fixed and the other is moveable.

Bootstrapping is an artifact of cladistics that BDIST has borrowed. While not necessarily a bad thing, borrowing from the evolutionists must be done with careful critical evaluation, to ensure that the good is separated from the bad. While some of its practitioners have acknowledged criticisms of the method from the evolutionists themselves, they spent little time rebutting them or examining them, instead choosing to simply accept the consensus of bootstrapping's value uncritically, and apply it to baraminology (Wood, 2008a). They have not addressed the underlying assumptions of the method, nor more than cursorily rebutted the criticisms of the method.

There are, however, serious issues with bootstrapping. It has four underlying assumptions as listed by Felsenstein, who is perhaps the primary popularizer of the method (Felsenstein, 1985):

1. Characters have been selected in an unbiased fashion by the taxonomist;
2. Characters have evolved independently;
3. Character evolution is randomly determined;
4. The phylogenetic program used generates the correct phylogeny and the most parsimonious tree is correct.

All of these assumptions are problematic. Everyone carries a bias and applies that bias to character selection (Winsor, 1994). Often certain characters are deliberately excluded from the dataset for a variety of reasons, which has the potential to bias the data (Sanderson, 1995). Other authors view bootstrapping as implicitly biased and a bad estimate of repeatability (Hillis and Bull, 1993). While in limited situations bootstrapping could be considered a measure of accuracy, bootstrap values cannot be compared from study to study as, due to each study's implicit bias, they will vary unpredictably. Further, as later commentators on his work point out, Felsenstein himself admitted that not all characters arise independently, even assuming evolution to be true (Kluge and Wolf, 1993). Further, the assumption of maximum parsimony is not something evolution is compelled to produce (Ridley, 1986). Parsimony is not even the only method cladists use. Character evolution is also not always random. Diversification in bird body sizes, for example, sometimes has been shown to be non-random (Maurer, 1998). This may explain why phylogenetic trees fail to predict diversity in characters except among close relatives (Scotland et al., 2014), as phylogenetics assumes random character evolution. Because its underlying assumptions are inconsistent with baraminology, bootstrapping fails as a measure of result robustness.

One reviewer of this paper has objected that, because bootstrapping is not being used for evolutionary purposes, its underlying assumptions can be ignored. This is incorrect. If statistical baraminology is going to use bootstrapping, it needs to meet the underlying assumptions of the method, or the bootstrapping results cannot be trusted. Wood used just that logic in replacing the Pearson coefficient with the Spearman coefficient in the updated BARCLAY method (Wood, 2020). As the reviewer pointed out, the assumptions of the bootstrapping model are not included in statistical baraminology. Therefore relying on bootstrapping to justify character selection within statistical baraminology is unjustified.

Character selection

Characters are the underlying force that drives the statistics behind taxonomic methods. The characters are the data being interpreted by statisticians using the statistics. Thus, selecting characters is critically important. However, with minimal exception, creation scientists never select the characters. The characters come preselected from the evolutionary community in their datasets, mostly accumulated for phylogenetic purposes. Therefore, it is crucial to know how they select their characters and what a character means to them.

To the evolutionist, a character can be any feature of an organism from morphological and anatomical, to ecological and behavioral (Gemeinholzer, 2008). Characters are defined as either evolutionarily stable or volatile, depending on whether they change with time or not and as either ancestral or derived depending on which is assumed to have appeared first. Characters are chosen to fit the purpose of the study at hand (Wiley, 1981) and different character types often produce discordant phylogenies (Ridley, 1986). This makes any result obtained by a statistical analysis of characters suspect as it is difficult to be certain that the correct characters were selected.

As an example of some of the problems with character sampling, an analysis of character selection across 512 phylogenetic studies discovered that systematists were usually very vague when it came to why they selected traits. Worse, they found that taxonomists were selecting characters differently and assuming that everyone else was making selections the same way they were (Poe and Wiens, 2000). Applied to baraminology, such a statement serves as a warning that characters from the same organisms can be vastly different depending on who is doing the measurements. The potential for bias is why critical examination, as detailed above, needs to be performed on data sets. Further, unless it is explicitly detailed in the paper, it should not be assumed that the secularist has used the same methods the reader would have used to obtain their data.

After characters have been selected, they are coded into a matrix where the state of each character is represented numerically. Coding can be done multiple ways, and each comes with its own problems (Strong and Lipscomb, 1999). The code can be represented multiple ways with ones for presence and zeroes for absence, or, more commonly, one number will represent one state of a character, (usually the presumed ancestral state), while a second number will represent a second state and so on (i.e., 1 = round, 2 = square, 3 = flat) (Gemeinholzer, 2008). These numbers are then converted into phylogenetic trees either by graphing by hand or, more commonly, using a computer program.

There are significant issues with a character-based system. One issue is how to assign discrete values to continuous character values, such as length. A larger issue is that numeric characters do not distinguish between traits which are diagnostic and those that are not. For example, the presence of mammary glands is diagnostic of a mammal, yet has the same weight as a non-diagnostic trait, such as teeth attached to the palate, which occurs in both reptiles and fish. This means traits which are truly unique to an organism or group of organisms, and thus could indicate discontinuity, can easily be lost in an unweighted system. They may simply be unable to overcome the background noise generated by the other traits which they either share or lack in common with another group in the analysis. This can lead to inaccurate clustering.

The best-case scenario would be to cover as many characters in as many species as possible. Adding more characters increases the resolution of a study and also decreases stochastic error. However, eliminating systematic error with more characters is not guaranteed. Adding more taxa to a study could make the reconstruction of species relationships more accurate. However, species selection must be even and not be skewed towards some groups over others. If one can choose between more characters or more taxa, choosing more taxa is a better option, at least in phylogenetic theory (Heath, 2008). Experiments need to be done to confirm this in baraminology.

The practitioners of the BDIST recognize that there is an issue with character selection. It was for this purpose bootstrapping was brought into the model, to see whether characters had been reliably selected (Wood, 2008a). However, as noted above, bootstrapping is rife with problems and cannot provide evidence of correct character selection.

Continuity and Discontinuity

The fundamental tenet of statistical baraminology states that species within a baramin are continuous with one another, and discontinuous with all other species. According to the BDIST, both continuity and discontinuity are necessary to define a baramin. Species must be shown to be continuous with one another, and discontinuous with all other species. Continuity is considered additive, not subtractive, evidence. Instead of demonstrating continuity, discontinuity between organisms must be demonstrated to show they are not in the same baramin. Just because continuity cannot be demonstrated does not mean discontinuity is present (Wood et al., 2003). Formally defined, discontinuity is "a significant, holistic difference between two organisms. Two organisms that are discontinuous with respect to each other are found in separate potentiality regions" (Wood et al., 2003).

Discontinuity is demonstrated in potentiality regions. These are particular regions of biological character space. Any possible character takes up a dimension of character space and has a unique position. Each unique design occupies a single point in this multi-dimensional space. Potentiality regions are areas within this space where various organismal designs can be found. Outside these potentiality regions, no designs can exist. These empty spaces form the borders of discontinuity. Finding these borders in multidimensional space is the work of the BDIST.

There are numerous underlying assumptions here. The most obvious is that discontinuity is a primary tool for identifying the baramin. This raises a question: how is this assumption different than the homology argument evolutionists like to wield? By definition, *discontinuity is difference*. This difference must be significant and holistic (Wood and Murray, 2003). Therefore, similarity within groups discontinuous from other groups is accepted as evidence of relationship.

A reviewer has objected that it is possible that similarity can exist within a baramin without being a product of ancestry. In some baramins, this might be possible, depending on how many members of the baramin were originally created and how they bred post-Fall. In the time since the Fall, particularly with the harsh Flood bottleneck, it seems unlikely, but the premise can be granted as theoretically possible. However, for any baramins that were on the Ark, all members of the baramin must share ancestry by default. Therefore, any similarity in those baramins will be a result of ancestry. Further, Wood et al. (2003) admitted that baramins were to be inferred from similarity. Therefore, at minimum, BDIST assumes similarity is important in determining baraminic relationship.

This argument is a twist on the homology argument, except it also suffers from the problem of character selection. The discontinuity argument assumes that continuity or lack of discontinuity is evidence for ancestry right up to the point where it is not. It is very difficult to define exactly where discontinuity begins without making character selections have weight. This is because characters are not all created equal. Thus, the anal scent glands, which can be viewed as evidence for continuity between Mustelidae and Mephitidae are not weighted as such and are given the same weight as other data that makes them discontinuous, such as DNA which is what was used to separate them, as they once were the same family (Eizirik et al., 2010). However, weighting one character over another introduces the possibility of picking weighted characters in an incorrect or arbitrary fashion which opens the model to criticism. This paradox is unescapable. In fact, one would have to know everything about the species under study to devise the perfect weighting scheme for characters. In reality, this is impossible.

A reviewer has objected that BDIST can correctly determine discontinuity without weighing characters. This argument is flawed because he assumes that BDIST produces an accurate measure of discontinuity, then uses that to argue that the BDIST has produced accurate measures of discontinuity. This is circular logic. If BDIST's accuracy is tested without assuming that it produces accurate results, as will be shown below, it will be demonstrated that it does not always produce an accurate measurement of discontinuity.

Worse, this argument assumes that discontinuity is only a prediction of creation science. Evolution predicts discontinuity as well, though not to the extent that a creation model does. Evolutionists have appealed to discontinuity to explain everything from the difference between modern humans and Neanderthals (Bertorelle et al., 2003) to the difference between two sub-species of the Ural field mouse, *Sylvaemus uralensis* (Chelomina and Atopkin, 2010). Discontinuity can be accommodated within the evolutionary models, something baraminologists stated as far back as 2009 (Wood and Garner, 2009). The only major difference is that evolution expects organisms can cross between potentiality regions over long periods of time.

On a philosophical level, discontinuity fails as well. A reviewer has claimed that discontinuity is measured not at the character level, but at the organismal level. This claim is innaccurate for several reasons. First, the BDIST relies on the BDC which measures how many taxa have a given character, then maps the average as distances in three dimensional space. In essence what this does is get an average, not of the whole organism, but of the characters in the dataset. Given that many disparate organisms share similar anatomical and morphological parts, what is really being mapped is not organismal similarity, but character similarity. Organismal continuity and/or discontinuity is inferred from character similarity or difference. It is not a direct result of the BDIST.

Second, traits themselves do not necessarily predict what the organism is. Given the following traits: aerobic respiration, streamlined body, dorsal fin, caudal fin, pectoral fins, dorsal spine, scales, lack an operculum, spiracle. That list of traits could apply to any number of species of shark. There is no way to know simply from reading it that it was written specifically about *Squalus acanthias*, the spiny dogfish, though the mention of a dorsal spine might provide a clue. Organisms are more than just a list of their parts. The arrangement of their parts matters. Because BDIST separates the parts from their arrangement, it is not able to measure continuity and discontinuity at the organismal level. It can only measure continuity and discontinuity at the level of the trait, which may not hold for the whole organism. While the practitioners of the BDIST may believe that the method is working at the organismal level, that is not, in fact, what is going on. They are making inferences about the organismal level, from the character level.

Holism and Significance

While the desire for statistical significance, which is applied to this model, is certainly understandable, in practice, it is meaningless. As Wood et al. (2003) point out, because significance is highly dependent on character selection, it was considered less valuable than the holism of the dataset. It is quite possible to have statistically significant results that are inaccurate if the data is limited or biased. Holism was meant to mitigate this issue. However, holism has not been used as intended.

Holism is the idea inherent within the BDIST methodology that datasets should include multiple types of characters (Wood et al., 2003). Ideally, this means that datasets containing different types of morphological data, molecular characters, ecological data, biochemical characters and so on are used. In practice however, this is not the case. Both Wood (Wood, 2002) and Robinson and Cavanaugh (Robinson and Cavanaugh, 1998a) strongly recommended not using molecular characters as they produce incorrect baraminic relationships. It is worth pointing out here that using multiple datasets does not constitute holism. Multiple data *types* are meant to represent holism.

Since most baraminologists are simply recycling secular datasets, it is often very difficult to use a holistic dataset. However, the further baraminology has progressed, the less holism has been applied. A reviewer has objected that holism is still alive and well because multiple datasets are being used. This is spurious for multiple reasons. First, as noted with Wood's (2008b) work on Felidae, many times the datasets are derived from one another and thus use the same characters with a few additions or subtractions. Such datasets add nothing to holism. Second, even if the datasets are not derived from one another, DNA data is rarely used if ever, and ecology data is uncommon. The most common types of data are morphometric and skeletal. By the BDIST's own definition of holism, this is not holistic.

The first use of BDC used four types of data: morphological, ecological, chromosomal, and molecular (Robinson and Cavanaugh, 1998a). Each of the character types had a range of different sub-types. For example, morphology included craniodental, and axial and appendicular skeleton character states. Thus, even when the dataset was revised to remove the molecular characters, the morphological characters were still holistic within the morphology character type. However, it did not take long before holism began to decline. Molecular data mostly went unused after 2002 due to Wood's strong recommendation not to use it (Wood, 2002).

By 2010, holism was all but dead. Wood (2010) published a BDIST analysis that clustered *Homo habilis*, *Homo rudolphensis*, and *Australopithecus sediba* into the human baramin based on craniodental and craniometric characters. This prompted a response by Menton et al. (2010) pointing out that the anatomy of *A. sebida* makes it an australopithecine rather than human.

Wood and O'Micks followed a similar pattern by tentatively assigning *Homo naledi* to the human baramin in 2016 based on craniodental characters, though, in fairness, this was all that was available at the time (Wood, 2016; O'Micks, 2016a). Thus, in spite of dental characters having been shown to be unreliable characters in hominids (Wood, 2013), O'Micks then followed up using a slightly modified BDIST by examining postcranial data and concluded that *H. naledi* was probably not human (O'Micks, 2017). In several follow-up papers, O'Micks demonstrated that, if BDIST is used, *H. naledi* is not in the human baramin, despite strong objections from Wood (O'Micks 2017a; 2017b; Wood, 2017).

Data Reduction Techniques Used in Baraminology

Baraminology studies ideally use data sets with large numbers of characters. Each character is regarded as a separate spatial dimension. As such, each species in a baraminology study is represented by a single point in n-dimensional hyperspace. Therefore, baraminologists can detect baramins in this n-dimensional space based on clustering patterns. Depicting species in one, two, or three dimensions is easy. But beyond three dimensions, this becomes complicated, because we are trying to depict n-dimensional clusters in only three or less dimensions.

The visualization of baramins have used several techniques, including Principle Component Analysis (PCA), Analysis of Patterns (ANOPA), and Multidimensional Scaling (MDS). The goal of these algorithms is to represent n-dimensional data (n being the number of characters in a baraminology data set) in only two or three dimensions. ANOPA and MDS approach these problems in different ways.

PCA

PCA is a widely used data reduction technique, which helps in understanding relationships between traits and discovering patterns within the data. It reduces a larger number of variables into a smaller set of variables with minimal information loss. In baraminology studies, variables represent traits in a baraminology data set. PCA selects the top few (usually 2–4) variables (called principal components), which explain the most variability in the data set, and plots species in 2D or 3D space along the axes of the principal components.

When using PCA there is a tradeoff concerning the number of traits used. If all traits are used in an analysis, the risk of overfitting and false positives increases. However, if only the top few traits are used, which explain the most variation, then information can be lost (Sainani, 2014). This is even more so if the data is highly variable, and the top few principal components can capture a lot less variability. That is why other techniques, such as ANOPA or MDS, are preferred (Wood and Murray, 2003).

ANOPA

For an n-dimensional data set, ANOPA defines a ‘centroid’ point which represents the average of all data points (species) in the data set. Then a vector t_0 is constructed between the centroid and the ‘outlier point,’ defined as the species farthest away from the centroid. The axis between the centroid and species i is the first dimension. Next, a vector d_2 is constructed perpendicularly from t_0 to point x_i. The angle α_r defines the angle of rotation between t_0 and d_2 for any given species. This way each species can be represented by three values: d_{t0}, d_2, and α_r. All species in the study can be depicted in a two- or three-dimensional plot using any two or three of these values. One dimensional ANOPA is also possible, if only the distance between the species and the centroids is analyzed. Clusters of species can then be determined based on the way they group in two- or three-dimensional space (Cavanaugh and Sternberg, 2004).

However, ANOPA has been criticized. It doesn’t provide any means for determining discrete, discontinuous groups (Bolnick, 2006). For example, a paper using ANOPA found that around 20,000 species of the family Asteraceae were discontinuous from all other organisms (Cavanaugh and Wood, 2002). A solution would be to try out any kind of clustering algorithm on three-dimensional data to resolve this problem.

MDS

MDS is a general statistics technique which aims at determining and depicting similarity between objects in a quantitative manner. In baraminology, MDS starts out from a character matrix with n species and m characters. A dissimilarity (or proximity) value, $\delta_{i,j}$ is calculated for each pair of species. Thus, the original m x n character matrix of m rows and n columns (generally called the configuration matrix) is transformed into an n x n proximity matrix. If n > 3, then the n species cannot be depicted in only a two or three dimensional MDS plot, therefore the proximity matrix must undergo dimension reduction. In the final output, species are depicted as objects, for example in three-dimensional space, with $d_{i,j}$ representing the baraminic distance between species i and j (De Leeuw, 2000). The inherent problem with MDS and other dimension reduction (scaling) algorithms is that information is lost and distorted during this process. The distortion of information is called stress. The stress function captures the amount of stress as the data undergoes during reduction:

$$S = \sqrt{\frac{\sum_{i,j}(\delta_{i,j} - d_{i,j})^2}{\sum_{i,j} {d_{i,j}}^2}}$$

It must be emphasized that scaled distances only approximate the true baraminic distances. The stress value describes the goodness of fit between these two sets of values (Wood, 2001). A stress value is calculated for each value of k > 0, where k represents the number of dimensions. Where the stress value is the lowest, that is the optimal number of dimensions. These stress values can be depicted on what is known as a ‘scree’ or ‘elbow plot.’ If the optimal value of k is much greater than three, there is a high chance that clusters will be distorted in the 3D MDS plot.

Dissimilarity values and distance values should show linear correlation; they would be equal in the case of a perfect fit. Smaller stress values correspond to a better fit. In general, stress values less than 0.1 correspond to a good fit. Where the elbow plot shows minimal stress is where the best fit exists between baraminic distances and scaled distances. Visually speaking, this is the ‘elbow’ in the elbow plot.

What must be said about MDS is that it is a descriptive technique, and statistical inference is almost completely absent from it. An MDS plot does not determine baraminic relationships. Sometimes a minimal stress value is not evident. Furthermore, objects will be placed on the MDS plot based on the primary dimension, which may or may not represent the clusters well, and like ANOPA, interpretation of clusters is subjective (Hout et al., 2013).

Testing BDIST

An internal critique

If the BDIST system is accurate, it should, given valid data, be able to detect both continuity and discontinuity within a dataset. Wilson (2020, personal communication) suggested it could be possible using the BDIST to detect discontinuity within breeds of domestic dogs. Thus, a test was devised, using data obtained from Jordana et al. (2006). Their dataset consisted of twenty-five dog taxa without an outgroup. The dataset consisted of 42 morphological and behavioral characters. These numbers are in line with other BDIST analysis such as that of Wood (2014) and Ingle and Aaron (2015).

Using a 0.95 relevance cut-off, all taxa and all characters were retained for analysis. Results were also obtained for cutoff values from 0.75 to 0.9, but they were very much like the results for a cutoff of 0.95. Based on this analysis, six separate groups are proposed (See Figure 1). The first consists largely of working dogs such as the Saint Bernard, Great Dane, the retrievers, and so on. There are nine breeds in this group and they divide fairly cleanly into two subgroups, with the Labrador Retriever and Pointer providing the overlap between the groups. Some of these breeds are also discontinuous with other groups.

The second group is very small, consisting of just the Beagle and Basset Hound. The third group consists of the herding dogs, including the German Shepherd and Shetland Sheepdog. Both of these groups are stand-alone groups. The German Shepherd does positively

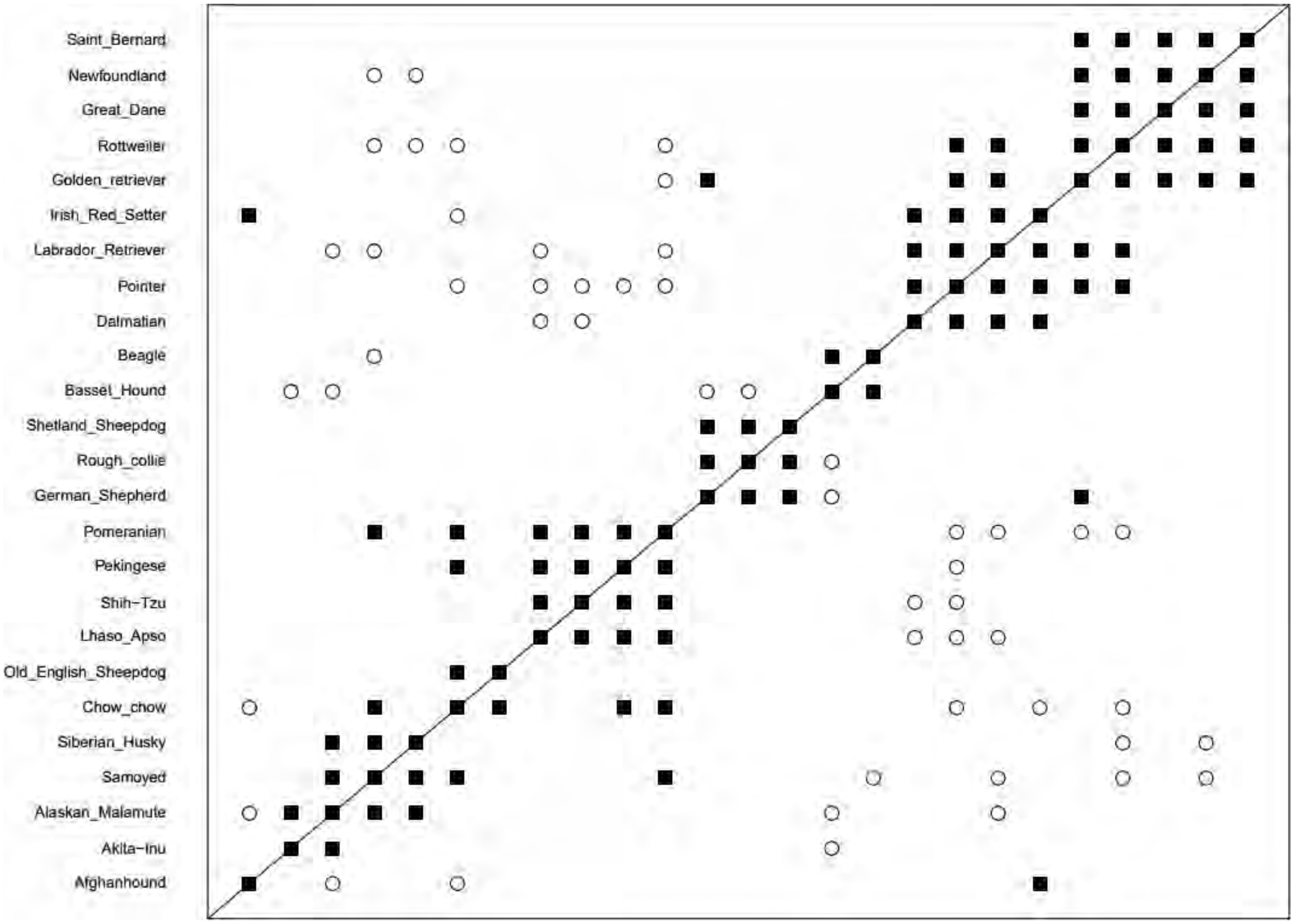

Figure 1. A baraminic distance correlation of the taxa from Jordana et al. and their clustering according to BDIST. Significant positive correlation indicated by filled squares. Significant negative correlation indicated by unfilled circles.

correlate with the Golden Retriever of the working dog group, but not with any other members of the working dog group.

The fourth group consists largely of the smaller toy dogs including the Shih-Tzu, Pekinese, and Pomeranian. The Pomeranian and Pekinese also correlate with the Chow Chow of group five so it is possible group five, which consists of just two breeds, could be merged into group four.

Group six consists of the cold-weather dogs such as the Siberian Husky, Alaskan Malalmute, and so on. Interestingly, the Chow-Chow also correlates with this group, leaving open the possibility that groups four through six could be merged. However, given MDS results (discussed below), this seems unlikely to be correct.

Perhaps more interesting than the potential groupings, given these are all breeds of domestic dogs, is what the BDIST views as significant negative correlation. Twenty-six taxon pairs are considered significantly negatively correlated. Bootstrap values are universally moderate to poor, with only a few in the 80% range and none above 90%. Keep in mind, these are domestic dog breeds. They are members of the same species, *Canis familiaris*, yet the BDIST is showing them as negatively correlated.

Multidimensional scaling is not definitive here, as the taxa show in a cloud of varying different distances, though there are some small apparent clusters (see Figure 2). Minimum stress occurs at nine dimensions. As Wood (2001) points out, this high-dimensional number indicates poor fit between the various data groups. Given how poorly most of the groups are defined, this is not surprising. However, with the strong correlation between the Beagle and Basset Hound and relatively robust bootstrapping results within that group, they could be tentatively placed in their own baramin and leave the remainder of the groups unresolved.

A reviewer has argued that the dogs cluster based on the MDS and thus the BDIST is perfectly validated by these results. This argument is purely subjective. In Figure 2, there are several potentiality regions splitting small clusters. While it is theoretically possible to argue that what Figure 2 indicates is a single cluster, it is equally valid to argue that there are multiple clusters with small breaks between them. MDS is a subjective tool. The reviewer may choose to interpret the results as he pleases, but given how poorly the data fits and the strong negative correlations between taxa, his interpretation seems less likely than the one presented here.

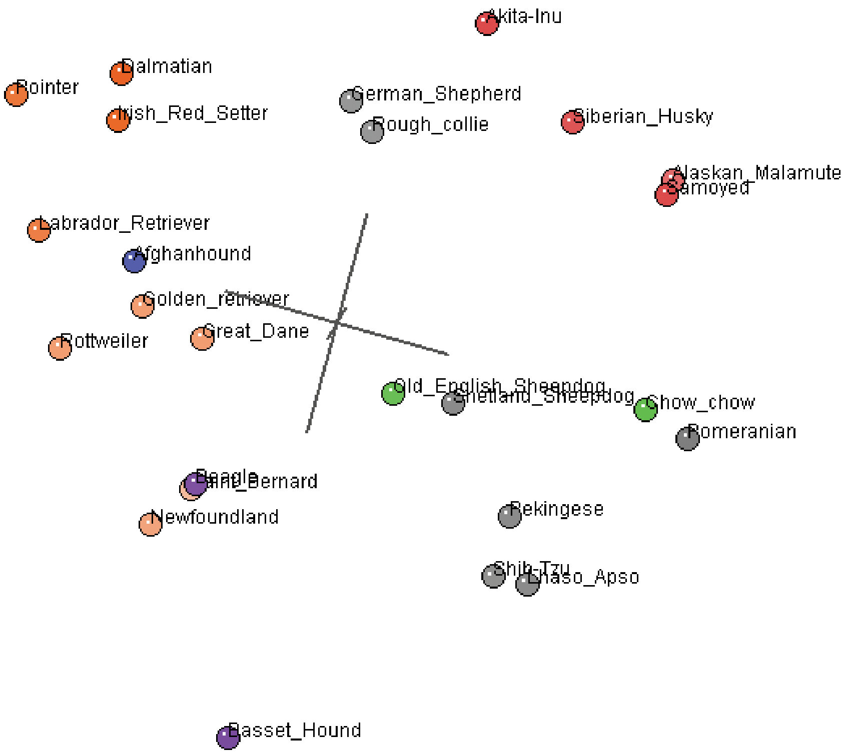

Figure 2. The MDS for the Jordana et al. dataset showing seven clusters. These clusters correspond to the clusters in the graphical output of Supplementary Data File X (Jordana et al., 1999).

Discussion

Of course, the inference drawn from these results, i.e., that different dog groups are unrelated, is incorrect. Empirical evidence from genetics, breeding records and morphology shows that these dogs are members of the same kind. In fact, they are the same species. There is no logical, empirical or Biblical reason to place these dogs in different baramin. Yet the BDIST results lend themselves to such an inference. That inference would be incorrect, but would be accepted if this was a group of organisms about which little was known.

The above analysis illustrates the problems with BDIST and really most purely statistical analysis. They are subjective on multiple levels. The first level of subjectivity is with the data itself, and the potential for bias in collection. The second is within the BDIST calculations, as the equations make assumptions that are not warranted. The third is within the MDS results as these are wholly subjective. The fourth is within the boostrapping convention, as the convention sets the cut-off and is thus subjective. The fifth is with the published baramins as they are interpretations of subjective results. None of these are empirical. While baraminology is a historical science, an empirical foundation would be helpful in ensuring robust results.

It could be argued that the BDIST results are not presenting the toy dogs as a holobaramin, but rather a monobaramin within a larger holobaramin. This is more logical than claiming holobaraminic status certainly. The issue is, many of the dog breeds in question show discontinuity between one another, not similarity. Since as a helpful reviewer pointed out, monobaramins are defined by similarity, not ancestry, it is impossible to argue for a single monobaraminic status here. Thus, explaining this as a monobaramin does not work.

Such aberrant results raise questions about the authenticity of the methodology. There are four options here, none of which are likely to salvage the current iterations of statistical baraminology as a workable methodology. The first option is there is some issue with the data. While this is a possibility, this opens the door to questioning *every* result of the BDIST that has borrowed data from the secular literature. BDIST must assume that the data collected from secular sources is always accurate, else its results are potentially flawed. This would mean that no baraminology study that has used secular data can be deemed empirical, even if it gives expected results. If only expected results are accepted from the method, then confirmation bias is at work and the results cannot be supported logically.

A second option requires rejecting the BDIST methodology. Given its prevalence, the general reluctance to change, and the reviews of this paper, this seems unlikely to occur, at least immediately. As will be shown below, BDC should have been reworked or reconsidered after its first use. Instead, it has become the foundation for the dominant model of baraminology.

The third logical option is accepting the above-presented results as valid. Obviously, this is incorrect. Multiple holobaramins within a single species is something that does not work either with empirical evidence or a Biblical understanding of a baramin.

A fourth potential option leaves some room to potentially salvage the methodology. It could be claimed that the above results are invalid because the taxa in question have undergone generations of artificial selection, making it difficult to determine true discontinuity. This is perhaps the best argument, and one worthy of examining.

Artificial selection, while it does produce a great deal of phenotypic variation as mutations and recessive traits are selected for, does not change a dog into something fundamentally different. For example, even though the Lhasa Apso and the Dalmatian share little in common, it is clear to any observer that both are dogs. The essential nature of the dog kind has not been changed (Joubert, 2011). Thus, discontinuity should not be observed within the canid kind, yet BDIST claims to detect it.

Other incorrect results

Were the above results the only instance of the BDIST producing demonstrably false results, it could be overlooked as an aberration. However, Wood (2012) admitted that the BDC can only detect discontinuity slightly more than half the time. The BDC and its later descendant program, the BDIST, have never been reliably able to determine created kinds.

The very first use of the BDC should have been a warning that all was not well with the methodology. The first use was an attempt to separate catarrhine primates from humans (Robinson and Cavanaugh, 1998a). This is a key test for the validity of the method because we know, Biblically, that apes and humans are not relatives (Genesis 1:26). The original dataset consisted of 204 characters, of which, over half were molecular.

The results were demonstrably false. Humans could not be reliably distinguished from most of the other hominoid primates. Only morphological and ecological data could make such a distinction, which required a post-hoc removal of over half the data from the dataset. Interestingly, no one has repeated this analysis with the newly revised BDIST, though ANOPA was applied to this group with some success (Cavanaugh, 2004). This early failure was an unheeded warning. Instead, it was interpreted as evidence that the genetic data did not need to be considered and the method remained unquestioned.

This first study was followed up the same year by a second study examining the felids. In this study, ecological data was unable to establish discontinuity between felids and the outgroups, while molecular data was (Robinson and Cavanaugh, 1998b). The authors readily accepted the molecular data here because it did not contradict the Scriptures and pointed them to the most logical conclusion, that felids are a holobaramin.

This inconsistency however, between studies, is alarming. It sets up the possibility of a bias accusation because the authors are selecting only data that provides the results they want. Also, illustrating how important character selection is, a later study indicated the felids were, in fact, not discontinuous from non-felids, though the author was quick to defer to the earlier study (Wood, 2008b). Because the results were contradictory, that one study determining felids were a distinct kind and the determined felids were not a distinct kind, it raises questions. Either there is an issue with one or both datasets, or there is an issue with the method.

A reviewer has raised the point that doing multiple studies with felids is an example of statistical baraminology being repeatable. This represents a fundamental misunderstanding of the word "repeatable" in science. When an experiment is deemed "repeatable" it means its results can be replicated by other researchers using similar methods. The felid results use the same method, yet gave disparate results. This is not replication in any scientific sense. It is a repeat of the study, but it does not replicate the results of the original, and, in fact, produces contradictory results. Either felids are a single created kind or they are part of a larger created kind. The two results are fundamentally incompatible.

Despite the change into the BDIST, statistical baraminology has continued to produce Biblically troubling results. A study of the Anserinae (geese and ducks) revealed discontinuity between Cyngini (swans) and the rest of the Anserini (Wood, 2008b). The study was quite robust, with 160 characters used, and low 3D stress for the MDS. Discontinuity surrounded both baramins in the BDIST display results, though MDS displayed a tetrahedral shape. The problem was, there are numerous known hybrids between Cyngini and Anserini, which seems to run afowl of the Biblical implications about bringing forth after their kind (Genesis 1:21). To Wood's credit, he acknowledged this issue and did not break them apart, but the method had failed another test.

A reviewer has objected to the above example, claiming that tetrahedral geometry of the MDS was the reason Wood did not split the Anserini and thus the BDIST worked as intended. This argument is inaccurate because MDS is a purely subjective tool that has no empirical power. Thus MDS cannot be empirically informative in any sense.

Further, the only previous example of tetrahedral shapes in an MDS plot came from Wood's study of Sulidae (gannets and boobies), where Wood (2005) post hoc rejected the dataset because it gave him unexpected results. While it is possible that the tetrahedral shape does indicate that there are issues with the data, this is far from confirmed, especially given the subjectivity of MDS. Rejecting the Anserini results based on tetrahedral geometry is also a post-hoc decision. If the method works, then these post-hoc rejections should not be required on a regular basis. This goes back to the lack of critical evaluation of the dataset. Because there is no critical evaluation, post hoc rejection of results is necessitated.

In 2010 an evolutionary scientist applied BDIST to a dataset of fossil theropods and birds (Senter, 2010). Using an aspect of the BDIST, multidimensional scaling, he was able to demonstrate common ancestry between birds and theropods. Predictably, this prompted a strong response from Wood, which the secular journal permitted him to publish. Wood (2011b) correctly pointed out that multidimensional scaling was not used to determine membership, merely to visualize relationship between taxa. While he conceded that Senter's analysis did lead to a continuum between Mesozoic birds and coelurosaurs, Wood presented an improved analysis of the dataset that pointed to discontinuity between birds and dinosaurs.

Senter (2011) then responded, admitting his original error and, using an improved version of the dataset, found eight very broad "kinds" of dinosaurs, all of which could be related using morphological intermediates. The analysis was robust, using over 100 taxa and nearly 400 characters. Senter actually apologized to Wood and Cavanaugh, who helped him with the study, for, in his mind, utterly destroying creation science. While Senter did not destroy creation science, his work was enough to undermine the BDIST. Senter demonstrated that *scientists can make the BDIST say anything they want it to say*. This subjectivity strips away any vestige of scientific respectability from BDIST. While the BDIST practitioners have published numerous dinosaur and fossil bird baraminologies since Senter's paper (see Cavanaugh, 2011; Wood et al., 2011; Garner et al., 2013), no one has attempted to directly rebut the Senter paper using an unedited BDIST and, indeed, some papers have used BDIST to reach similar conclusions (Doran et al., 2018; McLain et al., 2018).

Can the BDIST method be improved?

Diagnostic features

Another issue is the lack of diagnostic features, which can potentially cloud the analysis. This happens when, for many characters, there are only very few character states, and/or the great majority of species are in the same state for these characters. This kind of character uniformity makes it very likely that many species will match over many characters. This will decrease the baraminic distance between many pairs of species and will lump them together. If species are found in similar habitats and have similar diets, much of their anatomy and physiology may be the same even if they are not from the same baramin. It might be helpful to weigh features generally accepted by the taxonomic community as diagnostic of a group higher than non-diagnostic traits. An example would be increasing the weight of retractable claws in felids since they are much more valuable to identifying cats than habitat choice might be. Experiments would need to be done to determine exact weighing schemes of course.

The issue with weighing characters however, is the potential for bias. However, every attempt to analyze the data uses a weighing scheme, even when all characters are weighed the same (Wheeler, 1986). It is simply conventional to accept equal weighing. It would be useful to experiment with weighing diagnostic characters to see if the BDIST can be improved in that manner, though such would need to be done carefully.

If not BDIST, then what?

BDIST advocates might object that without it, there is no comprehensive baraminology method. This statement is incorrect. There are several other methods available. A system was developed to measure and determine kinds for Answers in Genesis' Ark Encounter and published by Lightner et al. (2011). This system was based mostly on morphology and the cognitum concept developed by Sanders (2010). However, it also incorporated the Marsh's hybridization ideas as the gold standard, based on numerous Biblical passages (incl. Genesis 1:11–12; 8:17–19), as well as using genetic data and some statistics. This is the most holistic method proposed to date, as well as one of the simplest to use, as it is far less labor intensive than some other systems.

There are, however, problems with this method. Organisms that appear similar to one person, may not to another. Further, Wood (2006) points out that hybridization works as an additive, not subtractive, criterion. Lack of hybridization data is not evidence of the organisms being different kinds. While this can potentially be overcome using embryological studies as suggested by Lightner (2007), it remains an issue at present due to lack of data. Perhaps embryological studies would be a good place to focus future baraminological research.

Molecular baraminology

Alternatively, molecular baraminology methods could be proposed. Online databases, such as the NCBI database/EBI/UniProt all contain millions, even billions of sequences. By 2014, the entire genomes of around 14,000 organisms had been sequenced (Land et al., 2015). By 2015, morphological traits comprised only a mere 2% of all characters in secular phylogenetic analyses. The number of nucleotide positions in molecular data sets has also increased greatly (see Figure 3; Lee and Palci, 2015). So much molecular data has been produced that we do not yet have the resources to even process all of it. It would be helpful to begin incorporating this untouched body of data into baraminology.

Although morphology studies will never go away, the area of molecular baraminology stands wide open before us. Up until recently, some baraminology studies have only examined mitochondrial DNA sequences (Robinson, 1997) or small sequences of DNA (Robinson and Cavanaugh, 1998). The mtDNA is only 16–20 Kbp, only a small fragment compared to the Mbp/Gbp-sized genomes of more complex organisms. Much more information can be extracted from the genome in order to assist in the determination of baraminic membership. Besides these, a handful of studies have appeared, which have examined whole proteomes, and which have analyzed and compared the whole genome sequence of different species (Yaugh, 2017; Cserhati, 2019; Cserhati and Alquist, 2019; Cserhati, 2020a).

The advantages of molecular baraminology studies are strong, compared to morphology studies (see Figure 3). As discussed previously, morphology studies are confounded many times by convergence. It is a well-known fact that the genotype largely defines the phenotype. The genotype contains the core information of the makeup of an organism. Whatever change is made in the genome is followed by changes in the phenotype (Cserhati and Tay, 2019). Furthermore, as opposed to morphology studies, where individual characters are subjectively interpreted, genome sequences constitute the raw hereditary material of an organism. Besides being less subjective, genetic studies are also rich in character data (i.e., the number of genes or nucleotides), and thus greatly reduces stochastic error (Heath, 2008). This, however, assumes that the genetic sequences were sequenced objectively and are not contaminated in anyway, which is not always the case.

A relatively new baraminology tool, the Gene Content Method (GCM) compares the overlapping orthologous protein content of different species. The Jaccard Coefficient Value (JCV), defined as the proportion of common orthologous proteins to all proteins between two species, is a measure of how similar two species are genetically. Genes code for proteins, which themselves fulfill functions in the cell, and which express the phenotype of an organism. Therefore, if two species have more genes/proteins in common, they likely belong to the same baramin. A smaller common gene/protein content is an indication that they belong to different baramins (O'Micks, 2017).

However, the coding sequence makes up only 1–2% of the genome, and there is much more genetic information to make use of than this. The ENCODE project found that virtually 100% of the human genome is associated with some biological function (ENCODE, 2012). That is why the Whole Genome K-mer Signature method was developed, in order to do just this (Cserhati, 2020b). It has the added advantage over the GCM in that protein sequences must be experimentally verified (otherwise researchers must rely on lower quality hypothetical or predicted proteins), whereas the whole genome sequence is generally the first thing that researchers determine when studying an organism. Whole genome sequences are thus easier to come by and provide holistic information about an organism.

The weaknesses of molecular studies are: (1) if the proteome is incomplete, or (2) if the genome sequence is low coverage, or (3) has a large percentage of undefined bases. This is akin to the problem of morphology studies which involve fragmented fossil remains (see Figure 3). Thus, care must be taken when viewing the results of molecular studies to ensure that overreliance is not placed on results of insufficient data. Further, the GCM allows users to select their preferred number of clusters. This has huge potential to bias the results and

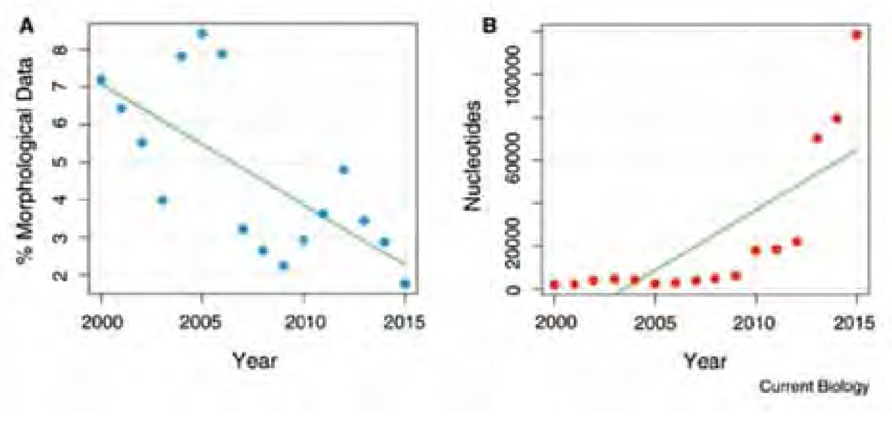

Figure 3. The decline of morphological data sets, and the rise of genetic information used in phylogenetic studies between 2000 and 2015. By 2015, only 2% of studies used morphological characters, whereas the number of nucleotides involved in these studies is increasing exponentially. Figure taken from Lee and Palci (2015).

result in the same selection of data to fit a desired result as the BDIST. Neither method is the answer as yet.

There is a place to combine molecular and morphological studies. Given that the essential nature of an organism has not changed from its creation, despite many variations it has undergone since then (Joubert, 2011), its morphology is indeed informative. Baraminology needs to adapt to the genetic revolution in science and begin incorporating DNA in its analysis, as well as developing new methods to replace the existing ones.

BARCLAY

Recently Wood (2020) has debuted a new baraminology algorithm termed BARCLAY. It has updated from the Pearson coefficient to the Spearman coefficient and incorporated Jaccard distance, along with two new output statistics, PAM and FANNY (Kaufman and Rousseeuw, 1990). The core of the model is still the BDC combined with bootstrapping and multidimensional scaling. Rerunning the domestic dog data presented earlier produced very similar results to those presented above for the traditional BDC. The criticisms presented of the BDIST remain valid for BARCLAY as do those presented against the GCM.

Summary

While the BDIST remains the most popular baraminology method, an honest assessment shows that it is rife with problems. The foundational calculation, the BDC, is flawed because all similarity is considered to be evidence of baraminic relationship. This rules out the possibility of homology being an artifact of design as it will be in many instances in a Biblical model.

Because statistical studies such as the BDIST are highly dependent on the data they are fed, character selection is key to ensuring accurate results. Yet baraminologists almost never select their own data, preferring to rely on the potentially biased character sets produced by evolutionists, which has led to discordant results in the past and undoubtedly will again. However, in molecular studies the DNA sequence is available and the same for all.

The discontinuity/continuity criterion is also limited. There is no reason to *a priori* assume that discontinuity/continuity is a primary criterion of the baramin, and such an assumption brings in a form of the homology problem. Discontinuity should exist between baramins, and continuity should exist within baramins, but it is not necessarily the *a priori* criterion which defines baramins. Attempting to define baramins holistically has its issues and, in practice, has been all but abandoned as a criterion.

The BDIST also fails an internal critique. It demonstrates significant negative correlation between domestic dog breeds as shown above. Further, its published results present contradictory and unbiblical results. It has been used to suggest evolution in dinosaurs and, undoubtedly, could be used to demonstrate evolution in other organisms as well if an evolutionist took the time to do so. As such, it is time for the BDIST to be critically re-evaluated. Changes need to be made to the model, be it diagnostic-character weighing or some other restructuring of the algorithm. BARCLAY is not the answer as it retains all the flaws inherent with BDIST. As it is currently constructed, the model simply does not work.

There is a wealth of potential in baraminology. New methods are rapidly developing. Ideas of Wise, ReMine, and Marsh could also be revisited. It is important to explore that potential and ensure baraminology does not become tied to a system which has a history of producing incorrect results.

References

Aaron, M. 2014. Discerning tyrants from usurpers: A statistical baraminological analysis of Tyrannosauroidea yielding the first dinosaur holobaramin. *Answers Research Journal* 7:463–481.

Bertorelle, G., D. Caramelli, C. Lalueza-Fox, C. Vernesi, M. Lari, A. Casoli, F. Mallegni, B. Chiarelli, I. Dupanloup, J. Bertranpetit, and G. Barbujani. 2003. Evidence for a genetic discontinuity between Neandertals and 24,000 year-old anatomically modern Europeans. *Proceedings of the National Academy of Sciences* 100:6593–6597.

Bolnick, D.I. 2006. ANOPA: 'Statistical' systematics for young-Earth creationists, *Reports of the National Center for Science Education* 26:22–31.

Brooks, D.R., and D.H. McLennan. 1991. *Phylogeny, Ecology and Behavior*. University of Chicago Press, Chicago, IL.

Cavanaugh, D.P. 2004. The cataharrine primates revisited: An ANOPA study. In Sanders, R.W. (editor). *'Discovering the Creator' Proceedings of the Third BSG (Baraminology Study Group) Conference*, R2:13.

Cavanaugh, D.P. 2011. An ANOPA study of coelurosaurian theropods. In Sanders, R.W. (editor). *Proceedings of CBS Annual Conference* 1:1.

Cavanaugh, D.P., and R.V. Sternberg. 2004. Analysis of morphological groupings using ANOPA, a pattern recognition and multivariate statistical method: A case study involving centrarchid fishes. *Journal of Biological Systems* 12(2):137–167.

Cavanaugh, D.P., and T.C. Wood. 2002. A baraminological analysis of the tribe Heliantheae *sensu lato* (Asteraceae) using analysis of pattern (ANOPA). *Occasional Papers of the Baraminological Study Group* 1:1–11.

Chelomina, G.N., and D.M. Atopkin. 2010. Molecular genetic evidence of a deep phylogenetic discontinuity between the Asian and European races of pygmy wood mouse based on the mitochondrial cytochrome *b* gene variation. *Molecular Biology* 44(5):699–708.

Cserhati, M. 2019. Baraminology data filtering method based on entropy measurement and its application in dinosaur and cephalopod data sets. *Journal of Creation* 33(3):55–65.

Cserhati, M. 2020a. A new baraminology method based on Whole Genome K-mer Signature analysis and its application to insect classification. *Journal of Creation* 34(1):86–95.

Cserhati, M. 2020b. Do lizards and snakes form separate apobaramins? *Journal of Creation* 34(1):96–101.

Cserhati, M., and J. Alquist. 2019. Baraminology suggests cryptic relationships among Caprimulgiformes. *Journal of Creation* 33:58–68.

Cserhati, M., and J. Tay. 2019. Comparison of morphology-based and genomics-based baraminology methods. *Journal of Creation* 33(3):10–15.

Cserhati, M., P. Xiao, and C. Guda. 2019. K-mer based motif analysis in insect species across *Anopheles*, *Drosophila* and *Glossina* genera and its application to species classification. *Computational and Mathematical Methods in Medicine* 2019:425–479. doi: 10.1155/2019/4259479.

Darwin, C. 1872. *On the Origin of Species by Means of Natural Selection, or the Preservation of the Favored Races in the Struggle for Life*. 6th edition. John Murray, London, UK.

De Leeuw, J. 2000. Multidimensional Scaling, UCLA Dept. of Statistics Papers, 1–9.

Doran, N.A., M.A. McLain, N. Young, and A. Sanderson. 2018. The Dinosauria: Baraminological and multivariate patterns. In Whitmore, J.H. (editor). *Proceedings of the Eighth International Conference on Creationism*. 8:404–457. Creation Science Fellowship, Pittsburgh, PA.

Eizirik, E., W.J. Murphy, K.Koepfli, W.E. Johnson, J.W. Dragoo, R.K. Wayne, and S.J. O'Brien. 2010. Pattern and timing of diversification of the mammalian order Carnivora inferred from multiple nuclear gene sequences. *Molecular Phylogenetics and Evolution* 56(1):49–63.

The ENCODE Project Consortium. 2012. An integrated encyclopedia of DNA elements in the human genome, *Nature* 489(7414):57–74.

Frair, W. 1967. Some molecular approaches to taxonomy. *Creation Research Society Quarterly* 4:18–22.

Garner, P.A., T.C. Wood, and M. Ross. 2013. Baraminological analysis of Jurassic and Cretaceous Avialae. In *Proceedings of the Seventh International Conference on Creationism*. Volume 7, Article 7. Creation Science Fellowship, Pittsburgh, PA.

Garner, P.A., and J. Asher. 2018. Baraminological analysis of Devonian and Carboniferous tetrapodomorphs. In Whitmore, J.H. (editor). *Proceedings of the Eighth International Conference on Creationism* 8:458–471. Creation Science Fellowship, Pittsburgh, PA.

Gemeinholzer, B. 2008. Phylogenetic networks. In Junker, B.H., and F. Schreiber (editors), *Analysis of Biological Networks*. Wiley-Interscience, Hoboken, NJ.

Gitt, W. 2005. *In the Beginning Was Information*. Master Books, Green Forest, AR.

Heath, T.A., D.J. Zwickl, J. Kim, and D.M. Hillis. 2008. Taxon sampling affects inferences of macroevolutionary processes from phylogenetic trees. *Systematic Biology* 57(1):160–166.

Hillis, D.M., and J.J. Bull. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Systematic Biology* 42(2):182–192.

Hout, M.C., M.H. Papesh, and S.D. Goldinger. 2013. Multidimensional scaling. *WIREs (Wiley Interdisciplinary Reviews) Cognitive Science* 4(1):93–103.

Ingle, M.E., and M. Aaron. 2015. A baraminic study of the blood flukes of family Schistosomatidae. *Answers Research Journal* 8:327–337.

Jordana, J., X. Manteca, and O. Ribo. 1999. Comparative analysis of morphological and behavioral characters in the domestic dog and their importance in the reconstruction of phylogenetic relationships in canids. *Genetics and Molecular Biology* 22(1):49–57.

Joubert, C. 2011. Created kinds and essential natures: A Biblical and philosophical response to evolutionists. *Answers Research Journal* 4:103–112.

Kaufman, L., and P.J. Rousseeuw. 1990. *Finding Groups in Data*. John Wiley & Sons, New York, NY.

Kluge, A.G., and A.J. Wolf. 1993. Cladistics: What's in a word? *Cladistics* 9(2):183–199.

Land, M., L. Hauser, S.R. Jun, I. Nookaew, M.R. Leuze, T.H. Ahn, T. Karpinets, O. Lund, G. Kora, T. Wassenaar, S. Poudel, and D.W. Ussery. 2015. Insights from 20 years of bacterial genome sequencing. *Functional & Integrative Genomics* 15(2):141–161.

Lee, M.S.Y., and A. Palci. 2015. Morphological phylogenetics in the genomic age. *Current Biology* 25(19):R922-R929.

Lightner, J.K. Identification of species within the cattle monobaramin (kind). *Journal of Creation* 21(1):119–122.

Lightner, J.K., T. Hennigan, G. Purdom, and B. Hodge. 2011. Determining the Ark kinds. *Answers Research Journal* 4:195–207.

McConnachie, M., and T.R. Brophy. 2008. A baraminological analysis of the landfowl (Aves: Galliformes). *Occassional Papers of the Baraminology Study Group* 11:9–10.

McLain, M.A., M. Petrone, and M. Speights. 2018. Feathered dinosaurs reconsidered: New insights from baraminology and ethnotaxonomy. In Whitmore, J.H. (editor). *Proceedings of the Eighth International Conference on Creationism* 8:472–515. Creation Science Fellowship, Pittsburgh, PA.

Marsh, F.L. 1941. *Fundamental Biology*. Self-published, Lincoln, NE.

Marsh, F.L. 1964. The Genesis kinds in the modern world. *Creation Research Society Quarterly* 1:30–38.

Maurer, B.A. 1998. The evolution of body size in birds. I. Evidence for non-random diversification. *Evolutionary Ecology* 12:925–934.

Mendel, G. 1866. Experiments in plant hybridization. *Proceedings of the Natural History Society of Brunn* 4:3–47.

Menton, D.N., A. Habermehl, and D.A. DeWitt. 2010. Baraminological analysis places *Homo habilis*, *Homo rudolpfensis*, and *Australopithecus sebida* in the human holobaramin: Discussion (of Wood, T.C. 2010). *Answers Research Journal* 3:153–158.

O'Micks, J. 2016a. Preliminary baraminological analysis of *Homo naledi* and its place within the human baramin. *Journal of Creation Theology and Science Series B: Life Sciences* 6:31–39.

O'Micks, J. 2016b. *Homo naledi* probably not part of the human holobaramin based on baraminic re-analysis including postcranial evidence. *Answers Research Journal* 9:263–272.

O'Micks J. 2017a. Rebutal to "Reply to O'Micks concerning the geology and taphonomy of the *Homo naledi* site" and "Identifying humans in the fossil record: A further response to O'Micks." *Answers Research Journal* 10:63–70.

O'Micks, J. 2017b. Further evidence that *Homo naledi* is not a member of the human holobaramin based on measurements of vertebrae and ribs. *Answers Research Journal* 10:103–113.

O'Micks, J. 2017c. Baraminological classification based on gene content similarity measurement. *Creation Research Society Quarterly 54(1)*:27–37.

Poe, S., and J.J. Wiens. 2000. Character selection and the methodology of morphological phylogenetics. In Wiens, J.J. (editor). *Phylogenetic Analysis of Morphological Data*. Smithsonian Institution Press, Washington, D.C.

ReMine, W. 1990. Discontinuity systematics: A new methodology of biosystematics relevant to the creation model. In Walsh, R.E. (editor). *Proceedings of the Second International Conference on Creationism* 2:207–213. Creation Science Fellowship, Pittsburgh, PA.

Ridley, M. 1986. *Evolution and Classification*. Longman Group Limited, London, UK.

Robinson, D.A. 1997. A mitochondrial DNA analysis of the Testudine apobaramin. *Creation Research Society Quarterly* 33(4):262–272.

Robinson, D.A., and D.P. Cavanaugh. 1998a. A quantitative approach to baraminology with examples from the catarrhine primates. *Creation Research Society Quarterly* 34(4):196–208.

Robinson, D.A., and D.P. Cavanaugh. 1998b. Evidence for a holobaraminic origin of cats. *Creation Research Society Quarterly* 35(1):1–14.

Sainani, K.L. 2014. Introduction to principal components analysis. *American Academy of Physical Medicine & Rehabilitation* 6(3):275–278.

Sanders, R.W. 2010. A quick method for developing a cognitum system exemplified using flowering plants. *Occasional Papers of the BSG (Baraminology Study Group)* 16:1–63.

Sanders, R.W. 2016. Evidence for holobaraminic status of the Verbenaceae (Verbena family). Journal of Creation Theology and Science, Series B: Life Science 6:81–90.

Sanderson, M.J. 1995. Objections to bootstrapping phylogenies: A critique. Systematic Biology 44(3):299–320.

Sanford, J. 2014. *Genetic Entropy*. FMS Publications, Livonia, NY.

Scotland, R.W., S. Kelly, and R. Grenyer. 2014. Phylogenetic trees do not reliably predict feature diversity. *Diversity and Distributions* 20(5):600–612.

Senter, P. 2010. Using creation science to demonstrate evolution: Application of a creationist method for visualizing gaps in the fossil record to a phylogenetic study of coelurosaurian dinosaurs. *Journal of Evolutionary Biology* 23(8):1732–1743.

Senter, P. 2011. Using creation science to demonstrate evolution 2: Morphological continuity within Dinosauria. *Journal of Evolutionary Biology* 24(10):2197–2216.

Siegler, H.R. The magnificence of kinds as demonstrated by canids. *Creation Research Society Quarterly* 11:94–97.

Strong, E.E., and D. Lipscomb. 1999. Character coding and inapplicable data. *Cladistics* 15(4):363–371.

Todd, S.C. A View from Kansas on that Evolution Debate. *Nature* 401:423.

Watson, J.D., and F.H. Crick. 1953. A Structure for Deoxyribose Nucleic Acid. *Nature* 171(4356):737–738.

Wheeler, Q.D. 1986. Character weighting and cladistic analysis. *Systematic Zoology* 35(1):102–109.

Wiley, E.O. 1981. *Phylogenetics.* John Wiley & Sons, New York, NY.

Winsor, M.P. 1994. The Lessons of History. In Scotland, R.W., D.J. Siebert, and D.M. Williams. *Models in Phylogeny Reconstruction*. Clarendon Press, Oxford, UK.

Wise, K. 1990. Baraminology: A young Earth creation biosystematic method. In Walsh, R.E. (editor). *Proceedings of the Second International Conference on Creationism* 2:345–358. Creation Science Fellowship, Pittsburgh, PA.

Wise, K. 1992. Practical baraminology. *Creation Ex Nihilo Technical Journal* 6:122–137.

Wood, T.C. 2002. A baraminology tutorial with examples from the grasses (Poaceae). *Technical Journal* 16(1):15–25.

Wood, T.C. 2005. Visualizing baraminic distances using classical multidimensional scaling. *Origins* 57:9–29.

Wood, T.C. 2006. The current status of baraminology. *Creation Research Society Quarterly* 43(3):149–158.

Wood, T.C. 2008a. Baraminic distance, bootstraps, and BDISTMDS. *Occasional Papers of the Baraminology Study Group* 12:1–17.

Wood, T.C. 2008b. *Issues in creation: Animal and plant baramins.* Wipf & Stock, Eugene, OR.

Wood, T.C. 2009. Natura Facit Saltum: The Case for Discontinuity. In Wood, T.C., and P.A. Garner. *Genesis Kinds: Creationism and the Origin of Species.* Wipf & Stock, Eugene, OR.

Wood, T.C. 2010. Baraminological analysis places *Homo habilis*, *Homo rudolphensis*, and *Australopithecus sebida* in the human holobaramin. *Answers Research Journal* 3:71–90.

Wood, T.C. 2011a. Baraminology, the image of God, and *Australopithecus sebida*. *Journal of Creation Theology and Science, Series B: Life Science* 1:6–14.

Wood, T.C. 2011b. Using creation science to demonstrate evolution? Senter's strategy revisited. *Journal of Evolutionary Biology* 24(4):914–918.

Wood, T.C. 2012. What can baraminic distance correlation really tell us? In Francis, J. (editor). *Proceedings of CBS Annual Conference* 2:5–6.

Wood, T.C. 2013. The value of dental characters for resolving the baraminic status of *Australopithecus sebida*. In Francis, J. (editor). *Proceedings of CBS Annual Conference* 3:4–5.

Wood, T.C. 2014. Two kinds of varmints: Preliminary baraminological analysis of racoons (*Procyon lotor*) and opossums (*Didelphis virginiana*). *Journal of Creation Theology and Science, Series B: Life Science* 4:12–18.

Wood, T.C. 2016. An evaluation of *Homo naledi* and "early" *Homo* from a young age creationist perspective. *Journal of Creation Theology and Science, Series B: Life Sciences* 6:14–30.

Wood, T.C. 2017. Identifying humans in the fossil record: A further response to O'Micks. *Answers Research Journal* 10:57–62.

Wood, T.C. 2020. Baraminology and cluster analysis. *Answers Research Journal*, in press.

Wood, T.C., and Murray, M.J. 2003. *Understanding the Pattern of Life: Origins and Organization of the Species.* Broadman & Holman, Nashville, TN.

Wood, T.C., M. Ross, and P.A. Garner. 2011. Preliminary baraminological analysis of Jurassic and Cretaceous Avialae. In Sanders, R.W. (editor). *Proceedings of CBS Annual Conference* 1:25–26.

Wood, T.C., K.P. Wise, R. Sanders, and N. Doran. 2003. A refined baramin concept. *Occasional Papers of the BSG (Baraminology Study Group)* 3:1–14.

Yaugh, A. 2017. Baraminological analysis of a set of Archaea species based on genomic data. *Creation Research Society Quarterly* 53:140–154.

Creation Research Society Quarterly 2022 58:193–203

Pinniped Molecular Baraminology

Matthew Cserhati and Emory Moynagh

Abstract

Pinnipeds are a group of semi-aquatic animals which live on land, but hunt for food in the water. As such, they constitute an apobaramin, similar to bats, which are the only flying mammals. Differentiating between seals (Phocidae), sea lions, fur seals (Otariidae), and walruses (Odobenidae) is therefore an interesting task for baraminology. A morphology-based baraminology study showed discontinuity between phocids and all other pinnipeds. Hybridization results also show that many different phocid genera are capable of interbreeding.

Using a gamut of molecular baraminology tools, the mitochondrial DNA, whole genome sequences and proteomes of several dozen pinniped species were studied. The analysis of mtDNA sequence similarity shows that Phocidae, Otariidae, and Odobenidae form their own distinct groups The whole genome analysis shows discontinuity between Otariidae and Phocidae and also Odobenidae. However, discontinuity between Odobenidae and Phocidae is not so clear. Looking at differences in gene content shows discontinuity between Otariidae and the other two pinniped groups. Discontinuity also exists between Odobenidae and the majority of phocids, except for *Leptonychotes weddelli*. However, a closer examination of orthology groups unique to *L. weddelli*, *Odobenus rosmarus*, and the outlier species, *Mustela erminea*, show that *L. weddelli* shows continuity with phocids, whereas *O. rosmarus* shows discontinuity with this group.

Ultimately, the morphological evidence, hybridization data, and the results from the molecular baraminology analyses support three separate pinniped holobaramins at the level of the family. There also appear to be several phocid lineages in the subfamily Monachinae, based on mtDNA analysis, such as *Lobodon*, *Mirounga*, and *Monachus*.

Key Words: seals, sea lions, fur seals, walrus, hybridization, mitochondrial DNA, whole genome analysis, gene content method

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Introduction

Pinnipeds are interesting animals, living both on land and in the sea. They are carnivorous and usually live along the coastlines in the Northern and Southern Hemispheres. The name 'pinniped' is derived from the Latin 'pinna,' which means feather, and 'pedis,' which means foot. Thus, these animals are 'feather-footed.' Their bodies are covered in fur, and have thick layers of fat to protect themselves from the cold. Pinnipeds make up about 28% of the diversity of marine mammals, made up of 34–36 species in three families: Phocidae (seals), Otariidae (fur seals and sea lions) and Odobenidae (walruses). In Figure 1 we can see an example of a seal (A), a walrus (B), a fur seal (C), and a sea lion (D). Some scientists estimate that in the past, more species existed than we have today.

Figure 1. A. seal (Phocidae), B. walrus (Odobenidae) C. fur seal (Otariidae) D. sea lion (Otariidae)
Animal images: The web references for the images of the pinnipeds in Figure 1 are as follows: seal (A): publicdomainpictures.net/en/view-image.php?image= 207005&picture=seal; walrus (B): commons.wikimedia.org/wiki/File:Close_up_of_ head_of_young_bull_walrus_marine_mammal_in_water_odobenus_rosmarus.jpg; fur seal (C): openfotos.com/view/fur-seal-1360; sea lion (D): goodfreephotos.com/animals/ mammals/california-sea-lion.jpg.php.

Walruses are characterized by their prominent, elongated upper-canine teeth, or tusks, and large size. Together with phocids, they do not have external ears, in contrast with otariids. Some argue for three species of extant walruses: *Odobenus rosmarus rosmarus* from the North Atlantic, *O. rosmarus divergens* from the North Pacific, and *O. rosmarus laptevi* from the Laptev sea. Two groups of walruses can be distinguished, namely the extinct Dusignathinae, and Odobeninae, which includes the living species and some more extinct species (Berta et al., 2015, pp. 27–50). A species of tuskless walrus, *Titanotaria orangensis*, has recently been discovered in the Capistrano Formation of Orange County, California (Magallanes et al., 2018).

Otariids and walruses have hind limbs that they can use to walk on land, whereas phocids do not. Both phocids and walruses use their hind limbs to propel themselves in the water, whereas otariids use their front legs. Phocids are characterized by thick mastoid bones, large endotympanic bones, an exerted pelvis, and large ankle bones. Within Otariidae, sea lions can be distinguished by their rounder snouts and shorter hair, as opposed to the more pointed snouts and thicker fur of fur seals.

Within Phocidae, there are two subfamilies, Phocinae, or the Northern seals, and Monachinae, or the Southern seals. Monachinae have 34 pairs of chromosomes, whereas Phocinae have either 32 or 34. The elephant seals, from the genus *Mirounga*, stand out among the other seals. There are two species, the Northern elephant seal (*Mirounga angustirostris*) and the Southern elephant seal (*Mirounga leonina*). They resemble walruses somewhat with their large, furless bodies, an elephant-like proboscis on the male, and the ability to pull themselves upright. They also have special whiskers, called vibrissae, to help them find food. Elephant seals differ from walruses based on their diet: they are deep-sea divers which feed on fish, cephalopods, sharks, and rays, whereas walruses prefer shallow water and eat shellfish, marine arthropods, some corals, and will also scavenge from other pinnipeds, birds, or even whales. Differences between walruses and elephant seals include facial features and flipper anatomy.

Based on these similarities and differences it is an interesting question as to whether elephant seals form a holobaramin with all other seals or with walruses. A 'holobaramin' denotes all species which constitute a single baramin, or created kind. Genetically, walruses have a diploid karyotype of 32 chromosomes, whereas Otariidae has 36. Within Phocidae, this number varies. In the genus *Phoca* the karyotype can be 32, whereas in *Erignathus* it can be 34. This suggests the presence of four possible pinniped holobaramins (Arnason, 1977). However, Árnason et al. propose that the 34 chromosome karyotype is ancestral to the 32 chromosome one, via chromosomal fusion (Arnason et al., 1977).

Pinnipeds also pose a very interesting question to the baraminologist. Bats are the only flying mammals, and thus display stark discontinuity with all other mammals. Similarly, since pinnipeds are semi-marine mammals, they also show discontinuity with all other mammals. Such a group is called an apobaramin, and may be composed on one or more holobaramins. Studying apobaramins is useful when determining the number of holobaramins within a set of species in a study. The big question here is, do pinnipeds form a single or multiple holobaramins?

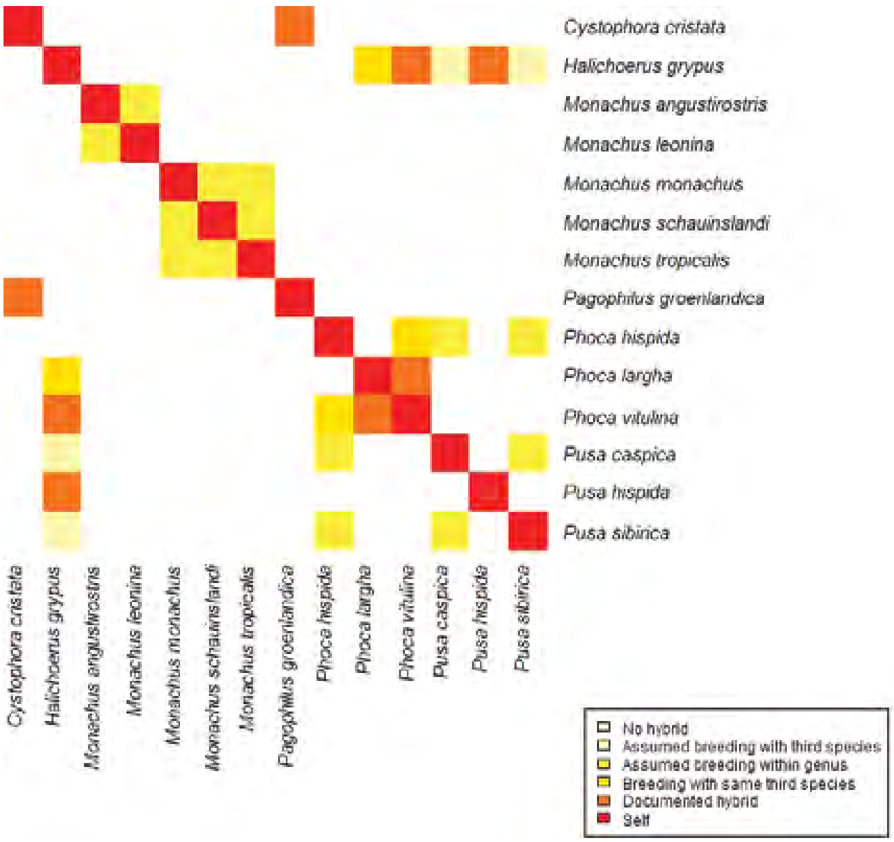


Figure 2. Hybridogram showing baraminic relationships between different species from the family Phocidae. All species can mate with themselves, as shown in red. Orange indicates documented hybridization between two given species. Dark yellow denotes two species both interbreeding with a third species. Yellow indicates breeding assumed within the same genus. Tan indicates that if a species can breed with another species, it is assumed that it can also breed with any other species from the genus that the second species belongs to. *Monachus tropicalis* is extinct.

Biblical Considerations

Pinnipeds are not specifically mentioned in the Bible, and it is also questionable as to which day they were created on, and whether they were on the Ark or not during the Flood in Genesis 6. Pinnipeds are adapted to moving around in the water, but mate and raise their young on land. Since they go into the water only temporarily to hunt for food, pinnipeds are most likely to have been created on Day 6 of Creation Week together with land animals. Thus, they could also have been taken on board the Ark during the Flood, especially since they breathe air through their lungs like other mammals. Due to their aquatic lifestyle, they could have possibly survived outside the Ark during the duration of the Deluge (Lightner et al., 2011). Whereas most seals live along ocean coastline, the existence of the Caspian seal (*Pusa caspica*) and the Baikal seal (*Phoca sibirica*) along the coasts of the inland Caspian Sea and Lake Baikal (McLaren, 1960) are testimonies to a global Flood that had once covered the Earth.

Previous Pinniped Baraminology and Phylogenetic Studies

Previous studies include analysis of a morphological data set including 196 characters for 21 pinniped species by Wood (2008, pp. 24–27). This study showed discontinuity between phocids and all other pinnipeds. While it also showed lack of continuity between the subfamilies Phocinae and Monachinae within Phocidae, it did not demonstrate any discontinuity between these two groups. This suggests that they are both monobaramins within the phocid holobaramin. A 'monobaramin' denotes either part of, or the entire holobaramin. This means it can also denote a specific lineage or subgroup within a holobaramin.

Similarly, Davis et al. (2004), who separate Odobenidae and Otariidae from Phocidae, show distinct differences between Monachinae and Phocinae. This was based on the analysis of the alignment and comparison of twelve protein-coding mitochondrial genes, including ATP synthase subunits 6 and 8, Cytochrome oxidase subunits I, II, and II, and NADH dehydrogenase subunits 1, 2, 3, 4, 4L, and 5.

Hybridization Data

Hybridization data is available for pinnipeds, but it is limited. Figure 2 shows the hybrid relationships between several species within Phocidae. There have been attempts to hybridize pinnipeds and non-pinnipeds, such as otters breeding with female seals (Heather et al., 2010), or male elephant seals attempting to breed with female fur seals (Best et al., 1981). However, in both cases, females usually died and no hybrids have been documented as yet. This is evidence that seals are discontinuous with otters (Mustelidae), and that probably otariids are discontinuous with phocids, suggesting that there are at least two holobaramins within pinnipeds.

Gray seals (*Halichoerus grypus*) hybridize with two other species: the harbor seal (*Phoca vitulina*) and the ringed seal (*Pusa hispida*) (Iverson et al., 1993; Savriama et al., 2018). Hybridization data also exists between the harp seal (*Pagophilus groenlandica*) and the hooded seal (*Cystophora cristatata*), producing live offspring (Moynagh, 2018). The harbor seal's breeding with the gray seal has been observed, but full-grown hybrids have not. However, there is no reason to doubt, based on Lightner's definition of hybridization success (i.e., several cell divisions in the zygote), that this is a successful hybridization (Lightner, 2007). Based on this, we can safely assume that the harbor seal and the ringed seal are related since they both breed with the gray seal. However, we can go a step further. Since breeding between species of different genera has been documented, we can extrapolate to state that all members of both genera are likely related. Thus, the gray seal is also related to the nerpa (*Pusa sibirica*) and the Caspian seal (*Pusa capsica*).

The genera *Pusa* and *Pagophilus* both used to be lumped into the genus *Phoca*. Therefore, it seems that several genera within Phocidae (*Phoca*, *Pagophilis*, *Pusa*, *Cystophora*, *Halichoerus*) are all related based on hybrid data, an indication of continuity within this family.

Principle of Analysis

The goal of this paper is to discern the number of baramins within the pinniped apobaramin. More specifically, do all pinnipeds make up a single holobaramin, or are phocids, otariids, and odobenids separate holobaramins within Pinnipedia? Do phocids belong to multiple holobaramins, as suggested by hybridization results? Are the subfamilies Monachinae and Phocinae separate baramins, or two separate lineages within Phocidae? As morphological comparisons might suggest, do walruses form a holobaramin with elephant seals?

Since morphological analyses have already been performed on pinnipeds, these studies were augmented with molecular studies to either challenge or confirm the previous results. The mitochondrial DNA (mtDNA) sequence is available for 27 pinniped species, and the whole genome sequence (WGS) for twelve. Therefore, these sequences could be compared with one another to elucidate molecular baraminic relationships between pinnipeds.

Materials and Methods

Sequences

MtDNA was downloaded for one species from the family Odobenidae, nine from Otariidae, and 17 from Phocidae from the National Center for Biotechnology Database (NCBI) Organelle Genome database at ncbi.nlm.nih.gov/genome/browse#!/organelles. The accession numbers for these sequences can be found in Supplementary data file 1, on the tab 'mtDNA.'

The proteomes for nine pinniped species and *M. erminea* were downloaded from the NCBI database. RefSeq proteins were selected for the comparison. The species' Latin name, family, number of proteins, mapped proteins, unique orthology groups, and taxid are available in the tab "Species, proteomes" in Supplementary File 3 online.

WGS for twelve pinniped species were also downloaded from the NCBI database at ncbi.nlm.nih.gov/genome. The accession number of these sequences are also listed in Supplementary data file 1, on the tab 'genomes.'

All supplemental data files and figures are available on github at github.com/csmatyi/pinnipeds.

Software

R version 4.0.3. was used to generate the heat maps in Figures 3, 4, and 5 using the heatmap command and the 'single' clustering method for mtDNA and gene content (GC) analysis, and the 'complete' method for the WGKS analysis. The fviz_nbclust function was used to create the elbow plots using the ‹wss› method. Significance levels were calculated in R using the ‹pnorm› function.

Protein sequences in the proteome data sets were mapped to Orthology Groups using the online Galaxy server

Figure 3 *(right)*. Heatmap showing baraminic relationships between Phocidae, Otariidae, Odobenidae, and *Mustela erminea*, the outlier species, based on mitochondrial DNA sequence similarity. Each colored pixel represents the global sequence similarity of a pair of species. Brighter, redder colors represent species which are more similar to one another, hence they are continuous with one another. Lighter, yellow colors represent species which are less similar to one another, and hence are discontinuous with one another.

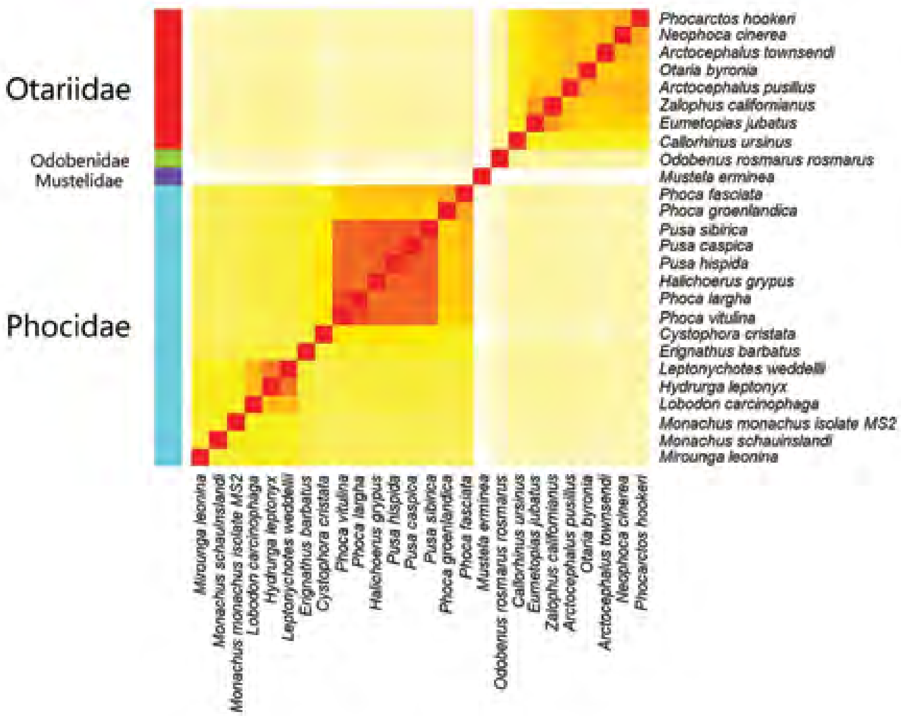
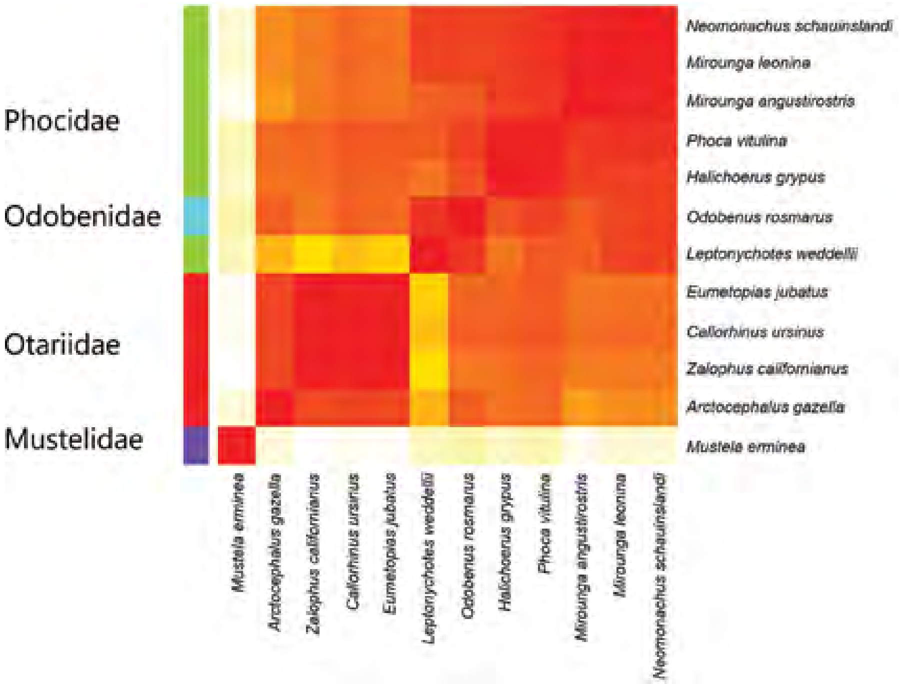


Figure 4 *(right)*. Heatmap showing baraminic relationships between Phocidae, Otariidae, Odobenidae, and *Mustela erminea*, based on the Whole Genome K-mer Signature analysis. Each colored pixel represents the Pearson Correlation Coefficient of a pair of species. Brighter, redder colors represent species which are more highly correlated with one another, hence they show continuity with one another. Lighter, yellow colors represent species which are less correlated with one another, and hence show discontinuity with one another.



tool at usegalaxy.org (Afgan et al., 2018). Comparisons between Orthology Group Identifiers (OGIs) between phocids and *L. weddelli*, *O. rosmarus*, and *M. erminea* were performed using the Venn diagram tool of the Vlaams Instituut voor Biotechnologie (VIB) at bioinformatics.psb.ugent.be/webtools/Venn.

Functional gene analysis

Functional analysis of the 119 proteins unique to *L. weddelli* was performed at the PANTHER database website at pantherdb.org. A tab-delimited PANTHER Generic Mapping file (NCBI accession plus PANTHER ID) was generated by performing an HMM search with them against all of the PANTHER HMM profiles, according to the protocol described in Mi et al. (2019). Version 3.3 (Nov 2019) of the HMM software was used (Eddy, 2011). The PANTHER HMM libraries were downloaded from ftp.pantherdb.org/panther_library/current_release (version 16.0), on March 30, 2021. Out of the 119 unique *L. weddelli* proteins, 112 were matched to 93 PANTHER functional IDs. These functional IDs are listed in Supplementary File 4 along with their functional classification. The Generic Mapping file was uploaded to the PANTHER database website for functional classification. Bar charts were produced showing the biological processes and protein classes that the 119 unique *L. weddelli* proteins mapped to.

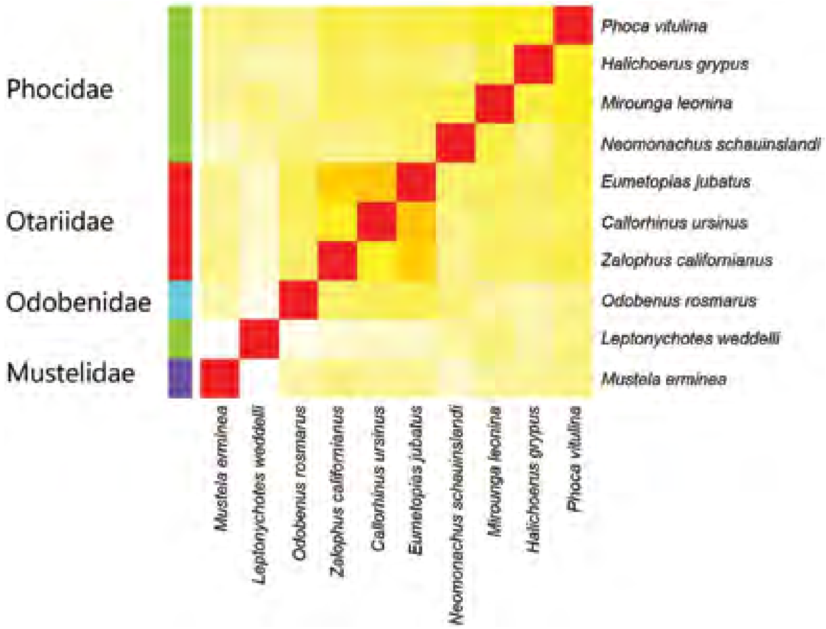


Figure 5. Heatmap showing baraminic relationships between Phocidae, Otariidae, Odobenidae, and *Mustela erminea*, based on the GC method analysis. Each colored pixel represents the Jaccard Coefficient Value of a pair of species. Brighter, redder colors represent species which are more similar to one another, hence they are continuous with one another. Lighter, yellow colors represent species which are less similar to one another, hence showing discontinuity with one another.

Results and Discussion

Mitochondrial analysis

A multiple alignment of 26 of the 27 pinniped mtDNA sequences was created and the sequence identity matrix was visualized in a heatmap in Figure 3. *Mustela erminea* (the short-tailed weasel) was used as an outlier. The identity matrix has a Hopkins clustering value of 0.784 which is good clustering quality.

The elbow plot in Supplementary Figure 1 shows a minimal total within sum of squares (TWSS) value at six clusters. However, the decrease from 0.279 at four clusters to 0.231 at five is an insignificant decrease of less than 5%. If we increase the number of predicted clusters to 5, then *O. rosmarus* clusters with *M. erminea*, and *Phoca groenlandica* and *Phoca fasciata*, are separated from the other *Phoca* species, clearly a bad clustering result. Thus, it appears that there are four baramins represented in the data set.

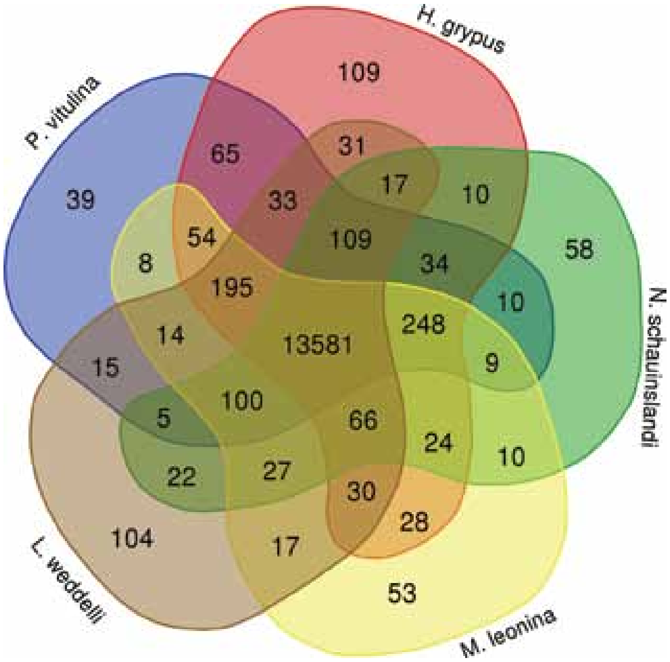


Figure 6. Venn diagram showing overlapping Orthology Group Identifiers between *P. vitulina*, *H. grypus*, *N. schauinslandi*, *M. leonina*, and *L. weddelli.*

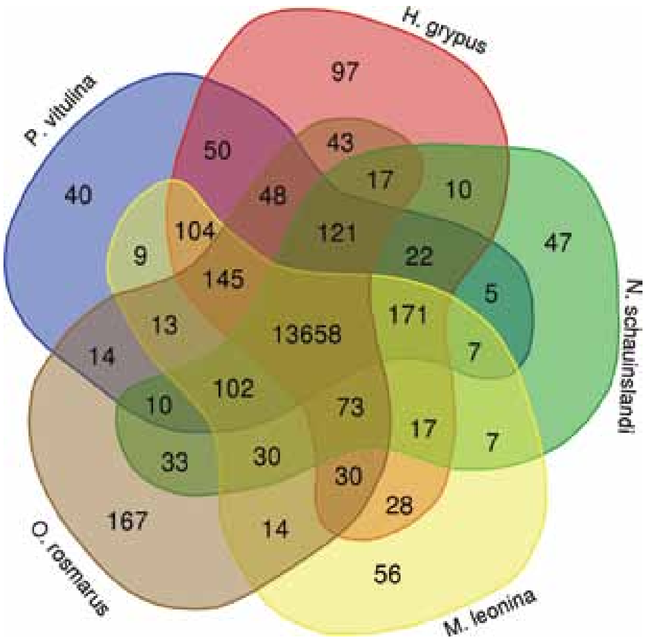


Figure 7. Venn diagram showing overlapping Orthology Group Identifiers between *P. vitulina*, *H. grypus*, *N. schauinslandi*, *M. leonina*, and *O. rosmarus.*

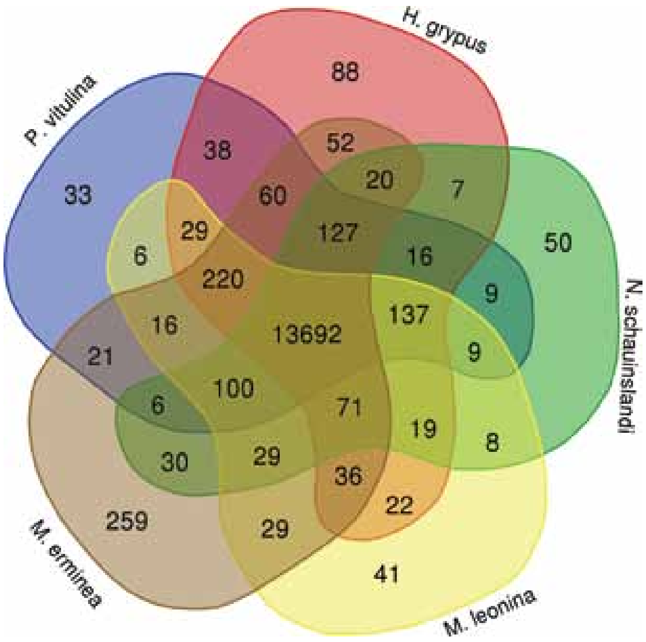


Figure 8. Venn diagram showing overlapping Orthology Group Identifiers between *P. vitulina*, *H. grypus*, *N. schauinslandi*, *M. leonina*, and *M. erminea.*

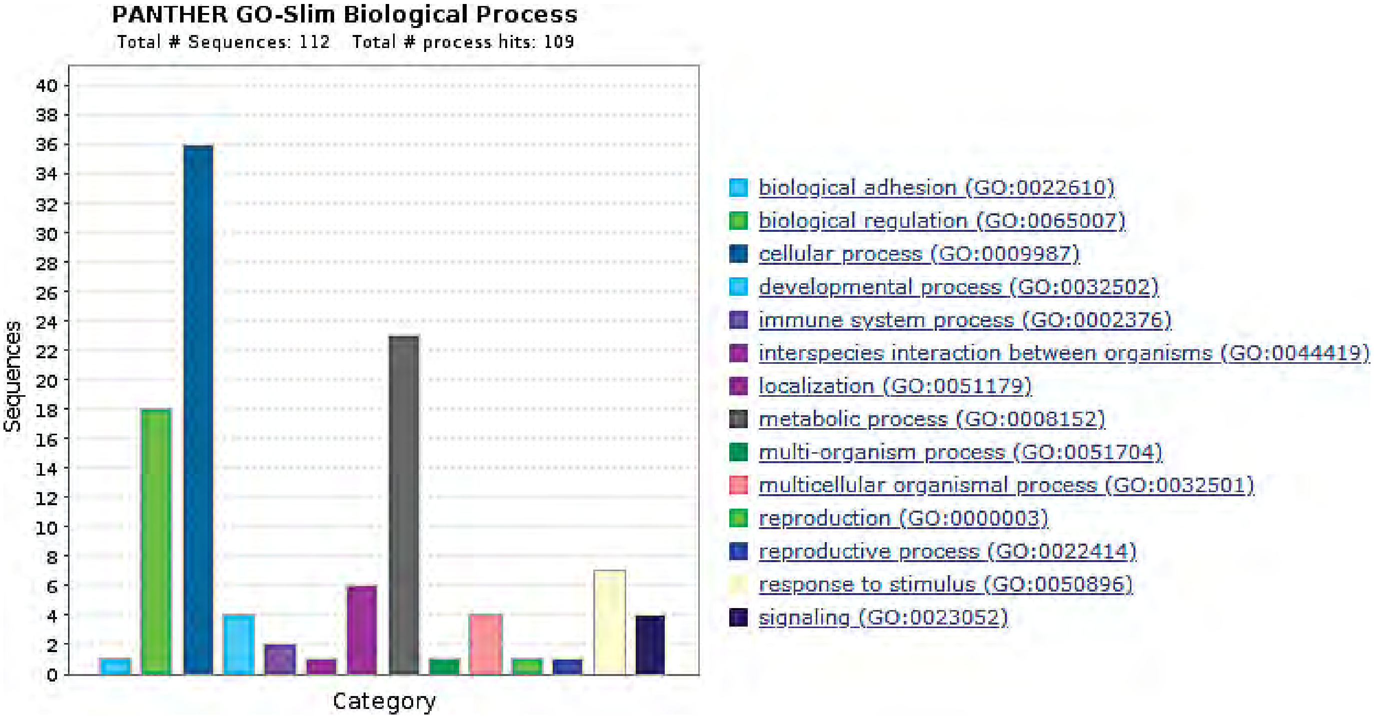


Figure 9. Different categories of PANTHER GO-Slim Biological Processes that the 119 unique *L. weddelli* proteins are enriched in.

The odobenid *O. rosmarus rosmarus* and the outlier, *M. erminea*, are the only singleton species within their own group.

The first larger group includes eight species of otarids: *Arctocephalus pusillus*, *Arctocephalus townsendi*, *Callorhinus ursinus*, *Eumetopias jubatus*, *Neophoca cinerea*, *Otaria byronia*, *Phocarctos hookeri*, and *Zalophus californianus*. This group is statistically significant at a p-value of 8.53E-26.

The second large cluster contains 16 phocids, including several species from ten genera in two subfamilies. From Phocinae: *Crystophora*, *Erignathus*, *Halicheorus*, *Phoca*, and *Pusa*. From Monachinae: *Hydrurga*, *Leptonychotes*, *Lobodon*, *Mirounga*, and *Monachus*. Apparently, Phocinae and Monachinae separate into two lineages based on the mtDNA results. Furthermore, three species of Lobodontine seals (the crabeater seal, *Lobodon carcinophaga*, the leopard seal, *Hydrurga leptonyx*, and the Weddell seal, *Leptonychotes weddelli*) also separate from the genera *Monachus* and *Mirounga*. Despite these different lineages, phocids apparently form a statistically significant holobaramin with a p-value of 4.83E-46.

Lastly, another mitogenomic study based on the alignments of the twelve heavy-chain mitochondrial genes (ATPase6, ATPase8, COI, COII, COIII, cytb, NADH1, NADH3, NADH4, NADH4L, NADH5, and NADH6) was performed by Arnason et al. (2002). 9,882 base pairs and 3,294 amino acids were aligned. These results showed significant discontinuity between pinnipeds and all other mammals, reinforcing the apobaraminic status of Pinnipedia. However, this study seemed to cluster Otariidae together with Odobenidae.

The sequence accession numbers and the results of the mtDNA analysis are available in Supplementary File 1.

Whole genome K-mer analysis

The WGS of six phocids (four otariids, *O. rosmarus*, and the outlier species, *M. erminea*) were downloaded from NCBI. A list of all species and the web address of their genome is listed in Supplementary File 2. The results of the WGKS analysis are also listed in this file: the Pearson Correlation Coefficient (PCC) matrix, the clusters, and the cluster statistics.

The PCC matrix has a Hopkins clustering value of 0.673, which denotes fair clustering. The PCC matrix was transformed into a heatmap to visualize baraminic relationships between the pinniped species and the outlier and can be seen in Figure 4. *M. erminea* clearly separates from all of the pinniped species. The four otariids also show statistically significant continuity within their own group and discontinuity with all other pinnipeds (p = 1.45E-4). The elbow plot in Supplementary Figure 2 shows a sharp drop between one to three

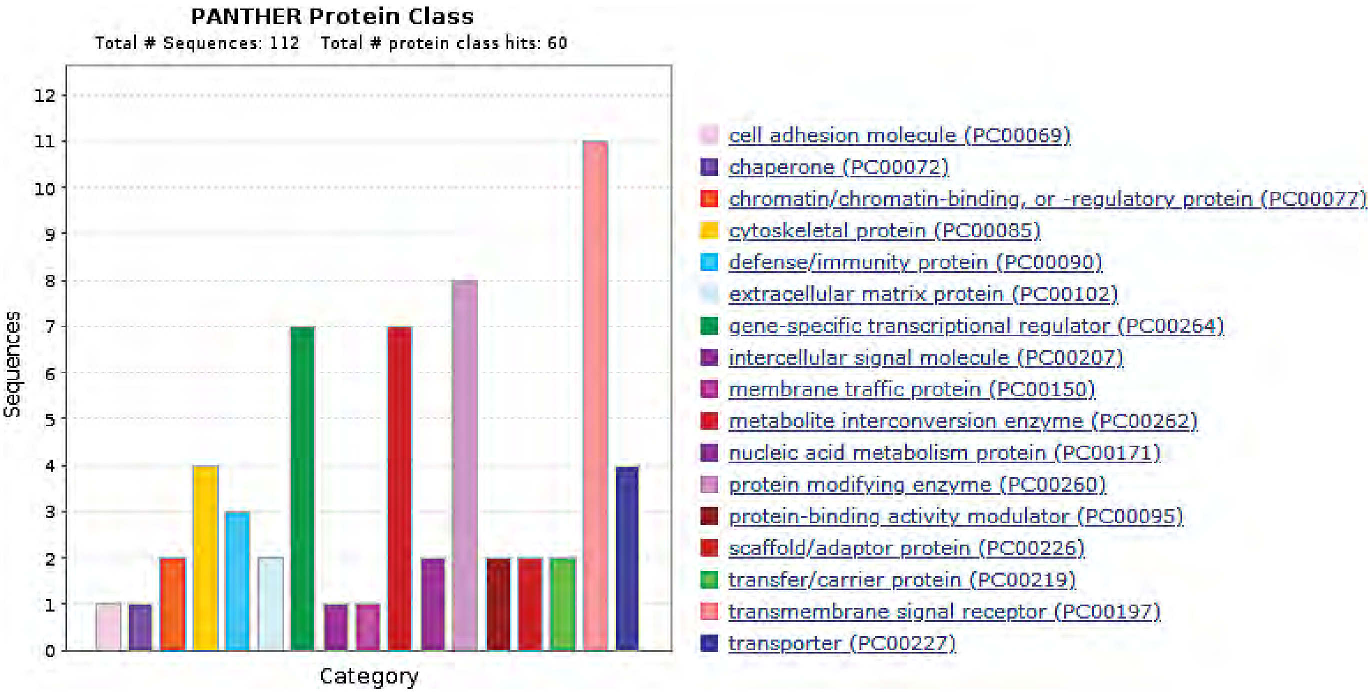


Figure 10. Different categories of PANTHER Protein Classes that the 119 unique *L. weddelli* proteins are enriched in.

clusters. However, the TWSS only decreases from 0.0015 to 0.0091 between three and four clusters. This difference (0.0076) is less than 5% of the TWSS value at one cluster (0.01835).

A more difficult question to answer is, do *O. rosmarus* and the phocids form a single holobaramin, or are they separate? The former result would contradict the mtDNA results where all three pinniped families were separate. To complicate things further, *O. rosmarus* is nested between *L. weddelli* and all other phocid species. Whereas *L. weddelli* has a mean PCC of 0.982±0.001 with the four otariids, it has a mean PCC value of 0.992±0.002 with the five other phocid species. However, it has a PCC value of 0.996 when paired with *O. rosmarus*. Supplementary Figure 2 seems to show an optimum of three clusters.

In order to clarify this discrepancy, further analysis is needed. Therefore, besides the WGKS algorithm, the Gene Content (GC) method was also used to analyze the pinniped species involved in this study.

Gene content analysis

The whole proteomes of five phocids (three otariids, *O. rosmarus*, and the outlier species, *M. erminea*) were downloaded from NCBI. The GC method was run according to the description in O›Micks (2017). The list of species, and the number of proteins, matched Orthology Groups (OG), Jaccard Coefficient Value (JCV) matrix, the putative clusters, and the cluster statistics are available in Supplementary File 3.

The Hopkins clustering statistic has a value of 0.529, which denotes acceptable, but not good clustering. The JCV matrix was visualized in a heatmap, seen in Figure 5. The elbow plot in Supplementary Figure 3 shows four optimal clusters. Statistics were calculated for five clusters. The three otariids (*C. ursinus*, *E. jubatus*, and *Z. californianus*) all form a statistically significant cluster, continuous among themselves and discontinuous with all other species. Four phocids (*H. grypus*, *M. leonina*, *N. schauinslandi*, and *P. vitulina*) group together, but are again conspicuously separated from *L. weddelli*, which was put into its own cluster, as was *O. rosmarus*.

Upon closer examination of the JCV matrix we can see that the mean JCV between *L. weddelli* and otariids is 0.937±0.001, whereas the mean JCV with phocids is 0.945±0.003. This would indicate that *L. weddelli* belongs to the phocid baramin. The JCV between *L. weddelli* and *O. rosmarus* is only 0.933. The mean JCV between *O. rosmarus* and all five phocids is 0.942±0.006. The mean JCV between *O. rosmarus* and the phocid species excluding *L. weddelli* is 0.945±0.003. This would seem to indicate that *O. rosmarus* forms a holobaramin with phocids. Just like with the WGKS results, the GC method also shows a discrepancy between *L. weddelli* and all other phocids.

The results of the GC analysis can be found in Supplementary File 3.

It is interesting to note that neither the mtDNA, nor the WGKS, nor the GC analysis showed that elephant seals are continuous with *O. rosmarus*. However, as we have seen here, the situation is not so clear with *L. weddelli*. Thus, closer attention was given to this species to see what genetic factors could be behind the special baraminic position of *L. weddelli*.

Examination of unique gene content of *L. weddelli*

In order to understand why *L. weddelli* is somewhat different from all other phocids genetically, those OGI were analyzed which belonged uniquely to *L. weddelli* compared to the phocids *H. grypus*, *M. leonina*, *N. schauinslandi*, and *P. vitulina*. *L. weddelli* had 104 such OGI›s mapped to 119 proteins, listed in Supplementary File 4.

Figure 6 shows the overlap of OGIs between *L. weddelli* and the other four phocids. As we can see, even another phocid species, *H. grypus* has more unique OGIs than does *L. weddelli* (109). When we compare the 104 unique OGIs of *L. weddelli* with the mean number of unique OGIs from the other phocids, we see that the z-score is only 1.28, which is statistically significant only at the 20.1% confidence level (see Table 1).

Figure 7 shows that *O. rosmarus* has 167 unique OGIs compared to the four

Table 1. Statistics showing differences in JCV values between four phocids and *Loptonychotes weddelli*, *Odobenus rosmarus*, and *Mustela erminea*.

Species	No. unique OGIs	Mean no. OGIs	St. dev.	Z-score	Conf. level
Leptonychotes weddelli	104	64.8	30.58	1.28	0.201
Odobenus rosmarus	167	60	25.52	4.19	2.79E-5 *
Mustela erminea	259	53	24.34	8.46	2.67E-16 *

*denotes statistically significant a difference between the given species and the four phocids

phocids. This corresponds to a z-score of 4.19, which is statistically significant at the 2.79E-3 % confidence level. This indicates that whereas *L. weddelli* does not contain too many discordant OGIs, *O. rosmarus* does. In comparison, as we can see in Figure 8, *M. erminea*, the outlier species, has 259 unique OGIs compared to the four phocids, corresponding to a z-score of 8.46 which is statistically significant at the 2.67E-14 % confidence level. Since *O. rosmarus* behaves just like the outlier *M. erminea*, this indicates that *L. weddelli* shows continuity with phocids, whereas *O. rosmarus* does not. This would mean that *L. weddelli* belongs to the phocid holobaramin, whereas *O. rosmarus* belongs to its own baramin.

The 119 unique *L. weddelli* proteins were analyzed at the PANTHER database according to the procedures described in the Materials and Methods section. Out of these 119 proteins, 112 mapped to 93 PANTHER functional categories. These were further analyzed for functional classification. Figures 9 and 10 show those biological classes and protein classes that the 119 unique genes were most enriched in. Figure 9 shows that many of the 119 unique genes mostly take part in biological regulation (GO:0065007), cellular processes (GO:0009987), and metabolic processes (GO:0008152). Figure 10 shows that these genes are most enriched in gene-specific transcriptional regulation (PC00264), metabolite interconversion (PC00262), protein modification (PC00260), and transmembrane signaling (PC00197).

Penso-Dolfin et al. (2020) analyzed 559 miRNA loci in *L. weddelli*, of which 146 (26.1%) were found to be unique to that species. These miRNA were expressed predominantly in the brain, the heart, muscle, and blood plasma. They were associated with physiological processes such as hypoxia, lipid metabolism, inflammatory signaling, Jak-stat signaling, and hypercortisolemia. The authors suggested that these physiological processes may aid in deep-sea diving. The Weddell seal is known to be able to dive down to 900 m, and stay submerged for at least 60 minutes, although another seal in this study, *M. leonina*, can dive up to 1000 m in depth. Figure 9 shows that both immune system (GO:0002376) and metabolic processes (GO:0008152) are associated with the 119 unique genes of *L. weddelli*. Figure 10 shows that several protein classes that these unique *L. weddelli* proteins belong to are also active in cell signaling: defense/immunity (PC00090), intercellular signaling (PC00207), membrane traffic (PC00150), metabolite interconversion (PC00262), and transmembrane signaling (PC00197).

The list of unique OGIs for *N. schauinslani*, *H. grypus*, *M. leonina*, *P. vitulina*, *L. weddelli*, *O. rosmarus*, and *M. erminea*, a list of the 119 unique *L. weddelli* proteins, and their PANTHER functional classification are available in Supplementary File 4.

Conclusion

Considering multiple lines of evidence, the three pinniped families each form a holobaramin. This is visible from the mtDNA results. The mtDNA analysis also shows that lobodontine and monachine seals, as well as seals from the genus *Mirounga* form a separate lineage from all other phocids. This is not so clear from the WGKS analysis, although these results show that otariids are fairly discontinuous with phocids and *O. rosmarus*. The GC method also shows that otariids separate from phocids and *O. rosmarus*, and that *O. rosmarus* also separates from phocids, except for *L. weddelli*. None of the studies show that *Mirounga* is in the same baramin as *O. rosmarus*. At best *O. rosmarus* shows genetic similarity with *L. weddelli*, although upon closer examination this does not seem to be the case, based on a statistically significant higher number of unique OGIs in the genome of *O. rosmarus* compared to *L. weddelli*.

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References

Afgan, E., D. Baker, B. Batut, M. van den Beek, D. Bouvier, M. Čech, J. Chilton, D. Clements, N. Coraor, B. Grüning, A. Guerler, J. Hillman-Jackson, V. Jalili, H. Rasche, N. Soranzo, J. Goecks, J. Taylor, A. Nekrutenko, and D. Blankenberg. 2018. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Research* 46(W1):W537–W544.

Arnason U. 1977. The relationship between the four principal pinniped karyotypes. *Hereditas* 87(2):227–242.

Arnason, U., J.A. Adegoke, K. Bodin, E.W. Born, Y.B. Esa, A. Gullberg, A., M. Nilsson, R.V. Short, X. Xu, and A. Janke. 2002. Mammalian mitogenomic relationships and the root of the eutherian tree. *Proceedings of the National Academy of Sciences of the United States of America* 99(12):8151–8156.

Berta, A., J.L. Sumich, and K.M. Kovacs. 2015. *Pinniped Evolution and Systematics*, in Marine Mammals, Evolutionary Biology, 3rd ed. Academic Press, San Diego, CA.

Best, P,B., M.A. Meyer, and R.W. Weeks. 1981. Interaction between a male elephant seal *Mirounga leonine* and Cape fur Seals *Arctocephalus pusillus*. *South African Journal of Zoology* 16:59–66.

Davis, C.S., I. Delisle, I. Stirling, D.B. Siniff, and C. Strobeck. 2004. A phylogeny of the extant Phocidae inferred from complete mitochondrial DNA coding regions. *Molecular Phylogenetics and Evolution* 33(2):363–377.

Eddy, S.R. 2011. Accelerated profile HMM searches. *PLoS Comput Biol* 7:e1002195.

Harris, H.S., S.C. Oates, M.M. Staedler, M.T. Tinker, D.A. Jessup, J.T. Harvey, and M.A. Miller. 2010. Lesions and behavior associated with forced copulation of juvenile Pacific harbor seals (*Phoca vitulina richardsi*) by southern sea otters (*Enhydra lutris nereis*). *Aquatic Mammals* 36(4):331–341.

Iverson, S.J., W.D. Bowen, D.J. Boness, and O.T. Oftedal. 1993. The effect of maternal size and milk energy output on pup growth in grey seals (*Halichoerus grypus*). *Physiological and Biochemical Zoology* 66(1):61–88.

Lightner, J.K. 2007. Identification of species within the cattle monobaramin (kind). *Journal of Creation* 21(1):119–122.

Lightner, J., T. Hennigan, G. Purdom, and B. Hodge. 2011. Determining the Ark kinds. *Answers Research Journal* 4(2011):195–201.

McLaren, I. 1960. On the origin of the Caspian and Baikal seals and the paleoclimatological implication. *American Journal of Science* 258(1):47–65.

Magallanes, I., J.F. Parham, G.P. Santos, and J. Velez-Juarbe. 2018. A new tuskless walrus from the Miocene of Orange County, California, with comments on the diversity and taxonomy of odobenids. *PeerJ* 6:e5708.

Mi, H., A. Muruganujan, X. Huang, D. Ebert, C. Mills, X. Guo, and P.D. Thomas. 2019. Protocol Update for Large-scale genome and gene function analysis with the PANTHER Classification System (v.14.0). *Nature Protocols* 14(3):703–721.

Moynagh, E. 2018. Applied Baraminology (Research Article), inhisimage.blog/2019/02/20/applied-baraminology-research-article.

O'Micks, J. 2017. Baraminology classification based on gene content similarity measurement. *Creation Research Society Quarterly* 54(1):27–37.

Penso-Dolfin, L., W. Haerty, A. Hindle, and F. Di Palma. 2020. MicroRNA profiling in the Weddell seal suggests novel regulatory mechanisms contributing to diving adaptation. *BMC Genomics* 21(1):303.

Savriama, Y., M. Valtonen, J. Kammonen, P. Rastas, O-P. Smolander, A. Lyyski, T. Hakkinen, I.J. Corfe, S. Gerber, I. Salazar-Ciudad, L. Paulin, L. Holm, A. Loytynoja, P. Auvinen, and J. Jernvall. 2018. Bracketing phenotypic limits of mammalian hybridization. *Royal Society Open Science* 5(11):180903.

Wood, T.C. 2008. *Animal and Plant Baramins*, Issues in Creation #3, Wipf and Stock Publishers, Eugene, OR.

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Petrified Ideas of the Williston Basin

Part II: Fossil Wood

Michael Oard and Peter Klevberg*

Abstract

"Petrified forests" are common tourist attractions, invariably used to promote uniformitarian thinking. One well-known example is in Theodore Roosevelt National Park near Medora, North Dakota, U.S.A. The petrified wood is contained in various strata of the "Paleogene" Fort Union Group in the Williston Basin, but in the park primarily in the lower Sentinel Butte Formation. This formation exhibits much evidence against uniformitarian hypotheses but which fits well with the Genesis Flood. The site shows laterally extensive and vertically limited horizons containing fossilized tree trunks, divorced from fine roots and branches, with no discernible rooting medium such as paleosols, and closely associated with bentonite, iron oxide, and coal. The stratigraphy and sedimentology of the area bespeak continuous, rapid deposition and powerful currents. The uniformitarian scientists also have the problem of how silicification occurs prior to the more rapid normal decay process typical of the supposed swamps which are the interpreted depositional environment for the Fort Union. Burial of vertical trees sinking from log mats and rapid silicification associated with volcanic activity during the Bibilical Flood (responsible for the bentonites) is a more plausible explanation.

Key Words: Petrified wood, Medora, North Dakota, Williston Basin, Fort Union Group, fossilization

Introduction

Many tourists pass through Medora, North Dakota, U.S.A. (Figure 1), each year, nearly all of them on the interstate highway. Many stop at the Painted Canyon overlook to gaze on the badlands (Figure 2). Those interested in seeing the park stop in Medora, and many drive the winding gravel road through colorful, grassy hills and wooded draws sprinkled with oil wells to the "Petrified Forest" (Figure 3). There, as at the highway overlook, they hear the usual story of millions of years and slow geologic processes. But a closer look shows the traditional story to be fiction. The State of North Dakota promotes evolutionary propaganda near Medora and at other locations: "Medora was a very swamp-like environment 55 million years ago. We find anything from crocodile bones,

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* Michael Oard, michael.j.oard@gmail.com; Peter Klevberg, grebvelk@yahoo.com

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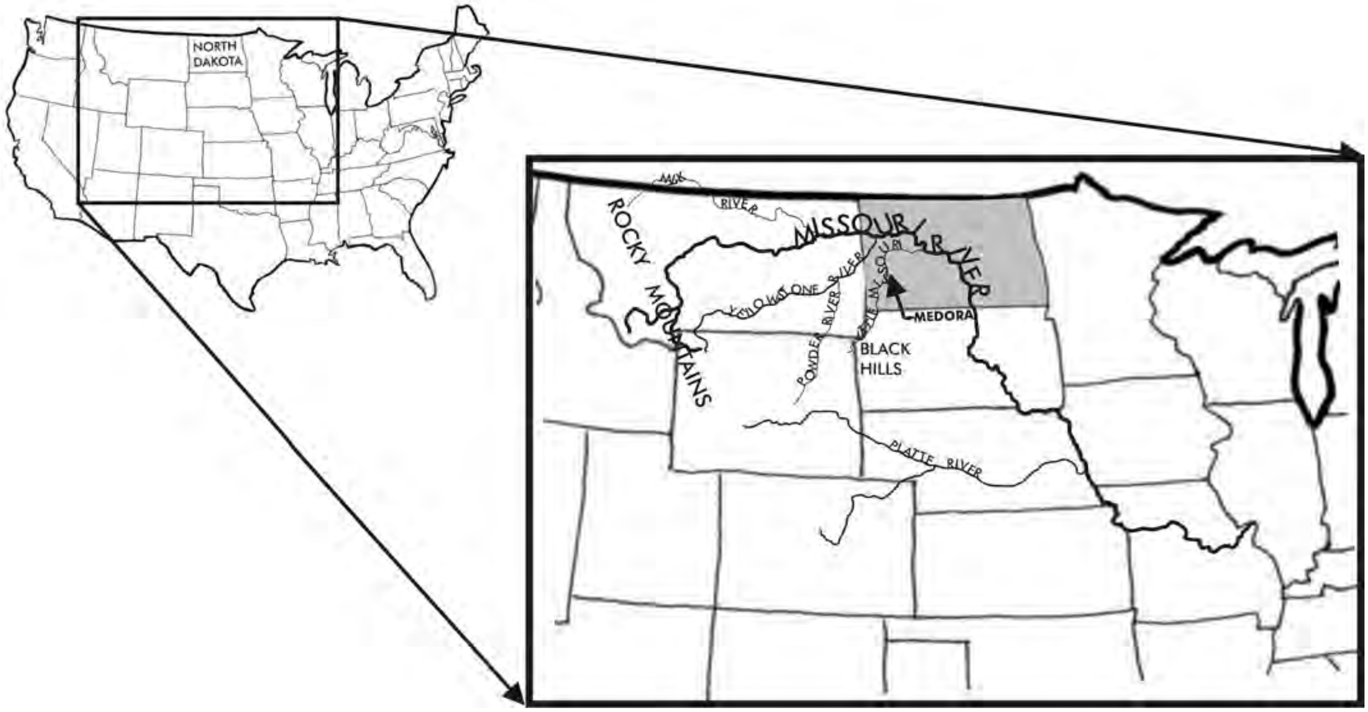

Figure 1. Study Area.

Figure 2. Painted Canyon from the Interstate 94 overlook.

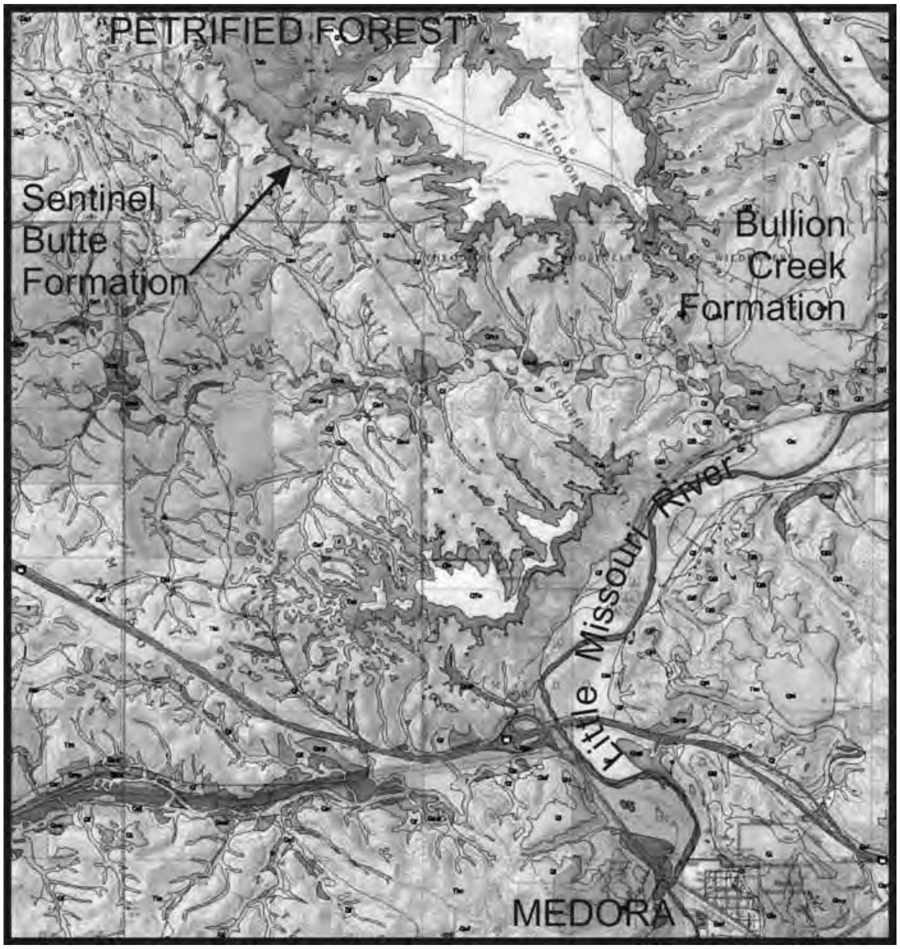

Figure 3. Portion of geologic map centered on Medora and the "Petrified Forest" (from Gonzalez and Biek, 2003). The Petrified Forest is located on the exposed Sentinel Butte strata (dark gray) on the west flank of the light-colored butte (Big Plateau) at the top of this figure.

fish, salamanders, turtles, champsosaurs, bald cypress branches and cones, snails, clams, mammals, and birds" (North Dakota Geological Survey, 2020). But were these plants and animals living here, or do the fossils only show that they died and their remains were buried here?

When visiting national parks, monuments, or other natural tourist areas, it is a good idea to put on one's "baloney detector," as advocated by the late Phillip Johnson (1997), one of the founders of the Intelligent Design Movement. When reading interpretations of geological observations, one should be skeptical, even as a uniformitarian. This study provides yet another example of why skepticism is in order whenever one reads "official" interpretations of local geology.

As another example, consider Devils Tower National Monument, Wyoming, U.S.A. Road signs propose that the hardened lava of the tower was exposed anywhere from over 40 million years to 2 million years ago, during which, hundreds of feet of material was eroded from the surrounding plains (Oard, 2008, 2009). But since the tower itself is eroding rapidly by block fall, it is strange that it has hardly changed diameter or height in all that time. It is more likely that the timeframe is wrong. Many have found numerous contradictions with uniformitarian interpretations at national parks and monuments. We often have better explanations from studying the geology of the Biblical Flood than is seen in government propaganda (Vail et al., 2008; Oard et al., 2010; Hergenrather et al., 2012).

A conference at Medora (Figure 4) during the summer of 2018, sponsored by the Institute for Biblical Authority (www.IBA777.org), Institute for Creation Research (www.storeICR.org), Montana Origins Research Effort (www.creationsciencedefense.org), and the Glendive Dinosaur & Fossil Museum (www.creationtruth.org), offered an opportunity to examine two spectacular Flood evidences in the badlands of Theodore Roosevelt National Park in southwest North Dakota. These are 1) well-rounded quartzite rocks likely spread from Idaho (Klevberg and Oard, 1998; Oard and Klevberg, 1998) and 2) vertical, petrified trees. The area, like the Badlands National Park (Figure 5) in northwest South Dakota, is famous for its badlands topography (Figures 4 and 5).

Theodore Roosevelt National Park, North Dakota, was named after President Theodore Roosevelt, who ranched in the area in the late 1800s and lost everything to droughts and blizzards. But, it prepared him to be president of the United States. As president, he was a conservationist and established numerous national parks and monuments in the United States.

We have already described the geology of the area in Part I (Klevberg and Oard, 2021), including general knowledge of the Williston Basin and its rate of sediment accumulation in both uniformitarian and diluvial models. We briefly described the geology of the Paleocene Fort Union Formation that contains this "Petrified Forest." Previously,

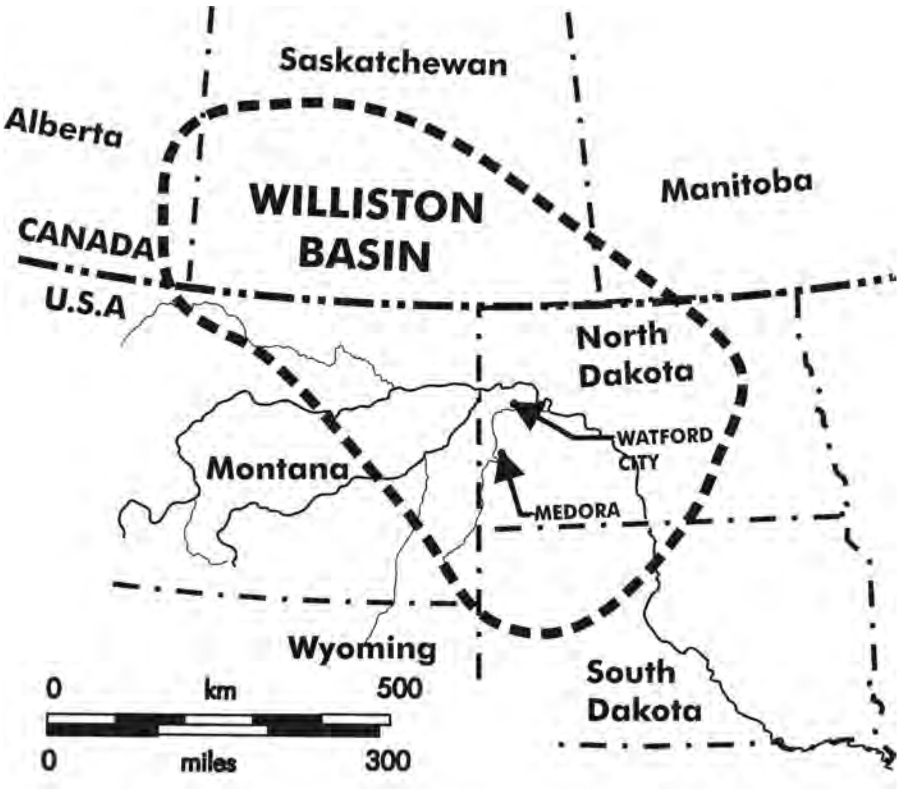

Figure 4. Map of the Williston Basin, the center of which is in western North Dakota. Medora, North Dakota, is located near the southern edge of the basin.

we emphasized the geomorphology of the area, including planation surfaces and well-rounded quartzite rocks likely transported from distant sources. This part will examine the "Petrified Forest" in Theodore Roosevelt National Park. The "Petrified Forest" has much to teach us far beyond the vicinity of Medora.

Figure 5. The badlands of Badlands National Park, southwest South Dakota.

Theodore Roosevelt National Park Petrified Forest

Southwest North Dakota and northwest South Dakota are famous for abundant petrified wood. Vertical petrified trees, called "petrified forests" by uniformitarians, occur in this area, another great location being the Black Hills Petrified Forest near Rapid City, South Dakota (Figure 4).

Fossil wood is plentiful throughout the North Dakota badlands, and the largest single fossil in North Dakota is a Bald Cypress stump (Figure 6) that was obtained from a location outside the two units of Theodore Roosevelt National Park. While on a field trip during the 2018 Medora creation conference, at the entrance to the south unit of the park, we discussed the plentiful information available on the "Petrified Forest." Here is an excellent representation of the Fort Union strata in the Williston Basin (Biek and Gonzalez, 2001), including the area near the north unit of the park where Klevberg has spent considerable time doing field research. We therefore reserve the term "Petrified Forest" for the west side of the Big Plateau (also known as Petrified Forest Plateau) on the west side of the Theodore Roosevelt National Park South Unit rather than other scattered deposits in the area. The Big Plateau includes the light-colored area at the top of Figure 3 (see Figure 4 for location of Medora, which is in the southeast corner of Figure 3).

Model Predictions

Uniformitarian geology would predict that vertical trees at Theodore Roosevelt National Park, as well as many other areas in the world, grew in place:

> Horizons of petrified wood are found in both units of the Park, and although they are all in the lower Sentinel Butte Formation, it is not known whether the horizons are truly correlative. They do indicate

Figure 6. North Dakota's single largest fossil is this petrified Bald Cypress stump exhibited in the Long X Visitor Center in Watford City (location of Watford City shown on Figure 4).

> that conditions favorable for the development and preservation of flood-plain forests were more favorable in early Sentinel Butte time than in earlier or later times. (Biek and Gonzalez, 2001, p. 17)

So, the standard uniformitarian explanation is that the forests grew in place for hundreds of years.

Since it appears that many, if not practically all, the vertical, petrified trees in the world are in strata from the Genesis Flood, diluvial geologists would predict that they did not grow in place as the required timescale would be much longer than the one-year period of the Biblical Flood. Instead, the trees fell through the Floodwater to sink vertically, with the heaviest, root end down, into the rapidly accumulating muddy sediments below, as demonstrated empirically at Spirit Lake by Morris and Austin (2003).

Is the "Petrified Forest" Really a Forest?

As we hiked in for a close examination of the "Petrified Forest," we discovered that indeed there were numerous petrified trees, many still vertical (Figure 7). Because of the intense erosion of the badlands, the bottom of the trees and presumably the material the trees grew in were well exposed. Many once-vertical trees were likely toppled because of this erosion. There were probably hundreds of trees represented at this location, which was one of two areas of abundant vertical petrified trees on the west side of the south unit of the park. Some trees exist in distinct layers.

The trees had a bulbous base and are Bald Cypress (*Taxodium distichum*), sequoia, or perhaps *Metasequoia glyptostroboides* (Dawn Redwood). Bald Cypress is native to the Mississippi Valley and eastern states. Sequoia trees

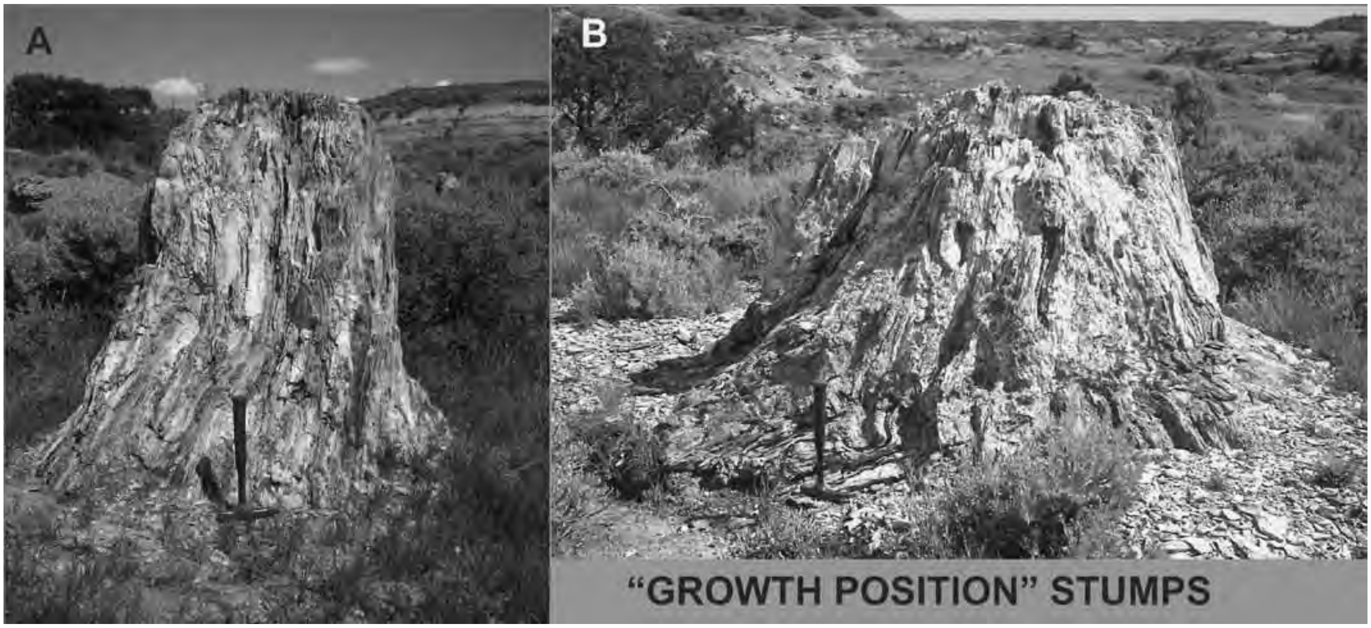

Figure 7. A: A vertically oriented stump from the "fossil forest" of Theodore Roosevelt National Park. While this looks very convincing, closer examination shows no soil or roots below the stump. B: View southeast from the center of the "Petrified Forest" showing one of the most convincing "in situ" stumps in the foreground with many petrified trees, some vertical, of the upper layer, northwest Theodore Roosevelt National Park, South Unit.

are limited to California today. Dawn Redwood is a common type of tree found as a fossil. It is interesting that at one time the Dawn Redwood was thought extinct—the latest it was thought to have lived was the Pliocene, over 2.5 million years ago—but it was found alive in 1941 growing in a remote area of southern China (Bartholomew et al., 1983). It is considered a 'living fossil,' and the question can be asked: Where are the remains of this common fossil tree between 2.5 million years ago and today? The same can be said for other living fossils.

When we examined the petrified trees, we notice that they were overwhelmingly stumps that were about 1 to 2 m tall. But the trees were truncated at the bottom with no roots (Figure 8) and the tops were also truncated and had likely been sheared off (they would be expected to be hollow or more irregular had they rotted). We might add that in other areas within southwest North Dakota and northwest South Dakota, many logs occur without stumps.

Moreover, since many of the petrified stumps were still on pedestals, as erosional remnants, we could see what material was below the stumps. It was the same altered volcanic ash as most of the rest of the badlands, and a recognizable soil profile was absent. With no roots and no soil, the area does not represent in situ tree growth, and the uniformitarian explanation is falsified. Uniformitarian scientists also acknowledge this lack of roots:

> The petrified stumps are up to about 6 feet high and 4 feet in diameter at chest height, but most are between 2 to 4 feet tall and 2 to 3 feet wide. Virtually all have fluted bases, and where in place, rest on a thin lignite or carbonaceous shale; no roots have been observed. Somewhat flattened trunks are less commonly found. The stumps were preserved where buried by flood-plain deposits; the upper parts of the trees simply rotted away. (Biek and Gonzalez, 2001, p. 19)

Paleosols are alleged to be present at the "Petrified Forest," and the two horizons are interpreted as "…two successive coniferous forests that developed on flood-plain sediments…" (Biek and Gonzalez, 2001, p. 21). The iron staining is interpreted as evidence of ponded water and remains of bivalves as evidence of continual submergence. Coal is, of course, interpreted as evidence of swamps. Examination of outcrops, however, shows no fossil soil profiles but rather distinct iron horizons and concretions associated with bentonite beds (altered volcanic ash) as illustrated by Figure 9. While in general, their observations are accurate (Figure 10), uniformitarians seemed to emphasize those associations of fossil wood and high-carbon sediments, even though the "Fossil Forest" does not rest on such shale. The problems with the "petrified forest" interpretation are similar to those found at Yellowstone (Coffin, 1997).

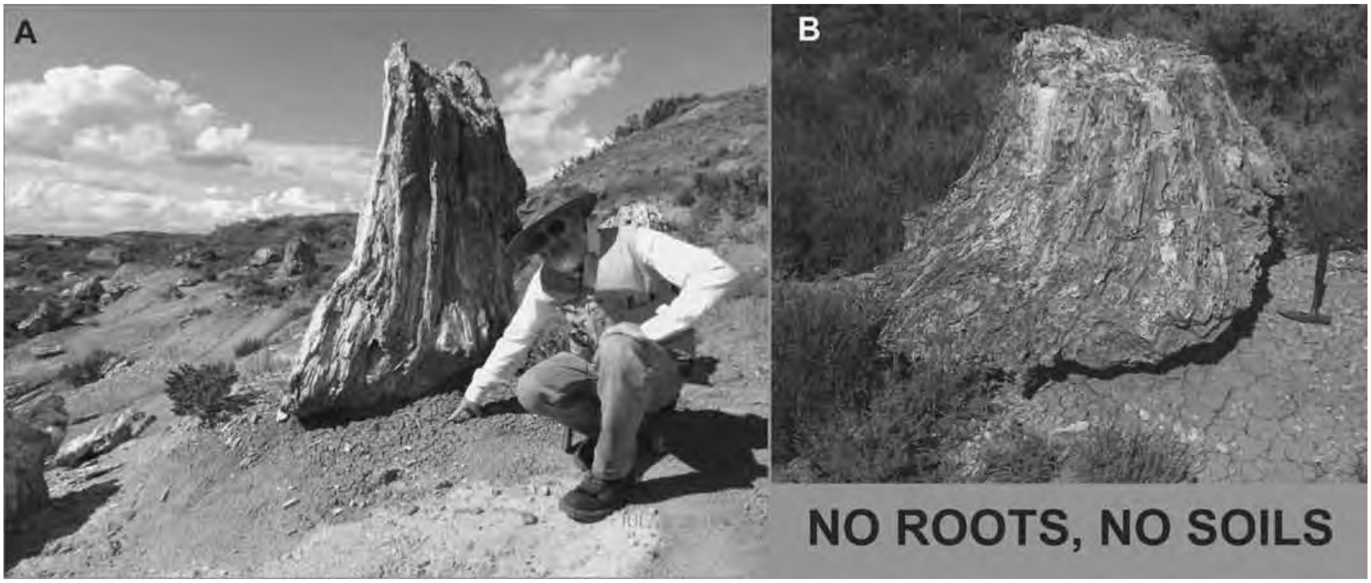

Figure 8. A: Portion of one layer of vertical petrified trees in the "fossil forest" of Theodore Roosevelt National Park. Peter Klevberg pointing to the lack of a soil under the vertical tree stump. B: Close up showing no soil below a stump from the overlying stump layer, which also had no roots.

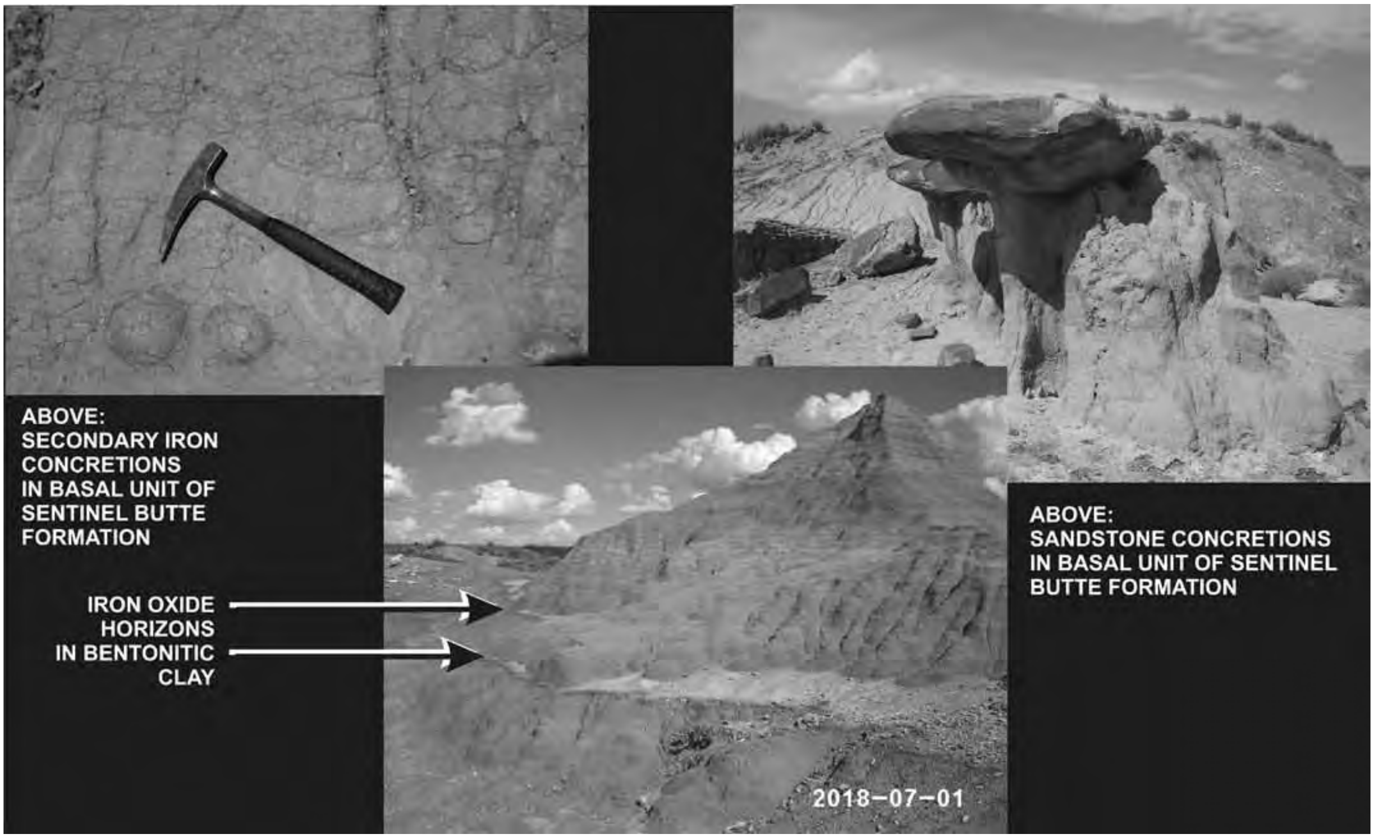

Figure 9. Iron oxide is notable in distinct horizons in bentonite beds and as concretions in sandstone and claystone. These examples are from the basal Sentinel Butte Formation in the "Petrified Forest" of Theodore Roosevelt National Park, South Unit.

The Yellowstone "Petrified Forests"

We have observed other areas with vertical, petrified trees that are almost always considered an in situ fossil forest. The so-called Yellowstone fossil forests probably represent the best example for secular scientists. In several steep to near-vertical slopes, numerous vertical and horizontal trees can be observed. As many as 65 layers of trees are claimed at Specimen Creek, northwest Yellowstone National Park (Figure 11). It is claimed that they represent tens of thousands of years of successive forests, much too long for the short timescale of the Biblical Flood. Some anti-Christian skeptics, once young-Earth creationists, claim they lost their Christian faith because of the Yellowstone "petrified forests" and consider them definitive proof against the Bible (Numbers, 2006).

In examining this and any other challenge, we must first examine the data, like a detective gathering clues in a forensic reconstruction. This forensic approach to geology must be used because no one was present to observe the events being studied. As unique, unobserved events, indirect clues are the best available evidence. As an aside, this is where Earth history and pure science diverge (Reed and Klevberg, 2014a, 2014b). Science investigates the timeless principles of the Universe; Earth history uses science indirectly, forensically. Without the ability to run controlled experiments or multiple observations, we are left with an inherent uncertainty, although the scientific method is still used in these forensic investigations. So, the analogy of detective work is widely accepted.

The first striking feature is the association of the trees and host rocks. The petrified trees are found in volcanic debris flows, called *lahars*. Numerous stacked trees are found in about a dozen locations with isolated trees in between. These rocks are the Absaroka Volcanics of the Absaroka Range, a thick series of volcanic breccia flows of mostly reworked andesite outcropping in northern and eastern Yellowstone Park and adjacent areas. (Breccia is a cemented rock composed of broken angular fragments. Andesite is a type of igneous rock, intermediate between black basalt and

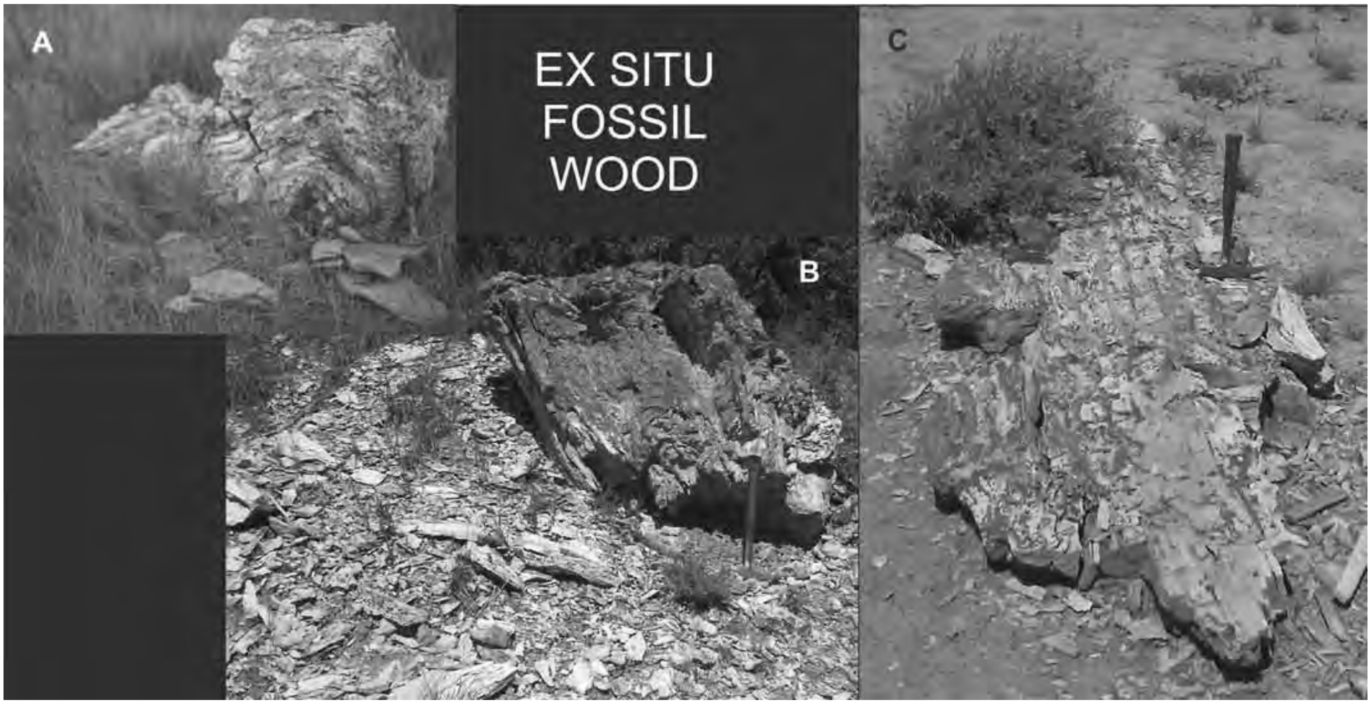

Figure 10. Other than stumps, petrified wood is found as: A. large pieces of stumps or burls, B. other fragments, and C. flattened logs. These are clearly not in growth position. Note Rock hammer for scale.

pale rhyolite, typically emitted by stratovolcanoes, or cone-shaped volcanoes.) Because breccia indicates reworking, the original andesite flow probably formed over a very large area nearby before breaking up and being redeposited in volcanic debris flows. The Absaroka Volcanics accumulated horizontal layers over more than 23,000 km^2, and the formation contains a volume of rock of about 30,000 km^3 (Feely and Cosca, 2003). The formation's thickness exceeds 1,830 m (6,000 ft.) in places (Sundell, 1993). This environment of deposition would be extremely inhospitable for tree growth.

Once again, the hypothesis of "petrified forests" is negated by the evidence. Forests are commonly rich ecosystems with a diversity of organisms and much organic matter in various states of decay. This is not what is observed in the fossil material. In examining the trees in depth, one finds that there are no soils, bark or

Figure 11. Numerous layers of vertical petrified trees at Specimen Creek, extreme northwest Yellowstone National Park.

Figure 12. Vertical tree with no roots in Absaroka Volcanics on Mount Hornaday, northeast Yellowstone National Park (David Anderson provides the scale).

Figure 13. Broken long root from a vertical stump at Specimen Creek, northwest Yellowstone National Park. (Perry Fishbaugh pointing to the end of the root.) The root of a growing tree crosses perpendicularly over the petrified root.

branches, long roots are mostly missing, there are no animal fossils. Tree rings correlate *between* different layers (Arct, 1979, 1991), and the 200 species of trees grow in widely divergent climates (Oard, 2014). Figure 12 shows a petrified tree within a lahar in Yellowstone National Park with no roots, while Figure 13 shows a rare example of a long root from a vertical petrified stump. The late Dr. Harold Coffin, who had extensively examined the Yellowstone petrified trees over dozens of years, thought they were best explained by sinking trees from a floating log mat during the Genesis Flood, similar to what has been observed on Spirit Lake north of Mount Saint Helens (Coffin, 1997). Figure 14 shows a schematic of the process. The analogy extends to volcanism also, which seems to be commonly associated with many of the fossil wood localities that appear to be diluvial in origin.

Other "Petrified Forests"

Oard has examined several other "petrified forests," such as at Ginkgo Petrified Forest State Park, near Vantage, Washington (Figure 15); a coal mine near Sutton, Alaska (Figure 16); massive stumps at Florissant, Colorado (Figure 17); and upright petrified trees in the western Bighorn Basin, Wyoming (Figure 18) (Oard, 2014). Many other areas of the world show such vertical petrified trees. The vertical trees near Sutton, Alaska, and Florissant, Colorado, have no roots and soils, just like the vertical trees in Theodore Roosevelt National Park.

The Problem of Silicification

Wood is petrified predominantly by various forms of silica (Hellawell et al., 2015). Petrification normally is the same as *replacement*—the complete replacement of the organic material by inorganic chemicals. But, in petrified wood, the organic structures often are not totally replaced. Some scientists believe that we should not use precise definitions for the state of the wood (Hellawell et al., 2015). Regardless, there is usually little organic matter left in petrified wood (Grimes et al., 2015). The numerous, huge logs in Petrified Forest National Park in Arizona (Figure 19) are a major exception in that the logs are just permineralized and not replaced (Akahane et al., 2004). *Permineralization* is the addition of silica or other lithification agents into the spaces between cells and within cells without replacing the organic matter. A minor form of petrification is by pyrite (FeS_2), but it requires very special conditions and must happen rapidly (Grimes et al., 2001).

Some claim that petrification should take millions of years, but like many slow processes observed today, time is only one variable (Daniels and Dayvault, 2006, p. 209). Moreover, could a log remain in the ground for millions of years without decaying away? It is now known that under the proper conditions *at present*, petrification can occur in years (Akahane et al., 2004). But of course as petrification proceeds and porosity decreases, the time to petrify increases, and this is where uniformitarian scientists still believe petrification must take a long time (Daniels and Dayvault, 2006, p. 181). Reed (personal communication) has observed worked wood from the Colonial Period settlements of the 18th century along the Black River Swamp in South Carolina that petrified within three centuries (Figure 20).

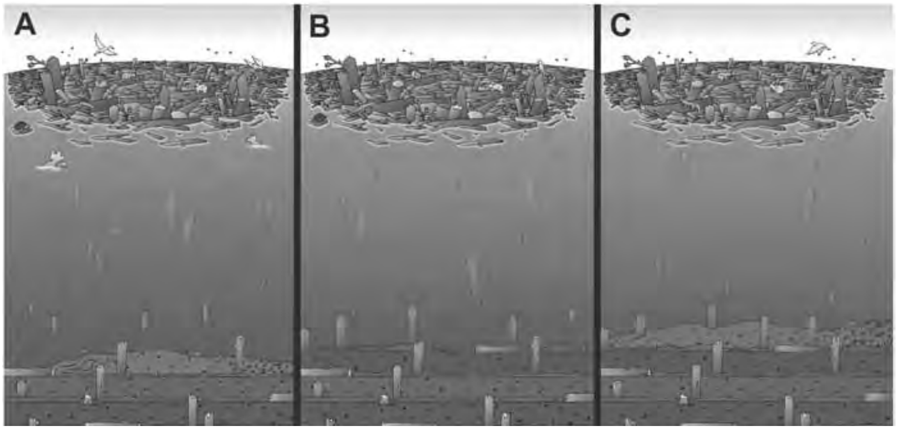

Figure 14. A log mat with trees sinking vertically to the bottom, while the bottom is collecting deposits horizontally from volcanic debris flows (courtesy of Keaton Halley). 'A' shows a log mat with many trees sinking vertically to the bottom. 'B' shows the vertical trees after sediment had been deposited. 'C' shows the next pulse of sediment spreading along the bottom of the Floodwaters.

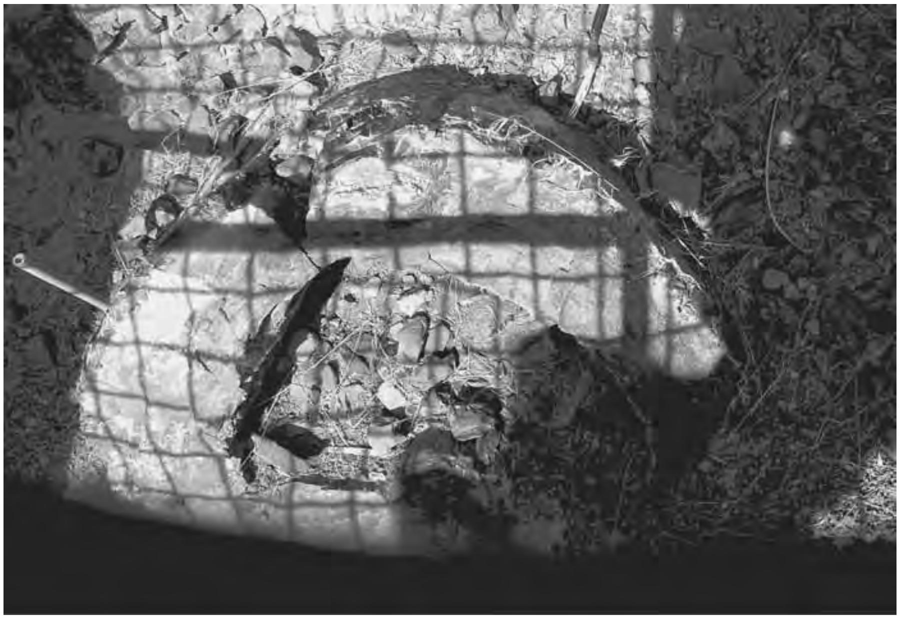

Figure 15. Tilted petrified log in a wire cage within the Columbia River Basalts at Ginkgo Petrified Forest State Park, Vantage, Washington. The log is hollow with rubble in it.

The specific way wood becomes petrified is not precisely known, but researchers are starting to understand it better (Mustoe, 2008). Hellawell et al. (2006, p. 79) exclaim: "Despite considerable progress made in the past, many details of fossilization by silicification remain unanswered…" One of the issues is to understand why silica is the predominant petrifying chemical. Researchers claim it is because wood has an affinity for silica (Ballhaus et al., 2012). Apparently, the shape of the wood first becomes 'templated' by amorphous silica, called opal-A (Mustoe, 2008). Then opal-A is replaced by opal-CT and chalcedony, other forms of silica, making opal-A actually rare in petrified wood. Some researchers had thought chalcedony replaced opal-CT, but apparently that is not the case. Quartz is also found in some petrified wood (Mustoe, 2008).

Figure 16. Two petrified trees, up to 4 m tall, from a coal mine north of Sutton, Alaska. Notice the lack of roots or a fossil soil profile.

Figure 17. Vertical Redwood tree at Florissant Fossil Beds National Monument in Florissant, Colorado. Some of the stumps in the area were over 3 m in diameter. Notice the lack of roots or a fossil soil profile.

Although researchers today are discovering that petrification does not take millions of years, they still believe it takes years to thousands of years or a long time (Daniels and Dayvault, 2006). Some admit that the time factor is still unknown. However, there are indications in the fossil record that the process can be much faster than researchers are willing to admit:

> The time scales of silicification cannot be quantified, but the silica precipitation rates observed and the excellent preservation states of cellular details in Chemnitz (Röβler, 2001) do suggest that much of the mineralization was accomplished within weeks to months after deposition of the pyroclastics. (Läbe et al., 2012, p. 841)

Chemnitz is a so-called fossil forest at Chemnitz, Germany. An experiment within hot springs in Yellowstone National Park, Wyoming, showed that significant silicification had already begun within one year (Channing and Edwards, 2004).

The fossil wood of the Rhynie chert, Scotland, with exceptionally preserved fossils in a supposed early Devonian chert, must have been petrified within a matter of weeks (Ballhaus et al., 2012). Petrification was so fast that "metabolic processes" were preserved:

> Silicification also replaced the organic cellular tissue with SiO_2; so thoroughly that many silicified trees consist of close to 100% SiO_2, so delicately that the minutest structural details of the wood cells are retained..., yet so rapidly (cf. Rhynie chert) that even metabolic processes on the subcellular scale can be arrested in time and then reconstructued.... (Ballhaus et al., 2012, p. 62)

Preservation of cells with visible details, including lack of decay, would require very fast fossilization indeed. Daniels and Dayvault (2006, p. 188) state:

Figure 18. One of many vertical petrified tree trunks at Dry Creek Petrified Environmental Education Area, about 24 km east of Buffalo, Wyoming. This metasequoia tree trunk is almost 1.5 m in diameter.

> The crystallization process overwhelms and obliterates antecedent components. So too do the microscopic details of the original wood diminish as the quartz crystallizes. It is remarkable that any original wood textures remain, much less that many microscopic cellular structures persist.

Very rapid petrification in the Rhynie chert wood also includes the petrification of very delicate plant structures (Kerp et al., 2004). Ballhaus et al. (2012, p. 63) even state:

> Finally, the amazing biological details preserved by the silica-rich hydrothermal solutions that formed the Lower Devonian Rhynie chert … is feasible only if the replacement

Figure 19. A petrified tree in Petrified Forest National Park, Arizona (Kumar Appaiah, Wikipedia-Commons CC-BY-SA-2.0).

Figure 20. Observed worked wood from the Colonial Period settlements of the 18th century along the Black River Swamp in South Carolina that petrified within a few centuries (photograph courtesy of John Reed).

> by silica occurred within a matter of weeks.

Some researchers think that silicification is aided by hot water in the environment (Läbe et al., 2012). The water possibly was in the vapor phase, since there are no fluid inclusions. In fact, silica is more soluble the higher the temperature and pressure (Manning, 1994), but of course dissolution of silica in ground water only works in rocks with high silica content in the first place such as volcanic ash (Davis, 1964), abundant in Theodore Roosevelt National Park. On the other hand, hot environments cause more rapid degradation of the wood, which also helps silica penetrate better (Channing et al., 2012). So, if hot silica-charged water or vapor is responsible for petrification, then the process must operate extremely fast before the wood degrades.

We have observed little, if any, degradation of the wood in petrified trees, reinforcing the rapidity of petrification. One would expect to see much rotting of the wood if the petrification process took even the thousands of years necessary for the uniformitarian model. Given the lack of silica in today's ground water, except in local areas such as volcanic areas or hot springs (Davis, 1964; Daniels and Dayvault, 2006), it is a mystery why so much well-preserved wood, showing little decay, even exists. Moreover, modern examples of wood petrifying are rare and show that the wood is only partially silicified, even in very special environments, such as the silica-rich hot springs of Yellowstone National Park (Hellawell et al., 2012). However, Yellowstone National Park really does not answer the question of why there is an abundance of petrified wood:

> Clearly, the Yellowstone Park situation is special and perhaps not generally applicable to the majority of environments in which silicified logs or wood are found in the fossil record. Fundamental parameters for silicification appear to be elevated concentrations in SiO_2 aqueous species and the rapid burial of a tree to isolate it from aerial oxygen. (Hellawell et al., 2012, p. 86)

Such a deduction would also apply to Theodore Roosevelt National Park trees.

Trees buried before the last major eruption of Mount Saint Helens only show incipient silicification (Karowe and Jefferson, 1987). Moreover, hot spring "environments" cannot account for the widespread petrified wood in the fossil record:

> However, the percentage of petrified wood that forms in hot spring environments is miniscule compared to the total volume of petrified wood in the world. Wood petrified in hot spring environments is not an accurate representation of the average time required for conversion of wood to stone in a sedimentary basin. (Daniels and Dayvault, 2006, p. 209)

So, the abundance of petrified wood is not readily explained by uniformitarianism. Those of today show rare silicification in hot-spring environments, although many fossil wood sites are associated with volcanic ash or volcaniclastic environments, which are high in silica (Daniels and Dayvault, 2006). However, the silica in the volcanic ash needs to be dissolved by much heat and enter the wood in hydrothermal solutions, since the solubility of quartz does not occur until a temperature of 70°C and increases exponentially above 70°C (Bjørlykke, 2014).

In summary, the petrification of wood requires specific conditions. The wood must first be buried rapidly (Ballhaus et al., 2012). Second, the wood must be buried in a water- or fluid-saturated environment, or else the wood rapidly decays in a matter of a few years (Daniels and Dayvault, 2006). And even if buried in a water-saturated environment, if it dries out, the wood will rot. Third, there must be an abundant source of silica (Daniels and Dayvault, 2006), which could occur in volcanic environments under the right conditions. Metasomatism (fluid-dominated metamorphism) altering igneous and metamorphic rock can also be a source of silica deeper down in the Earth (Manning, 1994), perhaps indicating the source of silica for the silica-rich water is from the mantle. Fourth, there are signs of very rapid petrification, which the researchers seem to downplay, especially since the fossil species are native to moister climates where rapid decay would result. The Genesis Flood provides a superior mechanism, while uniformitarianism does not.

Vertical Trees Explained by Sinking Logs During the Flood

The vertical trees in Theodore Roosevelt National Park and elsewhere cannot be explained by uniformitarianism. But the proposed model of floating log mats during the Biblical Flood (Figure 14), reinforced by the empirical observations at Spirit Lake (Morris and Austin, 2003), provides a good explanation of "petrified forests." The Deluge also appears to have been a time of significant volcanism, which would have provided one source of abundant silica. It also explains many related mysteries of the rocks and fossils, such as coal, insect fossils, amber, insects in amber, warm-climate plants and animal fossils at high latitudes, the mixture of plants from warm and cold climates, and postdiluvian biogeography (Oard, 2014). These log mats, floating on the Floodwaters, would often be of huge scale, both in extent and thickness, since the antediluvian biosphere had roughly ten times the amount of plants and trees, based on the estimated amount of coal (Archer, 2010). And just like at Mount Saint Helens, as the log mats drifted, some logs would have become waterlogged and sunk vertically.

With a focus on the petrified stumps at Theodore Roosevelt National Park, we can also surmise that violent volcanic explosions, such as occurred at Mount Saint Helens, would also blast away most of the trees leaving stumps that could later be transported and deposited. Roots could be lost during transport or by collisions with other trees in the log mats. Such a mechanism would also rub off bark and branches. So, diluvial log mats can explain the vertical petrified trees, including those at Theodore Roosevelt National Park. The trees were buried under hundreds of meters of wet sediments (see Part I). The pressure of the accumulating sediments would force the pore fluids to move under the pressure of compaction. Possibly the sediments became hot, more likely were deposited already hot, so that the silica in the volcanic ash and other sediments dissolved and rapidly moved within the hydrothermal flow. Alternatively, the hot, silica-rich hydrothermal flow could have come from deeper down in the thick sediments. This hot silica would petrify the wood quickly before it rotted.

Conclusions

Two significant evidences of the Genesis Flood have been presented in this series. The first is the nature of the Williston Basin in general and the Fort Union Group in particular. Gravel-capped planation surfaces are found here, as they are in many places of the world, and these indicate diluvial processes significantly different from processes we see today. Only large, energetic currents, such as the retreating Floodwaters, would erode the planation surfaces, and these currents would also be required to round and transport large quartzite clasts over hundreds of kilometers. The laterally extensive strata of the Fort Union Group are themselves a witness to the scale of the depositional event. The second evidence as presented in this paper is the fossil wood. We conclude that these physical evidences provide insight into Earth history.

We have examined a classically-interpreted "petrified forest" in Theodore Roosevelt National Park. Despite the uniformitarian claim of in situ growth, the vertical trees have no roots and no soils. Therefore, they did not grow in situ but can be readily explained by the Deluge. Catastrophic processes (e.g., lahars) probably initially sheared the trees off at about 1 to 2 m high. The stumps could have been subsequently transported, leaving the roots behind, perhaps as they were broken off in transport. If the stumps were uprooted like modern windfalls, most of the roots would be severed at various distances from the trunk. During flood transport, the roots could have been knocked off during turbulence with logs banging into other logs. Then the stumps would have sunk vertically, heavy-end down, from the log mats, as they became waterlogged.

The traditional story taught at Theodore Roosevelt National Park and other "petrified forests" is the growth of a forest over a significant time followed by its preservation and fossilization. However, what we actually observed were stumps that, although upright, lacked root systems and paleosols. While admittedly a matter of historical conjecture rather than scientific observation, the fossils can be evaluated in the light of science. Just as the eruption of Mount Saint Helens in 1980 blasted trees loose from the mountainside and into Spirit Lake, so these North Dakota fossil trees may have originated far from where they are now. While the stumps are of various heights, they are mostly upright. As the trees in Spirit Lake often became waterlogged and sank root-end down, so these stumps probably sank heavy-end first as they became waterlogged. This could explain the abundance of stumps and paucity of logs or smaller pieces in this "petrified forest." Abundant silica from the volcanic ash contributed to their petrification, and that altered ash (bentonite) is what we observe under the stumps. No soil horizons are observed because no soil horizons ever formed. This diluvial explanation fits the facts far better than the traditional story.

These same issues are seen in the "petrified forests" of Yellowstone National Park, as well as those in Arizona, Wyoming, Washington, and Alaska. Ring matches between different levels of fossil trees, polystrate tree trunks, very few roots, absence of bark, many species from different climatic zones–these all indicate that the trees were transported; they did not grow in place. Flood log mats (and in some cases, debris flows) can explain mixed assemblages of fossils and can readily explain the petrified trees, including those at Theodore Roosevelt National Park.

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References

Akahane, H., T. Furuno, H. Miyajima, T. Yoshikawa, and S. Yamamoto. 2004. Rapid wood silicification in hot spring water: An explanation of silicification of wood during the Earth's history. *Sedimentary Geology* 169(3–4):219–228.

Archer, D. 2010. *The Global Carbon Cycle*. Princeton University Press, Princeton, NJ.

Arct, M.J. 1979. Dendrochronology in the Yellowstone fossil forests. M.A. thesis, Loma Linda University, Loma Linda, CA.

Arct, M.J. 1991. Dendroecology in the fossil forests of the Specimen Creek area, Yellowstone National Park. Ph.D. dissertation, Loma Linda University, Loma Linda, CA.

Ballhaus, C., C.T. Gee, C. Bockrath, K. Greef, T. Mansfeldt, and D. Rhede. 2012. The silicification of trees in volcanic ash—an experimental study. *Geochimica et Cosmochimica Acta* 84:62–74.

Bartholomew, B., D.E. Boufford, and A. Spongberg. 1983. *Metasequoia glyptostroboides*—Its present status in central China. *Journal of the Arnold Arboretum* 64(1):105–128.

Biek, R.F., and M.A. Gonzalez. 2001. The geology of Theodore Roosevelt National Park, Billings and McKenzie Counties, North Dakota. *North Dakota Geological Survey Miscellaneous Series No. 86*. North Dakota Geological Survey, Bismarck, ND.

Bjørlykke, K. 2014. Relationships between depositional environments, burial history and rock properties. Some principal aspects of diagenetic process [sic] in sedimentary basins. *Sedimentary Geology* 301:1–14.

Channing, A., and D. Edwards. 2004. Experimental taphonomy: Silicification of plants in Yellowstone hot-spring environments. *Transactions of the Royal Society of Edinburgh: Earth Sciences* 94(4):503–521.

Coffin, H.G. 1997. The Yellowstone petrified "forests." *Origins* 24(1):5–44.

Daniels, F.J., and R.D. Dayvault. 2006. *Ancient Forests: A Closer Look at Fossil Wood*. Western Colorado Publishing Co., Grand Junction, CO, p. 209.

Davis, S.N. 1964. Silica in streams and ground water. *American Journal of Science* 262(7):870–891.

Feely, T.C., and M.A. Cosca. 2003. Time vs. composition trends of magmatism at Sunlight Volcano, Absaroka Volcanic Province, Wyoming. *GSA Bulletin* 115(6):714–728.

Gonzalez, M.A., and R.F. Biek. 2003. *Geology of the Medora, North Dakota, Quadrangle* (1:24,000). North Dakota Geological Survey, Bismarck, ND.

Grimes, S.T., F. Brock, D. Rickard, K.L. Davies, D. Edwards, E.E.G. Briggs, and R.J. Parkes. 2001. Understanding fossilization: Experimental pyritization of plants. *Geology* 29(2):123–126.

Hellawell, J., C. Ballhaus, C.T. Gee, G.E. Mustoe, T.J. Nagel, R. Wirth, J. Rethemeyer, F. Tomaschek, T. Geisler, K. Greef, and T. Mansfeldt. 2015. Incipient silification of recent conifer wood at a Yellowstone hot spring. *Geochimica et Cosmochimica Acta* 149:79–87.

Hergenrather, J., T. Vail, M. Oard, and D. Bokovoy. 2012. *Your Guide to Yellowstone and Grand Teton National Parks: A Different Perspective*. Master Books, Green Forest, AR.

Johnson, P.E. 1997. *Defeating Darwinism by Opening Minds*. InterVarsity Press, Downers Grove, IL.

Karowe, A.L., and T.H. Jefferson. 1987. Burial of trees by eruption of Mount St Helens, Washington: Implications for the interpretation of fossil forests. *Geological Magazine* 124(3):191–204.

Kerp, H., N.H. Trewin, and H. Hass. 2004. New gametophytes form the Early Devonian Rhynie chert. *Transactions of the Royal Society of Edinburgh: Earth Sciences* 94(04):411–428.

Klevberg, P., and M. Oard. 1998. Paleohydrology of the Cypress Hills Formation and Flaxville Gravel. In Walsh, R.E. (editor), *Proceedings of the Fourth International Conference on Creationism*, technical symposium sessions, pp. 361–378. Creation Science Fellowship, Pittsburgh, PA.

Klevberg, P., and M. Oard. 2021. Petrified ideas of the Williston Basin—Part I: Geologic setting. *Creation Research Society Quarterly* 58(2):85–103.

Läbe, S., C.T. Gee, C. Ballhaus, and T. Nagel. 2012. Experimental silicification of the tree fern *Dicksonia Antarctica* at high temperature with silica-enriched H_2O vapor. *Palaios* 27(11):835–841.

Manning, A. 2002. *Petrified Wood in the U.S.A.: Where to Collect It Where to See It*. Self-published.

Manning, C.E. 1994. The solubility of quartz in H_2O in the lower crust and upper mantle. *Geochimica et Cosmochimica Acta* 58(22):4831–4839.

Morris, J., and S.A. Austin. 2003. *Footprints in the Ash: The Explosive Story of Mount St Helens*. Master Books, Green Forest, AR.

Mustoe, G.E. 2008. Mineralogy and geochemistry of late Eocene silicified wood from Florissant Fossil Beds National Monument, Colorado. In Meyer, H.W., and D.M. Smith (editors), Paleontology of the Upper Eocene Florissant Formation, Colorado, *GSA Special Paper 435*. Geological Society of America, Boulder, CO, pp. 127–140.

North Dakota Geological Survey. 2020. https://www.dmr.nd.gov/ndfossil/digs/faqs/2018/Medora_FAQ_2018.pdf (accessed February 13, 2020).

Numbers, R.L. 2006. *The Creationists: From Scientific Creationism to Intelligent Design*, expanded edition. Harvard University Press, Cambridge, MA.

Oard, M.J. 2008. *Flood by Design: Receding Water Shapes the Earth's Surface*. Master Books, Green Forest, AR.

Oard, M.J. 2009. Devils Tower can be explained by floodwater runoff. *Journal of Creation* 23(2):124–127. https://creation.com/devils-tower-can-be-explained-by-floodwater-runoff.

Oard, M.J. (ebook). 2014. *The Genesis Flood and Floating Log Mats: Solving Geological Riddles*, Chapter 4. Creation Book Publishers, Powder Springs, GA.

Oard, M.J. 2019. The Florissant redwood trees deposited from a Flood log mat. *Journal of Creation* 33(3):85–93.

Oard, M.J., and P. Klevberg. 1998. A diluvial interpretation of the Cypress Hills Formation, Flaxville gravel, and related deposits. In Walsh, R.E. (editor) *Proceedings of the Fourth International Conference on Creationism*, technical symposium sessions, pp. 421–436. Creation Science Fellowship, Pittsburgh, PA.

Oard, M., T. Vail, D. Bokovoy, and J. Hergenrather. 2010. *Your Guide to Zion and Bryce Canyon National Parks: A Different Perspective*. Master Books, Green Forest, AR.

Reed, J.K., and P. Klevberg. 2014a. Beyond "origin & operation" science, part I: Critique of OS2. *Creation Research Society Quarterly* 50(4):237–251.

Reed, J.K., and P. Klevberg. 2014b. Beyond "origin & operation" science, part II: An alternative. *Creation Research Society Quarterly* 51(1):31–39.

Sundell, K.A. 1993. A geologic overview of the Absaroka Volcanic Province. In Snoke, A.W., J.R. Steidtmann, and S.M. Roberts (editors), *Geology of Wyoming: Geological Survey of Wyoming, Memoir No. 5*. Wyoming State Geological Survey, Laramie, WY, pp. 480–506.

Vail, T., M. Oard, D. Bokovoy, and J. Hergenrather. 2008. *Your Guide to the Grand Canyon: A Different Perspective*. Master Books, Green Forest, AR.

Letters to the Editor

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A Reply to the Heart Mountain Papers

As Dr. John Matthews (2021a,b) stated in his two part article in the *Creation Research Society Quarterly*, the Heart Mountains Detachment (HMD) is difficult for uniformitarian scientists to explain. Despite some who claim that the detachment moved very slowly, the majority of researchers seem to believe that the slide was catastrophic. Their debate centers on the exact mechanism and velocity of movement. There are widely different interpretations in the secular literature. Matthews does a good job in pointing out the difficulties with their various hypotheses for the sliding mechanism, as well as the difficulties explaining HMD from a creation science point of view.

I agree with Dr. Tim Clarey's (2021) editorial that the HMD is a slide. There are several reasons for my deduction. The Rocky Mountains of the United States are composed of high mountains separated by valleys and basins. At the peak of the Flood in northern Wyoming several kilometers of sedimentary rock layers were generally flat overlaying the granite and metamorphic rocks of the upper crust (Oard, 2013). As the mountains rose the valleys and basins sank according to Psalm 104:6–9 (Barrick, 2018, Barrick et al., 2020). This was a global shift that God used to drain the Floodwaters from continents into the sinking ocean basins (King, 1983). In Wyoming the greatest amount of differential vertical tectonics was about 13500 m (Oard, 2013). Practically all this tectonic activity occurred during the Cenozoic, which incidentally is a strong indication that the Flood/post-Flood boundary is in the late Cenozoic (Oard, 2014).

Varying amounts of sedimentary rocks were washed from the mountains during uplift. The continental crust and its capping sedimentary rocks sank where valleys and basins are located today. The valleys and basins filled with more sediments from the mountains. Floodwater currents also added sediments from afar to the valley fill. There is very little limestone in the valley fill in the Bighorn Basin, and since Heart Mountain and the McCulloch Buttes are relatively thick limestone and dolomite that rest on such valley fill, it is unlikely there was a thick layer of carbonate overlaying the Bighorn Basin. Heart Mountain and the McCulloch Buttes are the only two of the blocks that travelled up and then down the 500 m monocline north of Rattlesnake Mountain (Craddock et al., 2009). The HMD broke up into about 48 major and numerous minor blocks that never moved over the monocline. Erosion of more than 300 m ensued in the 110 km wide, 270 km long Bighorn Basin, placing this erosion within the Recessional Stage of the Flood (Walker, 1994). Thus, the location of these carbonate blocks is out of place; they are not valley fill which supports their transport in the HMD.

It appears that the HMD took place during the deposition of the Absaroka Volcanics, and associated volcanic lahars. Some uniformitarian scientists think there were 2–4 km of volcanic rock on top of the limestone (Aharonov and Anders, 2006), which is possible. Lahars also fill in the spaces between the blocks, west of the monocline, indicating continued emplacement of the Absaroka Volcanics after the HMD slid.

Besides the thin breccia on top of the slide plane that Clarey (2021) mentioned in his editorial, the slide plane can be easily traced west northwest to northeast Yellowstone Park, where limestone and dolomite that never broke away can be seen. This adds to evidence for a slide.

I have written on the HMD a number of times (Oard, 1996, 2006, 2010, 2018). I have reported mainly on the uniformitarian progress, or lack thereof, and suggested that the HMD happened in the Flood, just as Clarey (2021) believes. It can be pinpointed to very early in the Recessional Stage, occurring deep underwater. There are several reasons for this deduction. First, at least 2000 m of the Absaroka Volcanics were likely deposited by underwater volcanic debris flows, layer upon layer over 23,000 km^2. Second, the southern top of the Absaroka Volcanics represents a dissected planation surface that is a Flood runoff signature (Oard, 2013). Third, some valleys were eroded by about 1200 m within the Absaroka Volcanics. The planing would have occurred underwater during the Sheet Flow Phase and the deep valleys carved during the Channelized Flow Phase during the Recessive Stage of the Flood. Fourth, the Absaroka Volcanics are also the rocks in which the vertical, petrified trees of the "Yellowstone Fossils Forests" are found, indicating a log mat once floated above the depositing lahars (Coffin, 1997).

The evidence indicates that the limestone and dolomite blocks started off deep under the Floodwater, yet it is now found around 2,000 m above sea level. This much vertical uplift would be expected to have caused very large earthquakes which could have triggered brittle failure within the Bighorn Dolomite and possibly some renewed uplift on the monocline. The dolomite left behind and the sedimentary rock below are not deformed in most places, although it is significantly deformed in other places (Swanson et al., 2016). Clarey (2012) demonstrated that some of the HMD blocks were later transported piggy-back-style by the subsequent South Fork Fault system. This further deformed some of the HMD blocks.

The detachment layer within the dolomite could have formed and slid on a layer with high porewater pressure, since the sediments were just deposited during the Genesis Flood. In regard to the HMD moving southeast and not southwest (Prostka, 1978), the 10° southwest dip applies to the strata, but these strata likely had thick volcanic lahar flows preventing that direction of movement.

Michael J. Oard
Bozeman, MT

References

Aharonov, E. and M.H. Anders. 2006. Hot water: A solution to the Heart Mountain detachment problem? *Geology* 34:165–168.

Barrick, W.D. 2018. Exegetical analysis of Psalm 104:8 and its possible implications for interpreting the geologic record. In Whitmore, J.H. (editor), *Proceedings of the Eighth International Conference on Creationism*, pp. 95–102. Creation Science Fellowship, Pittsburgh, PA.

Barrick, W., M.J. Oard, and P. Price. 2020. Psalm 104:6–9 likely refers to Noah's Flood. *Journal of Creation* 34(1):102–109.

Clarey, T.L. 2012. South Fork fault as a gravity slide: Its break-away, timing, and emplacement, northwestern Wyoming, U.S.A. *Rocky Mountain Geology* 47(1):55–79.

Clarey, T.L. 2021. Heart Mountain fault papers. *Creation Research Society Quarterly* 58(1):4–7.

Coffin, H.G. 1997. The Yellowstone petrified 'forests.' *Origins* 24(1):5–39.

Craddock, J.P., D.H. Malone, J. Magloughlin, A.L. Cook, M.E. Rieser, and J.R. Doyle. 2009. Dynamics of the emplacement of the Heart Mountain allochthon at White Mountain: constraints from calcite twinning strains, anisotropy of magnetic susceptibility, and thermodynamic calculations. GSA *Bulletin* 121(5/6):919–938.

King, L.C. 1983. *Wandering Continents and Spreading Sea Floors on an Expanding Earth*. John Wiley and Sons, New York, NY.

Matthews, J. 2021a. The Heart Mountain conundrum, Part 1: Models of low-friction sliding have major problems. *Creation Research Society Quarterly* 57(4):269–275.

Matthews, J. 2021b. The Heart Mountain conundrum, Part II: A scientific critique of six unanswered uniformitarian questions. *Creation Research Society Quarterly* 58(1):8–5.

Oard, M.J. 1996 Possible analogue for the Heart Mountain detachment. *Journal of Creation* 10(1):3–4.

Oard, M.J. 2006. The Heart Mountain catastrophic slide. *Journal of Creation* 20(3):3–4.

Oard, M.J. 2010. The Heart Mountain slide becomes more catastrophic. *Journal of Creation* 24(2):11–12.

Oard, M.J. (ebook). 2013. *Earth's Surface Shaped by Genesis Flood Runoff*. http://Michael.oards.net/GenesisFloodRunoff.htm.

Oard, M.J. (ebook). 2014. *The Flood/Post-Flood Boundary Is in the Late Cenozoic with Little Post-Flood Catastrophism*. http://michael.oards.net/PostFloodBoundary.htm.

Oard, M.J. 2018. The Bighorn Basin, Wyoming—Monument to the Flood Part II: The Retreating Stage. *Creation Research Society Quarterly* 54(3):187–203.

Prostka, H. 1978. Heart Mountain fault and Absaroka Volcanism, Wyoming and Montana, U.S.A. In Voight, B. (editor), *Rockslides and Avalanches, 1 Natural Phenomena*, pp. 423–437. Elsevier, New York, NY.

Swanson, E., R.O. Wernicke, and T.A. Hauge. 2016. Episodic dissolution, precipitation, and slip along the Heart Mountain Detachment, Wyoming. *The Journal of Geology* 124:75–97.

Walker, T. 1994. A Biblical geological model. In Walsh, R.E. (editor), *Proceedings of the Third International Conference on Creationism*, technical symposium sessions, pp. 581–592. Creation Science Fellowship, Pittsburgh, Pennsylvania; biblicalgeology.net/.

Response to Letter to the Editor from Michael J. Oard

I thank Michael Oard (2021) for reading and promoting a discussion on my Heart Mountain papers and linking it to Dr. Tim Clarey's (2021) Editorial. I offer these comments, but inevitably my response is lengthy because of the need to address each point raised (the geological column, thin films, over-pressure, theology, paleo-reconstruction, and the South Fork fault.)

Although both mention a possible slide mechanism outside the three that I had challenged, my paper on overthrusting (Matthews, 2016) shows significant problems even if cohesion, tension, and other restraints are somehow removed from around the blocks that supposedly moved. Furthermore, there was no systematic discussion of the other 85% of my arguments that Heart Mountain Detachment (HMD) did not move (Matthews, 2021b).

Before getting into details, please note that this is a technical discussion. Mike and I have both worked well together on previous *CRSQ* papers (Oard et al., 2014; Oard and Matthews, 2015; Matthews and Oard, 2015). I am not immovable to the idea that HMD did move, but I want non-stratigraphic evidence. But whatever, the outcome will not change my mind about the geological column because my view of it is rooted in other data.

Geological Column: I hold similar views about the geologic column to Oard. For example, commenting on Snelling's (2009) writings, Oard (2011) says, "I don't believe…a case for a global geological column [has been made] in this book or elsewhere." Neither do I. However, I consider it walking a tight rope to say that the column is "A General Order with Many Exceptions" (Oard, 2010). Surely the phrase 'many exceptions' implies that we cannot use it even with caution since we have no *a priori* method for telling us where and when it works and when it fails (Matthews, 2011, 2016).

One of my major disappointments was the lack of engagement with the discussion about the column within the CRS forum (Reed and Oard, 2006) from those who support the column. Nor has there been any formal response to my articles challenging the column and the support it gets from supposed overthrusting (Matthews, 2011, 2016). The risk is that 'we are kicking the can down the road instead of picking it up and dealing with it properly.' If the column is bad, then we have in our hands the biggest challenge against evolution. Arguments from evolutionists using genetics and cladistics pale into insignificance because they rely on a timeline from the column. That surely is a major incentive for getting to the bottom of the story on the column by picking up the can.

Mechanisms: I have already shown that three suggestions (heat-generated CO_2, stress-generated high-pressure water, and melted calcite) attempting to explain the movement of HMD subaerially (and borrowed by creationists since they involve very short timescales) are totally inadequate. I also commented on the subaqueous suggestion by Oard (Matthews 2021a, 2021b). But first to Dr. Tim Clarey's (2021) suggestion that, just as a thin water layer could allow a sheet of plexiglass to slide, so could HMD.

There are four problems with applying this to HMD. Firstly, how did a convenient thin layer of water come into existence stretching perhaps 30 km within the middle of thick dolomite? Secondly, even if achieved, the supposed rapid movement, particularly when dealing with the individual blocks with vertical gaps, will shear any water layer and it will quickly be left behind resulting in grinding friction bringing movement to a halt. Thirdly, the surface tension forces are not adequate to support a mountain even during slow movement. Finally, how did the water layer stay beyond the monocline? These problems with this suggestion really belong to the 85% of issues that I have with HMD (Matthews, 2021b). No one has addressed them in blow-by-blow detail.

Over-pressure: Over-pressure of pore water is also offered as a possible mechanism for movement. The oil industry is concerned about over-pressures because of the dangers faced in oil recovery (e.g., the Deepwater Horizon accident, 2010.) Attempts to understand the causes of such pressures have been researched on both sides of the Atlantic. But what was found could never be used to explain overthrusting by an over-pressure mechanism within creationist or uniformitarian time-scales (Matthews, 2016, 2021c).

Summarizing, normal pore-pressure is ~10 kPa/m and is controlled by hydrostatic forces. Any sediments developing with a lower pressure will eventually become normal pressured because of compaction at the boundaries of the region and/or leakage into the region. Over-pressure is mostly produced by rapid burial of sediments. *Exhumation reduces over-pressure* (Poston and Berg, 1997)! Maximum over-pressure is ~22 kPa/m. Anything greater will breach the vertical stress and allow fluid to escape vertically. So natural geological events are already providing us with a delicate balance of pressures. To get anything above 22 kPa/m in order for sliding to take place without hefty gravity assistance is therefore impossible.

In this suggested Oard/Clarey explanation for movement, there is a lack of numerical data. And without numbers there is no explanation. While we cannot tie down exact numbers, I would argue that there isn't an envelope of physical space involving a combination of slope, friction, and pressure which explains movement as I now elaborate; see also Price and Cosgrove (1990).

In the scenario envisaged by Oard/Clarey, whilst leakage downwards cannot happen, edge and bulk horizontal leakage through high permeability unconsolidated material would, unless we adopt Murrell's (1981) idea of adding an impervious wrapper, or four-way closure to use oil-reservoir parlance. Within my overthrusting paper (Matthews, 2016), which is a summary of my 2009 notes and since updated (Matthews, 2021c), I show that a simple consideration of rock mechanics invalidates Murrell's idea. The Mohr stress circles simply move towards the failure curve. Furthermore, unconsolidated sedimentary layers generally do not suffer from diagenesis (which aids the consolidation). Yet, Heart Mountain is consolidated suggesting that it was never over-pressured. (Note also the earlier point that the suggested exhumation of HMD reduces over-pressure.) The McCulloch Peaks are somewhat less so and broken. Furthermore, Murrell's idea of a wrapper is not consistent with breakaway blocks with exposed vertical surfaces. This is not a way forward.

Theology: I regularly use NIV Bible translation in my private devotions; however, I am aware of the reluctance of the translators to treat the Genesis Flood as a global recent event. That is made clear by the way they suggest that Behemoth of Job 40:16 might have been an elephant or hippopotamus in spite of Job's contrary description of this animal. So, I accept that Psalm 104 refers to the Flood rather than Creation.

However, there are two points about how Barrick et al. (2020) are used as part of the explanation as to why Heart Mountain did move. Firstly, the geological column which Oard and I admit is not accurate, creeps in with Figures 2 and 3. Secondly, I cannot accept that mountains rose vertically, and valleys sank in a series of special convenient grabens and horsts without major folding. In fact, Figure 3 shows a 20–30° tilt. The consequences of this will be treated below.

Paleo-reconstruction: If we want to show that HMD moved, even though we don't know how, we have several options. Firstly, is to agree that the column is 100% robust. Although Clarey would agree, Oard and I don't. My reasons are clear and still awaiting challenge rather than pointing to correlations using data that have gone through a 'uniformitarian grinding mill' based heavily on inferred uniformitarian history using such things as imaginary 40,000-year orbital cycles (Ogg et al., 2016) and not a one-year Flood. Secondly, is to identify something unique about HMD (a sort of 'fingerprint') and find the corresponding 'hand that left the print' farther upstream. We can accept some distortion in the 'fingerprint' during movement. The best that can be found is a clastic dike in White Mountain (not HMD) which could potentially be related (but hasn't yet) back to its supposed original position on the slide plane either at the Crandall or Sunlight Volcanic Centers. The third option, which is not so reliable because it relies on several assumptions, is to attempt a formal paleo-reconstruction of the area to show that general movements occurred consistent with the idea of HMD having moved ~45 km.

Vertical tectonics is one of several contenders for paleo-reconstructing the history of the Flood and favored by Oard. The common choice amongst creationists seems to be catastrophic plate tectonics (CPT) (e.g., Clarey, 2016). I have reservations. Barrick et al. (2020) remind us that the first event that Genesis mentions in connection with the Flood is the opening of the fountains of the great deep. To that extent, the hydroplate model (Brown, 2008) seems relevant and specifically highlights the importance of those fountains and its explanation for limestone and possibly the trickier problem explaining dolomite (Krauskop and Bird, 1995, p. 79). Also, of course, CPT models generally require the robustness of the geological column as input data. My further reason for not rubber-stamping CPT is that whilst Baumgardner (2018) has tried to make a good case for rapid erosion by cavitation in order to ensure rapid deposition within CPT, the problems of (for example) flocculation (to separate sand from clay during such turbulence) is not explained within a one-year timescale.

Oard (2021) makes a good case based on his choice of vertical tectonics that because 'there is very little limestone [surely both carbonates?] in the valley' surrounding HMD substantiates the idea of movement. Otherwise, there would have been much more 'limestone' left around from the erosion of the extensive sheets of 'limestone' that would have existed on the now bare sliding surface. Without more evidence it is hard to be convinced. Also, Oard notes that the lahars may be responsible for preventing HMD from moving in the physical gradient direction. But equally they would prevent any movement!

South Fork Fault: This was briefly mentioned in my Latex pdf (Matthews, 2019). The idea that the movement of HMD provided a subsequent 'shock loading' releasing water from the gypsum layer to allow other movement faces two problems. Firstly, where are the calculations that show that anything closely to a sufficient pressure pulse reached the parts where it was needed? Secondly, even if it did, my calculations show that the water layer only survived for three seconds—totally inadequate for movement.

Note also, much of the analysis of the South Fork Fault relies on data from seismic and well logs but interpreted within (a supposed robust) geological column. Those using this type of analysis must show that the 'many exceptions' noted by Oard and myself have no effect on that analysis. This means that there are still fundamental questions about South Fork Fault and the inter-relational explanations offered for it with HMD.

Summary: Whilst a couple of ideas have been put forward by Oard and Clarey that might have explained how HMD could have moved, these are not robust ideas. Furthermore, 85% of the other essential parts of the explanation are missing. I don't believe that HMD moved.

John D. Matthews
United Kingdom

References

Barrick, W., M.J. Oard, and P. Price. 2020. Psalm 104:6–9 likely refers to Noah's Flood. *Journal of Creation* 34(1):102–109.

Baumgardner, J. 2018. Numerical modeling of the large-scale erosion, sediment transport, and deposition processes of the Genesis Flood. *Answers Research Journal* 11:149–170.

Brown, W. 2008. *In the Beginning (Eighth Edition)*. Center for Scientific Creation, Phoenix, AZ.

Clarey, T.L. 2016. Empirical data support seafloor spreading and Catastrophic Plate Tectonics. *Journal of Creation* 30(1):76–82.

Clarey, T.L. 2021. Heart Mountain fault papers. *Creation Research Society Quarterly* 58(1):4–7.

Krauskopf, K., and D. Bird. 1995. *Introduction to Geochemistry*. McGraw-Hill, Inc., New York, NY.

Matthews, J.D. 2011. The stratigraphic geological column—a dead end. *Journal of Creation* 25(1):98–103.

Matthews, J.D. 2016. The overthrusting paradox: A challenge to uniformitarian geology and evolution. *Journal of Creation* 30(2):83–91.

Matthews, J.D. 2019. The Heart Mountain detachment and slide—chemical, geological and physical analysis of the supposed event. Unpublished Latex pdf available from author—truthingeology@gmail.com.

Matthews, J. 2021a. The Heart Mountain conundrum, Part I: Models of low-friction sliding have major problems. *Creation Research Society Quarterly* 57(4):269–275.

Matthews, J.D. 2021b. The Heart Mountain conundrum, Part II: A scientific critique of six unanswered uniformitarian questions. *Creation Research Society Quarterly* 58(1):8–5.

Matthews, J.D. 2021c. Over-pressure—is not a viable explanation for over-thrusting. Unpublished Latex pdf available from author—truthingeology@gmail.com

Matthews, J.D., and M. Oard. 2015. Erosion of the Weald, Southeast England. Part II: A Flood explanation of the mystery and its implication. *Creation Research Society Quarterly* 52(1):22–33.

Murrell, S.A.F. 1981. The rock mechanics of thrust and nappe formation. In McClay, K., and N.J. Price (editors). *Thrust and Nappe Tectonicsrkg*. Special Publications 9:99–108. Geological Society, London, UK.

Oard, M.J. 2010. The geological column is a general Flood order with many exceptions. *Journal of Creation* 24(2):78–82.

Oard, M.J. 2011. A review of *Earth's Catastrophic Past: Geology, Creation & the Flood*, Volumes I and II by Andrew Snelling. *Journal of Creation* 25(10):33–40.

Oard, M.J. 2021. Letter to editor. *Creation Research Society Quarterly* 58(2):133–134.

Oard, M.J., and J.D. Matthews. 2015. Massive erosion at the English Weald. *Creation Research Society Quarterly* 51(4):165–176.

Oard, M.J., J.D. Matthews, and A. Sibley. 2014. The Jurassic Coast—Evidence for the Flood. Part I. *Creation Research Society Quarterly* 51(2):113–127.

Ogg, J.G., G.M. Ogg, and F.M. Gradstein. 2016. *A Concise Geologic Time Scale*. Elsevier, Oxford, UK.

Poston, S.W., and R.R. Berg. 1997. *Overpressured Gas Reservoirs*. Society of Petroleum Engineers, Richardson, TX.

Price, N.J., and J.W. Cosgrove. 1990. *Analysis of Geological Structures*. Cambridge University Press, Cambridge, UK.

Reed, J.K., and M.J. Oard. 2006. *The Geologic Column: Perspectives Within Diluvial Geology*. Creation Research Society Books, Chino Valley, AZ.

Snelling, A.A. 2009. *Earth's Catastrophic Past: Volume I*. Institute for Creation Research, Dallas, TX.

Errata

There was an error on page 16 in the first sentence of the second paragraph in the left-hand column in Peter Klevberg's paper "Cayuse Basin: A Study in Multiple Working Hypotheses," *CRSQ* 58(1): 16–29.

The sentence should read:

> "Cayuse Basin is owned by the Hughes Livestock Company."

The original incorrectly said Hayes Livestock Company.

Letters to the Editor

Further Thoughts on the Creation Model Controversy

I am surprised at the difference of opinion on what a creation scientists should be researching and publishing, as revealed by the letters from Bergman (2020) and Hill (2021). Not to belabor the point, I would like to add that creation scientists should be both challenging the claims of evolution, uniformitarianism, deep time, and naturalism and also developing our own models for observed data. Of course, I am aware the International Conference on Creationism is unique in that it *specifically* desires papers that build the Creation/Flood model.

I write on numerous challenges to uniformitarianism and deep time, and attempt to explain the data within a Flood and/or Ice Age model, whenever possible. I struggle with how a biologist would place the challenges to evolution and the amazing evidence of design within an overarching Creation model, except to point out that design indicates a Designer. I would be glad to be corrected on this impression. We cannot go back and explain how God supernaturally created, unlike using the Flood Model to explain geology, although we may be able to point out the cellular and genetic mechanisms He built in at Creation. Pointing out the incredible designs in the biological world and how they counter evolution is in itself valuable. I am personally edified by Bergman's work.

In some cases, I think we can develop sub-models within a larger Creation model, such as the ICR initiative that is working on explaining diversity from an internal, built-in response of an organism to environmental cues (Guliuzza, 2020). We can also study baraminology to help determine what the original Created kinds are, or at least those kinds that left the Ark.

Michael J. Oard

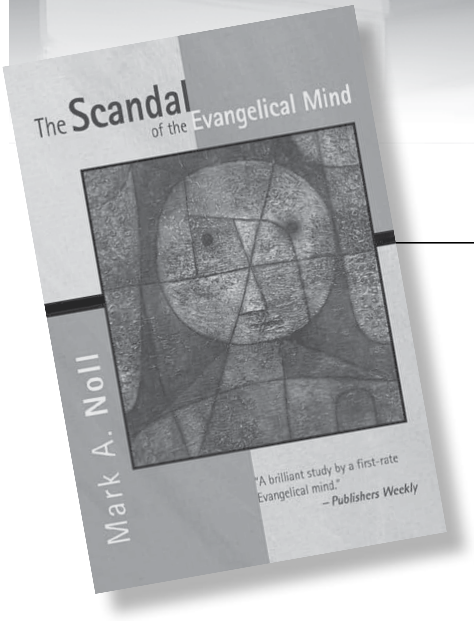
References

Bergman, J.R. 2020. Thoughts on the Creation Model Controversy. *Creation Research Society Quarterly* 57(2):153–154.

Guliuzza, R.J. 2020. The power of the next idea. *Acts & Facts* 49(11):5–7.

Hill, R. 2021. A response to "Thoughts on the Creation Model Controversy." *Creation Research Society Quarterly* 47(4):293–294.

Media Reviews



The Scandal of the Evangelical Mind

by Mark Noll

William B Eerdmans, Grand Rapids, 1996, 274 pages, $15.00

This is not a new book, first published in 1996 and *reviewed* that year in the December *CRSQ*. However, the book has had a long and influential life. Why should a pediatrician review it? And why now? First, I emerged from my medical training in 1967 as a theistic evolutionist, having been thoroughly indoctrinated in "the truth of evolution." What brought me back to Biblical creation was scientific evidence. Therefore, my attention was drawn to this book when it was quoted to me as the authoritative refutation of my creationist views.

I heard the author being interviewed by Ken Myers of *Mars Hill Audio*, describing creationism as consisting of pronouncements by rural pastors unqualified to discuss science. I emailed author Noll and asked if he had read young earth creationist writings. He replied that he reads only qualified experts in the field. I reminded him that he himself is considered a qualified expert although he had not gone to primary sources.

In 2021 I finally purchased the book. Most of it looks, to this non-historian, to be a masterful synthesis of church history, focusing briefly on the church fathers and the reformers. The book addresses evangelical phenomena beginning with the Whitefield and Wesley revivals and the first and second great awakenings in America. Noll laments the lack of serious scholarship within the revival movement and analyzes the possible factors that contributed. He draws on the writings of hundreds of experts as evidenced by 367 endnotes. He does not dwell on the Scopes Trial which might have precipitated an evaluation of "trial by media" coordinated by anti-creationists. Instead, Noll simply designates the trial as the end of the era dominated by William Jennings Bryan.

Noll takes a panoramic view, essentially from 30,000 feet, which does not swoop down to turn over rocks until it gets to the only young earth creationists referenced, Whitcomb and Morris. The author quotes from the introduction to 1961 *Genesis Flood*, highlighting the authors' goal of ascertaining what the Bible has to say about the Flood and orienting the data of the relevant sciences (p.201–202). To Noll, this sounds like pounding square pegs into round holes, and he never looks at the results of that change of orientation, either within the Flood book or the tsunami of research that followed. The only other ally of modern creationism mentioned is Phillip Johnson, applauded for addressing the philosophical overreach of naturalism (p.197), while ignoring Johnson's proposal that the validity of scientific evidence needs to be evaluated by legal standards.

Noll notes that the evangelical experience is based on conversion. Evangelical life is influenced by separation of church and state in America and a populist orientation that has tended to be suspicious of authority and leans towards anti-intellectualism. The flow of the book is that of a calm and disinterested scholar observing the currents of theology and practice until it comes to what certainly look like Noll's "pet peeves." Young earth creation, he claims, is an idea that was never defended until the 20th Century (p. 188–190). This even though Jesus believed in the Noahic Flood (Matthew 24:37–39). Also, Job hears God describe the behemoth, a sauropod dinosaur, as a real animal that Job would have observed (Job 40:15–24). Noll attributes recent creation to Seventh Day Adventist George McCready Price (p. 189), even though the Jewish calendar gives 5781 years from Adam to the present. Noll also neglects giving voice to young-earth theologians.

If God uses evolution and millions of years, then the geologic layers represent death before the time of Adam, thus before sin (Romans 5:12). If the death penalty only refers to spiritual death, then why is a blood sacrifice necessary? Why did Jesus have to take a body, suffer, and die? Or is God just a bad communicator?

Another issue that Noll approaches with less than scholarly detachment is "radical apocalyptic speculation," an intense interest in prophecy and a penchant for identifying current events with Biblical prophecies (p. 12–14). He opposes the rapture as a "wooden interpretation of 1 Thessalonians 4" (p. 143). Yet the disciples were told that Jesus was coming back in the manner He left (Acts 1:9–11). We are instructed to be ready because He could come at any time, and that although no one knows the day and hour except the Father (Matthew 24:36), we can know the times and seasons (Matthew 24:3–35). Noll claims that spiritual warfare, with events in the spiritual realm paralleling the physical, as depicted in the writings of Frank Peretti, implies a nearly Manichaean dualism (p. 140). Yet, unlike this heresy that proposes equally powerful good and evil gods, the Peretti novels represent a reasonable application of the facts of Scripture. For instance, Jesus cast out demons (Matthew 8:16–34) and stated that Satan wanted to sift Peter (Luke 22:31–32). Paul warned that we fight spiritual wickedness in high places for which we need spiritual armor and constant prayer (Ephesians 6:10–18). An angel described as coming to answer Daniel's question was detained by the Prince of Persia (Daniel 9:1–13). One of the churches addressed in Revelation is located where Satan has his throne (Revelation 2:12–13). And, of course, Satan is described in the end as defeated and cast into the lake of fire (Revelation 20:1–10).

Mark Noll is a graduate of Wheaton College and returned to teach there for 27 years after receiving graduate degrees from the University of Iowa and Trinity Evangelical School Divinity School and a church history Ph.D. from Vanderbilt University. Noll also taught at Notre Dame and Regent College.

Ross S. Olson, M.D.
rossolson1942@gmail.com

Instructions to Authors

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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.

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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.

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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.

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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.

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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, 1 W. Firestorm Way #145, Glendale, AZ 85306, 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 ☐ 2021 ☐ __________. *(Please type or print legibly.)*

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Phone (optional) ______________________ Email ______________________

Degree ______________________ Field ______________________

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I have read and subscribe to the CRS Statement of Belief. Signature ______________________

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	Paper**			**Paper-less‡**
☐ Voting ☐ Sustaining	USA	Canada Mexico	Other countries	
☐ Regular [per year]	☐ $43	☐ $63	☐ $80	☐ $33
☐ Senior [per year]	☐ $38	☐ $58	☐ $75	☐ $28
☐ Life member	☐ $500	☐ $500	☐ $500	☐ $500
☐ Student* [per year]	☐ $38	☐ $58	☐ $75	☐ $28
☐ Subscriber [per year]	☐ $46	☐ $66	☐ $83	☐ $36

* 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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34	☐	☐	☐	☐	46	☐	☐	☐	☐	58	☐	☐	☐	

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Mail to: Creation Research Society, 1 W. Firestorm Way #145, Glendale, AZ 85306, 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 Glendale, Arizona.

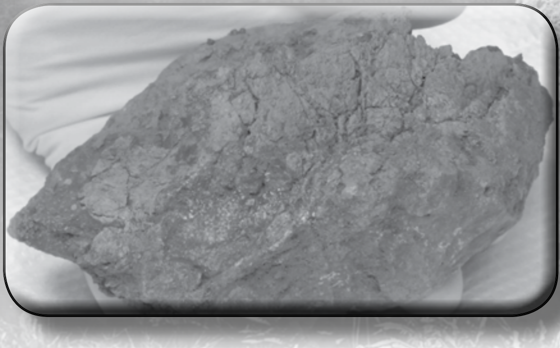
Membership—Voting membership is limited to scientists who have at least an earned graduate degree in a natural or applied science and subscribe to the Statement of Belief. Sustaining membership is available for those who do not meet the academic criterion for voting membership, but do subscribe to the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

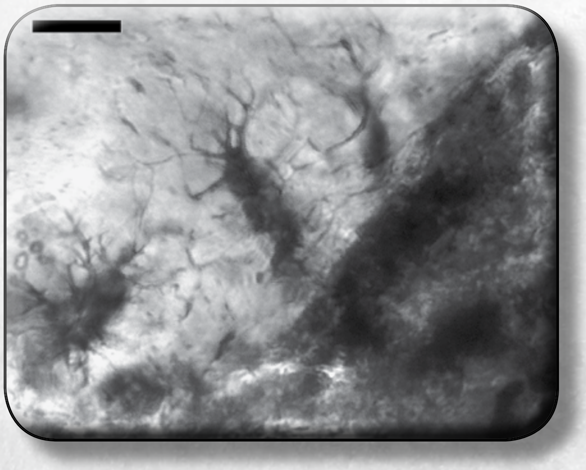
1. The Bible is the written Word of God, and because it is inspired throughout, all its assertions are historically and scientifically true in all the original autographs. To the student of nature this means that the account of origins in Genesis is a factual presentation of simple historical truths.
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

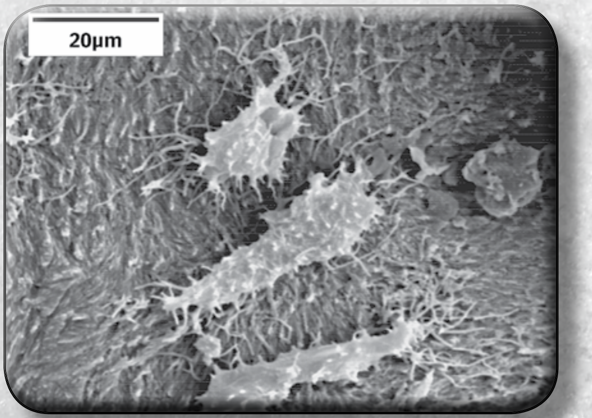
Investigation of Dinosaur Intact Natural Osteo-tissue



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.

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